National Veterinary Institute - DTU Orbit (02/07/2018)
National Veterinary Institute
Technical University of Denmark
Short name: DTU Veterinary

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Organisation profile
National Veterinary Institute DTU conducts research in infectious diseases in livestock and makes diagnoses in diseased animals. We give advice to public authorities and cooperate with them on the Danish veterinary contingency plan. We are reference laboratory in a number of areas.
National Veterinary Institute DTU encompasses all infectious animal diseases in farm livestock and companion animals.
Our main focus is on notifiable diseases, as well as other serious infectious diseases that affect farm livestock.
Our tasks concern:

Research

Innovation

Diagnostics

Surveillance

Consultancy

Risk assessment

Production of vaccines and sera

Dissemination of knowledge and education

We do research in diseases
The Institute does research in methods to detect, control and prevent infectious animal diseases. Our research activities cover a wide field, i.e. developmental and application-oriented projects as well as basic research.
The institute also hosts an international research centre for veterinary epidemiology, International EpiLab.

We diagnose
Veterinarians can submit samples from diseased animals to be diagnosed. For notifiable diseases the diagnosis is free, whereas we diagnose other diseases on commercial terms. All our diagnostic services are based on accredited or quality-assured analysis methods.

We manufacture vaccines and sera
For some animal diseases commercial vaccines and sera are not available. For the treatment of these diseases the National Veterinary Institute DTU manufactures vaccines and sera, if the disease is significant. Our production of vaccines and sera takes place on commercial terms.

We give advice to public authorities
The National Veterinary Institute DTU provides advisory services and risk assessment to public authorities, the industry and interest groups. Advisory services and risk assessment are both based on robust and sensitive research methods. In addition, we supply data for disease monitoring in Denmark and coordinate the national monitoring of veterinary drug use (Vetstat).

We are responsible for the Danish veterinary contingency plan
The National Veterinary Institute DTU is responsible for the laboratory component of the Danish veterinary contingency plan, which puts emergency procedures into action in the event of suspected or actual outbreaks of serious infectious animal diseases. In these cases our laboratories analyse samples from the animals. The contingency plan is supported by our activities in conjunction with a range of national monitoring programmes on animal diseases and zoonoses. Our research and diagnostics expertise is crucial for maintaining the high quality of the Danish veterinary contingency plan. The Danish Veterinary and Food Administration is responsible for the part of the contingency plan handling infection situations in Denmark.

We are reference laboratory
The institute is the Danish national reference laboratory for a long list of infectious animal diseases, and the EU and OIE reference laboratory for selected fish diseases.

We cover relevant subject areas
Professionally the institute covers all areas important to infectious diseases:

Pathology
Bacteriology
Virology
Parasitology
Immunology
Vaccinology
Serology
Epidemiology
Risk Assessment

We are 220
The institute employs about 220 staff members and consists of the management, the secretariat and the service division. Furthermore we have these five sections:
Virology – focusing on serious virus infections, including virus infections transmitted from animals to humans (zoonotic infections).

Immunology and vaccinology – including development and optimization of new vaccines and other biological products.

Epidemiology – including disease modeling and climate-related changes in disease spread.

Bacteriology, pathology and parasitology - focusing on fish bacteriology, non-food-borne bacterial zoonoses and activities with a view to reducing the use of antibiotics. We also work on methods for characterizing multi-bacterial societies.

Public sector consultancy, contingency and commercial diagnostics.

Organisational unit: Department

Publications:

Parasites in Myodes glareolus and their association with diet assessed by stable isotope analysis
Vertebrates are hosts to numerous parasites, belonging to many different taxa. These parasites differ in transmission, being through either direct contact, a faecal-oral route, ingestion of particular food items, vertical or sexual transmission, or by a vector. Assessing the impact of diet on parasitism can be difficult because analysis of faecal and stomach content are uncertain and labourious; and as with molecular methods, do not provide diet information over a longer period of time. We here explored whether the analysis of stable isotopes in hair provides insight into the impact of diet and the presence of parasites in the rodent Myodes glareolus. Twenty-one animals were examined for parasites and their hair analysed for stable isotopes (C and N). A positive correlation between δ15N and one species of intestinal parasite was observed in females. Furthermore, several ectoparasites were negatively correlated with δ15N, indicating that infections are further associated with foraging habits (size and layout of the home range, length and timing of foraging, interaction with other rodents, etc.) that set the rodents in direct contact with infected hosts. Although a limited number of animals were included, it seemed that the isotope values allowed for identification of the association between diet and parasite occurrence in this rodent. We therefore propose that this method is useful in providing further insight into host biology, feeding preferences and potential exposure to parasites species, contributing to the understanding of the complex relationship between hosts and parasites.

General information
State: Published
Organisations: National Veterinary Institute, Section for Diagnostics and Scientific Advice, University of Copenhagen, Norwegian Veterinary Institute, National Research Centre for the Working Environment
Authors: Lynggaard, C. (Ekstern), Woolsey, I. D. (Ekstern), Al-Sabi, M. N. S. (Intern), Bertram, N. (Ekstern), Jensen, P. M. (Ekstern)
Pages: 180-186
Publication date: 1 Aug 2018
Main Research Area: Technical/natural sciences

Publication information
Journal: International Journal for Parasitology: Parasites and Wildlife
Volume: 7
Issue number: 2
ISSN (Print): 2213-2244
Ratings:
Web of Science (2018): Indexed yes
Scopus rating (2017): CiteScore 3.07
Scopus rating (2016): CiteScore 3.03
Scopus rating (2015): CiteScore 2.7
Scopus rating (2014): CiteScore 1.32
Scopus rating (2013): CiteScore 0
Original language: English
Validation of a novel one-step reverse transcription polymerase chain reaction method for detecting viral haemorrhagic septicaemia virus

Viral haemorrhagic septicaemia (VHS) is one of the most serious viral diseases in salmonid and olive flounder farms. Various diagnostic methods for detecting VHS virus (VHSV) are described in the VHS chapter of the World Organization for Animal Health (OIE) Aquatic Diagnostic Manual. A conventional reverse transcription-PCR (cRT-PCR) targeting the viral nucleocapsid gene is recommended for the detection of VHSV and, to some extent, for genotypic classification. However, the recommended assay exhibits low sensitivity for the detection of VHSV genotype IVa isolates and often shows non-specific amplicons when the RNA template is extracted from non-infected fish cell lines. For these reasons, it is necessary to develop a new RT-PCR method for the foolproof detection of all VHSV genotypes and elimination of non-specific results. In this study, we selected five candidate primer sets that target the VHSV nucleoprotein (N) gene, and selected the most sensitive among them (3F/2R). We then established the optimal reaction conditions for these primers, and ensured that no non-specific amplification had occurred in the fish tissues, fish cell lines, or heterologous viruses. The analytical sensitivity of the novel cRT-PCR was compared to that of cell culture assays, real-time RT-PCR, and other cRT-PCR methods and was found to be as sensitive as or superior to the other methods for detecting all VHSV genotypes. Our newly developed cRT-PCR assay was tested with 80 isolates, representing a collection of all known VHSV genotypes worldwide. Clear and unique amplicons were amplified from all 80 VHSV isolates. The reproducibility, and partly the robustness, of the assay were confirmed by an inter-laboratory proficiency tests including nine laboratories. A high diagnostic sensitivity and specificity was confirmed on tissue material from affected fish. In conclusion a highly robust, sensitive and specific cRT-PCR for detection of VHSV was developed and validated.
Transcriptional profiles of PBMCs from pigs infected with three genetically diverse porcine reproductive and respiratory syndrome virus strains

Porcine reproductive and respiratory syndrome virus is the cause of reproductive failure in sows and respiratory disease in young pigs, which has been considered as one of the most costly diseases to the worldwide pig industry for almost 30 years. This study used microarray-based transcriptomic analysis of PBMCs from experimentally infected pigs to explore the patterns of immune dysregulation after infection with two East European PRRSV strains from subtype 2 (BOR and ILI) in comparison to a Danish subtype 1 strain (DAN). Transcriptional profiles were determined at day 7 post infection in three tested groups of pigs and analysed in comparison with the expression profile of control group. Microarray analysis revealed differential regulation (> 1.5-fold change) of 4253 and 7335 genes in groups infected with BOR and ILI strains, respectively, and of 12518 genes in pigs infected with Danish strain. Subtype 2 PRRSV strains showed greater induction of many genes, especially those involved in innate immunity, such as interferon stimulated antiviral genes and
inflammatory markers. Functional analysis of the microarray data revealed a significant up-regulation of genes involved in processes such as acute phase response, granulocyte and agranulocyte adhesion and diapedesis, as well as down-regulation of genes enrolled in pathways engaged in protein synthesis, cell division, as well as B and T cell signaling. This study provided an insight into the host response to three different PRRSV strains at a molecular level and demonstrated variability between strains of different pathogenicity level.

**General information**

State: Accepted/In press
Organisations: National Veterinary Institute, National Veterinary Research Institute, Warsaw University of Life Sciences (SGGW)
Authors: Rola-Łuszczak, M. (Ekstern), Materniak-Kornas, M. (Ekstern), Pluta, A. (Ekstern), Podgórska, K. (Ekstern), Nielsen, J. (Intern), Stadejek, T. (Ekstern), Kuźmak, J. (Ekstern)
Pages: 1-14
Publication date: 7 Jun 2018
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Molecular Biology Reports
ISSN (Print): 0301-4851
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.8 SJR 0.721 SNIP 0.689
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.84 SJR 0.736 SNIP 0.768
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.761 SNIP 0.75 CiteScore 1.83
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.753 SNIP 0.919 CiteScore 2.04
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.715 SNIP 0.853 CiteScore 1.97
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.658 SNIP 1.014 CiteScore 2.23
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.77 SNIP 1.13 CiteScore 2.17
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.449 SNIP 0.655
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.449 SNIP 0.606
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.541 SNIP 0.528
Scopus rating (2007): SJR 0.502 SNIP 0.425
Scopus rating (2006): SJR 0.546 SNIP 0.336
Scopus rating (2005): SJR 0.586 SNIP 0.46
Scopus rating (2004): SJR 0.543 SNIP 0.263
Scopus rating (2003): SJR 0.357 SNIP 0.166
Scopus rating (2002): SJR 0.729 SNIP 0.397
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.779 SNIP 0.259
Scopus rating (2000): SJR 1.251 SNIP 0.369
Scopus rating (1999): SJR 1.032 SNIP 0.581
Original language: English
Host immune response, Pig, PRRSV, Transcriptome analysis
Echinococcus multilocularis in Denmark 2012–2015: high local prevalence in red foxes

In Western Europe, the Echinococcus multilocularis lifecycle is predominantly sylvatic, typically involving red foxes (Vulpes vulpes) as the main definitive hosts with Microtus spp. and Arvicola spp. as intermediate hosts. During a 4-year surveillance study (2012–2015), Danish red foxes and raccoon dogs (n = 1345) were examined for E. multilocularis. Moreover, 134 insectivores and rodents collected in South Jutland during spring and summer 2016 were examined for the presence of metacestodes. The sedimentation and counting technique and molecular typing were used to identify E. multilocularis infections in the carnivores, while the rodent livers were examined macro- and microscopically for parasite lesions. Following morphological identification of E. multilocularis adult worms, the identity was verified by sequence analysis of the 12S rRNA gene in most cases (n = 13). Echinococcus multilocularis infection was demonstrated in 19 red foxes (Vulpes vulpes) originating from only two specific areas of South Jutland, namely Højer and Grindsted, and in two raccoon dogs (Nyctereutes procyonoides), originating from Højer. In Højer, 28.5% (CI 95% 11.7–45.3) of the examined red foxes were E. multilocularis positive per year. Moreover, positive red foxes were identified each year from 2012 to 2015, while E. multilocularis positive red foxes were only identified in Grindsted in 2013 (4.0%) and 2014 (6.4%). In contrast, all collected rodents were negative for E. multilocularis. We conclude that E. multilocularis is locally endemic in South Jutland with a high local prevalence in Højer.
Corrigendum: An analysis of natural T cell responses to predicted tumor neoepitopes [Front Immunol, 8, 1566, (2017)]
An outdated version of Supplementary Table 1 was uploaded to the final version of the paper for publication. This table has not been under peer review and does not include the information described in the paper such as the similarity measurement column. The correct Supplementary Table 1 has now been published in the original article. The authors apologize for this oversight. This error does not change the scientific conclusion of the article in any way. The original article has been updated.

General information
State: Published
Organisations: Department of Bio and Health Informatics, Cancer Genomics, Immunoinformatics and Machine Learning, Technical University of Denmark, National Veterinary Institute, T-cells & Cancer, Universidad Nacional de San Martin
Authors: Bjerregaard, A. M. (Intern), Nielsen, M. (Intern), Jurtz, V. (Intern), Barra, C. M. (Ekstern), Hadrup, S. R. (Intern), Szallasi, Z. (Intern), Eklund, A. C. (Intern)
Publication date: 14 May 2018
Main Research Area: Technical/natural sciences

Publication information
Journal: Frontiers in Immunology
Volume: 9
Issue number: MAY
ISSN (Print): 1664-3224
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
CD103$^+$ CD11b$^+$ mucosal classical dendritic cells initiate long-term switched antibody responses to flagellin

Antibody responses induced at mucosal and nonmucosal sites demonstrate a significant level of autonomy. Here, we demonstrate a key role for mucosal interferon regulatory factor-4 (IRF4)-dependent CD103$^+$ CD11b$^+$ (DP), classical dendritic cells (cDCs) in the induction of T-dependent immunoglobulin G (IgG) and immunoglobulin A (IgA) responses in the mesenteric lymph node (MLN) following systemic immunization with soluble flagellin (sFliC). In contrast, IRF8-dependent CD103$^+$ CD11b$^-$ (SP) are not required for these responses. The lack of this response correlated with a complete absence of sFliC-specific plasma cells in the MLN, small intestinal lamina propria, and surprisingly also the bone marrow (BM). Many sFliC-specific plasma cells accumulating in the BM of immunized wild-type mice expressed $\alpha_4\beta_7^+$, suggesting a mucosal origin. Collectively, these results suggest that mucosal DP cDC contribute to the generation of the sFliC-specific plasma cell pool in the BM and thus serve as a bridge linking the mucosal and systemic immune system.
Analysis of the dynamics of Staphylococcus aureus in two Danish dairy cattle herds

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, SEGES Livestock Innovation
Authors: Kirkeby, C. T. (Intern), Zervens, L. M. (Intern), Toft, N. (Intern), Farre, M. (Ekstern), Hisham Beshara Halasa, T. (Intern)
Number of pages: 1
Publication date: 2018
Event: Poster session presented at 2018 International Bovine Mastitis Conference, Milan, Italy.
Main Research Area: Technical/natural sciences

A new method for estimating transmission rates of mastitis-causing pathogens

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, Department of Applied Mathematics and Computer Science
Authors: Kirkeby, C. (Intern), Halasa, T. (Intern), Gussmann, M. K. (Intern), Græsbøll, K. (Intern)
Publication date: 2018
Main Research Area: Technical/natural sciences

A new report of the carnivore-transmitted Taenia ovis cysts infesting the heart muscles of sheep in Denmark

General information
State: Published
Ascaris Suum Infection Downregulates Inflammatory Pathways in the Pig Intestine In Vivo and in Human Dendritic Cells In Vitro.

Ascaris suum is a helminth parasite of pigs closely related to its human counterpart, A. lumbricoides, which infects almost 1 billion people. Ascaris is thought to modulate host immune and inflammatory responses, which may drive immune hyporesponsiveness during chronic infections. Using transcriptomic analysis, we show here that pigs with a chronic A. suum infection have a substantial suppression of inflammatory pathways in the intestinal mucosa, with a broad downregulation of genes encoding cytokines and antigen-processing and costimulatory molecules. A. suum body fluid (ABF) suppressed similar transcriptional pathways in human dendritic cells (DCs) in vitro. DCs exposed to ABF secreted minimal amounts of cytokines and had impaired production of cyclooxygenase-2, altered glucose metabolism, and reduced capacity to induce interferon-gamma production in T cells. Our in vivo and in vitro data provide an insight into mucosal immune modulation during Ascaris infection, and show that A. suum profoundly suppresses immune and inflammatory pathways.
A strain-, cow-, and herd-specific bio-economic simulation model of intramammary infections in dairy cattle herds

Intramammary infections (IMI) in dairy cattle lead to economic losses for farmers, both through reduced milk production and disease control measures. We present the first strain-, cow- and herd-specific bio-economic simulation model of intramammary infections in a dairy cattle herd. The model can be used to investigate the cost-effectiveness of different prevention and control strategies against IMI. The objective of this study was to describe a transmission framework, which simulates spread of IMI causing pathogens through different transmission modes. These include the traditional contagious and environmental spread and a new opportunistic transmission mode. In addition, the within-herd transmission dynamics of IMI causing pathogens were studied. Sensitivity analysis was conducted to investigate the influence of input parameters on model predictions. The results show that the model is able to represent various within-herd levels of IMI prevalence, depending on the simulated pathogens and their parameter settings. The parameters can be adjusted to include different combinations of IMI causing pathogens at different prevalence levels, representing herd-specific situations. The model is most sensitive to varying the transmission rate parameters and the strain-specific recovery rates from IMI. It can be used for investigating both short term operational and long term strategic decisions for the prevention and control of IMI in dairy cattle herds.

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, Seges Knowledge Centre for Agriculture
Authors: Gussmann, M. K. (Intern), Kirkeby, C. T. (Intern), Græsbøll, K. (Intern), Farre, M. (Ekstern), Hisham Beshara Halasa, T. (Intern)
Pages: 83-93
Publication date: 2018
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Theoretical Biology
Volume: 449
Blyindhold i rovfugle

General information
State: Published
Organisations: National Veterinary Institute, Diagnostic & Development, Aarhus University
Authors: Kanstrup, N. (Ekstern), Chriél, M. (Intern), Dietz, R. (Ekstern), Sonne, C. (Ekstern), Søndergaard, J. (Ekstern)
Number of pages: 23
Publication date: 2018

Publication information
Publisher: Dansk Jagtkakabede
Volume: 18-01
Original language: English
Main Research Area: Technical/natural sciences
Electronic versions: 180502_Blyindhold_i_rovfugle_RAPPORT.pdf
Source: PublicationPreSubmission
Source-ID: 147142141
Publication: Research › Report – Annual report year: 2018

Can we detect outbreaks at herd-level earlier when combining multiple data sources?
The aim of this study was to explore the potential of using multiple data sources for monitoring swine diseases

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology
Authors: Lopes Antunes, A. C. (Intern), Jensen, V. (Intern), Toft, N. (Intern)
Number of pages: 1
Publication date: 2018

Host publication information
Title of host publication: ISESSAH-InnovSur 2018 Conference Abstract Book
Article number: S2-P35
Main Research Area: Technical/natural sciences
Conference: ISESSAH-InnovSur 2018, Montpellier, France, 16/05/2018 - 16/05/2018
Outbreaks, Early warning, Big data, Swine
Electronic versions: InnovSur_2018_AbstractBook_ACLA.pdf

Relations
Activities:
Can we detect outbreaks at herd-level earlier when combining multiple data sources?
Source: PublicationPreSubmission
Source-ID: 148058332
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2018
Communications of Staphylococcus aureus and non-aureus Staphylococcus species from bovine intramammary infections and teat apex colonization

The role of non-aureus staphylococci (NAS) in the risk of acquisition of intramammary infections with Staphylococcus aureus is vague and still under debate. The objectives of this study were to (1) investigate the distribution patterns of NAS species from milk and teat skin in dairy herds with automatic milking systems, and (2) examine if the isolated NAS influences the expression of S. aureus virulence factors controlled by the accessory gene regulator (agr) quorum sensing system. In 8 herds, 14 to 20 cows with elevated somatic cell count were randomly selected for teat skin swabbing and aseptic quarter foremilk samples from right hind and left front quarters. Teat skin swabs were collected using the modified wet-dry method and milk samples were taken aseptically for bacterial culture. Colonies from quarters with suspicion of having NAS in milk or teat skin samples (or both) were subjected to MALDI-TOF assay for species identification. To investigate the interaction between S. aureus and NAS, 81 isolates NAS were subjected to a qualitative β-galactosidase reporter plate assay. In total, 373 NAS isolates were identified representing 105 from milk and 268 from teat skin of 284 quarters (= 142 cows). Sixteen different NAS species were identified, 15 species from teat skin and 10 species from milk. The most prevalent NAS species identified from milk were Staphylococcus epidermidis (50%), Staphylococcus haemolyticus (15%), and Staphylococcus chromogenes (11%), accounting for 76%. Meanwhile, the most prevalent NAS species from teat skin were Staphylococcus equorum (43%), S. haemolyticus (16%), and Staphylococcus cohnii (14%), accounting for 73%. Using reporter gene fusions monitoring transcriptional activity of key virulence factors and regulators, we found that out of 81 supernatants of NAS isolates, 77% reduced expression of hla, encoding α-hemolysin, 70% reduced expression of RNAIII, the key effector molecule of agr, and 61% reduced expression of spa encoding protein A of S. aureus, respectively. Our NAS isolates showed 3 main patterns: (1) downregulation effect such as S. chromogenes (milk) and Staphylococcus xylosus (milk and teat), (2) no effect such as Staphylococcus sciuri (teat) and S. vitulinus (teat), and the third pattern (c) variable effect such as S. epidermidis (milk and teat) and S. equorum (milk and teat). The pattern of cross-talk between NAS species and S. aureus virulence genes varied according to the involved NAS species, habitat type, and herd factors. The knowledge of how NAS influences S. aureus virulence factor expression could explain the varying protective effect of NAS on S. aureus intramammary infections.
Comparative analysis of adaptive immune responses following experimental infections of cattle with bovine viral diarrhoea virus-1 and an Atypical ruminant pestivirus

Atypical ruminant pestiviruses are closely related to the two bovine viral diarrhoea virus (BVDV) species, BVDV-1 and BVDV-2. While there is evidence of cross-protective immune responses between BVDV-1 and BVDV-2, despite antigenic differences, there is little information on the antigenic cross-reactivity with atypical ruminant pestiviruses. The aim of this
study was therefore to assess the specificity of antibody and T cell responses induced by experimental infection of calves with BVDV-1 strain Ho916, Th/04_KhonKaen (TKK), an Asiatic atypical ruminant pestivirus, or co-infection with both viruses. Homologous virus neutralization was observed in sera from both single virus infected and co-infected groups, while cross-neutralization was only observed in the TKK infected group. T cell IFN-γ responses to both viruses were observed in the TKK infected animals, whereas Ho916 infected calves responded better to homologous virus. Specifically, IFN-γ responses to viral non-structural protein, NS3, were observed in all infected groups while responses to viral glycoprotein, E2, were virus-specific. Broader antigen-specific cytokine responses were observed with similar trends between inoculation groups and virus species. The limited T cell and antibody immune reactivity of Ho916 inoculated animals to TKK suggests that animals vaccinated with current BVDV-1-based vaccines may not be protected against atypical ruminant pestiviruses.
Comparing low volume saphenous-obturator block with placebo and femoral-obturator block for anterior cruciate ligament reconstruction: a randomized controlled trial

BACKGROUND: Anterior cruciate ligament reconstruction (ACL-RC) is often associated with moderate to severe postoperative pain even with a multimodal analgesic regimen. We aimed to compare the analgesic efficacy of low volume saphenous-obturator block with placebo and femoral-obturator block in patients undergoing ACL-RC. METHODS: In a randomized controlled trial eighty-two patients undergoing ACL-RC with hamstring autograft were allocated to either low volume saphenous-obturator block, placebo block or femoral-obturator block. Ropivacaine 0.75% was used for active blocks and saline for placebo. Primary outcome was pain-scores at rest quantified as area-under-the-curve 0-6 hr postoperatively. Secondary outcomes were postoperative opioid consumption and pain localization in the knee.

RESULTS: No statistical difference existed between groups in area-under-the-curve 6 hr pain-scores. However, pain-scores were significantly lower in the two ropivacaine groups compared to placebo at emergence t=0 (P<0.018), at t=5 (P<0.042) and at t=6 hours (P<0.002) postoperatively. Furthermore, ropivacaine blocks exhibited significantly reduced total opioid consumption (15.81 and 18.44 mg) postoperatively compared with placebo (26.38 mg) (P<0.018). Patients receiving ropivacaine blocks localized pain in the posterolateral knee, whereas placebo block patients reported anteromedial and central pain. Other secondary outcomes were similar between groups. CONCLUSIONS: Low volume saphenous-obturator block is significantly more effective than placebo in reducing both early and late pain-scores as well as postoperative opioid consumption in patients undergoing ACL-RC. No statistical difference existed when comparing low volume saphenous-obturator block to femoral-obturator block regarding early and late pain-scores and postoperative opioid consumption.

General information
State: Published
Organisations: National Veterinary Institute, Bacteriology & Parasitology, University of Copenhagen, University of Toronto, Copenhagen University Hospital
Authors: Lenz, K. (Ekstern), Jensen, K. (Ekstern), Tanggaard, K. (Ekstern), Vazin, M. (Ekstern), Bendtsen, T. F. (Ekstern), Chan, V. (Ekstern), Krosggaard, M. R. (Ekstern), Strube, M. L. (Intern), Børglum, J. (Ekstern)
Pages: 168-177
Publication date: 2018
Main Research Area: Technical/natural sciences

Publication information
Journal: Minerva Anestesiologica
Volume: 84
Issue number: 2
Comparison of serum pools and oral fluid samples for detection of porcine circovirus type 2 by quantitative real-time PCR in finisher pigs

Porcine circovirus type 2 (PCV2) diagnostics in live pigs often involves pooled serum and/or oral fluid samples for group-level determination of viral load by quantitative real-time polymerase chain reaction (qPCR). The purpose of the study was to compare the PCV2 viral load determined by qPCR of paired samples at the pen level of pools of sera (SP) from 4 to 5 pigs and the collective oral fluid (OF) from around 30 pigs corresponding to one rope put in the same pen. Pigs in pens of 2 finishing herds were sampled by cross-sectional (Herd 1) and cross-sectional with follow-up (Herd 2) study designs. In Herd 1, 50 sample pairs consisting of SP from 4 to 5 pigs and OF from around 23 pigs were collected. In Herd 2, 65 sample pairs consisting of 4 (SP) and around 30 (OF) pigs were collected 4 times at 3-week intervals. A higher proportion of PCV2-positive pens (86% vs. 80% and 100% vs. 91%) and higher viral loads (mean difference: 2.10 and 1.83 log(10) PCV2 copies per ml) were found in OF versus SP in both herds. The OF cut-off value corresponding to a positive SP (>3 log(10) PCV2 copies per ml) was estimated to 6.5 and 7.36 log(10) PCV2 copies per ml for Herds 1 and 2, respectively. Significant correlations between SP and OF results were found in Herd 1 (rho=0.69) and the first sampling in Herd 2 (rho =0.39), but not for the subsequent consecutive 3 samplings in Herd 2. The proportion and viral loads of PCV2 positive pens were higher in collective OF (including up to 30 pigs) compared to SP (including 4-5 pigs) of the same pens. Also, OF seemed to detect the PCV2 infection earlier with OF values just below 6.5 (Herd 1) and 7.36 (Herd 2) log(10) being associated with a negative SP for the same pen. Nevertheless, a statistically significant correlation between SP and OF could not be found for all sampling time points, probably due to a high within-pen variation in individual pig viral load becoming very evident in SP of only four or five pigs. Consequently, the results imply that OF is well suited for detecting presence of PCV2 but less so for determining the specific viral load of pigs in a pen.

General information
State: Published
Organisations: National Veterinary Institute, Virology, MSD Animal Health Nordic, University of Copenhagen, Porcus Veterinary Pig Practice, SEGES Pig Research Center, OE-Vet
Authors: Nielsen, G. B. (Ekstern), Nielsen, J. P. (Ekstern), Haugegaard, J. (Ekstern), Leth, S. C. (Ekstern), Larsen, L. E. (Intern), Kristensen, C. S. (Ekstern), Pedersen, K. S. (Ekstern), Stege, H. (Ekstern), Hjulsager, C. K. (Ekstern), Houe, H. (Ekstern)
Number of pages: 10
Development of body mass and sexual size dimorphism in Danish red foxes (Vulpes vulpes)

In this study, we examine the development of body mass and sexual size dimorphism (SSD) in 178 juvenile wild Danish red foxes from 99 litters using piecewise analyses of regression lines for age versus weight. When fox cubs are younger than 100 days, only slight (SSD=1.7%) and no significant difference (t-test: t=1.2, p=0.24) was found in the mean weight of males (2.03± kg) and females (1.93± kg), and no significant difference was found in the slope of regression lines for males and females (F=0.97E-5, p = 0.99). In the growth period between 100 days of age and mating around 275 days of age, the regression line in males steepens more than that of females (difference in slopes, F=5.9, p<0.02) and the difference in mean weight of the sexes become highly significant (SSD=7.4%, difference in mean t=4.6, p=2.2E-5). After mating the growth curve levels off i.e. the slope of the regression lines for age versus weight is not significantly different from zero. Yearly variation was revealed in the growth rate of juvenile foxes (difference in slope for males; F=3.9, p<0.01 and females; F=8.6, p<0.001). Conclusion: SSD in red foxes mainly develop as a result of a faster grow rate in males between independence and maturity. Ontogony of red foxes may genetically be disposed to prevent males outcompeting females in the early stages of life (<100 days), when cubs are still fed by adults and the increase in SSD before mating, may be an adaption to selective forces benefitting larger males. The growth rate of juvenile foxes of both sexes is influenced by environmental variation in different years.

General information
State: Published
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Number of pages: 12
Pages: 36-47
Publication date: 2018
Effect of the nematophagous fungus Pochonia chlamydosporia on soil content of ascarid eggs and infection levels in exposed hens

The nematophagous fungus Pochonia chlamydosporia can degrade ascarid (e.g. Ascaridia galli) eggs in agar and soil in vitro. However, it has not been investigated how this translates to reduced infection levels in naturally exposed chickens. We thus tested the infectivity of soil artificially contaminated with A. galli (and a few Heterakis gallinarum) eggs and treated with P. chlamydosporia. Sterilised and non-sterilised soils were used to examine any influence of natural soil biota. Unembryonated eggs were mixed with sterilised (S)/non-sterilised (N) soil, either treated with the fungus (F) or left as untreated controls (C) and incubated (22 °C, 35 days) to allow eggs to embryonate and fungus to grow. Egg number in soil was estimated on days 0 and 35 post-incubation. Hens were exposed to the soil (SC/SF/NC/NF) four times over 12 days by mixing soil into the feed. On day 42 post-first-exposure (p.f.e.), the hens were euthanized and parasites were recovered. Serum A. galli IgY level and ascarid eggs per gram of faeces (EPG) were examined on days -1 and 36 (IgY) or 40 p.f.e. (EPG). Egg recovery in SF soil was substantially lower than in SC soil, but recovery was not significantly different between NF and NC soils. SF hens had a mean worm count of 76 whereas the other groups had means of 355-453. Early mature/mature A. galli were recovered from SF hens whereas hens in the other groups harboured mainly immature A. galli. Heterakis gallinarum counts were low overall, especially in SF. The SF post-exposure IgY response was significantly lower while EPG was significantly higher compared to the other groups. Pochonia chlamydosporia was very effective in reducing ascarid egg numbers in sterilised soil and thus worm burdens in the exposed hens. However, reduced exposure of hens shifted A. galli populations toward a higher proportion of mature worms and resulted in a higher faecal egg excretion within the study period. This highlights a fundamental problem in ascarid control: if not all eggs in the farm environment are inactivated, the resulting low level infections may result in higher contamination levels with associated negative long-term consequences.
Effects of Harmful Algal Blooms on Fish: Insights from Prymnesium parvum

Blooms of the planktonic alga Prymnesium parvum pose a global threat, causing fish kills worldwide. Early studies on the exposure of fish to P. parvum indicate that toxic effects are related to gill damage. The more strictly defined concept of adverse outcome pathways has been suggested as a replacement for the mode of action in toxicology studies. In this study, rainbow trout (Onchorhyncus mykiss) were exposed to P. parvum. During exposure, oxygen consumption was determined by respirometry, and ventilation and coughing rate were determined via video surveillance. Per breath oxygen consumption was calculated to assess the ventilation effort to obtain a unit of oxygen. A second experiment monitored fish behavior to assess recovery. The results indicated that oxygen consumption initially increased, but on average fell below the standard oxygen consumption at 70% relative exposure. Being a function of ventilation frequency and oxygen consumption, the per breath oxygen consumption decreased throughout exposure. Behavioral results determined that short-term P. parvum exposure subsequently caused the exposed fish to seek flow refuge immediately and to a greater extent than unexposed fish. The adverse outcome pathway of P. parvum on rainbow trout is that P. parvum acts as a gill irritant resulting in non-recoverable respiratory failure.
Effects of soluble immunostimulants on mucosal immune responses in rainbow trout immersion-vaccinated against Yersinia ruckeri

Immersion vaccination of rainbow trout against Yersinia ruckeri infection is an established method to prevent enteric red mouth disease (ERM) but the effect is inferior to injection vaccination and the duration of protection is limited to less than six months. Adjuvants in vaccines may in general elevate the immune response and the present work elucidates how ERM immersion vaccination of trout in combination with exposure to soluble adjuvants, Montanide™ IMS 1312 VG PR and β-glucan, affects immune reactions. The former adjuvant, when used alone, induced a slightly increased protection (not statistically significant) whereas β-glucan did not increase protection. Adjuvant-treated and non-exposed groups showed elevated plasma lysozyme activity after challenge with Y. ruckeri. Specific antibody production was not positively affected by combining adjuvant and vaccine. Overall expression of immune genes tested was generally manifold higher in gills compared to skin. Only genes encoding SAA and IL-17C1 were expressed at a higher level in skin. Dynamic differences between the gill and skin compartments were also recorded for genes encoding cytokines (TNF-α, IL-1β, IL-6, IL-10, IL-12, IL-17A/F2, IL-17C1, IL-17C2, IL-22), immunoglobulins (IgM, IgD, IgT), cell markers (CD8α, TCR-β) and acute phase reactants (SAA, lysozyme). These genes were upregulated 24h post-vaccination in fish gills exposed to both vaccine-adjuvant combinations when compared to fish exposed to vaccine alone. After a few weeks no vaccine induced reaction was seen and after challenge with bacteria mainly unvaccinated fish responded. Adjuvants used in combination with immersion vaccine clearly influences immune reactions and may improve duration and protection but further potency tests should be performed.
Yersinia ruckeri, Immersion vaccination, Adjuvant, Montanide™, β-glucan

DOIs: 10.1016/j.aquaculture.2018.04.011
Source: FindIt
Source-ID: 2411786389
Publication: Research - peer-review › Journal article – Annual report year: 2018
Efficacy and safety of simultaneous vaccination with two modified live virus vaccines against porcine reproductive and respiratory syndrome virus types 1 and 2 in pigs

The objective of the study was to compare responses of pigs vaccinated with a PRRS MLV vaccine against PRRSV-1 or PRRSV-2 with the responses of pigs vaccinated simultaneously with both vaccines. Furthermore, the efficacy of the two PRRSV MLV vaccination strategies was assessed following challenge. The experimental design included four groups of 4-weeks old SPF-pigs. On day 0 (DPV0), groups 1–3 (N = 18 per group) were vaccinated with modified live virus vaccines (MLV) containing PRRSV-1 virus (VAC-T1), PRRSV-2 virus (VAC-T2) or both (VAC-T1T2). One group was left unvaccinated (N = 12). On DPV 62, the pigs from groups 1–4 were mingled in new groups and challenged (DPC 0) with PRRSV-1, subtype 1, PRRSV-1, subtype 2 or PRRSV-2. On DPC 13/14 all pigs were necropsied. Samples were collected after vaccination and challenge. PRRSV was detected in all vaccinated pigs and the majority of the pigs were positive until DPV 28, but few of the pigs were still viremic 62 days after vaccination. Virus was detected in nasal swabs until DPV 7–14. No overt clinical signs were observed after challenge. PRRSV-2 vaccination resulted in a clear reduction in viral load in serum after PRRSV-2 challenge, whereas there was limited effect on the viral load in serum following challenge with the PRRSV-1 strains. Vaccination against PRRSV-1 had less impact on viremia following challenge. The protective effects of simultaneous vaccination with PRRSV Type 1 and 2 MLV vaccines and single PRRS MLV vaccination were comparable. None of the vaccines decreased the viral load in the lungs at necropsy. In conclusion, simultaneous vaccination with MLV vaccines containing PRRSV-1 and PRRSV-2 elicited responses comparable to single vaccination and the commercial PRRSV vaccines protected only partially against challenge with heterologous strains. Thus, simultaneous administration of the two vaccines is an option in herds with both PRRSV types.

General information
State: Published
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Pages: 227-236
Publication date: 2018
Main Research Area: Technical/natural sciences

Publication information
Journal: Vaccine
Volume: 36
Issue number: 2
ISSN (Print): 0264-410X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.19 SJR 1.863 SNIP 1.124
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.33 SJR 1.985 SNIP 1.142
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.073 SNIP 1.248 CiteScore 3.45
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.105 SNIP 1.218 CiteScore 3.57
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.752 SNIP 1.115 CiteScore 3.43
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.656 SNIP 1.154 CiteScore 3.56
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
Emerging skin diseases in aquaculture

Within the last decade skin diseases have become a major challenge for rainbow trout (Oncorhynchus mykiss) aquaculture in Europe and mariculture in the Mediterranean. The causes of these conditions remain largely elusive, however. A workshop was organised to focus on recent advances for some of the more notable skin disease problems affecting these aquaculture industries, namely red mark syndrome (RMS) and puffy skin disease (PSD) in rainbow trout and petechial rash (PR) in sea bream (Sparus aurata) and sea bass (Dicentrarchus labrax) and also some other skin diseases that are starting to emerge in Mediterranean aquaculture species. The target audience for the workshop was researchers with an interest and/or research focus on fish skin diseases or who had an interest in emerging fish diseases/pathogens.

General information
State: Published
Organisations: National Veterinary Institute, Public Sector Consultancy, Fish Diseases, Moredun Research Institute, Universitat Autonoma de Barcelona
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Pages: 122-129
Publication date: 2018
Epidemiology and genetic characterization of Peste des petits ruminants virus in Bangladesh

Peste des petits ruminants (PPR) is an acute, highly contagious disease responsible for high morbidity and mortality rates in susceptible sheep and goats. Adequate knowledge of the diversity of circulating strains of PPR virus will help livestock authorities choose appropriate vaccines. The objective of this study was to describe the epidemiology of PPR and characterize the strains circulating in Bangladesh. Veterinarians enrolled goats showing signs consistent with PPR, including diarrhoea, fever and respiratory distress, from three veterinary hospitals. Post-treatment follow up was carried out to ascertain health outcomes of the goats. Faecal and throat swab samples were collected from the goats and tested for PPRV RNA using real-time reverse transcription polymerase chain reaction (rRT-PCR). Nucleotide sequence-based phylogenetic analyses of two structural genes, the nucleocapsid (N gene), and the haemagglutinin (H gene) were studied to determine the genetic variations of PPRV strains. Of the 539 goats enrolled, 38% (203/539) had detectable RNA for PPRV. We were able to follow up with 91% (184/203) of the PPRV infected goats; 44 of them died (24%). PPRV was more frequently identified in the summer (45%) than in the rainy season (29%) (Odds ratio = 1.9, 95% confidence interval: 1.3–3.1). Bangladeshi strains were phylogenetically similar to the lineage IV PPRV strains; showing particularly strong affiliation with Tibetan and Indian strains. PPR is a common viral infection of the goats in Bangladesh, with a high case-fatality rate. This study confirms the circulation of lineage IV PPRV in the country with unique amino acid substitutions in N and H proteins and provides baseline data for vaccine development and implementation.

Epidemiology, biology and therapy of Merkel cell carcinoma: conclusions from the EU project IMMOMEC

Merkel cell carcinoma (MCC) is a highly aggressive, often lethal neuroendocrine cancer. Its carcinogenesis may be either caused by the clonal integration of the Merkel cell polyomavirus into the host genome or by UV-induced mutations. Notably, virally-encoded oncoproteins and UV-induced mutations affect comparable signaling pathways such as RB restriction of cell cycle progression or p53 inactivation. Despite its low incidence, MCC recently received much attention based on its exquisite immunogenicity and the resulting major success of immune modulating therapies. Here, we summarize current knowledge on epidemiology, biology and therapy of MCC as conclusion of the project 'Immune Modulating strategies for treatment of Merkel Cell Carcinoma', which was funded over a 5-year period by the European Commission to investigate innovative immunotherapies for MCC.
Evaluating the impact of transmission mode, calibration level and farmer compliance in simulation models of paratuberculosis in dairy herds

Simulation models can predict the outcome of different strategies for the control and eradication of paratuberculosis (PTB) in dairy herds. Two main transmission modes have previously been used to simulate the spread of PTB: direct (contact between animals) and indirect (through the environment). In addition, previous models were calibrated to either low or high within-herd prevalence levels, which we refer to as normal and low hygiene levels, respectively. We simulated both direct and indirect transmission with the same model in both normal and low hygiene level scenarios. The effectiveness of a test-and-cull strategy was dependent on the calibration level of the simulation model, and eradication occurred less frequently with the more biologically plausible indirect transmission mode. The results were compared to within-herd prevalence records from 314 dairy herds. The prevalence in 50% of the herds varied less than 0.9% per year on average, and less than 4% in 90% of the herds. We therefore conclude that the normal-hygiene scenario best describes most dairy herds in Denmark. Finally, we simulated different levels of farmer compliance with a test-and-cull strategy and found that a 60% compliance level was not sufficient to reach eradication within 10 years.
Evaluation of a multiplex immunoassay for bovine respiratory syncytial virus and bovine coronavirus antibodies in bulk tank milk against two indirect ELISAs using latent class analysis

Bovine respiratory syncytial virus (BRSV) and bovine coronavirus (BCV) are responsible for respiratory disease and diarrhea in cattle worldwide. The Norwegian control program against these infections is based on herd-level diagnosis using a new multiplex immunoassay. The objective of this study was to estimate sensitivity and specificity across different cut-off values for the MVD-Enferplex BCV/BRSV multiplex, by comparing them to a commercially available ELISA, the SVANOVIR® BCV-Ab and SVANOVIR® BRSV-Ab, respectively. We analyzed bulk tank milk samples from 360 herds in a low- and 360 herds in a high-prevalence area. As none of the tests were considered perfect, estimation of test characteristics was performed using Bayesian latent class models. At the manufacturers’ recommended cut-off values, the median sensitivity for the BRSV multiplex and the BRSV ELISA was 94.4 [89.8–98.7 95% Posterior Credibility Interval (PCI)] and 99.8 [98.7–100 95% PCI], respectively. The median specificity for the BRSV multiplex was 90.6 [85.5–94.4 95% PCI], but only 57.4 [50.5–64.4 95% PCI] for the BRSV ELISA. However, increasing the cut-off of the BRSV ELISA increased specificity without compromising sensitivity. For the BCV multiplex we found that by using only one of the three antigens included in the test, the specificity increased, without concurrent loss in sensitivity. At the recommended cut-off this resulted in a sensitivity of 99.9 [99.3–100 95% PCI] and specificity of 93.7 [88.8–97.8 95% PCI] for the multiplex and a sensitivity of 99.5 [98.1–100 95% PCI] and a specificity of 99.6 [97.6–100 95% PCI] for the BCV ELISA.
Evaluation of ELISA and haemagglutination inhibition as screening tests in serosurveillance for H5/H7 avian influenza in commercial chicken flocks

Avian influenza virus (AIV) subtypes H5 and H7 can infect poultry causing low pathogenicity (LP) AI, but these LPAIVs may mutate to highly pathogenic AIV in chickens or turkeys causing high mortality, hence H5/H7 subtypes demand statutory intervention. Serological surveillance in the European Union provides evidence of H5/H7 AIV exposure in apparently healthy poultry. To identify the most sensitive screening method as the first step in an algorithm to provide evidence of H5/H7 AIV infection, the standard approach of H5/H7 antibody testing by haemagglutination inhibition (HI) was compared with an ELISA, which detects antibodies to all subtypes. Sera (n = 1055) from 74 commercial chicken flocks were tested by both methods. A Bayesian approach served to estimate diagnostic test sensitivities and specificities, without assuming any ‘gold standard’. Sensitivity and specificity of the ELISA was 97% and 99.8%, and for H5/H7 HI 43% and 99.8%, respectively, although H5/H7 HI sensitivity varied considerably between infected flocks. ELISA therefore
provides superior sensitivity for the screening of chicken flocks as part of an algorithm, which subsequently utilises H5/H7 HI to identify infection by these two subtypes. With the calculated sensitivity and specificity, testing nine sera per flock is sufficient to detect a flock seroprevalence of 30% with 95% probability.
Evidence of No Association Between Human Papillomavirus and Breast Cancer

Background: Globally, breast cancer is the most frequent cancer among women. Studies reported an increased risk of breast cancer among women with prior cervical dysplasia. This study aimed to describe the prevalence of human papillomavirus (HPV) in breast cancer and explore if women with prior cervical neoplasia carry an increased risk of HPV-positive breast cancer compared to women without.

Methods: This case–control study identified 193 Danish women diagnosed with breast cancer (1998–2012) at Aarhus University Hospital or Copenhagen University Hospital Herlev. Cases were 93 women with cervical intraepithelial neoplasia grade 3 or worse (CIN3+) prior to breast cancer. Controls were 100 women without prior cervical dysplasia. HPV testing and genotyping were done using SPF10 PCR-DEIA-LiPA25 and an in-house semi-Q-PCR assay.

Results: Overall HPV prevalence in breast cancer for the assays was 1.55% (95% CI 0.32–4.48) and 0.52% (95% CI 0.01–2.85). There was no difference in HPV prevalence between cases and controls (2.15 vs. 1.00%, p = 0.61 and 1.08 vs. 0.00%, p = 0.48). HPV prevalence in CIN3+ was 94.62% (95% CI 0.88–0.98). Concordance between the assays was 98.60%.

Conclusion: HPV prevalence in breast cancer is very low suggesting no etiological correlation between HPV and breast cancer.

General information
State: Published
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Publication date: 2018
Main Research Area: Technical/natural sciences

Publication information
Journal: Frontiers in Oncology
Volume: 8
Article number: 209
Ratings:
We report Taenia ovis infection in Danish sheep for the first time. In spring 2016, the metocestode stage of T. ovis was at slaughter observed in heart muscles, diaphragm and skeletal muscles from approx. a third of all sheep from one specific farm localised in South Jutland. The diagnosis was confirmed by molecular typing of the mitochondrial cytochrome c oxidase I (cox1) gene. Three newly imported dogs were suspected but the definitive host was unidentifiable. The finding is not regulated in the meat control procedures. However, infected meat is usually condemned due to aesthetic reasons causing economic losses. Thus, finding of T. ovis is of concern to sheep meat producers in the area, as the infection could have spread further on to other farms.
Flavobacteria, a Never Ending Threat for Fish: a Review

Purpose of Review
In this review, we summarized the most recent findings on the partial and full genome and the phylogenetic structure of genomovars, as well as on virulence factors, vaccine development, and treatment methods of the two fish pathogenic bacteria Flavobacterium psychrophilum and F. columnare. Both species have a widespread distribution and are the causative agents of devastating diseases of both farmed and wild fish. For minimizing the impact of these infections, knowledge on biology and epidemiology of these pathogens is essential. Recent Findings
Recent investigations have demonstrated a wide variability with regard to strains and genotypes. For both pathogens, new host species and geographic areas have been identified. For some isolates, a certain degree of host specificity could be demonstrated. Attempts have been undertaken to standardize methods for testing bacteria for resistance to antibiotics. Further, newly developed vaccines and a number of new treatment methods yielded promising results, but fully convincing and generally accepted prophylactic or therapeutic methods are not yet available. Summary
In summary, despite intense research in the two species and considerable increase in understanding the host-pathogen relationship, there is still no generally applicable method to reduce the devastating effect of these bacteria species on farmed and wild fish populations.

General information
State: Published
Porcine circovirus 3 (PCV3) is a new species of the Circovirus genus, which has recently been associated with different clinical syndromes. Its presence has been reported in different countries of North and South America, Asia and recently also Europe (Poland). However, different from the other continents, no European PCV3 sequence is currently available in public databases. There is a strong need of epidemiological data and full-genome sequences from Europe because of its relevance in the understanding of PCV3 molecular epidemiology and control. To fill this lack of information, samples collected in Denmark, Italy and Spain in 2016 and 2017 were screened for PCV3. Of the Danish samples, 36 of 38 the lymph nodes, six of 20 serum samples and two of 20 lung samples tested positive. Similarly, 10 of 29 lungs, 20 of 29 organ pools, six of 33 sera and one of eight nasal swabs tested PCV3 positive in Italy. Fourteen of 94 serum pools from seven of 14 Spanish farms were also positive. Despite the convenience nature of the sampling prevents any precise prevalence estimation, the preliminary screening of the data from three European countries confirmed a rather wide PCV3 distribution in Europe. Furthermore, the analysis of the six obtained complete European PCV3 genomes and their comparison with the public available sequences seems to support a remarkable worldwide PCV3 circulation. These results underline once more the urgency of more extensive epidemiological studies to refine the current knowledge on PCV3 evolution, transmission, spreading patterns and impact on pig health.
Europe, Porcine circovirus 3, Full genome, Molecular epidemiology

Porcine epidemic diarrhoea virus, strain CV777, was initially characterized in 1978 as the causative agent of a disease first identified in the UK in 1971. This coronavirus has been widely distributed among laboratories and has been passaged both within pigs and in cell culture. To determine the variability between different stocks of the PEDV strain CV777,
sequencing of the full-length genome (ca. 28kb) has been performed in 6 different laboratories, using different protocols. Not surprisingly, each of the different full genome sequences were distinct from each other and from the reference sequence (Accession number AF353511) but they are >99% identical. Unique and shared differences between sequences were identified. The coding region for the surface-exposed spike protein showed the highest proportion of variability including both point mutations and small deletions. The predicted expression of the ORF3 gene product was more dramatically affected in three different variants of this virus through either loss of the initiation codon or gain of a premature termination codon. The genome of one isolate had a substantially rearranged 5´-terminal sequence. This rearrangement was validated through the analysis of sub-genomic mRNAs from infected cells. It is clearly important to know the features of the specific sample of CV777 being used for experimental studies.

General information
State: Published
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Number of pages: 17
Pages: e0193682
Publication date: 2018
Main Research Area: Technical/natural sciences

Publication information
Journal: P L o S One
Volume: 13
Issue number: 3
ISSN (Print): 1932-6203
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.01 SJR 1.164 SNIP 1.111
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.11 SJR 1.236 SNIP 1.101
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.427 SNIP 1.136 CiteScore 3.32
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.559 SNIP 1.148 CiteScore 3.54
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.772 SNIP 1.153 CiteScore 3.94
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.982 SNIP 1.156 CiteScore 4.15
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 2.425 SNIP 1.233 CiteScore 4.58
ISI indexed (2011): ISI indexed no
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.705 SNIP 1.178
Web of Science (2010): Indexed yes
Genomic Diversity and Evolution of the Fish Pathogen Flavobacterium psychrophilum

Flavobacterium psychrophilum, the etiological agent of rainbow trout fry syndrome and bacterial cold-water disease in salmonid fish, is currently one of the main bacterial pathogens hampering the productivity of salmonid farming worldwide. In this study, the genomic diversity of the F. psychrophilum species is analyzed using a set of 41 genomes, including 30 newly sequenced isolates. These were selected on the basis of available MLST data with the two-fold objective of maximizing the coverage of the species diversity and of allowing a focus on the main clonal complex (CC-ST10) infecting farmed rainbow trout (Oncorhynchus mykiss) worldwide. The results reveal a bacterial species harboring a limited genomic diversity both in terms of nucleotide diversity, with similar to 0.3% nucleotide divergence inside CDSs in pairwise genome comparisons, and in terms of gene repertoire, with the core genome accounting for similar to 80% of the genes in each genome. The pan-genome seems nevertheless "open" according to the scaling exponent of a power-law fitted on the rate of new gene discovery when genomes are added one-by-one. Recombination is a key component of the evolutionary process of the species as seen in the high level of apparent homoplasy in the core genome. Using a Hidden Markov Model to delineate recombination tracts in pairs of closely related genomes, the average recombination tract length was estimated to similar to 4.0 Kbp and the typical ratio of the contributions of recombination and mutations to nucleotide-level differentiation (r/m) was estimated to similar to 13. Within CC-ST10, evolutionary distances computed on non-recombined regions and comparisons between 22 isolates sampled up to 27 years apart suggest a most recent common ancestor in the second half of the nineteenth century in North America with subsequent diversification and transmission of this clonal complex coinciding with the worldwide expansion of rainbow trout farming. With the goal to promote the development of tools for the genetic manipulation of F. psychrophilum, a particular attention was also paid to plasmids. Their extraction and sequencing to completion revealed plasmid diversity that remained hidden to classical plasmid profiling due to size similarities.
Genomic investigation of Danish Staphylococcus aureus isolates from bulk tank milk and dairy cows with clinical mastitis

Staphylococcus aureus is one of the most common pathogens that cause mastitis in dairy cows. Various subtypes, virulence genes and pathogenicity islands have been associated with isolates from bulk tank milk and clinical mastitis. So far, no Danish cattle associated S. aureus isolates have been whole-genome sequenced and further analyzed. Thus, the main objective was to investigate the population structure and genomic content of isolates from bulk tank milk and clinical mastitis, using whole-genome sequencing. This may reveal the origin of strains that cause clinical mastitis. S. aureus isolates from bulk tank milk (n=94) and clinical mastitis (n=63) were collected from 91 and 24 different farms, respectively and whole-genome sequenced. The genomic content was analyzed and a phylogenetic tree based on single nucleotide polymorphisms was constructed. In general, the isolates from both bulk tank milk and clinical mastitis were of similar genetic background. This suggests that dairy cows are natural carriers of the S. aureus subtypes that cause mastitis if the right conditions are present and that a broad range of subtypes cause mastitis. A phylogenetic cluster that mostly consisted of ST151 isolates carried three pathogenicity islands that were primarily found in this group. The prevalence of resistance genes was generally low. However, the first ST398 methicillin resistant S. aureus isolate from a Danish dairy cow with clinical mastitis was detected.

Genomic investigation of Danish Staphylococcus aureus isolates from bulk tank milk and dairy cows with clinical mastitis

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How cancer specific T-cell recognition and functionality is affected by combination of radio- and immunotherapeutic strategies

General information
State: Published
Organisations: National Veterinary Institute, T-cells & Cancer, Cancer Genomics, Immunoinformatics and Machine Learning, Technical University of Denmark
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Pages: S21-S21
Publication date: 2018
Main Research Area: Technical/natural sciences

Publication information
Journal: European Journal of Cancer
Volume: 92
Issue number: Suppl. 1
Article number: P08.01
ISSN (Print): 0959-8049
Ratings:
  BFI (2018): BFI-level 1
  Web of Science (2018): Indexed yes
  BFI (2017): BFI-level 1
  Scopus rating (2017): SNIP 1.987 SJR 2.963 CiteScore 6.01
  Web of Science (2017): Indexed Yes
  BFI (2016): BFI-level 1
  Scopus rating (2016): CiteScore 6.1 SJR 3.105 SNIP 2.196
  BFI (2015): BFI-level 1
  Scopus rating (2015): SJR 3.177 SNIP 2.1 CiteScore 5.89
  BFI (2014): BFI-level 1
  Scopus rating (2014): SJR 2.608 SNIP 1.866 CiteScore 5.1
  Web of Science (2014): Indexed yes
  BFI (2013): BFI-level 1
  Scopus rating (2013): SJR 2.864 SNIP 2.061 CiteScore 5.65
  ISI indexed (2013): ISI indexed yes
  BFI (2012): BFI-level 1
  Scopus rating (2012): SJR 2.894 SNIP 2.141 CiteScore 5.79
  ISI indexed (2012): ISI indexed yes
  BFI (2011): BFI-level 1
  Scopus rating (2011): SJR 2.514 SNIP 1.893 CiteScore 5.19
  ISI indexed (2011): ISI indexed yes
  Web of Science (2011): Indexed yes
  BFI (2010): BFI-level 1
  Scopus rating (2010): SJR 2.205 SNIP 1.555
  BFI (2009): BFI-level 1
  Scopus rating (2009): SJR 1.974 SNIP 1.521
  BFI (2008): BFI-level 1
  Scopus rating (2008): SJR 2.161 SNIP 1.578
  Scopus rating (2007): SJR 2.102 SNIP 1.557
  Scopus rating (2006): SJR 1.706 SNIP 1.593
IFN-λ and microRNAs are important modulators of the pulmonary innate immune response against influenza A (H1N2) infection in pigs

The innate immune system is paramount in the response to and clearance of influenza A virus (IAV) infection in non-immune individuals. Known factors include type I and III interferons and antiviral pathogen recognition receptors, and the cascades of antiviral and pro- and anti-inflammatory gene expression they induce. MicroRNAs (miRNAs) are increasingly recognized to participate in post-transcriptional modulation of these responses, but the temporal dynamics of how these players of the antiviral innate immune response collaborate to combat infection remain poorly characterized. We quantified the expression of miRNAs and protein coding genes in the lungs of pigs 1, 3, and 14 days after challenge with swine IAV (H1N2). Through RT-qPCR we observed a 400-fold relative increase in IFN-lambda 3 gene expression on day 1 after challenge, and a strong interferon-mediated antiviral response was observed on days 1 and 3 accompanied by up-regulation of genes related to the pro-inflammatory response and apoptosis. Using small RNA sequencing and qPCR validation we found 27 miRNAs that were differentially expressed after challenge, with the highest number of regulated miRNAs observed on day 3. In contrast, the number of protein coding genes found to be regulated due to IAV infection peaked on day 1. Pulmonary miRNAs may thus be aimed at fine-tuning the initial rapid inflammatory response after IAV infection. Specifically, we found five miRNAs (ssc-miR-15a, ssc-miR-18a, ssc-miR-21, ssc-miR-29b, and hsa-miR-590-3p)-four known porcine miRNAs and one novel porcine miRNA candidate-to be potential modulators of viral pathogen recognition and apoptosis. A total of 11 miRNAs remained differentially expressed 14 days after challenge, at which point the infection had cleared. In conclusion, the results suggested a role for miRNAs both during acute infection as well as later, with the potential to influence lung homeostasis and susceptibility to secondary infections in the lungs of pigs after IAV infection.

General information
State: Published
Organisations: Department of Biotechnology and Biomedicine, National Veterinary Institute, Innate Immunology, Virology, University of Copenhagen, Robert Koch Institute
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Number of pages: 23
Publication date: 2018
Main Research Area: Technical/natural sciences

Publication information
Journal: PLoS One
Volume: 13
Issue number: 4
Article number: e0194765
ISSN (Print): 1932-6203
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.01 SJR 1.164 SNIP 1.111
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.11 SJR 1.236 SNIP 1.101
Web of Science (2016): Indexed yes
Immunity to gastrointestinal nematode infections
Numerous species of nematodes have evolved to inhabit the gastrointestinal tract of animals and humans, with over a billion of the world's population infected with at least one species. These large multicellular pathogens present a considerable and complex challenge to the host immune system given that individuals are continually exposed to infective stages, as well as the high prevalence in endemic areas. This review summarizes our current understanding of host-parasite interactions, detailing induction of protective immunity, mechanisms of resistance, and resolution of the response. It is clear from studies of well-defined laboratory model systems that these responses are dominated by innate and adaptive type 2 cytokine responses, regulating cellular and soluble effectors that serve to disrupt the niche in which the parasites live by strengthening the physical mucosal barrier and ultimately promoting tissue repair.

General information
State: Published
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Pages: 304-315
Publication date: 2018
Main Research Area: Technical/natural sciences

Publication information
Journal: Mucosal Immunology
Increased reproductive output of Danish red fox females following an outbreak of canine distemper

A decline in the Danish population of red foxes Vulpes vulpes due to an outbreak of canine distemper (CDV) in 2012 gave us the opportunity to test the hypothesis that the reproductive performance of foxes increases when the population density declines. The reproductive performance of 280 female foxes from two periods (mainly shot or road killed) in 1997-2000 and 2012-16, were compared. Game Bag Records of Jutland (GBRJ) were used as an estimate of population density. After a drop in GBRJ in 2013 due to the CDV epidemic, the mean litter size (based on dark placental scars from partum to oestrus) became significantly larger than in previous years; F=4.3, p=0.03, Hc=8.1, p<0.02. In 2015-2016, after population decline the mean litter size was 8.2 (±2.5 SD) and in the breeding seasons before population decline in 1997-1999 and 2012-2013 the mean litter size was 5.6 (±2.1 SD) and 5.7 (±2.0 SD), respectively. During the period 1997-1999, barrenness was relatively high especially in yearlings, and the reproducing yearling foxes made up only 6% of the breeding females compared to 2012-13 and 2015-16 where breeding yearling females made up 53% and 61%, respectively. Age related differences in litter size and productivity were found in years with a relatively high population density, when older females in their third and fourth breeding seasons had the largest litter sizes and highest productivity. This was in contrast to the years with low population size, when no age-related reproduction was found, and when young females had relatively large litter sizes and high productivity. Rump fat thickness (RFT) of the breeding females was significantly higher in breeding females than in barren females, and the RFT was positively correlated to the number of embryos (R2=41%). This study confirms that the number of barren females drops, and the proportion of yearling females and litter size increase with reduced population density. Hence, culling or epidemics in fox populations increase production, most probably due to reduced competition among foxes, but will not change population size permanently. The present level of culling and traditional hunting in Denmark has no long-term effect on population size.
Infection of pigs with African swine fever virus via ingestion of stable flies (Stomoxys calcitrans)

Within Eastern Europe, African swine fever virus (ASFV) has unexpectedly spread to farms with high biosecurity. In an attempt to explain this process, pigs were allowed to ingest flies that had fed on ASFV-spiked blood, which had a realistic titre for an infected pig. Some of the pigs became infected with the virus. Thus, ingestion of blood-sucking flies, having fed on ASFV-infected wild boar before entering stables, represents a potential route for disease transmission.
Interplay between daily rhythmic serum-mediated bacterial killing activity and immune defence factors in rainbow trout (Oncorhynchus mykiss)

Circadian rhythm is emerging as an important regulator of immune functions. However, there is a paucity of information on the influence of this biological phenomenon in the antimicrobial factors in teleost fish. This study investigated the dynamics and interplay of serum-mediated bacterial killing activity and immune defence factors throughout the light:dark (LD) cycle in rainbow trout (Oncorhynchus mykiss). The juvenile fish came from two different emergence time fractions (i.e., late and early) that were believed to exhibit behavioural and physiological differences. Serum collected during the day from fish (mean ± SD: 39.8 ± 6.3 g) reared under 14L:10D photoperiod demonstrated bactericidal activity against Flavobacterium psychrophilum, Yersinia ruckeri and Aeromonas salmonicida subsp. salmonicida of varying magnitude, but no significant differences between the emergence fractions were observed. A day-night comparison in the same batch of fish revealed time-of-day dependence in the bactericidal activity against F. psychrophilum and Y. ruckeri amongst emergence fractions.

A group of fish (63.3 ± 4.7 g) from each fraction was entrained to 12L:12D photoperiod for 21 days to investigate whether serum bactericidal activity exhibit daily rhythm. Serum-mediated bacterial killing activity against F. psychrophilum and Y. ruckeri displayed significant daily rhythm in both emergence fractions, where the peak of activity was identified during the light phase. Moreover, several serum defence factors manifested variations during the LD cycle, where anti-protease (ANTI) and myeloperoxidase (MPO) activities exhibited significant daily oscillation. However, there were no remarkable differences in the daily changes of serum factors amongst emergence fractions. Acrophase analysis revealed that the peaks of activity of alkaline phosphatase (only in late fraction), ANTI, lysozyme (only in early fraction) and MPO were identified during the light phase and corresponded with the period when serum-mediated bacterial killing activity was also at its highest. The daily dynamics of bactericidal activity and immune defence factors displayed positive correlation, particularly between MPO and, the two pathogens (i.e., F. psychrophilum and Y. ruckeri). Taken together, the study revealed that serum-mediated bacterial killing activity and immune defence factors remarkably varied during the LD cycle in rainbow trout. In addition, the two emergence fractions displayed nearly comparable immunological profiles.

General information
State: Published
Latent class analysis of real time qPCR and bacteriological culturing for the diagnosis of Streptococcus agalactiae in cow composite milk samples

Streptococcus agalactiae (S. agalactiae) has re-emerged as a mastitis pathogen among Norwegian dairy cows. The Norwegian cattle health services recommend that infected herds implement measures to eradicate S. agalactiae, this includes a screening of milk samples from all lactating cows. The performance of the qPCR-test currently in use for this purpose has not been evaluated under field conditions. The objective of this study was to estimate the sensitivity and specificity of the real-time qPCR assay in use in Norway (Mastitis 4 qPCR, DNA Diagnostics A/S, Risskov, Denmark) and compare it to conventional bacteriological culturing for detection of S. agalactiae in milk samples. Because none of these tests are considered a perfect reference test, the evaluation was performed using latent class models in a Bayesian analysis. Aseptically collected cow-composite milk samples from 578 cows belonging to 6 herds were cultured and tested by qPCR. While 37 (6.4%) samples were positive for S. agalactiae by bacteriological culture, 66 (11.4%) samples were positive by qPCR. The within-herd prevalence in the six herds, as estimated by the latent class models ranged from 7.7 to 50.8%. At the recommended cut-off (cycle threshold 37), the sensitivity of the qPCR was significantly higher at 95.3 (95% posterior probability interval [PPI] [84.2; 99.6]) than that of bacteriological culture at 58.2 (95% PPI [43.8; 74.4]). However, bacterial culture had a higher specificity of 99.7 (95% PPI [98.5; 100.0]) compared to the qPCR at 98.5 (95% PPI [94.6; 99.9]). The median estimated negative predictive values of qPCR was consistently higher than those of the BC at all estimated prevalences, and the superiority of the qPCR increased with increasing within-herd prevalence. The median positive predictive values of BC was in general higher than the estimates for the qPCR, however, at the highest prevalence the predictive ability of both tests were similar.

General information
State: Published
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Pages: 119-123
Publication date: 2018
Main Research Area: Technical/natural sciences

Publication information
Journal: Preventive Veterinary Medicine
Volume: 154
ISSN (Print): 0167-5877
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 1.31 SJR 1.144 CiteScore 2.26
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.2 SJR 1.249 SNIP 1.361
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.282 SNIP 1.177 CiteScore 2.1
Web of Science (2015): Indexed yes
Bone mineral density (BMD) assessed by DXA is used to evaluate bone health. In children, total body (TB) measurements are commonly used; in older individuals, BMD at the lumbar spine (LS) and femoral neck (FN) is used to diagnose osteoporosis. To date, genetic variants in more than 60 loci have been identified as associated with BMD. To investigate the genetic determinants of TB-BMD variation along the life course and test for age-specific effects, we performed a meta-analysis of 30 genome-wide association studies (GWASs) of TB-BMD including 66,628 individuals overall and divided across five age strata, each spanning 15 years. We identified variants associated with TB-BMD at 80 loci, of which 36...
have not been previously identified; overall, they explain approximately 10% of the TB-BMD variance when combining all age groups and influence the risk of fracture. Pathway and enrichment analysis of the association signals showed clustering within gene sets implicated in the regulation of cell growth and SMAD proteins, overexpressed in the musculoskeletal system, and enriched in enhancer and promoter regions. These findings reveal TB-BMD as a relevant trait for genetic studies of osteoporosis, enabling the identification of variants and pathways influencing different bone compartments. Only variants in ESR1 and close proximity to RANKL showed a clear effect dependency on age. This most likely indicates that the majority of genetic variants identified influence BMD early in life and that their effect can be captured throughout the life course.

**General information**

**State:** Published

**Organisations:** Department of Bio and Health Informatics, National Veterinary Institute, Immunoinformatics and Machine Learning, T-cells & Cancer, Wake Forest School of Medicine, Erasmus University Rotterdam, University of Queensland, University of Cambridge, The Children's Hospital of Philadelphia, University of Copenhagen, Leiden University, Federal University of Pelotas, California Pacific Medical Center, University of Eastern Finland, McGill University, Sir Charles Gairdner Hospital, Boston University, University of Gothenburg, deCODE/Amgen, Wayne State University, National Institute on Aging, University of Western Australia, University of Edinburgh, Hebrew SeniorLife, Lund University, University of California at Davis, King's College London, The Ohio State University, The National University Hospital of Iceland, Oregon Health and Science University, University of Washington, University of Ioannina, Mayo Clinic, Imperial College London, Garvan Institute of Medical Research, University of Rochester, University of Bristol


**Pages:** 88-102

**Publication date:** 2018

**Main Research Area:** Technical/natural sciences

**Publication information**

**Journal:** American Journal of Human Genetics

**Volume:** 102

**Issue number:** 1

**ISSN (Print):** 0002-9297

**Ratings:**

- BFI (2018): BFI-level 2
- Web of Science (2018): Indexed yes
- BFI (2017): BFI-level 2
- Scopus rating (2017): SNIP 2.428 SJR 7.45 CiteScore 8.34
- Web of Science (2017): Indexed Yes
- BFI (2016): BFI-level 2
- Scopus rating (2016): CiteScore 8.43 SJR 7.504 SNIP 2.536
- BFI (2015): BFI-level 2
- Scopus rating (2015): SJR 8.755 SNIP 3.01 CiteScore 9.71
- Web of Science (2015): Indexed yes
- BFI (2014): BFI-level 2
- Scopus rating (2014): SJR 8.801 SNIP 3.195 CiteScore 9.66
- Web of Science (2014): Indexed yes
- BFI (2013): BFI-level 2
**Methicillin-resistant Staphylococcus aureus in Danish production animals**

Methicillin-resistant Staphylococcus aureus (MRSA) is recognized as one of the most common multiresistant bacteria found in both human and veterinary medicine, and the newly emerged livestock-associated MRSA clonal complex 398 (LA-MRSA CC398) pose a risk of zoonotic infections in humans. An increase in the occurrence of MRSA CC398 positive carriers in Denmark has been observed in the general community, where a proportion of cases occur in people without livestock exposure. This development threatens the national low levels of MRSA in humans and the sustainability of the domestic ‘search-and-destroy’ control policies. To arrest this development it seems important to contain MRSA CC398 within pig farms, which are the primary reservoir of MRSA CC398, followed by attempts to lower the within farm level of MRSA CC398. Quantitative methods for MRSA CC398 within farms are needed in order to assess the effect of intervention strategies. However, S. aureus has on multiple occasions proven difficult to control and has illustrated its ability to adapt to new niches and disseminate with great success to new reservoirs. This PhD project presents an evaluation of the feasibility to measure MRSA CC398 within pig herds in a quantitative and reproducible manner using swab and air samples, and an assessment of MRSA CC398 loads within different units of the pig production. We found nasal swab samples to be more reproducible than skin swab samples. Further, nasal samples were found to be a better proxy for airborne MRSA CC398 compared to skin samples, however, the correlation was found insufficient to recommend that air samples would be enough for complete quantification of MRSA CC398 within production units. The highest levels of MRSA CC398 within pig farms were seen in the farrowing and weaning unit which means, that the highest risk for farmers to become colonized with MRSA CC398 occurs when working within these two units. Unfortunately, these two units are where the most intense human-to-pig contact occurs which is worrisome, as human carriage are known to play a role in dissemination of MRSA CC398 into naive animal productions. Focus was consequently turned to investigate the emergence of possible new animal reservoirs in Denmark. We investigated if Danish veal and dairy herds constitute a reservoir of MRSA CC398. Both production lines was found positive for MRSA CC398 in low prevalence, however veal calf was thought merely to be contaminated, whereas indications of dairy herds as a persistent reservoir was observed. The Danish mink production has gained our attention for some time throughout the present study period, as human cases of MRSA CC398 in people with mink contact, have been seen since 2009 and infections in mink caused by MRSA CC398...
was first observed in 2013. Consequently, we wanted to determine the degree of MRSA CC398 positive farms and to identify where the bacterium most often could be detected. A total of one third of the screened farms were found positive for MRSA CC398 with the bacterium most often found on the paws and in the pharynx, which poses a human health hazard to farmers, who risk getting bites and scratches when handling the animals. Based on results from phylogenetic analysis of isolates from both the cattle and mink production, we suggested a spillover from the pig production to be the primary source of introduction. In mink, results pointed to an introduction via contaminated feed. The introduction into mink has subsequently led to increased carriage and infections in people with contact to mink, observed since 2011. The results obtained as part of this PhD project, emphasize the importance of lowering the levels of MRSA CC398 within farms to reduce dissemination and emergence of new reservoirs. Further, the results illustrated the need for continued screening of low prevalence MRSA CC398 positive productions and possibly unknown positive productions. This is needed in order to try and take control of the development, emergence and spread of MRSA CC398, with the subsequent goal of preventing the emergence of reservoirs with possible relevance to human health.

Microclimatic temperatures at Danish cattle farms, 2000–2016: quantifying the temporal and spatial variation in the transmission potential of Schmallenberg virus

Microclimatic temperatures provide better estimates of vector-borne disease transmission parameters than standard meteorological temperatures, as the microclimate represent the actual temperatures to which the vectors are exposed. The objectives of this study were to quantify farm-level geographic variations and temporal patterns in the extrinsic incubation period (EIP) of Schmallenberg virus transmitted by Culicoides in Denmark through generation of microclimatic temperatures surrounding all Danish cattle farms.

Methods

We calculated the hourly microclimatic temperatures at potential vector-resting sites within a 500 m radius of 22,004 Danish cattle farms for the months April to November from 2000 to 2016. We then modeled the daily EIP of Schmallenberg virus at each farm, assuming vectors choose resting sites either randomly or based on temperatures (warmest or coolest available) every hour. The results of the model output are presented as 17-year averages. Results: The difference between the warmest and coolest microhabitats at the same farm was on average 3.7 °C (5th and 95th percentiles: 1.0 °C to 7.8 °C). The mean EIP of Schmallenberg virus (5th and 95th percentiles) for all cattle farms during spring, summer, and autumn was: 23 (18–33), 14 (12–18) and 51 (48–55) days, respectively, assuming Culicoides select resting sites randomly. These estimated EIP values were considerably shorter than those estimated using standard meteorological temperatures obtained from a numerical weather prediction model for the same periods: 43 (39–52), 21 (17–24) and 57 (55–58) days, respectively. When assuming that vectors actively select the coolest resting sites at a farm, the EIP was 2.3 (range: 1.1 to 4.1) times longer compared to that of the warmest sites at the same farm. Conclusions: We estimated a wide range of EIP in different microclimatic habitats surrounding Danish cattle farms, stressing the importance of identifying the specific resting sites of vectors when modeling vector-borne disease transmission. We found a large variation in the EIP among different farms, suggesting disease transmission may vary substantially between regions, even within a small country. Our findings could be useful for designing risk-based surveillance, and in the control and prevention of emerging and re-emerging vector-borne diseases.
Migrating birds and carnivores introduce ticks and tick borne pathogens to Denmark – but are they also a public health risk?

Since the end of the ice age, spring migrating birds from Africa and Europe and autumn migrating birds from Northern Scandinavia have entered Denmark, and recently a small wave of long migrating carnivores have started arriving in Denmark from Central Europe. Theoretically, migrating birds could introduce new tick species as well as tick-associated pathogens to Denmark. These migrating animals may also carry ticks and pathogens which already exist in native tick populations.
populations in Denmark. The potential supplement of native ticks and existing pathogens to the established high density tick populations in Danish forest and nature areas can be expected to be of little practical importance. However, some of the infected ticks, introduced by migrating birds, may be deposited in private gardens and public parks that are otherwise not able to sustain a viable tick population. Migrating birds may therefore introduce a low level risk of tick borne infections to urban areas. Also the recent unexpected wave of long migrating golden jackals (Canis aureus) and grey wolves (Canis lupus), arriving at the Danish peninsula of Jutland, constitutes an emerging risk of introduction of especially Dermacentor spp ticks and their associated pathogens from Germany and Central Europe. Here, we present the results of screening migrating birds and a golden jackal for ticks as well as ticks collected by flagging in selected urban areas in Denmark. The collected ticks were screened for exotic tick species and 38 different tick borne pathogens. We show that the risk is not just theoretical and we suggest that these introductions may have a practical public health impact.

**General information**
State: Published
Organisations: National Veterinary Institute, Epidemiology, Diagnostic & Development, Bacteriology & Parasitology, Technical University of Denmark, University of Copenhagen
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Number of pages: 1
Publication date: 2018
Main Research Area: Technical/natural sciences
Electronic versions:
Nordick_NordTick_Abstract_Rene_B_dker_DTU_For_oral_presentation_on_session_1_i_samverkan_med_ScandTick_Innovation_tisdag_10_april.pdf
Source: PublicationPreSubmission
Source-ID: 146296245
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2018

**Modeling the Effects of Duration and Size of the Control Zones on the Consequences of a Hypothetical African Swine Fever Epidemic in Denmark**
African swine fever (ASF) is a notifiable infectious disease. The disease is endemic in certain regions in Eastern Europe constituting a risk of ASF spread toward Western Europe. Therefore, as part of contingency planning, it is important to continuously explore strategies that can effectively control an epidemic of ASF. A previously published and well documented simulation model for ASF virus spread between herds was used to examine the epidemiologic and economic impacts of the duration and size of the control zones around affected herds. In the current study, scenarios were run, where the duration of the protection and surveillance zones were reduced from 50 and 45 days to 35 and 25 days or to 35 and 25 days, respectively. These scenarios were run with or without enlargement of the surveillance zone around detected herds from 10 to 15 km. The scenarios were also run with only clinical or clinical and serological surveillance of herds within the zones. Sensitivity analysis was conducted on influential input parameters in the model. The model predicts that reducing the duration of the protection and surveillance zones has no impact on the epidemiological consequences of the epidemics, while it may result in a substantial reduction in the total economic losses. In addition, the model predicts that increasing the size of the surveillance zone from 10 to 15 km may reduce both the epidemic duration and the total economic losses, in case of large epidemics. The ranking of the control strategies by the total costs of the epidemics was not influenced by changes of input parameters in the sensitivity analyses.

**General information**
State: Published
Organisations: National Veterinary Institute, Epidemiology, Virology, Ministry of Environment and Food
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Number of pages: 7
Publication date: 2018
Main Research Area: Technical/natural sciences

**Publication information**
Journal: Frontiers in Veterinary Science
Volume: 5
Article number: 49
ISSN (Print): 2297-1769
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.94
Original language: English
African swine fever, Control, Model, Simulation, Surveillance
Modifications to the foot-and-mouth disease virus 2A peptide; influence on polyprotein processing and virus replication

Foot-and-mouth disease virus (FMDV) has a positive-sense ssRNA genome that includes a single, large, open reading frame encoding a polyprotein. The co-translational "cleavage" of this polyprotein at the 2A/2B junction is mediated by the 2A peptide (18 residues in length) using a non-proteolytic mechanism termed "ribosome skipping" or "StopGo". Multiple variants of the 2A polypeptide with this property among the picornaviruses share a conserved C-terminal motif (D(V/I)E(S/T)NPG↓P). The impact of 2A modifications within this motif on FMDV protein synthesis, polyprotein processing and virus viability were investigated. Amino acid substitutions are tolerated at residues E14, S15 and N16 within the 2A sequence of infectious FMDVs despite their reported "cleavage" efficiencies at the 2A/2B junction of only ca. 30-50% compared to wt. In contrast, no viruses were rescued containing substitutions at residues P17, G18 or P19 that displayed little or no "cleavage" activity in vitro, but wt revertants were obtained. The 2A substitutions impaired the replication of a FMDV replicon. Using transient expression assays, it was shown that certain amino acid substitutions at residues E14, S15, N16 and P19 resulted in partial "cleavage" of a protease-free polyprotein indicating that these specific residues are not essential for co-translational "cleavage". Immunofluorescence studies, using full-length FMDV RNA transcripts encoding mutant 2A peptides, indicated that the 2A peptide remained attached to adjacent proteins, presumably 2B. These results show that efficient "cleavage" at the 2A/2B junction is required for optimal virus replication. However, maximal StopGo activity does not appear to be essential for the viability of FMDV. ImportanceFoot-and-mouth disease virus (FMDV) causes one of the most economically important diseases of farm animals. Co-translational "cleavage" of the FMDV polyprotein precursor at the 2A/2B junction, termed StopGo, is mediated by the short 2A peptide through a non-proteolytic mechanism which leads to release of the nascent protein and continued translation of the downstream sequence. Improved understanding of this process will not only give a better insight into how this peptide influences the FMDV replication cycle but may also assist the application of this sequence in biotechnology for the production of multiple proteins from a single mRNA. Our data show that single amino acid substitutions in the 2A peptide can have a major influence on viral protein synthesis, virus viability and polyprotein processing. It also indicates that efficient "cleavage" at the 2A/2B junction is required for optimal virus replication. However, maximal StopGo activity is not essential for the viability of FMDV.
Molecular epidemiology, evolution and phylogeny of foot-and-mouth disease virus

Foot-and-mouth disease virus (FMDV) is responsible for one of the most economically important infectious diseases of livestock. The virus spreads very easily and continues to affect many countries (mainly in Africa and Asia). The risks associated with the introduction of FMDV result in major barriers to trade in animals and their products. Seven antigenically distinct forms of the virus are known, called serotypes, but serotype C has not been detected anywhere for many years and may now be extinct. The serotypes have been further divided into topotypes (except for serotype Asia-1
viruses, which comprise a single topotype), genotypes, lineages and sub-lineages, which are usually restricted to specific geographical regions. However, sometimes, trans-regional spread of some strains occurs. Due to the error-prone replication of the RNA genome, the virus continuously evolves and new strains frequently arise (e.g. with modified antigenicity). Using nucleotide sequencing technologies, this rapid evolution of the viral genome can be followed. This allows the tracing of virus transmission pathways within an outbreak of disease if (near) full-length genome sequences can be generated. Furthermore, the movement of distinct virus lineages, from one country to another can be analyzed. Some important examples of the spread of new strains of FMD virus are described.
Multiband modulation spectroscopy for determination of sex and species of mosquitoes in flight

We present a dual-wavelength polarimetric measurement method to distinguish species and sexes of disease transmitting mosquitoes in flight. By measuring co- and de-polarized backscattered light at 808 and 1550 nm, the degree of linear polarization, wingbeat frequency, reflectance, spectral ratio and glossiness of mosquitoes can be retrieved. Body and wing contributions to these signals can be separated. Whereas the optical cross-section is sensitive to the aspect of observation, thus the heading direction of the insect in flight, we demonstrate that polarimetric- and spectral- band ratios are largely invariant to the aspect of observation. We show that wing glossiness, as well as wing- and body-spectral ratios are particularly efficient in distinguishing Anopheles coluzzii and Anopheles arabiensis, two closely related species of malaria vectors. Spectral- and polarimetric ratios relate to microstructural and melanization features of the wing and body of these species. We conclude that multiband modulation spectroscopy is a useful expansion of the parameter space that can be used to improve specificity of entomological lidars.
Necrotizing enterocolitis is associated with acute brain responses in preterm pigs

BACKGROUND: Necrotizing enterocolitis (NEC) is an acute gut inflammatory disorder that occurs in preterm infants in the first weeks after birth. Infants surviving NEC often show impaired neurodevelopment. The mechanisms linking NEC lesions with later neurodevelopment are poorly understood but may include proinflammatory signaling in the immature brain. Using preterm pigs as a model for preterm infants, we hypothesized that severe intestinal NEC lesions are associated with acute effects on the developing hippocampus.

METHODS: Cesarean-delivered preterm pigs (n = 117) were reared for 8 days and spontaneously developed variable severity of NEC lesions. Neonatal arousal, physical activity, and in vitro neuritogenic effects of cerebrospinal fluid (CSF) were investigated in pigs showing NEC lesions in the colon (Co-NEC) or in the small intestine (Si-NEC). Hippocampal transcriptome analysis and qPCR were used to assess gene expressions and their relation to biological processes, including neuroinflammation, and neural plasticity. Microglia activation was quantified by stereology. The neuritogenic response to selected proteins was investigated in primary cultures of hippocampal neurons.

RESULTS: NEC development rapidly reduced the physical activity of pigs, especially when lesions occurred in the small intestine. Si-NEC and Co-NEC were associated with 27 and 12 hippocampal differentially expressed genes (DEGs), respectively. These included genes related to neuroinflammation (i.e., S100A8, S100A9, IL8, IL6, MMP8, SAA, TAGLN2) and hypoxia (i.e., PDK4, IER3, TXNIP, AGER), and they were all upregulated in Si-NEC pigs. Genes related to protection against oxidative stress (HBB, ALAS2) and oligodendrocytes (OPALIN) were downregulated in Si-NEC pigs. CSF collected from NEC pigs promoted neurite outgrowth in vitro, and the S100A9 and S100A8/S100A9 proteins may mediate the neuritogenic effects of NEC-related CSF on hippocampal neurons. NEC lesions did not affect total microglial cell number but markedly increased the proportion of Iba1-positive amoeboid microglial cells.

CONCLUSIONS: NEC lesions, especially when present in the small intestine, are associated with changes to hippocampal gene expression that potentially mediate neuroinflammation and disturbed neural circuit formation via enhanced neuronal differentiation. Early brain-protective interventions may be critical for preterm infants affected by intestinal NEC lesions to reduce their later neurological dysfunctions.
Novel Platforms for the Development of a Universal influenza vaccine

Despite advancements in immunotherapeutic approaches, influenza continues to cause severe illness, particularly among immunocompromised individuals, young children, and elderly adults. Vaccination is the most effective way to reduce rates of morbidity and mortality caused by influenza viruses. Frequent genetic shift and drift among influenzavirus strains with the resultant disparity between circulating and vaccine virus strains limits the effectiveness of the available conventional influenza vaccines. One approach to overcome this limitation is to develop a universal influenza vaccine that could provide protection against all subtypes of influenza viruses. Moreover, the development of a novel or improved universal influenza vaccines may be greatly facilitated by new technologies including virus-like particles, T-cell-inducing peptides and recombinant proteins, synthetic viruses, broadly neutralizing antibodies, and nucleic acid-based vaccines. This review discusses recent scientific advances in the development of next-generation universal influenza vaccines.
Oral Supplementation with Bovine Colostrum Prevents Septic Shock and Brain Barrier Disruption During Bloodstream Infection in Preterm Newborn Pigs

Preterm infants have increased risk of neonatal sepsis, potentially inducing brain injury, and they may benefit from early initiation of enteral milk feeding. Using preterm pigs as models, we hypothesized that early provision of bovine colostrum to parentally nourished newborns protects against sepsis and neuroinflammation during bloodstream infection. Preterm newborn pigs were administered $10^8$ CFU/kg of intra-arterial Staphylococcus epidermidis (SE, an opportunistic pathogen often causing sepsis in preterm infants), followed by administration of total parenteral nutrition (TPN, SE + TPN, $n = 15$) or oral provision of bovine colostrum with supplementary parenteral nutrition (SE + COL, $n = 14$), and compared with uninfected, TPN-nourished controls (CON + TPN, $n = 11$). SE-infected animals showed multiple signs of sepsis, including lethargy, hypotension, respiratory acidosis, internal organ hemorrhages, cellular responses (leukopenia, thrombocytopenia), brain barrier disruption and neuroinflammation. At 24 h, colostrum supplementation reduced the SE abundance in blood and cerebrospinal fluid (CSF, both $p < 0.05$). Further, colostrum feeding normalized arterial blood pressure (38.5 ± 1.20 vs 30.6 ± 3.79 mmHg), pH (7.37 ± 0.02 vs 7.10 ± 0.07) and lactate (1.01 ± 0.11 vs 4.20 ± 1.20 mM, all $p < 0.05$), and increased motor activity, to levels in controls ($p < 0.001$). Finally, colostrum-fed animals showed reduced blood-CSF barrier permeability and CSF leukocyte levels, and this was accompanied by normalized gene expression of tight junction proteins (Occludin, Claudin-5, both $p < 0.05$) and reduced expression of leukocyte chemotactants (CXCL9-11, all $p < 0.01$). Early oral supplementation with bovine colostrum prevents septic shock and ameliorates brain barrier disruption and neuroinflammation during bloodstream infection in preterm pigs. Bovine colostrum supplementation may improve resistance against systemic infection in immature, immune-compromised preterm infants.

General information
State: Accepted/In press
Organisations: National Veterinary Institute, Innate Immunology, University of Copenhagen
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Partial validation of a TaqMan real-time quantitative PCR for the detection of ranaviruses

Ranaviruses are globally emerging pathogens negatively impacting wild and cultured fish, amphibians, and reptiles. Although conventional and diagnostic real-time PCR (qPCR) assays have been developed to detect ranaviruses, these assays often have not been tested against the known diversity of ranaviruses. Here we report the development and partial validation of a TaqMan real-time qPCR assay. The primers and TaqMan probe targeted a conserved region of the major capsid protein (MCP) gene. A series of experiments using a 10-fold dilution series of Frog virus 3 (FV3) MCP plasmid DNA revealed linearity over a range of 7 orders of magnitude (10^7-10^1), a mean correlation coefficient (R^2) of >0.99, and a mean efficiency of 96%. The coefficient of variation of intra- and inter-assay variability ranged from <0.1-3.5% and from 1.1-2.3%, respectively. The analytical sensitivity was determined to be 10 plasmid copies of FV3 DNA. The qPCR assay detected a panel of 33 different ranaviral isolates originating from fish, amphibian, and reptile hosts from all continents excluding Africa and Antarctica, thereby representing the global diversity of ranaviruses. The assay did not amplify highly divergent ranaviruses, members of other iridovirus genera, or members of the alloherpesvirus genus Cyprinivirus. DNA from fish tissue homogenates previously determined to be positive or negative for the ranavirus Epizootic hematopoietic necrosis virus by virus isolation demonstrated a diagnostic sensitivity of 95% and a diagnostic specificity of 100%. The reported qPCR assay provides an improved expedient diagnostic tool and can be used to elucidate important aspects of ranaviral pathogenesis and epidemiology in clinically and subclinically affected fish, amphibians, and reptiles.

General information
State: Published
Organisations: National Veterinary Institute, University of Florida, University of Sydney, James Cook University Queensland, Utrecht University
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Pages: 105-116
Publication date: 2018
Main Research Area: Technical/natural sciences
Pathology and bacteria related to digital dermatitis in dairy cattle in all year round grazing system in Brazil

Digital dermatitis (DD) is one of the main causes of lameness in dairy cattle worldwide, and it is frequently reported in high-yielding, free stall dairy herds from regions with a temperate climate. However, DD is also observed with high
prevalence in grazing cattle with a low milk yield in tropical regions. To clarify whether these differences have an impact on the etiology of the disease, we studied DD lesions from all year round grazing cattle of mixed breed in Brazil using high-throughput 16S rRNA gene sequencing and fluorescent in situ hybridization. The study included samples from 66 skin lesions and 5 healthy skins collected from five farms. Both techniques showed Treponema spp. to be the most abundant bacteria, present in all but one of the samples with minimal epidermal alterations. We identified eleven different Treponema strains belonging to the six major phylotypes of Treponema which have all previously been identified in DD lesions. Furthermore, we identify Dichelobacter nodosus in DD lesions by gene sequencing and also by fluorescent in situ hybridization in almost half of biopsy specimens in areas with mild epithelial damage and together with Treponema. The present data support the hypothesis that Treponema constitutes the main pathogen responsible for DD, independent of the environment and region where cows are kept, and it further suggests D. nodosus as another potentially important pathogen.

General information
State: Published
Organisations: National Veterinary Institute, Bacteriology & Parasitology, Research Group for Genomic Epidemiology, Pathology, Federal University of Minas Gerais
Number of pages: 15
Publication date: 2018
Main Research Area: Technical/natural sciences

Publication information
Journal: P L o S One
Volume: 13
Issue number: 3
Article number: e0193870
ISSN (Print): 1932-6203
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.01 SJR 1.164 SNIP 1.111
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.11 SJR 1.236 SNIP 1.101
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.427 SNIP 1.136 CiteScore 3.32
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.559 SNIP 1.148 CiteScore 3.54
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.772 SNIP 1.153 CiteScore 3.94
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.982 SNIP 1.156 CiteScore 4.15
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 2.425 SNIP 1.233 CiteScore 4.58
ISI indexed (2011): ISI indexed no
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.705 SNIP 1.178
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Påvisning af PCV2: Notat nr 1807


General information
State: Published
Organisations: National Veterinary Institute, Virology, MSD Animal Health Copenhagen, Danish Agriculture and Food Council, Technical University of Denmark, University of Copenhagen
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Number of pages: 4
Publication date: 2018

Publication information
Publisher: SEGES Svineproduktion
Volume: 2018
Edition: 1807
Original language: Danish
Main Research Area: Technical/natural sciences
Electronic versions:
Notat_1807_1_.pdf
Links:
http://svineproduktion.dk/publikationer/kilder/notater/2018/1807
Source: FindIt
Persistence of antimicrobial resistance genes from sows to finisher pigs

Antimicrobial resistance in pigs has been under scrutiny for many years. However, many questions remain unanswered, including whether the initial antimicrobial resistance level of a pig will influence the antimicrobial resistance found at slaughter. Faecal samples from finishers pigs from 681 farms and from sows from 82 farms were collected, and levels of seven antimicrobial resistance genes, ermB, ermF, sulI, sulII, tet(M), tet(O), and tet(W), were quantified by high-capacity qPCR. There were 40 pairs of observations where the finishers were born in the farms of the sows. The objective of this study was to evaluate whether the levels of AMR genes found in finisher pigs at slaughter were associated with the levels in the farm where the finishers were born, and whether the levels of the AMR genes were equal in the sow and finisher pig populations. We found a significant positive correlation between the levels of AMR genes in finishers and the sows in the farms where the pigs were born for some of the genes (ermB (ρ = 0.47, p-value = 0.002), ermF (ρ = 0.41, p-value = 0.03), and tet(O) (ρ = 0.33, p-value = 0.04)). Furthermore, there were significant differences between AMR gene levels for the sow and finisher populations for ermB, ermF, sulI, sulII, tet(O), and tet(W), though not for tet(M).
Pigs are useful for the molecular study of bone inflammation and regeneration in humans

Pigs are used with increased frequency to model different kinds of orthopedic surgical conditions. In order to show the full potential of porcine models in orthopedic research, it is therefore required to examine the expression of bone regulatory genes in pigs affected by orthopedic surgery and compare it to the expression in humans and mice as mice, are one of the most applied animal species in orthopedics today. In the present study, the local molecular response to drilling of a tibial implant cavity, and the subsequent insertion of a steel implant was examined in a porcine model. Pigs were euthanized five days after drilling of the bone. The molecular response of 73 different genes was analyzed using a high-throughput quantitative polymerase chain reaction platform and compared to histopathology. Histologically, it was found that bone remodeling was initiated on day 5 after surgery and was associated with upregulation of several genes involved in bone degradation and formation (CTSK, ACP5, IBSP, RANK, RANKL and COL1A1). Interleukin-6 and several acute-phase proteins (C3, SAA and ITIH4) were significantly upregulated, indicating their importance in the initial process of healing and osseointegration. All tested bone morphogenic proteins (BMP2, -4 and -7) including their inhibitor noggin were also significantly upregulated. Surprisingly, vascular endothelial growth factor A was not found to be regulated five days after surgery while several other vascular growth factors (ANGPT1, ANGPT2 and PTN) were upregulated. The pig was found to be a useful model for elucidation of bone regulatory genes in humans.

General information
State: Accepted/In press
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Number of pages: 11
Publication date: 2018
Main Research Area: Technical/natural sciences

Publication information
Journal: Laboratory Animals
Piscine orthoreovirus infection in Atlantic salmon (Salmo salar) protects against subsequent challenge with infectious hematopoietic necrosis virus (IHNV)

Infectious hematopoietic necrosis virus (IHNV) is endemic in farmed rainbow trout in continental Europe and in various salmonid fish species at the Pacific coast of North America. IHN has never occurred in European Atlantic salmon (Salmo salar) farms, but is considered as a major threat for the European salmon industry. Another virus, Piscine orthoreovirus (PRV), is widespread in the sea phase of Atlantic salmon, and is identified as the causative agent of heart and skeletal muscle inflammation. The aim of this study was to investigate the interactions between a primary PRV infection and a secondary IHNV infection under experimental conditions. A PRV cohabitation challenge was performed with Atlantic salmon. At peak of PRV viremia the fish were challenged by immersion with an IHNV genogroup E isolate. Clinical signs
and morbidity were monitored. Target organs were sampled at selected time points to assess viral loads of both pathogens. Antiviral immune response and presence of histopathological findings were also investigated. Whereas the PRV-negative/IHNV positive group suffered significant decrease in survival caused by IHNV, the PRV infected groups did not suffer any morbidity and showed negligible levels of IHNV infection. Antiviral response genes were induced, as measured in spleen samples, from PRV infected fish prior to IHNV challenge. In conclusion, PRV-infection protects Atlantic salmon against IHNV infection and morbidity, most likely by inducing a protective innate antiviral response.

**General information**

State: Published
Organisations: National Institute of Aquatic Resources, National Veterinary Institute, Fish Diseases, Norwegian Veterinary Institute, Norwegian University of Life Sciences
Number of pages: 12
Publication date: 2018
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Veterinary Research
Volume: 49
Issue number: 1
Article number: 30
ISSN (Print): 0928-4249
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 1.139 SJR 1.266
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): SJR 1.44 SNIP 1.303
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.537 SNIP 1.153 CiteScore 2.66
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.453 SNIP 1.423 CiteScore 2.46
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.681 SNIP 1.701 CiteScore 3.13
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.461 SNIP 1.45 CiteScore 2.97
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.712 SNIP 1.655 CiteScore 3.85
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.531 SNIP 1.606
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.489 SNIP 1.689
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.578 SNIP 2.002
Web of Science (2008): Indexed yes
Prevalence of Onchocerca in Danish wild deer

General information
State: Published
Organisations: National Veterinary Institute, Bacteriology & Parasitology, Epidemiology, Diagnostic & Development
Authors: Petersen, H. H. (Intern), Hansen, M. F. (Intern), Nielsen, S. T. (Intern), Chriél, M. (Intern)
Publication date: 2018
Event: Abstract from Joint Spring Symposium 2018: Danish Society for Parasitology and Danish Society, Frederiksberg, Denmark.
Main Research Area: Technical/natural sciences
Electronic versions:
DSP_2018_Onchocerca_abstract.pdf. Embargo ended: 08/04/2018
Source: PublicationPreSubmission
Source-ID: 144762107
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2018

Rapid Protective Effects of Early BCG on Neonatal Mortality Among Low Birth Weight Boys: Observations From Randomized Trials

Background. Three randomized trials (RCTs) in low-weight (<2.5 kg) infants have shown that Bacille Calmette-Guérin (BCG) vaccine nonspecifically reduces all-cause mortality in the neonatal period. Methods. Using data from 3 RCTs of early BCG (n = 6583) we examined potential sex differences in the timing of the mortality reduction in the neonatal period, presenting metaestimates of the main outcome mortality rate ratios (MRR) for BCG-vaccinated and controls. Results. Among controls, boys had a particularly high mortality during the first week after randomization: male–female MRR 2.71 (95% CI, 1.70–4.50). During the first week, BCG had a marked beneficial effect for boys, reducing mortality 3-fold (MRR [BCG/no BCG] = 0.36 [0.20–0.67]). In weeks 2–4 the effect waned for boys (MRR = 0.91 [0.51–1.69]). In girls, the pattern was opposite with a limited effect in the first week (MRR = 0.85 [0.46–1.54]), but a significant reduction in weeks 2–4 (MRR = 0.56 [0.31–1.00]). This was consistent in all 3 trials. Verbal autopsies linked early benefit to fewer sepsis-related deaths among BCG-vaccinated boys. Discussion. The marked reduction in mortality in the days after BCG vaccination in boys emphasizes the importance of providing BCG soon after birth. Trial registration numbers: ClinicalTrials.gov (NCT00146302) and ClinicalTrials.gov (NCT00625482).
Recognition of microbial viability via TLR8 drives $T_{FH}$ cell differentiation and vaccine responses

Live attenuated vaccines are generally highly efficacious and often superior to inactivated vaccines, yet the underlying mechanisms of this remain largely unclear. Here we identify recognition of microbial viability as a potent stimulus for follicular helper T cell ($T_{FH}$ cell) differentiation and vaccine responses. Antigen-presenting cells (APCs) distinguished viable bacteria from dead bacteria through Toll-like receptor 8 (TLR8)-dependent detection of bacterial RNA. In contrast to dead bacteria and other TLR ligands, live bacteria, bacterial RNA and synthetic TLR8 agonists induced a specific cytokine profile in human and porcine APCs, thereby promoting $T_{FH}$ cell differentiation. In domestic pigs, immunization with a live bacterial vaccine induced robust $T_{FH}$ cell and antibody responses, but immunization with its heat-killed counterpart did not. Finally, a hypermorphic TLR8 polymorphism was associated with protective immunity elicited by vaccination with bacillus Calmette-Guérin (BCG) in a human cohort. We have thus identified TLR8 as an important driver of $T_{FH}$ cell differentiation and a promising target for $T_{FH}$ cell-skewing vaccine adjuvants.
Recognition of microbial viability via TLR-8 is a critical driver of T follicular helper cell differentiation and vaccine responses

General information
State: Published
Organisations: National Veterinary Institute, Adaptive Immunology, Charité-Universitätsmedizin Berlin
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Pages: 8-8
Publication date: 2018
Conference: 15th International Symposium on Dendritic Cells, Aachen, Germany, 10/06/2017 - 10/06/2017
Main Research Area: Technical/natural sciences

Publication information
Journal: European Journal of Immunology
Volume: 48
Issue number: S1
Article number: T-12
ISSN (Print): 0014-2980
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.59 SJR 2.206 SNIP 0.92
Secondary immune response of rainbow trout following repeated immersion vaccination

Teleosts are able to raise a protective immune response, comprising both innate and adaptive elements, against various pathogens. This is the basis for a widespread use of vaccines, administered as injection or immersion, in the aquaculture industry. It has been described that repeated injection vaccination of fish raises a secondary immune response, consisting of rapid, accelerated and increased antibody reaction. This study reports how rainbow trout responds to repeated immersion vaccination against yersiniosis (ERM) caused by the bacterial pathogen Yersinia ruckeri. It was found that rainbow trout does not raise a classical secondary response following repeated immersion vaccination. Serum antibody titres were merely slightly increased even after three immunizations, using 30-s immersion into a bacterin consisting of...
formalin-inactivated Y. ruckeri (serotype O1, biotypes 1 and 2), performed over a 3-month period. The densities of IgM-positive lymphocytes in spleen of fish immunized three times were increased compared to control fish, but no general trend for an increase with the number of immunizations was noted. The lack of a classical secondary response following repeated immersion vaccination may partly be explained by limited uptake of antigen by immersion compared to injection.

**General information**

State: Published  
Organisations: National Veterinary Institute, Innate Immunology, Bacteriology & Parasitology, University of Copenhagen  
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Pages: 117-123  
Publication date: 2018  
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Journal of Fish Diseases  
Volume: 41  
Issue number: 1  
ISSN (Print): 0140-7775  
Ratings:  
BFI (2018): BFI-level 1  
Web of Science (2018): Indexed yes  
BFI (2017): BFI-level 1  
Scopus rating (2017): CiteScore 1.82  
Web of Science (2017): Indexed yes  
BFI (2016): BFI-level 1  
Scopus rating (2016): CiteScore 2.12  
Web of Science (2016): Indexed yes  
BFI (2015): BFI-level 1  
Scopus rating (2015): CiteScore 1.71  
Web of Science (2015): Indexed yes  
BFI (2014): BFI-level 1  
Scopus rating (2014): CiteScore 1.99  
Web of Science (2014): Indexed yes  
BFI (2013): BFI-level 1  
Scopus rating (2013): CiteScore 1.74  
ISI indexed (2013): ISI indexed yes  
Web of Science (2013): Indexed yes  
BFI (2012): BFI-level 1  
Scopus rating (2012): CiteScore 1.7  
ISI indexed (2012): ISI indexed yes  
Web of Science (2012): Indexed yes  
BFI (2011): BFI-level 1  
Scopus rating (2011): CiteScore 2.09  
ISI indexed (2011): ISI indexed yes  
Web of Science (2011): Indexed yes  
BFI (2010): BFI-level 1  
Web of Science (2010): Indexed yes  
BFI (2009): BFI-level 1  
Web of Science (2009): Indexed yes  
BFI (2008): BFI-level 2  
Web of Science (2008): Indexed yes  
Web of Science (2007): Indexed yes  
Web of Science (2006): Indexed yes  
Web of Science (2005): Indexed yes  
Web of Science (2004): Indexed yes  
Web of Science (2003): Indexed yes
Selection of functional 2A sequences within foot-and-mouth disease virus; requirements for the NPGP motif with a distinct codon bias

Foot-and-mouth disease virus (FMDV) has a positive-sense ssRNA genome including a single, large, open reading frame. Splitting of the encoded polyprotein at the 2A/2B junction is mediated by the 2A peptide (18 residues long) which induces a non-proteolytic, co-translational, "cleavage" at its own C-terminus. A conserved feature among variants of 2A is the C-terminal motif N16P17G18/P19 where P19 is the first residue of 2B. It has been shown previously that certain amino acid substitutions can be tolerated at residues E14, S15 and N16 within the 2A sequence of infectious FMDVs but no variants at residues P17, G18 or P19 have been identified. In this study, using highly degenerate primers, we analysed if any other residues can be present at each position of the NPG/P motif within infectious FMDV. No alternative forms of this motif were found to be encoded by rescued FMDVs after 2, 3 or 4 passages. However, surprisingly, a clear codon preference for the wt nucleotide sequence encoding the NPGP motif within these viruses was observed. Indeed, the codons selected to code for P17 and P19 within this motif were distinct; thus the synonymous codons are not equivalent.
Serological evidence of exposure to Toxoplasma gondii in extensively farmed wild boars (Sus scrofa) in Denmark

General information
State: Published
Organisations: National Veterinary Institute, Bacteriology & Parasitology, University of Copenhagen, University of Latvia, Statens Serum Institute, Københavns Universitet
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Number of pages: 1
Publication date: 2018
Event: Abstract from Joint Spring Symposium 2018: Danish Society for Parasitology and Danish Society, Frederiksberg, Denmark.
Main Research Area: Technical/natural sciences
Electronic versions:
DSP_2018_Serological_evidence_of_exposure_to_Toxoplasma_gondii...pdf. Embargo ended: 08/04/2018
Source: PublicationPreSubmission
Source-ID: 144762076
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2018

Short time window for transmissibility of African swine fever virus from a contaminated environment
Since the introduction of African swine fever virus (ASFV) into the Baltic states and Poland in 2014, the disease has continued to spread within these regions. In 2017, the virus spread further west and the first cases of disease were reported in the Czech Republic and Romania, in wild boar and domestic pigs, respectively. To control further spread, knowledge of different modes of transmission, including indirect transmission via a contaminated environment, is crucial. Up until now, such an indirect mode of transmission has not been demonstrated. In this study, transmission via an environment contaminated with excretions from ASFV-infected pigs was investigated. Following euthanasia of pigs that were infected with an isolate of ASFV from Poland (POL/2015/Podlaskie/Lindholm), healthy pigs were introduced into the pens, in which the ASFV-infected pigs had been housed. Introduction was performed at 1, 3, 5 or 7 days, following euthanasia of the infected pig groups. Pigs, that were introduced into the contaminated environment after 1 day, developed clinical disease within 1 week, and both ASFV DNA and infectious virus were isolated from their blood. However, pigs introduced into the contaminated pens after 3, 5 or 7 days did not develop any signs of ASFV infection and no viral DNA was detected in blood samples obtained from these pigs within the following 3 weeks. Thus, it was shown that exposure of pigs to an environment contaminated with ASFV can result in infection. However, the time window for transmissibility of ASFV seems very limited, and, within our experimental system, there appears to be a rapid decrease in the infectivity of ASFV in the environment.
Spatial and temporal variation in the abundance of Culicoides biting midges (Diptera: Ceratopogonidae) in nine European countries

Biting midges of the genus Culicoides (Diptera: Ceratopogonidae) are vectors of bluetongue virus (BTV), African horse sickness virus and Schmallenberg virus (SBV). Outbreaks of both BTV and SBV have affected large parts of Europe. The spread of these diseases depends largely on vector distribution and abundance. The aim of this analysis was to identify and quantify major spatial patterns and temporal trends in the distribution and seasonal variation of observed Culicoides abundance in nine countries in Europe. We gathered existing Culicoides data from Spain, France, Germany, Switzerland, Austria, Denmark, Sweden, Norway and Poland. In total, 31,429 Culicoides trap collections were available from 904 ruminant farms across these countries between 2007 and 2013. The Obsoletus ensemble was distributed widely in Europe and accounted for 83% of all 8,842,998 Culicoides specimens in the dataset, with the highest mean monthly abundance recorded in France, Germany and southern Norway. The Pulicaris ensemble accounted for only 12% of the specimens and had a relatively southerly and easterly spatial distribution compared to the Obsoletus ensemble. Culicoides imicola Kieffer was only found in Spain and the southernmost part of France. There was a clear spatial trend in the accumulated annual abundance from southern to northern Europe, with the Obsoletus ensemble steadily increasing from 4000 per year in southern Europe to 500,000 in Scandinavia. The Pulicaris ensemble showed a very different pattern, with an increase in the accumulated annual abundance from 1600 in Spain, peaking at 41,000 in northern Germany and then decreasing again toward northern latitudes. For the two species ensembles and C. imicola, the season began between January and April, with later start dates and increasingly shorter vector seasons at more northerly latitudes. We present the first maps of seasonal Culicoides abundance in large parts of Europe covering a gradient from southern Spain to northern Scandinavia. The identified temporal trends and spatial patterns are useful for planning the allocation of resources for international prevention and surveillance programmes in the European Union.

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, Department of Applied Mathematics and Computer Science, Statistics and Data Analysis, University of Oldenburg, CIRAD, Universite de Strasbourg, EID Méditerranée, University of the Balearic Islands, University of Zaragoza, University of Zurich, Avia-GIS NV, Aarhus University, Roskilde University, National Veterinary Institute Sweden, Bernhard Nocht Institute for Tropical Medicine, Friedrich Loeffler Institute, National Veterinary Research Institute, National Veterinary Institute, Institute for Veterinary Public Health
Number of pages: 18
Publication date: 2018
Main Research Area: Technical/natural sciences

Publication information
Journal: Parasites & Vectors
Volume: 11
Article number: 112
ISSN (Print): 1756-3305
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SJR 1.702 SNIP 1.295 CiteScore 3.29
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.23 SJR 1.534 SNIP 1.313
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Livestock-associated methicillin-resistant Staphylococcus aureus (LA-MRSA) is an opportunistic human pathogen with main reservoir in pigs. Since LA-MRSA first was identified in Denmark in 2007 among isolates collected at two Danish pig farms in 2003, the occurrence have increased dramatically and reached a prevalence of 88% positive farms in 2016. Meanwhile a similar increase in human infections have been observed; most infections are still observed among people with livestock contact, but the development in number of infections among people without livestock contact have followed a similar increasing trend. Given the high prevalence of LA-MRSA positive farms, total eradication of LA-MRSA in the Danish pig population does not seem feasible, and thus a strong need for exploring options to control the spread of LA-MRSA in Danish pig herds exists. At present it is still not known how LA-MRSA managed to spread so quickly in the Danish pig population and a lot still needs to be understood regarding which factors that determine whether a farm becomes LA-MRSA positive or not. In the first part of this thesis two studies were conducted with the aim of identifying herd-level risk factors for: 1) herds testing MRSA positive (study 1), and 2) more specifically for herds changing status from negative to positive during 2014-2016 (study 2). The studies were based on data harvested in questionnaire-based phone interviews with farmers and supplemented with data for antimicrobial use, movement of pigs and location of neighbouring farms extracted from three national registers. Three risk factors already identified in other studies were confirmed. LA-MRSA positive status was associated with large herd size and with number of pig suppliers. In addition, sow herds tested LA-MRSA positive less frequently than herds without sows, and therefore data from sow herds were analysed separately. In univariable analysis, the following factors were associated with sow herds testing LA-MRSA positive: use of wet feed in the sow units; higher weights of piglets at weaning; availability of a delivery room on the farm; cleaning of aisles after pigs were moved; number of pigs per weaner section; number of pigs purchased in the past year, and factors related to rodent control and human traffic in the herd. In herds without sows, the univariable analysis showed...
that the presence of other animal species on the farm; negative pressure ventilation; full sectioning; frequent visits from the veterinarian; peroral use of tetracyclines for weaners; number of pigs purchased in the past year, and factors related to rodent control and human traffic in the herd were significantly associated with LA-MRSA status. Similar to what have been observed in other studies, many of the factors significantly associated with LA-MRSA status in study 1 was also significantly associated with herd size, and thus it was not possible to identify whether herd size itself or the related factors were the “true” risk factors. The number of observations in study 2 was small, but three variables (the number of pig suppliers, use of group medication in water vs. administration through feed, and having a company contract for mouse control) were associated with changing LA-MRSA status in the univariable analysis. Before the implementation of a national control strategy can be decided upon, it is also essential to understand how LA-MRSA spreads and persists within a pig herd, once it has been introduced. In the second part of this thesis a mechanistic model for spread of LA-MRSA within a pig herd was therefore build and subsequently used for studying transmission dynamics and within-farm prevalence after simulating different introductions of LA-MRSA on a farm. With the current parameterisation of the model, spread of LA-MRSA throughout the farm mainly followed the movement of pigs. The later in the production process LA-MRSA was introduced, the longer it took to spread to the whole farm. After spread of LA-MRSA had reached a steady state, the prevalence of LA-MRSA shedders was predicted to be highest in the farrowing unit, and lowest in the mating unit, independent of where and how LA-MRSA was introduced. Thus the farrowing unit might the area with most potential for intervention against spread of LA-MRSA. Introduction of a low number of intermittently shedding pigs was predicted to frequently result in LA-MRSA not establishing itself in the her. Increasing the duration of carriage led to an increased median prevalence, less variance and fewer iterations where LA-MRSA did not become established in the herd. When removing the possibility of pigs becoming persistent shedders, LA-MRSA more frequently faded out and did not become established within the herd. Not much is known regarding successful interventions against LA-MRSA within pig herds. Consequently the mechanistic model for spread of LA-MRSA within a farm were used for simulating on-farm interventions within four different areas: 1) Reduced antimicrobial consumption, 2) Reduced number of pigs within each section, 3) Reduced mixing of pigs from different litters, batches or pens, and 4) Improved internal biosecurity. It is believed that a reduction in the within-farm LA-MRSA prevalence will result in less spread between farms and reduce the risk of transmission to humans working on the farm. Reducing the transmission rates after LA-MRSA had become fully established within the herd, resulted in a marked prevalence decrease in the prevalence of LA-MRSA positive pigs within the different stable units, albeit LA-MRSA rarely disappeared completely. This indicates that while reducing antimicrobial consumption might be an important step towards reducing the LA-MRSA occurrence within the herd, other preventive or intervention measures should also be implemented in order to completely clear a herd from LA-MRSA. Implementation of the other interventions after LA-MRSA had become established within a herd only resulted in marginal changes in the median within-herd prevalence. However, in relation to being able to achieve or maintain a low level of antimicrobial consumption, these factors might still be of importance. The results of the sensitivity analysis indicated that the assumptions regarding the existence of pigs persistently shedding MRSA have a noticeable influence on the model results. A secondary of objective of building the simulation model was to identify knowledge gaps regarding spread and control of LA-MRSA. Several knowledge gaps related to infection dynamics exist, including influence of the environment, LA-MRSA load and persistent carriage. Regarding control of LA-MRSA, the main problem is currently a lack of evidence for major effect of any type of intervention other than reducing antimicrobial consumption. In conclusion, the work presented in this thesis have resulted in: 1) Confirmation of already known risk factors for farms testing LA-MRSA positive (herd type, herd size, number of pig suppliers) and identification of a number of potential new risk factors, albeit many of these were related to herd size, and it therefore was impossible to conclude, whether herd size itself or these factors were the true risk factors. 2) Construction of a mechanistic model for spread of LA-MRSA within a pig herd that can be used for simulating LA-MRSA within herd dynamics following different introductions. The code for the model is publicly available, and the herd part of the model can potentially be re-used together with epidemic models for other pathogens. 3) Simulation of within-herd interventions: Reduced antimicrobial consumption, reduced number of pigs within each section, reduced mixing of pigs, and improved internal biosecurity, of which only reduced antimicrobial consumption had a marked effect on the within-herd prevalence. More intervention scenarios can be simulated, when data becomes available. 4) The observation that once LA-MRSA has become established within a herd, it will spread to all compartments within the farm and be very hard to get rid of.

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology
Authors: Sørensen, A. I. V. (Intern)
Number of pages: 205
Publication date: 2018

Publication information
Place of publication: Kgs. Lyngby
Publisher: DTU Veterinærinstituttet
Original language: English
Main Research Area: Technical/natural sciences
Electronic versions:
Phd_thesis_Ana_Irene_Vedel_S_rensen.pdf
Staphylococcus aureus and Streptococcus agalactiae in milk and teat skin from cows in automatic milking systems

General information
State: Published
Organisations: National Veterinary Institute, Bacteriology & Parasitology, University of Applied Sciences and Arts Hannover, Københavns Universitet, University of Copenhagen
Authors: Svennesen, L. (Ekstern), Mahmmod, Y. (Ekstern), Pedersen, K. (Intern), Krömker, V. (Ekstern), Klaas, I. C. (Ekstern)
Publication date: 2018
Main Research Area: Technical/natural sciences
Electronic versions: Poster_NMC_Arizona_2018_Line_150118.ppt
Source: PublicationPreSubmission
Source-ID: 142550667
Publication: Research - peer-review › Poster – Annual report year: 2018

Stress and disease resilience differences related to emergence time for first feeding in farmed rainbow trout (Oncorhynchus mykiss)

Salmonid individuals show a relatively high variability in the time required to abandon the gravel nest where they hatch, the so-called "emergence time". Different behavioral and physiological traits have been shown to be associated to that emergence time in wild salmonids. In general, early- and late-emerging fish have traits resembling those of proactive and reactive stress coping styles, respectively. Proactive fish are considered to be more resilient to stress and probably to disease, so it was hypothesized that fish with different emergence time have different ability to resist repeated episodes of stress without suffering deleterious effects on their welfare or health status. In this study, rainbow trout eyed eggs were hatched and larvae were fractionated according to their emergence time (Early fraction: first 20 % of fish to emerge; Intermediate fraction: mid 20 %; Late fraction: last 20 %). When the fish were four months old, part of the fish were exposed to a daily repeated stress protocol for 15 days. The next day, both naïve and repeatedly-stressed fish were exposed to an acute stress challenge. Different plasma (cortisol, glucose, lactate) as well as CNS (serotonergic activity) stress markers were assessed to evaluate the stress resilience of the different fractions. Furthermore, an intraperitoneal infection challenge with Flavobacterium psychrophilum was carried out to assess the disease resilience of the different emergence fractions. Altogether, the results showed that fish from different fractions displayed different activation of the hypothalamus-pituitary-interrenal axis, pointing to a higher stress resilience in the fish with shorter emergence times. However, those differences were not reflected in the ability of the different fractions to grow and perform well in terms of growth, or in the ability to overcome the infection with the bacteria, which was similar for all the emergence fractions. This suggests that discriminating fish according to emergence time would probably have little effect in improving the
performance and the welfare of farmed fish.

**General information**
State: Accepted/In press
Organisations: National Institute of Aquatic Resources, Section for Aquaculture, National Veterinary Institute, Fish Diseases
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Publication date: 2018
Main Research Area: Technical/natural sciences

**Publication information**
Journal: Journal of Experimental Biology
Article number: jeb.174623
ISSN (Print): 0022-0949
Ratings:
  - BFI (2018): BFI-level 2
  - Web of Science (2018): Indexed yes
  - BFI (2017): BFI-level 2
  - Scopus rating (2017): SNIP 1.306 SJR 1.611 CiteScore 2.6
  - Web of Science (2017): Indexed yes
  - BFI (2016): BFI-level 2
  - Scopus rating (2016): CiteScore 2.62 SJR 1.824 SNIP 1.27
  - Web of Science (2016): Indexed yes
  - BFI (2015): BFI-level 2
  - Scopus rating (2015): SJR 1.821 SNIP 1.211 CiteScore 2.4
  - Web of Science (2015): Indexed yes
  - BFI (2014): BFI-level 2
  - Scopus rating (2014): SJR 1.742 SNIP 1.315 CiteScore 2.51
  - Web of Science (2014): Indexed yes
  - BFI (2013): BFI-level 2
  - Scopus rating (2013): SJR 1.733 SNIP 1.314 CiteScore 2.75
  - ISI indexed (2013): ISI indexed yes
  - Web of Science (2013): Indexed yes
  - BFI (2012): BFI-level 2
  - Scopus rating (2012): SJR 1.627 SNIP 1.372 CiteScore 2.91
  - ISI indexed (2012): ISI indexed yes
  - BFI (2011): BFI-level 2
  - Scopus rating (2011): SJR 1.553 SNIP 1.321 CiteScore 2.77
  - ISI indexed (2011): ISI indexed yes
  - Web of Science (2011): Indexed yes
  - BFI (2010): BFI-level 2
  - Scopus rating (2010): SJR 1.491 SNIP 1.332
  - Web of Science (2010): Indexed yes
  - BFI (2009): BFI-level 2
  - Scopus rating (2009): SJR 1.775 SNIP 1.356
  - BFI (2008): BFI-level 2
  - Scopus rating (2008): SJR 1.915 SNIP 1.384
  - Web of Science (2008): Indexed yes
  - Scopus rating (2007): SJR 1.599 SNIP 1.397
  - Web of Science (2007): Indexed yes
  - Scopus rating (2006): SJR 1.449 SNIP 1.358
  - Web of Science (2006): Indexed yes
  - Scopus rating (2005): SJR 1.619 SNIP 1.299
  - Web of Science (2005): Indexed yes
  - Scopus rating (2004): SJR 1.527 SNIP 1.329
  - Web of Science (2004): Indexed yes
Subtyping of Swine Influenza Viruses Using a High-Throughput Real-Time PCR Platform

Influenza A viruses (IAVs) are important human and animal pathogens with high impact on human and animal health. In Denmark, a passive surveillance program for IAV in pigs has been performed since 2011, where screening tests and subsequent subtyping are performed by reverse transcription quantitative real-time PCR (RT-qPCR). A disadvantage of the current subtyping system is that several assays are needed to cover the wide range of circulating subtypes, which makes the system expensive and time-consuming. Therefore, the aim of the present study was to develop a high-throughput method, which could improve surveillance of swine influenza viruses (swIAVs) and lower the costs of virus subtyping. Twelve qPCR assays specific for various hemagglutinin and neuraminidase gene lineages relevant for swIAV and six assays specific for the internal genes of IAV were developed and optimized for the high-throughput qPCR platform BioMark (Fluidigm). The qPCR assays were validated and optimized to run under the same reaction conditions using a 48.48 dynamic array (48.48DA). The sensitivity and specificity was assessed by testing virus isolates and field samples with known subtypes. The results revealed a performance of the swIAV 48.48DA similar to conventional real-time analysis, and furthermore, the specificity of swIAV 48.48DA was very high and without cross reactions between the assays. This high-throughput system provides a cost-effective alternative for subtyping of swIAVs.

General information
State: Published
Organisations: National Veterinary Institute, Virology, Department of Biotechnology and Biomedicine, Innate Immunology, Friedrich Loeffler Institute
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Number of pages: 12
Publication date: 2018
Main Research Area: Technical/natural sciences

Publication information
Journal: Frontiers in Cellular and Infection Microbiology
Volume: 8
Article number: 165
ISSN (Print): 2235-2988
Ratings:
Web of Science (2018): Indexed yes
Scopus rating (2017): SJR 1.703 SNIP 1.097 CiteScore 3.97
Web of Science (2017): Indexed yes
Scopus rating (2016): CiteScore 4.07 SJR 2.311 SNIP 1.305
Scopus rating (2015): SJR 2.365 SNIP 1.406 CiteScore 4.13
Web of Science (2015): Indexed yes
Scopus rating (2014): SJR 1.699 SNIP 0.998 CiteScore 3.02
Scopus rating (2013): SJR 1.376 SNIP 0.3 CiteScore 2.43
ISI indexed (2013): ISI indexed no
Scopus rating (2012): SJR 0.256 SNIP 0.189
Original language: English
Electronic versions:
Goecke_2018_Subtyping_of_swine_influenza_viruse.pdf
Survival and localization of African swine fever virus in stable flies (Stomoxys calcitrans) after feeding on viremic blood using a membrane feeder

Since 2014, African swine fever virus (ASFV) has been spreading within Eastern Europe. Within affected regions, the virus has infected some farms with high biosecurity and a marked seasonality of outbreaks in domestic pigs has been observed. ASFV transmission from stable flies, Stomoxys calcitrans, has previously been shown both mechanically and via ingestion of whole flies. Hence, blood-feeding flies may offer one explanation for the introductions into high biosecurity farms and for the observed seasonality. The aim of this study was to further elucidate the potential role of stable flies in ASFV transmission. Different parts of flies were analyzed for the presence of viral DNA and infectious virus at different time points following in vitro feeding of the flies on blood from an ASFV-infected pig. Using qPCR, ASFV DNA was detectable in mouth parts of flies for at least 12 h and remained in head and body samples from the flies for up to three days following feeding. Infectious virus was detected in fly body samples prepared at 3 h and 12 h after feeding. The presence of infectious ASFV in stable flies following feeding on viremic blood means that such flies are capable of transporting infectious virus. The detection of ASFV DNA in the flies for up to three days following feeding suggests that qPCR analysis of blood-feeding flies during ASFV outbreaks could be a useful method to elucidate the role of these flies in ASFV transmission under field conditions.
African swine fever virus, Blood-feeding flies in vitro feeding, Stomoxys calcitrans

DOI: 10.1016/j.vetmic.2018.06.010
Source: FindIt
Source-ID: 2435897821
Publication: Research - peer-review » Journal article – Annual report year: 2018

SVEPM 2017-Recent developments and contemporary foci in veterinary epidemiology and economics, Society of Veterinary Epidemiology and Preventive Medicine conference Inverness, Scotland 29-31 March 2017

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, University of Liverpool, Utrecht University
Authors: McIntyre, K. M. (Ekstern), van den Borne, B. H. P. (Ekstern), Calvo Artavia, F. F. (Intern), van Schaik, G. (Ekstern)
Number of pages: 2
Pages: 133-134
Publication date: 2018
Main Research Area: Technical/natural sciences

Publication information
Journal: Preventive Veterinary Medicine
Volume: 150
T-cell Responses in the Microenvironment of Primary Renal Cell Carcinoma-Implications for Adoptive Cell Therapy

In vitro expansion of large numbers of highly potent tumor-reactive T cells appears a prerequisite for effective adoptive cell therapy (ACT) with autologous tumor-infiltrating lymphocytes (TIL) as shown in metastatic melanoma (MM). We therefore sought to determine whether renal cell carcinomas (RCC) are infiltrated with tumor-reactive T cells that could be efficiently employed for adoptive transfer immunotherapy. TILs and autologous tumor cell lines (TCL) were successfully generated from 22 (92%) and 17 (77%) of 24 consecutive primary RCC specimens and compared with those generated from metastatic melanoma. Immune recognition of autologous TCLs or fresh tumor digests was observed in CD8(+) TILs from 82% of patients (18/22). Cytotoxicity assays confirmed the tumoricidal capacity of RCC-TILs. The overall expansion capacity of RCC-TILs was similar to MM-TILs. However, the magnitude, polyfunctionality, and ability to expand in classical expansion protocols of CD8(+) T-cell responses was lower compared with MM-TILs. The RCC-TILs that did react to the tumor were functional, and antigen presentation and processing of RCC tumors was similar to MM-TILs. Direct recognition of tumors with cytokine-induced overexpression of human leukocyte antigen class II was observed from CD4(+) T cells (6/12; 50%). Thus, TILs from primary RCC specimens could be isolated, expanded, and could recognize tumors. However, immune responses of expanded CD8(+) RCC-TILs were typically weaker than MM-TILs and displayed a mono-/oligofunctional pattern. The ability to select and expand polyfunctional T cells may be critical in developing effective ACT with TILs for RCC. In summary, TILs isolated from primary RCC specimens could recognize tumors. However, their immune responses were weaker than MM-TILs and displayed a mono-/oligofunctional pattern. The ability to select and expand polyfunctional T cells may improve cell therapy for RCC. (C) 2018 AACR.

The Detection and Phylogenetic Analysis of Bovine Hepacivirus in China

Hepacivirus has been identified in cattle in Africa, Europe, and South America. In this survey of bovine hepacivirus (BovHepV) in 131 serum samples from Chinese cattle herds using RT-PCR, five of 131 sera were BovHepV positive, with the infection rate of 3.82%. Phylogenetic analysis based on the partial NS3 coding sequence showed that the BovHepV of the five positive samples clustered with other BovHepV but formed a separate branch. The results indicated that these new BovHepV represent emerging and novel strains. Further investigations are necessary to determine the epidemiology
and viral pathogenesis of these BovHepV strains, as well as the potential threat to ruminant and livestock workers in
China.

**General information**

**State:** Published  
**Organisations:** National Veterinary Institute, Virology, Technical University of Denmark, Xichang College  
**Authors:** Deng, Y. (Ekstern), Guan, S. H. (Ekstern), Wang, S. (Ekstern), Hao, G. (Ekstern), Rasmussen, T. B. (Intern)  
**Number of pages:** 4  
**Publication date:** 2018  
**Main Research Area:** Technical/natural sciences

**Publication information**

**Journal:** Journal of Biomedicine and Biotechnology  
**Volume:** 2018  
**Article number:** 6216853  
**ISSN (Print):** 1110-7243  
**Ratings:**  
- BFI (2018): BFI-level 1  
- Web of Science (2018): Indexed yes  
- BFI (2017): BFI-level 1  
- Scopus rating (2017): SJR 0.935 SNIP 0.984 CiteScore 2.55  
- Web of Science (2017): Indexed Yes  
- BFI (2016): BFI-level 1  
- Scopus rating (2016): CiteScore 2.32 SJR 0.885 SNIP 0.919  
- BFI (2015): BFI-level 1  
- Scopus rating (2015): SJR 0.854 SNIP 0.799 CiteScore 1.77  
- Web of Science (2015): Indexed yes  
- BFI (2014): BFI-level 1  
- Scopus rating (2014): SJR 0.797 SNIP 0.777 CiteScore 1.29  
- Web of Science (2014): Indexed yes  
- BFI (2013): BFI-level 1  
- Scopus rating (2013): SJR 1.175 SNIP 0.973  
- ISI indexed (2013): ISI indexed yes  
- BFI (2012): BFI-level 1  
- Scopus rating (2012): SJR 1.084 SNIP 0.872  
- ISI indexed (2012): ISI indexed yes  
- BFI (2011): BFI-level 1  
- Scopus rating (2011): SJR 0.887 SNIP 0.704  
- ISI indexed (2011): ISI indexed yes  
- Web of Science (2011): Indexed yes  
- BFI (2010): BFI-level 1  
- Scopus rating (2010): SJR 0.526 SNIP 0.488  
- Web of Science (2010): Indexed yes  
- BFI (2009): BFI-level 1  
- Scopus rating (2009): SJR 0.967 SNIP 0.834  
- BFI (2008): BFI-level 1  
- Scopus rating (2008): SJR 1.245 SNIP 0.773  
- Scopus rating (2007): SJR 0.972 SNIP 0.867  
- Scopus rating (2006): SJR 0.746 SNIP 0.864  
- Scopus rating (2005): SJR 0.619 SNIP 0.826  
- Scopus rating (2004): SJR 0.675 SNIP 0.481  
- Scopus rating (2003): SJR 0.34 SNIP 0.344  
- Scopus rating (2002): SJR 0.185 SNIP 0.266

**Original language:** English  
**Electronic versions:**  
- Deng_2018_The_detection_and_phylogenetic_anal.pdf  
**DOIs:**
The diet of feral raccoon dog (Nyctereutes procyonoides) and native badger (Meles meles) and red fox (Vulpes vulpes) in Denmark

The raccoon dog (Nyctereutes procyonoides) is an East Asian Canid that has been introduced in Europe. Introduction of alien species is an increasing conservation issue. We examined the diet of a recently established raccoon dog population in Denmark by analysing stomach content in 249 carcasses collected in 2008–2016. Raccoon dog diet was compared to the diet of native badger (Meles meles) and red fox (Vulpes vulpes) in Denmark. The most common food for raccoon dogs were invertebrates (frequency of occurrence, FO 69%), small mammals (FO 68%), birds (FO 41%), fruits (FO 38%), amphibians (FO 36%) and carrions (FO 34%). The occurrence of invertebrates was highest during spring and summer, while fruits, cereals and carrions were eaten most often during autumn and winter. As expected, raccoon dog shared the major food categories with badger and red fox, but generally, it had a wider dietary niche. Overall, dietary overlap between raccoon dog and badger was 0.74 (Pianka index, Ojk). The dietary overlap with red fox was relatively high in all seasons, peaking in summer (Ojk 0.87) and dropping in winter (Ojk 0.79). Despite the dietary overlap between the alien raccoon dog and native red fox and badger, the species may coexist due to partitioning of feeding habitats and/or because the red fox is limited by other factors, e.g. diseases and anthropogenic activities. The introduced raccoon dog seems to fit a dietary niche between badger and red foxes in human-dominated landscapes in north-western Europe.

General information
State: Accepted/In press
Organisations: National Veterinary Institute, Diagnostic & Development, Aarhus University, Aalborg University
Authors: Elmeros, M. (Ekstern), Mikkelsen, D. M. G. (Ekstern), Nørgaard, L. S. (Ekstern), Pertoldi, C. (Ekstern), Jensen, T. H. (Ekstern), Chriél, M. (Intern)
Number of pages: 9
Publication date: 2018
Main Research Area: Technical/natural sciences

Publication information
Journal: Mammal Research
ISSN (Print): 2199-241x
Ratings:
Web of Science (2018): Indexed yes
Scopus rating (2017): SNIP 0.816 SJR 0.7 CiteScore 1.4
Web of Science (2017): Indexed Yes
Scopus rating (2016): CiteScore 1.1 SJR 0.611 SNIP 0.891
Scopus rating (2015): SJR 0.547 SNIP 0.621
Web of Science (2015): Indexed yes
Scopus rating (2014): SJR 0.51 SNIP 0.894
Scopus rating (2013): SJR 0.476 SNIP 0.842
Scopus rating (2012): SJR 0.466 SNIP 0.793
Scopus rating (2011): SJR 0.373 SNIP 0.66
Scopus rating (2010): SJR 0.425 SNIP 0.718
Scopus rating (2009): SJR 0.48 SNIP 0.873
Scopus rating (2008): SJR 0.711 SNIP 0.772
Scopus rating (2007): SJR 0.402 SNIP 0.776
Scopus rating (2006): SJR 0.306 SNIP 0.496
Scopus rating (2005): SJR 0.356 SNIP 0.6
Scopus rating (2004): SJR 0.378 SNIP 0.829
Scopus rating (2003): SJR 0.544 SNIP 0.949
Scopus rating (2002): SJR 0.611 SNIP 1.106
Scopus rating (2001): SJR 0.478 SNIP 0.679
Scopus rating (2000): SJR 0.716 SNIP 0.693
Scopus rating (1999): SJR 0.735 SNIP 0.949
The role of the transcription factors Bcl6 and Blimp-1 in intestinal dendritic cell subset specification

General information
State: Published
Organisations: National Veterinary Institute, Mucosal Immunology
Authors: Kifagi, C. (Intern), Lahl, K. (Intern)
Pages: 192-193
Publication date: 2018
Conference: 15th International Symposium on Dendritic Cells, Aachen, Germany, 10/06/2017 - 10/06/2017
Main Research Area: Technical/natural sciences

Publication information
Journal: European Journal of Immunology
Volume: 48
Issue number: S1
Article number: P–306
ISSN (Print): 0014-2980
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.59 SJR 2.206 SNIP 0.92
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.61 SJR 2.525 SNIP 0.927
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.588 SNIP 0.965 CiteScore 3.85
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.672 SNIP 0.972 CiteScore 3.83
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 2.876 SNIP 1.05 CiteScore 4.3
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 2.989 SNIP 1.063 CiteScore 4.62
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 3.255 SNIP 1.025 CiteScore 4.69
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 3.363 SNIP 0.99
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 3.188 SNIP 1.007
The role of TLR3/TRIF and type I IFN signaling in the migration of intestinal DC subsets in response to poly(I:C)

General information
State: Published
Organisations: National Veterinary Institute, Mucosal Immunology, T-cells & Molecular Mechanisms, Bayer Pharma ag, Technical University of Munich, Lund University
Authors: Garcia Lopez, A. (Intern), Bekiaris, V. (Intern), Müller-Luda, K. (Ekstern), Hütter, J. (Ekstern), Holzmann, B. (Ekstern), Agace, W. (Intern), Lahl, K. (Intern)
Pages: 150-150
Publication date: 2018
Conference: 15th International Symposium on Dendritic Cells, Aachen, Germany, 10/06/2017 - 10/06/2017
Main Research Area: Technical/natural sciences

Publication information
Journal: European Journal of Immunology
Volume: 48
Issue number: S1
Article number: P–227
ISSN (Print): 0014-2980
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.59 SJR 2.206 SNIP 0.92
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.61 SJR 2.525 SNIP 0.927
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.588 SNIP 0.965 CiteScore 3.85
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.672 SNIP 0.972 CiteScore 3.83
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Toxoplasma gondii antibodies in extensively farmed wild boars (Sus scrofa) in Denmark

General information
State: Published
Organisations: National Veterinary Institute, Bacteriology & Parasitology, Statens Serum Institut, University of Copenhagen, University of Latvia, Københavns Universitet
Authors: Petersen, H. H. (Intern), Jokelainen, P. (Ekstern), Laforet, C. K. (Ekstern), Deksne, G. (Ekstern), Johansen, M. V. (Ekstern), Lassen, B. (Ekstern)
Number of pages: 1
Publication date: 2018
Event: Abstract from Thirteenth Workshop of National Reference Laboratories for Parasites, Rome, Italy.
Main Research Area: Technical/natural sciences
Electronic versions:
EUERP_2018_Toxoplasma_gondii_antibodies_in_farmed_wild_boars_final_version.pdf
Source: PublicationPreSubmission
Source-ID: 146181619
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2018
Validation of real-time PCR and bacteriological culture for identification of Streptococcus agalactiae and Staphylococcus aureus in milk and on teat skin in herds with automatic milking system

General information
State: Published
Organisations: National Veterinary Institute, Bacteriology & Parasitology, University of Copenhagen
Authors: Skjølstrup, N. K. (Ekstern), Mathiasen, L. R. (Ekstern), Klaas, I. C. (Ekstern), Svønnesen, L. (Ekstern), Mahmmod, Y. (Ekstern), Pedersen, K. (Intern)
Publication date: 2018
Main Research Area: Technical/natural sciences
Electronic versions:
PosterNannaNMC170118.pdf
Source: PublicationPreSubmission
Source-ID: 143275457
Publication: Research › Poster – Annual report year: 2018

Variability in body mass and sexual dimorphism in Danish red foxes (Vulpes vulpes) in relation to population density
For the first time, temporal variability in body size and sexual dimorphism is revealed in foxes Vulpes vulpes from the same geographical area at over time. The weights and lengths of 552 Danish foxes were documented during three different periods: 1965–1977, 2012–2014 and the winter of 2015/2016. During the first and the third periods, the fox population was below the carrying capacity due to hunting pressure and canine distemper, respectively. Adult males were significantly (p < 0.01) heavier (mean weight: 7.7 kg and 7.5 kg respectively) in periods of low population density, i.e. 1965–1977 and compared to 2015/2016, compared to 2012–2014, when population density was high (the mean weight: 6.8 kg). However, no significant differences were found in the weight of females. Hence, sexual dimorphism ranged from 7.6 to 3.6 in adult foxes in low and high-density periods, respectively. During the winters of 2012–2014, no difference in body fat measured by rump fat thickness (RFT) was found between age groups and genders in contrast to 2015/2016, when RFT was significantly (p < 0.001) larger in adult females (mean RFT: 0.77 cm) than in adult males (mean RFT = 0.58 cm).

General information
State: Published
Organisations: National Veterinary Institute, Pathology, Diagnostic & Development, Aalborg Zoo
Authors: Pagh, S. (Ekstern), Hansen, M. S. (Intern), Jensen, B. (Ekstern), Pertoldi, C. (Ekstern), Chriél, M. (Intern)
Pages: 1-9
Publication date: 2018
Main Research Area: Technical/natural sciences
Publication information
Journal: Zoology and Ecology
Volume: 28
Issue number: 1
ISSN (Print): 2165-8005
Ratings:
Web of Science (2018): Indexed yes
Scopus rating (2017): SNIP 0.605 SJR 0.24 CiteScore 0.54
Scopus rating (2016): CiteScore 0.56 SNIP 0.645 SJR 0.309
Scopus rating (2015): CiteScore 0.52 SNIP 0.696 SJR 0.291
Scopus rating (2014): CiteScore 0.39 SNIP 0.487 SJR 0.249
Scopus rating (2013): CiteScore 0 SNIP 0.468 SJR 0.212
Scopus rating (2012): SNIP 0.373 SJR 0.214
Scopus rating (2011): SNIP 0.791 SJR 0.297
Scopus rating (2010): SNIP 0.641 SJR 0.248
Scopus rating (2009): SNIP 0.607 SJR 0.227
Scopus rating (2008): SNIP 0.455 SJR 0.323
Scopus rating (2007): SNIP 0.658 SJR 0.23
Scopus rating (2006): SNIP 0.096 SJR 0.192
Scopus rating (2005): SNIP 0.025 SJR 0.126
Scopus rating (2004): SNIP 0.015 SJR 0.126
Scopus rating (2003): SNIP 0.065 SJR 0.109
Scopus rating (2002): SNIP 0.079 SJR 0.1
Virulence marker candidates in N-protein of viral haemorrhagic septicaemia virus (VHSV): virulence variability within VHSV Ib clones

Four major genotypes of viral haemorrhagic septicaemia virus (VHSV), which have been isolated from many marine and freshwater fish species, are known to differ in virulence. While fast and low-cost genotyping systems based on monoclonal antibodies (MAbs) have been developed for typing of VHSV virulence, there is a need for supplementing the knowledge. In particular, 2 field isolates from viral haemorrhagic septicaemia (VHS) outbreaks in sea-reared rainbow trout Oncorhynchus mykiss in Sweden, SE-SVA-14 and SE-SVA-1033 (both genotype Ib), have yielded contradictory reactions. In the present study, upon cloning by limited dilution, both isolates appeared to be heterogeneous in terms of reactivity with nucleo (N)-protein-specific MAbs as well their gene sequences. Infection trials in rainbow trout further revealed differences in the virulence of these virus clones derived from the same primary isolate. Based on a comparative analysis of the entire genome of the clones tested, we suggest that the differences in virulence are tentatively linked to substitutions of amino acids (aa) in the N-protein region covered by aa 43-46 and aa position 168, or a combination of the two. The fact that such minor naturally occurring genetic differences affect the virulence implies that even low-virulent VHSV isolates in the marine environment should be considered as a potential threat for the trout farming industry. The described MAbs can represent useful tools for initial risk assessment of disease outbreaks in farmed trout by marine VHSV isolates.
Kit-of-parts for use in a prime-boost vaccination strategy to protect cloven-footed animals against foot-and-mouth disease virus infection

The present invention relates to a kit-of-parts for use in immunizing an animal against foot-and-mouth disease virus (FMDV) infection. In particular, the present invention relates to a kit-of-parts containing a priming composition and a boosting composition for use in a prime-boost FMDV-vaccination strategy.

General information
Binding of hydrophobic antigens to surfaces
A first aspect of the present invention is a method of detecting antibodies comprising the steps of: i) providing a first group of beads comprising a surface modified with C1-C10 alkyl groups comprising amine, ammonium, ether and/or hydroxyl groups, ii) contacting said first group of beads with a first hydrophobic antigen to provide a first group of bead-antigen conjugates by adsorption of the first hydrophobic antigen on the first group of beads, iii) isolating said bead-antigen conjugates, iv) contacting said bead-antigen conjugates with a sample to bind antibodies therein to provide bead-antigen-antibody conjugates, and v) detecting said bead-antigen-antibody conjugates. Further aspects include an antibody detection kit, a bead-antigen conjugate and a composition comprising at least two different groups of bead-antigen-conjugates.

1,2-Fucosyllactose Does Not Improve Intestinal Function or Prevent Escherichia coli F18 Diarrhea in Newborn Pigs
Objectives: Infectious diarrhea, a leading cause of morbidity and deaths, is less prevalent in breastfed infants compared with infants fed infant formula. The dominant human milk oligosaccharide (HMO), α-1,2-fucosyllactose (2′-FL), has structural homology to bacterial adhesion sites in the intestine and may in part explain the protective effects of human milk. We hypothesized that 2′-FL prevents diarrhea via competitive inhibition of pathogen adhesion in a pig model for sensitive newborn infants. Methods: Intestinal cell studies were coupled with studies on cesarean-delivered newborn pigs (n=24) without (control) or with inoculation of enterotoxigenic Escherichia coli F18 (7.5×1010/day for 8 days) fed either no (F18) or 10 g/L 2′-FL (2FL-F18). Results: In vitro studies revealed decreased pathogen adhesion to intestinal epithelial cells with 2′-FL (5 g/L; P<0.001). F18 pigs showed more diarrhea than control pigs (P<0.01). Administration of 2′-FL to F18 pigs failed to prevent diarrhea, although the relative weight loss tended to be reduced (~19 vs ~124 g/kg, P=0.12), higher villi were observed in the distal small intestine (P<0.05), and a trend toward increased proportion of mucosa and activities of some brush border enzymes in the proximal small intestine. In situ abundance of α-1,2-fucose and E coli was similar between groups, whereas sequencing showed higher abundance of Enterobacteriaceae in F18, Enterococcus in control and Lachnospiraceae in 2FL-F18 pigs. Conclusions: 2′-FL inhibited in vitro adhesion of E coli F18 to epithelial
cells, but had limited effects on diarrhea and mucosal health in newborn pigs challenged with E coli F18
A combined UHV-STM-flow cell set-up for electrochemical/electrocatalytic studies of structurally well-defined UHV prepared model electrodes

We describe the construction and discuss the performance of a novel combined ultrahigh vacuum (UHV)-electrochemistry set-up, allowing the controlled preparation and structural characterization of complex nanostructured electrode surfaces by high resolution scanning tunnelling microscopy (STM) under UHV conditions on the one hand and, after electrode transfer under clean conditions, electrochemical measurements under continuous, controlled electrolyte mass transport conditions on the other. Electrochemical measurements can be coupled with online product detection, either using an additional collector electrode or by differential electrochemical mass spectrometry (DEMS). The potential of the set-up will be illustrated in two electrocatalytic reactions on complex, but structurally well-defined bimetallic electrode surfaces, O₂ reduction on PtₓAg₁₋ₓ/Pt(111) monolayer surface alloys and bulk CO oxidation on Pt monolayer island modified Ru(0001) electrodes. We will particularly demonstrate the importance of structural characterization after the electrochemical measurements for identifying structural modifications induced by the electrochemical environment and thus avoiding misleading conclusions about the structure-activity relationships.
A Cow- and Herd-specific Bio-Economic Model of Intramammary Infections in Dairy Cows

Introduction. Mastitis, or intramammary infection (IMI), is one of the most significant diseases in dairy herds worldwide. It is caused by environmental and contagious bacteria. Simulation models have proven useful for evaluating the effect of different control strategies. However, previous published models are not cow-specific and therefore not so detailed in the simulation of host-pathogen interactions. If a simulation model is to be used by dairy farmers as a decision-making tool, it needs to be cow-specific because daily management decisions are made on cow level. Furthermore, as IMI is often caused by more than one pathogen in the same herd, such a simulation model should also be pathogen-specific to account for different transmission characteristics and treatment effects. Moreover, as different strains of pathogens can have different transmission routes (i.e. environmental, contagious or mixed), the model should be able to reflect this diversity. Our objective was thus to create a pathogen-, cow- and herd-specific bio-economic simulation model that could simulate multiple pathogens and strains at the same time within a dairy herd. This model should be able to simulate realistic scenarios for specific herds, thus being a tool for decision-making for individual farmers. Methods We used an existing mechanistic, stochastic simulation model framework to create an IMI simulation model. This mechanistic model simulates a dairy herd in great detail; i.e. with individual lactation curves for all cows, continuous movement of cows between farm sections and continuous culling decisions made by the farmer. We expanded the model to simulate the individual quarters of cows. This procedure made it possible for cows to have up to four different infections at a time, one per quarter. We implemented two different transmission modes, namely environmental transmission based on a continuous reservoir of pathogens in the farm, and contagious IMI originating from other infected animals in the herd. Currently, the environmental pathogen included is Escherichia coli, and the contagious pathogens are Staphylococcus aureus, Streptococcus agalactiae and Streptococcus uberis. The contagious transmission is simulating transmission, e.g. via milk liners, and depends on the number of quarters with contagious pathogens in the herd. We chose to focus on these four pathogens because they are common in Danish dairy farms. We modelled the increase in somatic cell count (SCC) due to subclinical infection. The reduction in milk yield for individual cows is then based on their SSC. Thus we are able to estimate the economic consequences of each IMI pathogen in the herd, simulate different control scenarios and estimate their epidemiological and economic effects.
Acquired Immune Resistance Follows Complete Tumor Regression without Loss of Target Antigens or IFN gamma Signaling

Cancer immunotherapy can result in durable tumor regressions in some patients. However, patients who initially respond often experience tumor progression. Here, we report mechanistic evidence of tumoral immune escape in an exemplary clinical case: a patient with metastatic melanoma who developed disease recurrence following an initial, unequivocal radiologic complete regression after T-cell-based immunotherapy. Functional cytotoxic T-cell responses, including responses to one mutant neoantigen, were amplified effectively with therapy and generated durable immunologic memory. However, these immune responses, including apparently effective surveillance of the tumor mutanome, did not prevent recurrence. Alterations of the MHC class I antigen-processing and presentation machinery (APM) in resistant cancer cells, but not antigen loss or impaired IFN gamma signaling, led to impaired recognition by tumor-specific CD8(+) T cells. Our results suggest that future immunotherapy combinations should take into account targeting cancer cells with intact and impaired MHC class I-related APM. Loss of target antigens or impaired IFN gamma signaling does not appear to be mandatory for tumor relapse after a complete radiologic regression. Personalized studies to uncover mechanisms leading to disease recurrence within each individual patient are warranted.
A cross-sectional field study on potential associations between feed quality measures and usage of antimicrobials in commercial mink (Neovison vison)

Feed quality is generally assumed to affect health status in animal production. In previous studies, the feed producer has been found to affect the occurrence of gastrointestinal disease and antimicrobial use in Mink (Neovison vison). Mink are fed with moist, freshly produced feed, based on perishable ingredients. The objective of this study was to investigate the potential effect of specific feed parameters on antimicrobial use on herd level. The study was cross-sectional, including 1472 mink herds, responsible for 97% of oral antimicrobials prescribed for Danish mink during the study period, 2012-2014. Data were obtained from the national veterinary prescription database (VetStat), Kopenhagen Fur database, and the Voluntary Feed Control (Mink producers Organization). All feed batches subject to feed control were included. A multi-variable variance analysis was carried out analysing the effect of the feed parameters total volatile nitrogen, dry matter, crude protein and fat; total bacterial count (21 °C), and counts of sulphite producing bacteria (21 °C), Clostridium spp., faecal cocci (FC) (44 °C), yeast, and mould; presence of Salmonella spp. and Clostridium perfringens (dichotome). Three outcome variables were applied: prescription of oral antimicrobial on herd level within time slots of 3, 5 or 7 days after feeding. Two binomial models were developed, adjusting for significant effects (p < 0.0001) of Ps. aeruginosa infection, herd size, month (season) and year. Antimicrobial prescription was significantly (p < 0.0001) associated with FC (all time slots, both models). A negative association (p < 0.0001) with crude protein on antimicrobial prescription within a 7 day slot suggested an association between low content of crude protein and antimicrobial use. The associations need to be confirmed in controlled studies, and ideally, potential causalities should be investigated. The perspective of such findings could be the development of tests for control of feed ingredients prior to use in the feed production.
General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, Department of Applied Mathematics and Computer Science, Diagnostic & Development, Kopenhagen Fur
Authors: Jensen, V. F. (Intern), Sommer, H. M. (Intern), Struve, T. (Ekstern), Clausen, J. (Ekstern), Chrié, M. (Intern)
Pages: 54–60
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Preventive Veterinary Medicine
Volume: 143
ISSN (Print): 0167-5877
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 1.31 SJR 1.144 CiteScore 2.26
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.2 SJR 1.249 SNIP 1.361
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.282 SNIP 1.177 CiteScore 2.1
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.27 SNIP 1.407 CiteScore 2.37
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.264 SNIP 1.529 CiteScore 2.49
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.265 SNIP 1.436 CiteScore 2.45
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.194 SNIP 1.295 CiteScore 2.24
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.156 SNIP 1.284
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.032 SNIP 1.338
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.056 SNIP 1.258
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.009 SNIP 1.353
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.06 SNIP 1.277
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.931 SNIP 1.414
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.812 SNIP 1.146
A cross-sectional study of oral antibacterial treatment patterns in relation to specific diarrhoeal pathogens in weaner pigs

According to international guidelines, the use of antibacterials should be evidence based and prudent. This register-based, cross-sectional study investigates the potential effect of laboratory findings on the patterns of antibacterial oral (batch) medication of weaner pigs, and the level of compliance with national guidelines for antibacterial use. The study population includes 1,736 weaner herds (~65% of all Danish weaner pigs) that were subject to laboratory analysis from the National Veterinary Institute on Brachyspira pilosicoli, Lawsonia intracellularis, and E. coli (F4 and F18) in 2014. Antibacterial prescription data were obtained from the national database, VetStat. These showed that antibacterial prescriptions for use in weaner pigs was 8.6% lower in spring 2015 compared to spring 2014. The antibacterial use per pig tended (p = 0.08) to decrease more in herds with negative laboratory results compared to herds with a moderate or massive occurrence of either of the pathogens. Irrespective of the laboratory findings on diarrhoeal pathogens, tetracyclines were the most frequently used antibacterials by a substantial margin, both 3 months prior to and 2-5 months after laboratory analysis. According to the national guidelines, tetracyclines are the second or third-choice antibacterial for treatment of diarrhoeal pathogens, due to resistance and co-resistance patterns. Compliance with the guidelines increased in 14% of the herds, mostly following identification of B. pilosicoli within the herd. Between 10% and 20% of the herds did not use batch treatment, despite the presence of moderate–massive amounts of the pathogens.

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, Diagnostic & Development
Authors: Jensen, V. F. (Intern), Jorsal, S. E. L. (Intern), Toft, N. (Intern)
Pages: 18-24
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Veterinary Microbiology
Volume: 203
ISSN (Print): 0378-1135
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.7 SJR 1.175 SNIP 1.241
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.363 SNIP 1.206
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.413 SNIP 1.21 CiteScore 2.56
A mechanistic model for spread of livestock-associated methicillin-resistant Staphylococcus aureus (LA-MRSA) within a pig herd

Before an efficient control strategy for livestock-associated methicillin resistant *Staphylococcus aureus* (LA-MRSA) in pigs can be decided upon, it is necessary to obtain a better understanding of how LA-MRSA spreads and persists within a pig herd, once it is introduced. We here present a mechanistic stochastic discrete-event simulation model for spread of LA-MRSA within a farrow-to-finish sow herd to aid in this. The model was individual-based and included three different
disease compartments: susceptible, intermittent or persistent shedder of MRSA. The model was used for studying transmission dynamics and within-farm prevalence after different introductions of LA-MRSA into a farm. The spread of LA-MRSA throughout the farm mainly followed the movement of pigs. After spread of LA-MRSA had reached equilibrium, the prevalence of LA-MRSA shedders was predicted to be highest in the farrowing unit, independent of how LA-MRSA was introduced. LA-MRSA took longer to spread to the whole herd if introduced in the finisher stable, rather than by gilts in the mating stable. The more LA-MRSA positive animals introduced, the shorter time before the prevalence in the herd stabilised. Introduction of a low number of intermittently shedding pigs was predicted to frequently result in LA-MRSA fading out. The model is a potential decision support tool for assessments of short and long term consequences of proposed intervention strategies or surveillance options for LA-MRSA within pig herds.

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, Bacteriology & Parasitology, Statens Serum Institut
Authors: Sørensen, A. I. V. (Intern), Toft, N. (Intern), Boklund, A. (Intern), Espinosa-Gongora, C. (Intern), Græsbøll, K. (Intern), Larsen, J. (Ekstern), Hisham Beshara Halasa, T. (Intern)
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: P L o S One
Volume: 12
Issue number: 11
Article number: e0188429
ISSN (Print): 1932-6203
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.01 SJR 1.164 SNIP 1.111
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.11 SJR 1.236 SNIP 1.101
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.427 SNIP 1.136 CiteScore 3.32
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.559 SNIP 1.148 CiteScore 3.54
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.772 SNIP 1.153 CiteScore 3.94
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.982 SNIP 1.156 CiteScore 4.15
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 2.425 SNIP 1.233 CiteScore 4.58
ISI indexed (2011): ISI indexed no
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.705 SNIP 1.178
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 2.614 SNIP 1.046
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
A meta-proteomics approach to study the interspecies interactions affecting microbial biofilm development in a model community

Microbial biofilms are omnipresent in nature and relevant to a broad spectrum of industries ranging from bioremediation and food production to biomedical applications. To date little is understood about how multi-species biofilm communities develop and function on a molecular level, due to the complexity of these biological systems. Here we apply a meta-proteomics approach to investigate the mechanisms influencing biofilm formation in a model consortium of four bacterial soil isolates; Stenotrophomonas rhizophila, Xanthomonas retroflexus, Microbacterium oxydans and Paenibacillus amylolyticus. Protein abundances in community and single species biofilms were compared to describe occurring interspecies interactions and the resulting changes in active metabolic pathways. To obtain full taxonomic resolution between closely related species and empower correct protein quantification, we developed a novel pipeline for generating reduced reference proteomes for spectral database searches. Meta-proteomics profiling indicated that community development is dependent on cooperative interactions between community members facilitating cross-feeding on specific amino acids. Opposite regulation patterns of fermentation and nitrogen pathways in Paenibacillus amylolyticus and Xanthomonas retroflexus may, however, indicate that competition for limited resources also affects community development. Overall our results demonstrate the multitude of pathways involved in biofilm formation in mixed communities.

General information
State: Published
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Number of pages: 13
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Scientific Reports
Volume: 7
Issue number: 1
Article number: 16483
ISSN (Print): 2045-2322
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.36 SJR 1.533 SNIP 1.245
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.63 SJR 1.692 SNIP 1.354
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.034 SNIP 1.597 CiteScore 5.3
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.163 SNIP 1.554 CiteScore 4.75
Web of Science (2014): Indexed yes
A multivariate dynamic linear model for early warnings of diarrhea and pen fouling in slaughter pigs

We present a method for providing early, but indiscriminant, predictions of diarrhea and pen fouling in grower/finisher pigs. We collected data on dispensed feed amount, water flow, drinking bouts frequency, temperature at two positions per pen, and section level humidity from 12 pens (6 double pens) over three full growth periods. The separate data series were co-modeled at pen level with time steps of one hour, using a multivariate dynamic linear model. The step-wise forecast errors of the model were unified using Cholesky decomposition. An alarm was raised if the unified error exceeded a set threshold a sufficient number of times, consecutively. Using this method with a 7 day prediction window, we achieved an area under the receiver operating characteristics curve of 0.84. Shorter prediction windows yielded lower performances, but longer prediction windows did not affect the performance.

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, University of Copenhagen
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Number of pages: 12
Pages: 51-62
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Computers and Electronics in Agriculture
Volume: 135
ISSN (Print): 0168-1699
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.563 SJR 0.814 CiteScore 3.27
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.873 SNIP 1.861 CiteScore 3.27
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.816 SNIP 1.895 CiteScore 2.99
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.961 SNIP 2.123 CiteScore 2.71
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
An Analysis of Natural T Cell Responses to Predicted Tumor Neoeptopes

Personalization of cancer immunotherapies such as therapeutic vaccines and adoptive T-cell therapy may benefit from efficient identification and targeting of patient-specific neoeptopes. However, current neoeptope prediction methods based on sequencing and predictions of epitope processing and presentation result in a low rate of validation, suggesting that the determinants of peptide immunogenicity are not well understood. We gathered published data on human neopeptides originating from single amino acid substitutions for which T cell reactivity had been experimentally tested, including both immunogenic and non-immunogenic neopeptides. Out of 1,948 neopeptide-HLA (human leukocyte antigen) combinations from 13 publications, 53 were reported to elicit a T cell response. From these data, we found an enrichment for responses among peptides of length 9. Even though the peptides had been pre-selected based on presumed likelihood of being immunogenic, we found using NetMHCpan-4.0 that immunogenic neopeptides were predicted to bind significantly more strongly to HLA compared to non-immunogenic peptides. Investigation of the HLA binding strength of the immunogenic peptides revealed that the vast majority (96%) shared very strong predicted binding to HLA and that the binding strength was comparable to that observed for pathogen-derived epitopes. Finally, we found that neopeptide dissimilarity to self is a predictor of immunogenicity in situations where neo- and normal peptides share comparable predicted binding strength. In conclusion, these results suggest new strategies for prioritization of mutated peptides, but new data will be needed to confirm their value.

General information
State: Published
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Publication date: 2017
An expression tag toolbox for microbial production of membrane bound plant cytochromes P450

Membrane-associated Cytochromes P450 (P450s) are one of the most important enzyme families for biosynthesis of plant-derived medicinal compounds. However, the hydrophobic nature of P450s makes their use in robust cell factories a challenge. Here we explore a small library of N-terminal expression tag chimeras of the model plant P450 CYP79A1 in different Escherichia coli strains. Using a high-throughput screening platform based on C-terminal GFP fusions, we identify several highly expressing and robustly performing chimeric designs. Analysis of long-term cultures by flow cytometry showed homogeneous populations for some of the conditions. Three chimeric designs were chosen for a more complex combinatorial assembly of a multigene pathway consisting of two P450s and a redox partner. Cells expressing these recombinant enzymes catalysed the conversion of the substrate to highly different ratios of the intermediate and the final product of the pathway. Finally, the effect of a robustly performing expression tag was explored with a library of 49 different P450s from medicinal plants and nearly half of these were improved in expression by more than 2-fold. The developed toolbox serves as platform to tune P450 performance in microbial cells, thereby facilitating recombinant production of complex plant P450-derived biochemicals.

General information
State: Published
Organisations: Novo Nordisk Foundation Center for Biosustainability, National Veterinary Institute, T-cells & Cancer, Research Groups, Loop, Microbial Evolution and Synthetic Biology, University of Copenhagen
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Pages: 751-760
Publication date: 2017
Main Research Area: Technical/natural sciences
Animal prevalence of livestock-associated methicillin-resistant Staphylococcus aureus in five Danish mink farms

Background. Livestock-associated methicillin-resistant Staphylococcus aureus (LA-MRSA) was for the first time isolated from Danish mink in 2013. Subsequent testing of all mink submitted for clinical diagnosis in Denmark, found 34 % (20/58) mink positive for LA-MRSA. In addition, 40 % (20/50) of screened healthy Danish mink farms were found positive. LA-MRSA in mink is believed to originate from contaminated slaughter-offal in the mink feed. Objective. The objective of the present study was to identify the animal-prevalence of LA-MRSA in five Danish mink farms. Materials and Methods. We collected 1,500 mink carcasses from five Danish mink farms. Farmers were asked to collect 100 mink for each of the three consecutive months following the whelping period (May-July 2017). From each carcass, the right forepaw and a pharyngeal-swab was collected for investigation of MRSA by enrichment, followed by screening on selective agar. Results. By July 1st 2017, 20 mink (5 adult, 15 mink kits) from one farm, were all tested negative. Results from the remaining mink will be presented at the conference. Discussion and Conclusion. In the preliminary results of this study, all mink tested negative. This finding may be explained by an overall low animal-prevalence in the farm. Another explanation could be the high proportion of young mink kits (15/20) tested. All mink kits were <5 weeks of age and had therefore not yet started feeding, which may reduce the likelihood of MRSA carriage. Perspectives. The anatomical location of LA-MRSA on mink (pharynx and paws) poses a human health hazard to farmers, who handle the animals and are at risk of bites and scratches from infected sites. To what extent LA-MRSA has dispersed in the environment of LA-MRSA positive mink farms remains for investigation.

Animal prevalence of livestock-associated methicillin-resistant Staphylococcus aureus in five Danish mink (Neovison vison) farms

Background. Livestock-associated methicillin-resistant Staphylococcus aureus (LA-MRSA) was for the first time isolated from Danish mink in 2013. Subsequent testing of all mink submitted for clinical diagnosis in Denmark, found 34 % (20/58) mink positive for LA-MRSA. In addition, 40 % (20/50) of screened healthy Danish mink farms were found positive. LA-MRSA in mink is believed to originate from contaminated slaughter-offal in the mink feed. Objective. The objective of the present study was to identify the animal-prevalence of LA-MRSA in five Danish mink farms. Materials and Methods. We collected 1,500 mink carcasses from five Danish mink farms. Farmers were asked to collect 100 mink for each of the three consecutive months following the whelping period (May-July 2017). From each carcass, the right forepaw and a pharyngeal-swab was collected for investigation of MRSA by enrichment, followed by screening on selective agar. Results. By July 1st 2017, 20 mink (5 adult, 15 mink kits) from one farm, were all tested negative. Results from the remaining mink will be presented at the conference. Discussion and Conclusion. In the preliminary results of this study, all mink tested negative. This finding may be explained by an overall low animal-prevalence in the farm. Another explanation could be the high proportion of young mink kits (15/20) tested. All mink kits were <5 weeks of age and had therefore not yet started feeding, which may reduce the likelihood of MRSA carriage. Perspectives. The anatomical location of LA-MRSA on mink (pharynx and paws) poses a human health hazard to farmers, who handle the animals and are at risk of bites and scratches from infected sites. To what extent LA-MRSA has dispersed in the environment of LA-MRSA positive mink farms remains for investigation.
A novel 3D skin explant model to study anaerobic bacterial infection

Skin infection studies are often limited by financial and ethical constraints, and alternatives, such as monolayer cell culture, do not reflect many cellular processes limiting their application. For a more functional replacement, 3D skin culture models offer many advantages such as the maintenance of the tissue structure and the cell types present in the host environment. A 3D skin culture model can be set up using tissues acquired from surgical procedures or post slaughter, making it a cost effective and attractive alternative to animal experimentation. The majority of 3D culture models have been established for aerobic pathogens, but currently there are no models for anaerobic skin infections. Footrot is an anaerobic bacterial infection which affects the ovine interdigital skin causing a substantial animal welfare and financial impact worldwide. *Dichelobacter nodosus* is a Gram-negative anaerobic bacterium and the causative agent of footrot. The mechanism of infection and host immune response to *D. nodosus* is poorly understood. Here we present a novel 3D skin ex vivo model to study anaerobic bacterial infections using ovine skin explants infected with *D. nodosus*. Our results demonstrate that *D. nodosus* can invade the skin explant, and that altered expression of key inflammatory markers could be quantified in the culture media. The viability of explants was assessed by tissue integrity (histopathological features) and cell death (DNA fragmentation) over 76 h showing the model was stable for 28 h. *D. nodosus* was quantified in all infected skin explants by qPCR and the bacterium was visualized invading the epidermis by Fluorescent in situ Hybridization. Measurement of pro-inflammatory cytokines/chemokines in the culture media revealed that the explants released IL1β in response to bacteria. In contrast, levels of CXCL8 production were no different to mock-infected explants. The 3D skin model realistically simulates the interdigital skin and has demonstrated that *D. nodosus* invades the skin and triggered an early cellular inflammatory response to this bacterium. This novel model is the first of its kind for investigating an anaerobic bacterial infection.

General information

State: Published
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Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information

Journal: Frontiers in Cellular and Infection Microbiology
Volume: 7
Article number: 404
ISSN (Print): 2235-2988
Ratings:
Web of Science (2018): Indexed yes
Scopus rating (2017): SJR 1.703 SNIP 1.097 CiteScore 3.97
Web of Science (2017): Indexed yes
Scopus rating (2016): CiteScore 4.07 SJR 2.311 SNIP 1.305
Scopus rating (2015): SJR 2.365 SNIP 1.406 CiteScore 4.13
Web of Science (2015): Indexed yes
Scopus rating (2014): SJR 1.699 SNIP 0.998 CiteScore 3.02
Scopus rating (2013): SJR 1.376 SNIP 0.3 CiteScore 2.43
ISI indexed (2013): ISI indexed no
Scopus rating (2012): SJR 0.256 SNIP 0.189
Original language: English
Skin culture, Ex vivo model, Footrot, Bacterial infection, *Dichelobacter nodosus*, Ovine pro-inflammatory cytokines
Electronic versions:
fcimb_07_00404.pdf
DOIs:
10.3389/fcimb.2017.00404

Bibliographical note

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Publication: Research - peer-review › Journal article – Annual report year: 2017

A novel porcine model of implant associated osteomyelitis: a comprehensive analysis of local, regional and systemic response

Pigs are favorable experimental animals for infectious diseases in humans. However, implant associated osteomyelitis (IAO) models in pigs have only been evaluated using high-inoculum infection (>10⁶ CFU) models in 1975 and 1993. Therefore, the aim of this paper was to present a new low inoculum porcine model of human IAO based on 42 experimental pigs. The model was created by drilling an implant cavity in the tibial bone followed by insertion of a small
steel implant and simultaneous inoculation of Staphylococcus aureus bacteria (n = 32) or saline (n = 10). The infected pigs were either inoculated with $10^4$ CFU (n = 26) or $10^2$ and $10^3$ CFU (n = 6). All animals were euthanized five days after insertion of implants. Pigs receiving the high-inoculum infections showed a significantly higher volume of bone lesion, number of neutrophils around the implant, concentrations of acute phase proteins in serum and enlargement of regional lymph nodes. A positive correlation was present between a high number of surrounding neutrophils and high values of all other parameters. Furthermore, a threshold of 40 neutrophils per 10 high power fields for the histopathological diagnosis of high grade IAO was defined. In conclusion: this paper describes a novel low-inoculum S. aureus porcine model of IAO which was demonstrated to be reliable, reproducible and discriminative to human IAO, and represents a requested and valuable tool in orthopedic research. This article is protected by copyright. All rights reserved.

**General information**

**State:** Published  
**Organisations:** National Veterinary Institute, Section for Immunology and Vaccinology, LEO Pharma A/S, University of Copenhagen, Copenhagen University Hospital, Aarhus University  
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**Pages:** 2211-2221  
**Publication date:** 2017  
**Main Research Area:** Technical/natural sciences

**Publication information**

**Journal:** Journal of Orthopaedic Research  
**Volume:** 35  
**Issue number:** 10  
**ISSN (Print):** 0736-0266  
**Ratings:**  
BFI (2018): BFI-level 2  
Web of Science (2018): Indexed yes  
BFI (2017): BFI-level 2  
Scopus rating (2017): SNIP 1.167 SJR 1.181 CiteScore 3.03  
Web of Science (2017): Indexed yes  
BFI (2016): BFI-level 2  
Scopus rating (2016): CiteScore 2.8 SJR 1.237 SNIP 1.106  
BFI (2015): BFI-level 2  
Scopus rating (2015): SJR 1.478 SNIP 1.357 CiteScore 3.22  
BFI (2014): BFI-level 2  
Scopus rating (2014): SJR 1.404 SNIP 1.404 CiteScore 3.14  
BFI (2013): BFI-level 2  
Scopus rating (2013): SJR 1.487 SNIP 1.343 CiteScore 3.21  
BFI (2012): BFI-level 2  
Scopus rating (2012): SJR 1.455 SNIP 1.388 CiteScore 3.31  
BFI (2011): BFI-level 2  
Scopus rating (2011): SJR 1.456 SNIP 1.404 CiteScore 3.15  
BFI (2010): BFI-level 2  
Scopus rating (2010): SJR 1.623 SNIP 1.524  
BFI (2009): BFI-level 2  
Scopus rating (2009): SJR 1.486 SNIP 1.378  
BFI (2008): BFI-level 1  
Scopus rating (2008): SJR 1.579 SNIP 1.369  
Scopus rating (2007): SJR 1.561 SNIP 1.445  
Scopus rating (2006): SJR 1.817 SNIP 1.811  
Scopus rating (2005): SJR 1.794 SNIP 1.794  
Scopus rating (2004): SJR 1.45 SNIP 1.499  
Scopus rating (2003): SJR 1.385 SNIP 1.251  
Scopus rating (2002): SJR 1.531 SNIP 1.062  
Scopus rating (2001): SJR 1.503 SNIP 1.518  
Scopus rating (2000): SJR 1.44 SNIP 1.882
Anthelmintic effects of forage chicory (Cichorium intybus) against free-living and parasitic stages of Cooperia oncophora

Chicory shows great promise as an anthelmintic forage for grazing ruminants that can reduce reliance on anti-parasitic drugs. Recently, we reported potent anthelmintic effects of chicory-based diets in infected cattle with significant reductions in worm burdens of the abomasal nematode Ostertagia ostertagi, whilst no apparent activity was observed against the small intestinal parasite Cooperia oncophora. To explore this discrepancy, we investigated direct anthelmintic effects of forage chicory against C. oncophora in vitro. Chicory leaves (cultivar ‘Spadona’) were extracted with methanol in a Soxhlet apparatus and the resulting extract was purified by solid-phase extraction to concentrate bioactive phytochemicals such as sesquiterpene lactones. C. oncophora eggs and adult worms from mono-infected donor calves were exposed to decreasing concentrations of the chicory extract. In an egg hatch assay, the chicory extract induced a marked and dose-dependent inhibition of egg hatching, with 95% inhibition at 2500 μg extract/mL (EC50 = 619 [95% CI: 530–722] μg extract/mL). In the adult motility inhibition assays, the chicory extract induced a potent and dose-dependent worm paralysis. At 12 h of incubation, worms exposed to chicory showed a total paralysis at ≥500 μg extract/mL, while after 48 h of incubation a complete inhibition of worm motility was observed at ≥250 μg extract/mL (EC50 = 80 [95% CI: 67–95] μg extract/mL). We have demonstrated that forage chicory can induce potent inhibitory effects on the egg hatching and exert direct anthelmintic activity against parasitic stages of C. oncophora. These results suggest that the previously reported absence of in vivo effects of chicory towards C. oncophora in infected animals may be related with host-mediated factors and/or inhibitory digestive conditions, rather than an inherent inactivity of chicory and its bioactive phytochemicals.
Antimicrobial peptide CAP18 and its effect on Yersinia ruckeri infections in rainbow trout Oncorhynchus mykiss (Walbaum): comparing administration by injection and oral routes

The antimicrobial peptide CAP18 has been demonstrated to have a strong in vitro bactericidal effect on Yersinia ruckeri, but its activity in vivo has not been described. In this work, we investigated whether CAP18 protects rainbow trout Oncorhynchus mykiss (Walbaum) against enteric red mouth disease caused by this pathogen either following i.p. injection or by oral administration (in feed). It was found that injection of CAP18 into juvenile rainbow trout before exposure to Y. ruckeri was associated with lowered mortality compared to non-medicated fish although it was less effective than the conventional antibiotic oxolinic acid. Oral administration of CAP18 to trout did not prevent infection. The proteolytic effect of secretions on the peptide CAP18 in the fish gastrointestinal tract is suggested to account for the inferior effect of oral administration.

General information
State: Published
Organisations: National Food Institute, Research Group for Gut Microbiology and Immunology, Research Group for Genomic Epidemiology, National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Copenhagen, Aalborg University, BioMar A/S
Authors: Chettri, J. K. (Intern), Mehrdana, F. (Ekstern), Hansen, E. B. (Intern), Ebbensgaard, A. E. (Intern), Overgaard, M. T. (Ekstern), Lauritsen, A. H. (Ekstern), Dalsgaard, I. (Intern), Buchmann, K. (Ekstern)
Pages: 97-104
Antimicrobial reduction measures applied in Danish pig herds following the introduction of the "Yellow Card" antimicrobial scheme

Following introduction of the antimicrobial restrictive "Yellow Card Scheme" in summer 2010, a rapid decrease in the Danish national pig antimicrobial consumption was observed. The aims of this study were to (i) investigate which measures had been implemented to reduce the antimicrobial consumption according to farmers and veterinarians and (ii) where possible, investigate if said measures were reflected in the herds' antimicrobial purchase data. Based on national register data from VetStat and the Central Husbandry Register, the study population was selected among Danish pig herds which had decreased their annual antimicrobial consumption with ≥10% following the introduction of the Yellow Card Scheme comparing June 1, 2009–May 31, 2010 to June 1, 2010–May 31, 2011. Subsequently, questionnaire surveys of both farmers and veterinarians were carried out, resulting in responses from 179 farmers accounting for 202 herds (response ratio: 83%) and 58 veterinarians accounting for 140 herds. Prior to the introduction of the Yellow Card Scheme, 24% of the participating herds had an antimicrobial consumption for one or more age groups which exceeded the Yellow Card Scheme threshold values on antimicrobial consumption, while 50% of the herds had an antimicrobial consumption below the national average. The measures most frequently stated as having contributed to the antimicrobial reduction were increased use of vaccines (52% of farmers; 35% of the veterinarians), less use of group medication (44% of the farmers; 58% of the veterinarians) and staff education (22% of the farmers; 26% of the veterinarians). Reduced usage of antimicrobials for oral use accounted for 89% of the total reduction in antimicrobial use. Among the farmers, 13% also stated that change in choice of product had contributed to reducing their antimicrobial consumption. However, when analyzing purchase data, no general trend was seen towards a larger purchase of products with a higher registered dosage per kg animal compared to similar products. The findings of this study indicate that implementation of antimicrobial restrictive legislation at herd-level may lead to a variety of antimicrobial reducing initiatives in both herds with a high- and herds with a low previous level of antimicrobial consumption.

General information
State: Published
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Pages: 9-16
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Preventive Veterinary Medicine
Volume: 138
ISSN (Print): 0167-5877
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 1.31 SJR 1.144 CiteScore 2.26
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.2 SJR 1.249 SNIP 1.361
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.282 SNIP 1.177 CiteScore 2.1
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.27 SNIP 1.407 CiteScore 2.37
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.264 SNIP 1.529 CiteScore 2.49
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.265 SNIP 1.436 CiteScore 2.45
Antimicrobial resistance among pathogenic bacteria from mink (Neovison vison) in Denmark

Background: For proper treatment of bacterial infections in mink, knowledge of the causative agents and their antimicrobial susceptibility patterns is crucial. The used antimicrobials are in general not registered for mink, i.e. most usage is "off-label". In this study, we report the patterns of antimicrobial resistance among pathogenic bacteria isolated from Danish mink during the period 2014-2016. The aim of this investigation was to provide data on antimicrobial resistance and consumption, to serve as background knowledge for new veterinary guidelines for prudent and optimal antimicrobial usage in mink. Results: A total number of 308 *Escherichia coli* isolates, 41 *Pseudomonas aeruginosa*, 36 *Streptococcus canis*, 30 *Streptococcus dysgalactiae*, 55 *Staphylococcus delphini*, 9 *Staphylococcus aureus*, and 20 *Staphylococcus schleiferi* were included in this study. Among *E. coli*, resistance was observed more frequently among the hemolytic isolates than among the non-hemolytic ones. The highest frequency of resistance was found to ampicillin, 82.3% and 48.0% of the hemolytic of the non-hemolytic isolates, respectively. The majority of the *P. aeruginosa* isolates were only sensitive to ciprofloxacin and gentamicin. Among the 9 *S. aureus*, one isolate was resistant to cefoxitin indicating it was a methicillin-resistant *Staphylococcus aureus*. Both β-hemolytic *Streptococcus* species showed high levels of resistance to tetracycline and erythromycin. The antimicrobial consumption increased significantly during 2007-2012, and fluctuated at a high level during 2012-2016, except for a temporary drop in 2013-2014. The majority of the prescribed antimicrobials were aminopenicillins followed by tetracyclines and macrolides. Conclusions: The study showed that antimicrobial resistance was common in most pathogenic bacteria from mink, in particular hemolytic *E. coli*. There is a need of guidelines for prudent use of antimicrobials for mink.
Antimicrobial resistance in Danish pigs: A cross sectional study of the association between antimicrobial resistance and geography, exposure to antimicrobials, and trade

Antimicrobial resistance is a worldwide problem of paramount importance for both humans and animals. To combat the emergence of antimicrobial resistance, the problem must be targeted in all major reservoirs as it is assumed that a high level of AMR genes in environmental reservoirs can increase the risk of human pathogens becoming resistant. Pigs might constitute an important reservoir. Therefore, it is important to manage antimicrobial resistance in pigs. Before effective actions can be initiated, it is crucial to know which factors are associated with the levels of antimicrobial resistance in pigs. The Danish pig farm is an ideal place to study AMR, as the pigs are all kept together in a confined space and managed in a similar manner. Furthermore, movements of pigs between farms and the purchase of antimicrobials for use at the farm are registered in national databases, thus facilitating the collection of information on relevant factors. The aim of this PhD project was to study the relationship between the levels of antimicrobial resistance genes and three factors in Danish pig farms: the geographical location of the farm, the exposure to antimicrobials, and the trade patterns. Data collection was necessary in order to fulfill the aim of the project, and early in the project it became evident that a thorough consideration of how the data should be collected was needed. This resulted in three different projects, each contributing to the planning process. Throughout the entire PhD project, the focus was on seven antimicrobial resistance genes - ermB, ermF, sul, sulII, tet(M), tet(O), and tet(W). The levels of these genes were determined using a quantitative real-time polymerase chain reaction (qPCR). The erm genes confer resistance against macrolides, the sul genes confer resistance against sulfonamides, and the tet genes confer resistance against tetracyclines. It was necessary to determine the minimum number of individual faecal samples that should be pooled together to represent the average level of antimicrobial resistance genes in the farm. It was estimated that a sample pooled from individual samples from five pigs was optimal. The pooling method was optimised, and was found to have strong agreement with previously used pooling methods. Samples were collected from 687 Danish pig farms in February and March 2015. However, 6 farms did not fulfil the criteria for the target population and were excluded. The samples were collected at five abattoirs located on Zealand and in Jutland. The sample material was faeces, and it was collected by squeezing a small amount out of the rectum at the slaughter line. After collection the samples were sent to the laboratory. The samples were pooled into one aliquot per farm and DNA was extracted from the faecal material. The antimicrobial resistance gene levels were then measured using quantitative real-time PCR. As the samples were collected at the abattoir it was not possible to know in advance which farms were available for sampling. Consequently, it was not possible to estimate whether the sampled farms were representative of the target and study populations prior to sampling. However, an evaluation of the representativeness of sampled farms (in terms of farm size and geographical location) was carried out post-sampling. It was found that the sampled farms were larger than nonsampled farms. Furthermore, there was an undersampled area in the western part of Jutland and an oversampled area in the northern part of Jutland. A simulation study showed that the sampling procedure would inevitably result in a bias towards larger farms and with some non-randomness in the spatial distribution. One of the aims of this PhD project was to estimate the quantitative relationship between the antimicrobial resistance gene levels and antimicrobial exposure. Previous studies have indicated that antimicrobial exposure in early periods of a pig’s life can influence the antimicrobial resistance genes levels found later in life. In order to quantify the relationship, an estimate of the antimicrobial exposure throughout the entire lifetime of a slaughter pig was required. An algorithm to estimate the LEA was therefore developed. Previous studies have shown that livestock farms in close proximity share common pathogens.
Furthermore, there have been indications that phenotypic antimicrobial resistance can be spatially clustered. Therefore, the spatial pattern of the antimicrobial resistance gene levels was assessed, and both areas with high levels and areas with low levels of some of the genes were found. However, it was concluded that the geographical location of the farm had only a minor effect on the antimicrobial resistance gene levels. Antimicrobial exposure is the most important risk factor for the development of antimicrobial resistance. However, previous studies of the relationship between antimicrobial resistance and antimicrobial exposure have focused on phenotypic antimicrobial resistance in a small number of farms. In this PhD project, the focus was on genotypic antimicrobial resistance. The quantitative relationship between the levels of seven antimicrobial resistance genes and the lifetime exposure of 11 different antimicrobial classes was estimated. It was found that some antimicrobial classes had a positive correlation with the levels of some antimicrobial resistance genes, but a negative correlation with other antimicrobial resistance genes. In conclusion, it was found that even though exposure to antimicrobials was associated with the antimicrobial resistance gene levels, it could only explain 10% - 42% of the variation in the gene levels. The microflora of a pig is established soon after birth. The source of the microflora is bacteria in the environment and from the sow. It has been shown that antimicrobial exposure of the sow will influence the antimicrobial resistance levels in the piglet. Therefore, the correlation between the levels of antimicrobial resistance genes in finisher farms and that of the sow farms with which they had trade connections was assessed. A significant correlation was found for most of the antimicrobial resistance genes with correlation coefficients ranging from 0.06 to 0.47. Of the three factors that were studied in this PhD project, only the antimicrobial exposure and the level of antimicrobial resistance in the sow farm with a trade connection were found to have a considerable effect on the antimicrobial resistance genes. However, it became apparent during the project that many other factors could affect the levels of antimicrobial resistance genes. This could lay the foundation for future studies.
Apolipoprotein E deficiency increases remnant lipoproteins and accelerates progressive atherosclerosis, but not xanthoma formation, in gene modified minipigs

Summary: Deficiency of apolipoprotein E (APOE) causes familial dysbetalipoproteinemia in humans resulting in a higher risk of atherosclerotic disease. In mice, APOE deficiency results in a severe atherosclerosis phenotype, but it is unknown to what extent this is unique to mice. In this study, APOE was targeted in Yucatan minipigs. APOE−/− minipigs displayed increased plasma cholesterol and accumulation of apolipoprotein B-48–containing chylomicron remnants on low-fat diet, which was significantly accentuated upon feeding a high-fat, high-cholesterol diet. APOE−/− minipigs displayed accelerated progressive atherosclerosis but not xanthoma formation. This indicates that remnant lipoproteinemia does not induce early lesions but is atherogenic in pre-existing atherosclerosis.

General information

State: Published
Organisations: National Veterinary Institute, Innate Immunology, Aarhus University, Rigshospitalet, University of Copenhagen
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Pages: 591-600
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information

Journal: JACC: Basic to Translational Science
Volume: 2
Issue number: 5
ISSN (Print): 2452-302X
Ratings:
Scopus rating (2017): SNIP 0.844 SJR 1.529 CiteScore 2.32
Original language: English
Apolipoprotein E, Atherosclerosis, Pig, Remnant cholesterol dysbetalipoproteinemia

Electronic versions:
befo_1_s2.0_S2452302X17301444_main_oa.pdf
DOI:s:
10.1016/j.jacbts.2017.06.004

Bibliographical note
This is an open access article under the CC BY-NC-ND license.

Source: FindIt
Source-ID: 2392831943
Publication: Research - peer-review › Journal article – Annual report year: 2017

A polyphenol-enriched diet and Ascaris suum infection modulate mucosal immune responses and gut microbiota composition in pigs

Polyphenols are a class of bioactive plant secondary metabolites that are thought to have beneficial effects on gut health, such as modulation of mucosal immune and inflammatory responses and regulation of parasite burdens. Here, we examined the interactions between a polyphenol-rich diet supplement and infection with the enteric nematode Ascaris suum in pigs. Pigs were fed either a basal diet or the same diet supplemented with grape pomace (GP), an industrial by-product rich in polyphenols such as oligomeric proanthocyanidins. Half of the animals in each group were then inoculated with A. suum for 14 days to assess parasite establishment, acquisition of local and systemic immune responses and effects on the gut microbiome. Despite in vitro anthelmintic activity of GP-extracts, numbers of parasite larvae in the intestine were not altered by GP-supplementation. However, the bioactive diet significantly increased numbers of eosinophils induced by A. suum infection in the duodenum, jejunum and ileum, and modulated gene expression in the jejunal mucosa of infected pigs. Both GP-supplementation and A. suum infection induced significant and apparently similar changes in the composition of the prokaryotic gut microbiota, and both also decreased concentrations of isobutyric and
isovaleric acid (branched-chain short chain fatty acids) in the colon. Our results demonstrate that while a polyphenol-enriched diet in pigs may not directly influence A. suum establishment, it significantly modulates the subsequent host response to helminth infection. Our results suggest an influence of diet on immune function which may potentially be exploited to enhance immunity to helminths.

General information
State: Published
Organisations: National Veterinary Institute, Innate Immunology, University of Copenhagen, University Malaysia Pahang, Aarhus University
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Number of pages: 21
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: P L o S One
Volume: 12
Issue number: 10
Article number: e0186546
ISSN (Print): 1932-6203
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.01 SJR 1.164 SNIP 1.111
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.11 SJR 1.236 SNIP 1.101
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.427 SNIP 1.136 CiteScore 3.32
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.559 SNIP 1.148 CiteScore 3.54
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.772 SNIP 1.153 CiteScore 3.94
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.982 SNIP 1.156 CiteScore 4.15
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 2.425 SNIP 1.233 CiteScore 4.58
ISI indexed (2011): ISI indexed no
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.705 SNIP 1.178
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 2.614 SNIP 1.046
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 2.506 SNIP 1.006
Web of Science (2008): Indexed yes
Seizures are common in dogs and can be caused by non-epileptic conditions or epilepsy. The clinical course of newly diagnosed epilepsy is sparsely documented. The objective of this study was to prospectively investigate causes for seizures (epileptic and non-epileptic) in a cohort of dogs with new-onset untreated seizures, and for those dogs with newly diagnosed epilepsy to investigate epilepsy type, seizure type and the course of disease over time, including the risk of seizure recurrence. Untreated client-owned dogs experiencing new-onset seizures were prospectively enrolled in a longitudinal observational study including clinical investigations and long-term monitoring at the Copenhagen University Hospital for Companion Animals. A baseline clinical assessment was followed by investigator/owner contact every eight weeks from inclusion to death or end of study. Inclusion of dogs was conducted from November 2010 to September 2012, and the study terminated in June 2014. One hundred and six dogs were included in the study. Seventy-nine dogs (74.5%) were diagnosed with epilepsy: 61 dogs (77.2%) with idiopathic epilepsy, 13 dogs (16.5%) with structural epilepsy and five dogs (6.3%) with suspected structural epilepsy. A non-epileptic cause for seizures was identified in 13 dogs and suspected in 10 dogs. Four dogs in which no cause for seizures was identified experienced only one seizure during the study. In dogs with idiopathic epilepsy 60% had their second epileptic seizure within three months of seizure onset. Twenty-six dogs with idiopathic epilepsy (43%) completed the study without receiving antiepileptic treatment. The natural course of idiopathic epilepsy (uninfluenced by drugs) was illustrated by highly individual and fluctuating seizure patterns, including long periods of remission. Cluster seizures motivated early treatment. In a few dogs with a high seizure frequency owners declined treatment against the investigators advice. Epilepsy is the most likely diagnosis in dogs presenting with new-onset seizures. The course of idiopathic epilepsy is highly individual and might not necessarily require long-term treatment. This must be considered when advising owners about what to expect with regard to treatment and prognosis.
Arcanobacterium phocae infection in mink (Neovison vison), seals (Phoca vitulina, Halichoerus grypus) and otters (Lutra lutra)

Infectious skin disorders are not uncommon in mink. Such disorders are important as they have a negative impact on animal health and welfare as well as on the quality and value of the fur. This study presents the isolation of Arcanobacterium phocae from mink with severe skin lesions and other pathological conditions, and from wild seals and otters. In 2015, A. phocae was isolated for the first time in Denmark from outbreaks of dermatitis in mink farms. The outbreaks affected at least 12 farms. Originating from these 12 farms, 23 animals cultured positive for A. phocae. The main clinical findings were necrotizing pododermatitis or dermatitis located to other body sites, such as the lumbar and cervical regions. A. phocae could be isolated from skin lesions and in nine animals also from liver, spleen and lung, indicating a systemic spread. The bacterium was also, for the first time in Denmark, detected in dead seals (n = 9) (lungs, throat or wounds) and otters (n = 2) (throat and foot). An infectious skin disorder in mink associated with A. phocae has started to occur in Danish farmed mink. The origin of the infection has not been identified and it is still not clear what the pathogenesis or the port of entry for A. phocae infections are.

General information
State: Published
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Number of pages: 6
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Acta Veterinaria Scandinavica
Volume: 59
Issue number: 1
A Robust Statistical Model to Predict the Future Value of the Milk Production of Dairy Cows Using Herd Recording Data

The future value of an individual dairy cow depends greatly on its projected milk yield. In developed countries with developed dairy industry infrastructures, facilities exist to record individual cow production and reproduction outcomes consistently and accurately. Accurate prediction of the future value of a dairy cow requires further detailed knowledge of the costs associated with feed, management practices, production systems, and disease. Here, we present a method to predict the future value of the milk production of a dairy cow based on herd recording data only. The method consists of several steps to evaluate lifetime milk production and individual cow somatic cell counts and to finally predict the average production for each day that the cow is alive. Herd recording data from 610 Danish Holstein herds were used to train and test a model predicting milk production (including factors associated with milk yield, somatic cell count, and the survival of individual cows). All estimated parameters were either herd- or cow-specific. The model prediction deviated, on average, less than 0.5 kg from the future average milk production of dairy cows in multiple herds after adjusting for the effect of somatic cell count. We conclude that estimates of future average production can be used on a day-to-day basis to rank cows for culling, or can be implemented in simulation models of within-herd disease spread to make operational decisions, such as culling versus treatment. An advantage of the approach presented in this paper is that it requires no specific knowledge of disease status or any other information beyond herd recorded milk yields, somatic cell counts, and reproductive status.

General information
State: Published
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Number of pages: 9
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Frontiers in Veterinary Science
Volume: 4
Article number: 13
ISSN (Print): 2297-1769
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.94
Original language: English
lactation curve, modeling, prediction, production parameters, simulation, Journal Article
Electronic versions:
fvets_04_00013.pdf
DOIs:
10.3389/fvets.2017.00013
Source: FindIt
Source-ID: 2355032853
Publication: Research - peer-review › Journal article – Annual report year: 2017

A simulation study to evaluate the performance of five statistical monitoring methods when applied to different time-series components in the context of control programs for endemic diseases

Disease monitoring and surveillance play a crucial role in control and eradication programs, as it is important to track implemented strategies in order to reduce and/or eliminate a specific disease. The objectives of this study were to assess the performance of different statistical monitoring methods for endemic disease control program scenarios, and to explore what impact of variation (noise) in the data had on the performance of these monitoring methods. We simulated 16 different scenarios of changes in weekly sero-prevalence. The changes included different combinations of increases, decreases and constant sero-prevalence levels (referred as events). Two space-state models were used to model the time series, and different statistical monitoring methods (such as univariate process control algorithms—Shewart Control Chart, Tabular Cumulative Sums, and the V-mask- and monitoring of the trend component–based on 99% confidence intervals and the trend sign) were tested. Performance was evaluated based on the number of iterations in which an alarm was
raised for a given week after the changes were introduced. Results revealed that the Shewhart Control Chart was better at detecting increases over decreases in sero-prevalence, whereas the opposite was observed for the Tabular Cumulative Sums. The trend-based methods detected the first event well, but performance was poorer when adapting to several consecutive events. The V-Mask method seemed to perform most consistently, and the impact of noise in the baseline was greater for the Shewhart Control Chart and Tabular Cumulative Sums than for the V-Mask and trend-based methods. The performance of the different statistical monitoring methods varied when monitoring increases and decreases in disease sero-prevalence. Combining two of more methods might improve the potential scope of surveillance systems, allowing them to fulfill different objectives due to their complementary advantages.
Association between selected antimicrobial resistance genes and antimicrobial exposure in Danish pig farms

Bacterial antimicrobial resistance (AMR) in pigs is an important public health concern due to its possible transfer to humans. We aimed at quantifying the relationship between the lifetime exposure of antimicrobials and seven antimicrobial resistance genes in Danish slaughter pig farms. AMR gene levels were quantified by qPCR of total-community DNA in faecal samples obtained from 681 batches of slaughter pigs. The lifetime exposure to antimicrobials was estimated at batch level for the piglet, weaner, and finisher periods individually for the sampled batches. We showed that the effect of antimicrobial exposure on the levels of AMR genes was complex and unique for each individual gene. Several antimicrobial classes had both negative and positive correlations with the AMR genes. From 10-42% of the variation in AMR gene levels could be explained in the final regression models, indicating that antimicrobial exposure is not the only important determinant of the AMR gene levels.
Associations between Antibacterial Treatment and the Prevalence of Tail-Biting-Related Sequelae in Danish Finishers at Slaughter

Secondary infections as a result of tail biting cause substantial economic losses in pig production and are a subject of concern for animal welfare. The use of first-choice antibacterial agents in the treatment of tail biting in finishing pigs is hypothesized to be negatively correlated with the development of systemic infection. This would be expected to reduce the prevalence of post-mortem pyemic sequelae (such as osteomyelitis and abscesses) in finishers with tail-bite lesions. We performed a register-based study that included three Danish databases, holding information on the purchase of antibacterials at herd level (VetStat), herd demographics (Central Husbandry Register), and relevant observations at slaughter (meat inspection data). We included all finishers from indoor production finisher herds that met the inclusion criterion of at least one slaughtered finisher with a recorded tail-bite observation during 2015 at the single largest Danish abattoir. The final dataset held 1,070 herds with one or more tail-bite observations, from which 14,411 of 2,906,626 finishers (0.50%) had an individual record of a tail bite. Within this group of finishers with tail-bite observations, the recorded tail-biting-related sequelae included osteomyelitis (8.1%), abscesses in the hindquarters (10.5%), abscesses in the forequarters (2.3%), abscesses in the mid-section of the carcass (2.9%), abscesses in the limbs (2.4%), and chronic arthritis (0.5%).

Due to a high-herd prevalence (>25%), osteomyelitis and abscesses in the hindquarters were selected for further analysis. The occurrence of osteomyelitis and hindquarter abscesses in individual finishers with tail-bite observations was described using a generalized linear mixed effects model with binomial response and logit link. Herd was included as a random effect, while herd size and various antibacterial treatments were tested for inclusion in the model as fixed effects. The final models indicated a significant association between herd size and both osteomyelitis (p = 0.014) and hindquarter abscesses (p < 0.001), with larger herds (2,001–12,000 registered finisher pigs) showing a reduced risk. Further, a negative association was found between the occurrence of hindquarter abscesses and the use of oral pleuromutilin (p = 0.022). The significant association with herd size highlights the potential importance of management factors in reducing the occurrence of tail-bite lesions in finishing pigs.

General information
State: Published
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Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Frontiers in Veterinary Science
Volume: 4
Article number: 182
ISSN (Print): 2297-1769
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.94
Original language: English
Slaughter remarks, Pigs, Swine, Meat inspection, Hierarchical model, Antibiotic use, Antimicrobial use, Abattoir
Electronic versions:
Fertner_2017.pdf
DOIs:
10.3389/fvets.2017.00182

Bibliographical note
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Automated Analysis of Flow Cytometry Data to Reduce Inter-Lab Variation in the Detection of Major Histocompatibility Complex Multimer-Binding T Cells

Manual analysis of flow cytometry data and subjective gate-border decisions taken by individuals continue to be a source of variation in the assessment of antigen-specific T cells when comparing data across laboratories, and also over time in individual labs. Therefore, strategies to provide automated analysis of major histocompatibility complex (MHC) multimer-binding T cells represent an attractive solution to decrease subjectivity and technical variation. The challenge of using an automated analysis approach is that MHC multimer-binding T cell populations are often rare and therefore difficult to detect. We used a highly heterogeneous dataset from a recent MHC multimer proficiency panel to assess if MHC multimer-binding CD8(+ T cells could be analyzed with computational solutions currently available, and if such analyses would reduce the technical variation across different laboratories. We used three different methods, FLOW Clustering without K (FLOCK), Scalable Weighted Iterative Flow-clustering Technique (SWIFT), and ReFlow to analyze flow cytometry data files from 28 laboratories. Each laboratory screened for antigen-responsive T cell populations with frequency ranging from 0.01 to 1.5% of lymphocytes within samples from two donors. Experience from this analysis shows that all three programs can be used for the identification of high to intermediate frequency of MHC multimer-binding T cell populations, with results very similar to that of manual gating. For the less frequent populations (
Automated identification of MHC multimer binding T cells

General information
State: Published
Organisations: National Veterinary Institute, T-cells & Cancer
Number of pages: 1
Pages: 283-283
Publication date: 2017
Conference: 44th Annual Meeting of the Scandinavian Society of Immunology, Stockholm, Sweden, 17/10/2017 - 17/10/2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Scandinavian Journal of Immunology
Volume: 86
Issue number: 4
ISSN (Print): 0300-9475
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.621 SJR 0.891 CiteScore 2.11
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.03 SJR 0.979 SNIP 0.644
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.933 SNIP 0.679 CiteScore 1.97
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.901 SNIP 0.665 CiteScore 1.91
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.875 SNIP 0.709 CiteScore 2.05
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.89 SNIP 0.742 CiteScore 2.16
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.865 SNIP 0.654 CiteScore 2.06
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.859 SNIP 0.621
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.973 SNIP 0.659
Web of Science (2009): Indexed yes
Bacterial invasion of the uterus and oviducts in bovine pyometra

Pyometra is a common disease of cattle that causes infertility and thereby financial losses to the cattle industry. Bacteria involved in the development and progression of pyometra have been investigated by microbial culture but their tissue invading abilities, which is an important aspect of bacterial pathogenicity and development of lesions, have not been investigated. Bacterial invasion of the uterus and oviducts was studied in 21 cows diagnosed with pyometra at the time of slaughter by applying fluorescence in situ hybridization using probes targeting 16S ribosomal RNA of Fusobacterium necrophorum, Porphyromonas levii, Trueperella pyogenes and the overall bacterial domain Bacteria. Fusobacterium necrophorum and P. levii were found to invade the endometrium, especially if the endometrium was ulcerated, and penetrated deep into the lamina propria. These species co-localized within the tissue thus indicating a synergism. Trueperella pyogenes did not invade the uterine tissue. In addition to endometrial lesions, most cows with pyometra also had salpingitis but without significant bacterial invasion of the oviductal wall.

General information
State: Published
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Number of pages: 6
Pages: 93-98
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Theriogenology
Volume: 93
ISSN (Print): 0093-691X
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 1.338 SJR 0.936 CiteScore 2.27
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 1.99 SJR 0.786 SNIP 1.192
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 0.862 SNIP 1.244 CiteScore 1.86
BFI (2014): BFI-level 2
Batch medication of intestinal infections in nursery pigs—A randomised clinical trial on the efficacy of treatment strategy, type of antibiotic and bacterial load on average daily weight gain

Introduction Previous research projects have demonstrated the need for better diagnostic tools to support decisions on medication strategies for infections caused by Escherichia coli F4 (F4) and F18 (F18), Lawsonia intracellularis (LI) and Brachyspira pilosicoli (PILO). This study was carried out as a randomised clinical trial in three Danish pig herds and included 1047 nursery pigs, distributed over 10 batches and 78 pens. The objectives of this study were: (1) to assess the effect of four 5-day treatment strategies (initiated at clinical outbreak of diarrhoea or at fixed time points 14, 21, or 28 days after weaning) on average daily weight gain (ADG); (2) to compare the effect of treatment with doxycycline or tylosine on diarrhoea prevalence, pathogenic bacterial load, and ADG; (3) to evaluate PCR testing of faecal pen floor samples as a diagnostic tool for determining the optimal time of treatment. Results (1) The four treatment strategies had a significant overall effect on ADG (p = 0.01). Pigs starting treatment 14 days after weaning had a significantly higher ADG (42 g) compared to pigs treated on day 28 (p = 0.01). (2) When measured 2 days after treatment, doxycycline treatment resulted in fewer LI-positive pens (p = 0.004), lower excretion levels of LI (p = 0.013), and fewer pens with a high level of LI (p = 0.031) compared to pens treated with tylosine. There was no significant difference in F4, F18 and PILO levels after treatment with the two antibiotic compounds. There was a significant difference (p = 0.04) of mean diarrhoea prevalence, pathogenic bacterial load, and ADG; (3) to evaluate PCR testing of faecal pen floor samples as a diagnostic tool for determining the optimal time of treatment. Results (1) The four treatment strategies had a significant overall effect on ADG (p = 0.01). Pigs starting treatment 14 days after weaning had a significantly higher ADG (42 g) compared to pigs treated on day 28 (p = 0.01). (2) When measured 2 days after treatment, doxycycline treatment resulted in fewer LI-positive pens (p = 0.004), lower excretion levels of LI (p = 0.013), and fewer pens with a high level of LI (p = 0.031) compared to pens treated with tylosine. There was no significant difference in F4, F18 and PILO levels after treatment with the two antibiotic compounds. There was a significant difference (p = 0.04) of mean diarrhoea prevalence on day 21 of the study between pens treated with tylosine (0.254, 95% CI: 0.184–0.324), and doxycycline (0.167, 95% CI: 0.124–0.210). The type of antibiotic compound was not found to have a significant effect on ADG (p = 0.209). (3) Pigs starting treatment on day 14 in pens where F4, F18, LI or PILO were detected by qPCR on the pen floor had a statistically significant increase in ADG (66 g) compared to pigs treated on day 14 in pens where no enteric pathogens were detected (p = 0.04). Conclusions The results of this study showed that the highest ADG was achieved when treatment was initiated 14 days after weaning in pens where intestinal pathogens were detected. Doxycycline was more effective in reducing diarrhoea and LI excretion levels than treatment with tylosine.
Batf3-dependent classical dendritic cells are required for mounting optimal rotavirus-specific IgA immune responses

General information
State: Published
Organisations: National Veterinary Institute, Mucosal Immunology, Lund University
Authors: Nakawesi, J. (Ekstern), Hütter, J. (Intern), Lahl, K. (Intern)
Pages: 281
Publication date: 2017
Conference: 44th Annual Meeting of the Scandinavian Society of Immunology, Stockholm, Sweden, 17/10/2017 - 17/10/2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Scandinavian Journal of Immunology
Volume: 86
Issue number: 4
ISSN (Print): 0300-9475
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.621 SJR 0.891 CiteScore 2.11
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.03 SJR 0.979 SNIP 0.644
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.933 SNIP 0.679 CiteScore 1.97
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.901 SNIP 0.665 CiteScore 1.91
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.875 SNIP 0.709 CiteScore 2.05
ISI indexed (2013): ISI indexed yes
Big data - modelling of midges in Europa using machine learning techniques and satellite imagery

Biting midges (Diptera, Ceratopogonidae) of the genus Culicoides are important vectors of pathogens causing diseases in free living and production animals and can lead to large economic losses in many European countries. In Europe, Culicoides imicola and the Obsoletus group are considered to be the main vectors of bluetongue virus that mostly affects ruminants such as cattle and sheep. Spatio-temporal modelling of vector distribution and abundance allows us to identify high risk areas for virus transmission and can aid in applying effective surveillance and control measures.

We used presence-absence and monthly abundance data of Culicoides from 1005 sites across 9 countries (Spain, France, Denmark, Poland, Switzerland, Austria, Poland, Sweden, Norway) collected between the years 2007 and 2013. The dataset included information on the vector species abundance (number of specimens caught per night), GPS coordinates of each trap, start and end dates of trapping. We used 120 environmental predictor variables together with Random Forest machine learning algorithms to predict the overall species distribution (probability of occurrence) and monthly abundance in Europe. We generated maps for every month of the year, to visualize the abundance of C. imicola and the Obsoletus group in Europe as well as distribution maps showing the probability of occurrence.

We were able to create predictive maps of both Culicoides sp. occurrence and abundance using Random Forest models, and although the variance was large, the predicted abundance values for each site had a positive correlation with the observed abundance. We found relatively large spatial variations in probability of occurrence and abundance for both C. imicola and the Obsoletus group. For C. imicola probability of occurrence and abundance was higher in southern Spain, where as the Obsoletus group had higher probability of occurrence and abundance in central and northern Europe such as France and Germany. Temporal variation was also observed with higher abundance occurring during summer months and low or no abundance during winter months for both C. imicola and the Obsoletus group, although abundance was generally higher for a longer period of time for C. imicola than for the Obsoletus group.
Using machine learning techniques, we were able to model the spatial distribution in Europe for C. imicola and the Obsoletus group in terms of abundance and suitability (probability of occurrence). Our maps corresponded well with the previously reported distribution for C. imicola and the Obsoletus group. The observed seasonal variation was also consistent with reported population dynamics for Culicoides, as it depends on environmental factors such as temperature and rainfall. Longer seasonal abundance for C. imicula compared to the Obsoletus group can be explained by the species distribution, as C. imicula is limited to the southern parts of Europe where the warm season lasts longer, whereas the Obsoletus group is found further north. The outputs obtained here will be used as input for epidemiological models and can be helpful for determining high risk areas for disease transmission.

Biosecurity Conditions in Small Commercial Chicken Farms, Bangladesh 2011-2012

In Bangladesh, highly pathogenic avian influenza H5N1 is endemic in poultry. This study aimed to understand the biosecurity conditions and farmers' perception of avian influenza biosecurity in Bangladeshi small commercial chicken farms. During 2011-2012, we conducted observations, in-depth interviews and group discussions with poultry farmers in 16 farms and in-depth interviews with seven local feed vendors from two districts. None of the farms were completely segregated from people, backyard poultry, other animals, households, other poultry farms or large trees. Wild birds and rodents accessed the farms for poultry feed. Farmers usually did not allow the buyers to bring egg trays inside their sheds. Spraying disinfectant in the shed and removing feces were the only regular cleaning and disinfection activities observed. All farmers sold or used untreated feces as fish feed or fertilizer. Farmers were more concerned about Newcastle disease and infectious bursal disease than about avian influenza. Farmers' understanding about biosecurity and avian influenza was influenced by local vendors. While we seldom observed flock segregation, some farmers used measures that involved additional cost or effort to protect their flocks. These farmers could be motivated by interventions to protect their investment from diseases they consider harmful. Future interventions could explore the feasibility and effectiveness of low-cost alternative biosecurity measures.
Blood Donor Disclosure - Rates of filled antibiotic Prescriptions Before 4,978,751 Blood Donations in Denmark

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Section for Immunology and Vaccinology, Institut for Klinisk Medicin - Klinisk Immunologisk Afdeling, SKS, Statens Serum Institut, Klinisk Immunologi, University of Southern Denmark, Karolinska Institute and University Hospital, Psychiatric Center Copenhagen, Rigshospitalet, University of Copenhagen
Authors: Erikstrup, C. (Ekstern), Hjalgrim, H. (Ekstern), Pedersen, O. B. V. (Ekstern), Petersen, M. (Intern), Sørensen, E. H. (Ekstern), Rostgaard, K. (Ekstern), Nielsen, K. R. (Ekstern), Paarup, H. M. (Ekstern), Edgren, G. (Ekstern), Ullum, H. (Ekstern), Custer, B. (Ekstern)
Publication date: 2017
Conference: 27th Regional Congress of the International Society of Blood Transfusion, København, Denmark, 17/06/2017 - 17/06/2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Vox Sanguinis
Volume: 112
Issue number: S1
Article number: 4C-S30-01
CD4\(^+\)CD8\(^+\) double-positive T cells in skin-draining lymph nodes respond to inflammatory signals from the skin

CD4\(^+\)CD8\(^+\) double-positive (DP), mature, peripheral T cells are readily detectable in a variety of species and tissues. Despite a common association with autoimmune and malignant skin disorders, however, little is understood about their role or function. Herein, we show that DP T cells are readily detectable in the blood, spleen, and peripheral lymph nodes of naive C57BL/6 mice. DP T cells were also present in Jα\(^{-}\) and CD1d\(^{-}\) mice, indicating that these cells are not NK-T cells. After skin administration of CASAC adjuvant, but not Quil A adjuvant, both total DP T cells and skin-infiltrating DP T cells increased in number. We explored the possibility that DP T cells could represent aggregates between CD4\(^+\) and CD8\(^+\) single-positive T cells and found strong evidence that a large proportion of apparent DP T cells were indeed aggregates. However, the existence of true CD4\(^+\)CD8\(^+\) DP T cells was confirmed by Amnis Image-Stream (Millipore Sigma, Billerica, MA, USA) imaging. Multiple rounds of FACS sorting separated true DP cells from aggregates and indicated that conventional analyses may lead to ~10-fold overestimation of DP T cell numbers. The high degree of aggregate contamination and overestimation of DP abundance using conventional analysis techniques may explain discrepancies reported in the literature for DP T cell origin, phenotype, and function.
Characterization of Campylobacter jejuni and Campylobacter coli Broiler Isolates by Whole-Genome Sequencing

Campylobacter has been the most commonly reported cause of bacterial diarrheal disease in humans in the European Union since 2005. Most broiler batches at slaughter are colonized with Campylobacter, and the major source of infection is contaminated poultry meat. The aim of this study was to characterize a selection of Campylobacter jejuni and Campylobacter coli isolates from broilers through whole-genome sequencing (WGS). A total of 16 isolates (C. jejuni = 12 and C. coli = 4) from five broiler farms from Catalonia (northeastern Spain) were analyzed. A phylogenetic analysis based on 8420 single-nucleotide polymorphisms showed two main cluster grouping strains by species. Phenotypic resistances to quinolones (100%), tetracycline (81%), streptomycin (75%), erythromycin (56%), and gentamicin (13%) were found. All the isolates carried the C257T point mutation in the subunit A of the DNA gyrase gene (Thr86Ile) conferring resistance to quinolones, while all the isolates showing resistance to tetracycline carried the tet(O) gene. The genes aph(3′)-III and aadE conferring resistance to aminoglycosides were identified in the two isolates (one C. jejuni and one C. coli) resistant to streptomycin and gentamicin. The point mutation A2075G on the 23S rDNA conferring high resistance to macrolides was detected in three C. coli isolates. The CmeABC multidrug efflux pump was also detected, both in C. jejuni and C. coli isolates. All C. jejuni and C. coli isolates were positive for most of the 34 virulence-associated genes studied related to motility, chemotaxis, adhesion, and invasion. Interestingly, the wlaN gene involved in the Guillain–Barré syndrome was found in two isolates. The results underline the power of WGS for investigation of virulence, clonality, and antimicrobial resistance in Campylobacter.

General information
State: Published
Organisations: National Veterinary Institute, Bacteriology & Parasitology, Universitat Autonoma de Barcelona
Authors: Cantero, G. (Ekstern), Correa-Fiz, F. (Ekstern), Ronco, T. (Intern), Strube, M. L. (Intern), Cerdà-Cuéllar, M. (Ekstern), Pedersen, K. (Intern)
Pages: 145-152
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Foodborne Pathogens and Disease
Volume: 15
Issue number: 3
ISSN (Print): 1535-3141
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.016 SJR 1.063 CiteScore 2.47
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.46 SJR 1.062 SNIP 1.08
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.064 SNIP 1.035 CiteScore 2.41
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.953 SNIP 1.051 CiteScore 2.16
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.184 SNIP 1.129 CiteScore 2.41
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.185 SNIP 1.144 CiteScore 2.55
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.118 SNIP 1.037 CiteScore 2.33
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Characterization of C. jejuni and C. coli broiler isolates by whole genome sequencing

Campylobacter is the most commonly reported cause of bacterial diarrhoeal disease in humans in the EU since 2005. The major source of infection is contaminated poultry meat with most broiler batches at slaughter colonized with Campylobacter. C. jejuni and C. coli are responsible for the isolates vast majority of infections, which may subsequently lead to serious neuropathologies such as Guillain-Barré syndrome. The aim of this study was to take advantage of whole genome sequencing (WGS) to in-depth characterize a subset of 16 C. jejuni and C. coli isolates from broilers from five farms.

General information
State: Published
Organisations: National Veterinary Institute, Bacteriology & Parasitology, Universitat Autonoma de Barcelona
Authors: Cantero, G. (Ekstern), Correa-Fiz, F. (Ekstern), Ronco, T. (Intern), Strube, M. L. (Intern), Cerdà-Cuéllar, M. (Ekstern), Pedersen, K. (Intern)
Publication date: 2017
Event: Poster session presented at 19th International Workshop on Campylobacter, Helicobacter and Related Organisms, Nantes, France.
Main Research Area: Technical/natural sciences
Electronic versions:
Poster_WGS_FINAL_CHRO2017.pdf
Source: PublicationPreSubmission
Source-ID: 135023239
Publication: Research - peer-review › Poster – Annual report year: 2017

Characterization of C. jejuni and C. coli broiler isolates by whole genome sequencing

General information
State: Published
Organisations: National Veterinary Institute, Bacteriology & Parasitology, CReSA - Centre for Animal Health Research, Centre de Recerca en Sanitat Animal
Authors: Guillermo, C. (Ekstern), Florencia, C. (Ekstern), Ronco, T. (Intern), Strube, M. L. (Intern), Cerdà-Cuéllar, M. (Ekstern), Pedersen, K. (Intern)
Pages: 299-299
Publication date: 2017

Host publication information
Title of host publication: 19th International Workshop on Campylobacter, Helicobacter and Related Organisms: CHRO 2017 - Abstract Book
Place of publication: Nantes, France
Main Research Area: Technical/natural sciences
Conference: 19th International Workshop on Campylobacter, Helicobacter and Related Organisms, Nantes, France, 10/09/2017 - 10/09/2017
Electronic versions:
Characterization of leukocytes in distinct human intestinal compartments

General information
State: Published
Organisations: National Veterinary Institute, Mucosal Immunology, Herlev and Gentofte Hospital
Number of pages: 2
Pages: 298-299
Publication date: 2017
Conference: 44th Annual Meeting of the Scandinavian Society of Immunology, Stockholm, Sweden, 17/10/2017 - 17/10/2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Scandinavian Journal of Immunology
Volume: 86
Issue number: 4
Article number: A-31498
ISSN (Print): 0300-9475
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.621 SJR 0.891 CiteScore 2.11
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.03 SJR 0.979 SNIP 0.644
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.933 SNIP 0.679 CiteScore 1.97
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.901 SNIP 0.665 CiteScore 1.91
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.875 SNIP 0.709 CiteScore 2.05
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.89 SNIP 0.742 CiteScore 2.16
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.865 SNIP 0.654 CiteScore 2.06
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.859 SNIP 0.621
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.973 SNIP 0.659
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Characterization of Salmonella spp. from wastewater used for food production in Morogoro, Tanzania

Wastewater use for crop irrigation and aquaculture is commonly practiced by communities situated close to wastewater treatment ponds. The objective of this study was to characterize Salmonella spp. and their antimicrobial susceptibility patterns among isolates from wastewater and Tilapia fish. A total of 123 Salmonella spp. isolates were isolated from 52 water and 21 fish intestinal samples. Genotyping of Salmonella spp. isolates was done by Pulsed-field Gel Electrophoresis (PFGE). Antimicrobial susceptibility testing was done by the minimal inhibitory concentration (MIC) technique. A total of 123 Salmonella spp. isolates represented 13 different serovars and 22 PFGE groups. Salmonella serovars showed resistance to 8 out of 14 antimicrobials; sulfamethaxazole (94%), streptomycin (61%), tetracycline (22%), ciprofloxacin and nalidixic acid (17%), trimethoprim (11%); gentamycin and chloramphenicol (6%). Salmonella Kentucky, S. Chandans, S. Durban and S. Kiambu showed multiple antimicrobial resistance to 7, 6 and 3 antimicrobials, respectively. This study has demonstrated that wastewater at the study sites is contaminated with Salmonella spp. which are resistant to common antimicrobials used for treatment of diseases in humans. Wastewater may, therefore, contaminate pristine surface water bodies and foodstuffs including fish and irrigated crops as well as food handlers.

General information
State: Published
Organisations: National Veterinary Institute, Bacteriology & Parasitology, Sokoine University of Agriculture, University of Copenhagen
Authors: Mhongole, O. J. (Ekstern), Mdegela, R. H. (Ekstern), Lughano J. M. Kusiluk (Ekstern), Forslund, A. (Intern), Dalsgaard, A. (Ekstern)
Number of pages: 7
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: World Journal of Microbiology and Biotechnology
Volume: 33
Issue number: 42
ISSN (Print): 0959-3993
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.81 SJR 0.604 CiteScore 2.14
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.99 SJR 0.621 SNIP 0.88
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.635 SNIP 0.941 CiteScore 1.83
During 2001 to 2016 a total of 203 bovines were submitted to the institute with clinical suspicion of having BSE. In two cases BSE was confirmed. The most common differential diagnosis was listeriosis, found in 54% of the cases. Listeriosis was characterized by multifocal, necrotizing, non-suppurative encephalitis confined to the brainstem region.

**CNS histopathology on 203 bovines with clinical suspicion of BSE in Denmark 2001 to 2016**

During 2001 to 2016 a total of 203 bovines were submitted to the institute with clinical suspicion of having BSE. In two cases BSE was confirmed. The most common differential diagnosis was listeriosis, found in 54% of the cases. Listeriosis was characterized by multifocal, necrotizing, non-suppurative encephalitis confined to the brainstem region.

**General information**

State: Published
Organisations: National Veterinary Institute, Pathology
Authors: Jensen, T. K. (Intern)
Publication date: 2017
Event:
Main Research Area: Technical/natural sciences
Electronic versions:
DTU_VET_2016_BSE_poster.pdf
Source: PublicationPreSubmission
Source-ID: 128736484
Publication: Research - peer-review › Poster – Annual report year: 2017
**Coccidia infections in Danish farmed mink**

Although Danish farmed mink are frequently infected with Coccidia, knowledge of factors affecting the infection is scarce. Thus, we studied age, geographical and season-related factors affecting coccidia prevalence. Unsporulated oocysts excretion was quantified microscopically (n=4142) every 7-14th day (April-October 2016) from bitches and cups on 30 farms (n=335 mink) from South- or North Jutland, or Zealand. Minimum once, 60.9% (n=204) mink excreted *Eimeria*, 56.7% (n=190) *Isospora* and 29.9% (n=70) excreted both coccidia. Positive mink were identified on all farms. *Eimeria* prevalence was higher on the Zealand farms (25.4±2.2%, P<0.0001) compared to South- and North Jutland farms (5.4±2.9%, 7.5±4.1%). *Isospora* prevalence was similar regardless of farm locality (12.2±3.5%, 9.2±7.1%).

Eimeria prevalence peaked in June-July (12.6%-24.9%), while *Isospora* prevalence peaked in July-August (12.1%-27.6%). More cups (19.5%) than bitches (4.6%) were *Isospora* positive, while *Eimeria* prevalence was similar for cups (15.7%) and bitches (10.5%). For cups, *Eimeria* prevalence peaked when cups were 7-11 weeks old and again when 18-24 weeks old. *Isospora* prevalence peaked in cups 13-15 weeks old. Three *Eimeria* types were characterized by size and wall thickness (unverified by PCR); A, B and C. Types B and C (40.9%, 39.8%) were more prevalent than A (19.3%). Bitches were primarily infected with type B (50.4%), while type C (48.0%) predominated in cups. Type B infections dominated in mink from Zealand (56.5±13.7%), while mink from Jutland were primarily infected with type C (55.6±28.6%; 81.9±19.4%).

Farmed mink showed high coccidia prevalence with seasonal- and age-related *Isospora* prevalence, and seasonal- and geographical-related *Eimeria* prevalence.

**General information**
- **State:** Published
- **Organisations:** National Veterinary Institute, Bacteriology & Parasitology, Diagnostic & Development, Pathology
- **Authors:** Petersen, H. H. (Intern), Chriél, M. (Intern), Hansen, M. S. (Intern)
- **Publication date:** 2017
- **Event:** Abstract from 26th International Conference of World Association for the Advancement of Veterinary Parasitology (WAAVP), Kuala Lumpur, Malaysia.
- **Main Research Area:** Technical/natural sciences
- **Electronic versions:** WAAVP_2017_Coccidiose_in_Danish_farmed_mink.pdf
- **Source:** PublicationPreSubmission
- **Source-ID:** 136854741
- **Publication:** Research - peer-review › Conference abstract for conference – Annual report year: 2017
Colonization of the bovine uterus by Candida kefyr

Background. While fungal infections of the bovine uterus are well-known diseases in pregnant cattle, very limited knowledge exists on the presence and significance of fungi in the uterus of non-pregnant cows. Presence of fungi in the uterine lumen of postpartum (pp) cows has been reported, but little attention has been paid to this as most studies of the bovine pp uterus have focused on bacteria. Case presentation. Microscopy of uterine lavage cytology slides of three cows from one herd revealed the presence of numerous yeast-like organisms, which were located either free in the fluid or within macrophages. Two of the cows were around 30 days pp, while the third was 7 months pp. None of the cows had been treated with antibiotics. Culturing of the flush samples was unsuccessful, but Sanger sequencing of DNA extracted from an endometrial biopsy of one of the cows revealed the presence of Candida kefyr (Kluyveromyces marxianus). Fluorescence in situ hybridization examination of endometrial tissue sections of two cows using probes targeting 18S rRNA of the K. marxianus group was performed and revealed the presence of yeast cells on the endometrium. Histology was performed and demonstrated hyphal and non-hyphal yeast-like organisms on the surface of endometrium and in the crypts. Tissue invasion was restricted to the superficial part of the epithelium and although endometrial inflammation was present, this was mild and considered as not being caused by the fungi. One of the cows became pregnant and delivered a normal calf at term, while the two others were not bred. Conclusions. Candida kefyr is commonly isolated from milk of cows with mastitis, but has not been reported in association with other diseases of cattle. The infection was present as a monoculture in all three cows, but the fungi had only colonized the uterine lumen and the endometrial surface. Only a mild non-suppurative endometrial inflammation was present, but within the uterine luminal content, many macrophages having phagocytized yeast cells were present. Re-examination of the cows did not reveal a persistent infection, so the infection probably resolved spontaneously.

General information
State: Published
Organisations: National Veterinary Institute, Bacteriology & Parasitology, Pathology, University of Copenhagen
Authors: Christensen Karstrup, C. (Ekstern), Aalbæk, B. (Ekstern), Schou, K. K. (Intern), Jensen, T. K. (Intern), Pedersen, H. G. (Ekstern), Agerholm, J. S. (Ekstern)
PUBLICATION DATE: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Acta Veterinaria Scandinavica (Online)
Volume: 59
Article number: 61
ISSN (Print): 0044-605X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.077 SJR 0.655 CiteScore 1.45
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.01 SJR 0.641 SNIP 0.826
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.644 SNIP 1.641 CiteScore 0.98
BFI (2014): BFI-level 1
Combining radiotherapy with immunotherapy: the past, the present and the future

The advent of immunotherapy is currently revolutionizing the field of oncology, where different drugs are used to stimulate different steps in a failing cancer immune response chain. This review gives a basic overview of the immune response against cancer, as well as the historical and current evidence on the interaction of radiotherapy with the immune system and the different forms of immunotherapy. Furthermore the review elaborates on the many open questions on how to exploit this interaction to the full extent in clinical practice.

General information
Comparison of antimicrobial resistance in E. coli isolated from rectal and floor samples in pens with diarrhoeic nursery pigs in Denmark

Introduction. The prudent use of antibiotics in veterinary medicine necessitates the selection of antibiotic compounds with narrow-spectrums targeted against the specific pathogens involved. The same pathotype of enterotoxigenic E. coli (ETEC) was recently found both in diarrhoeic pigs and in samples from the pen floor where the pigs were housed. The first objective of this study was to compare resistance profiles from ETEC isolates and Non-ETEC isolates. The second objective was to evaluate the agreement between resistance profiles of ETEC isolated from pen floor samples and from individual rectal samples from pigs. Across three Danish pig herds, faecal samples were collected from the floors of 31 pens that had a within-pen diarrhoea prevalence of >25%, and from rectal samples of 93 diarrhoeic nursery pigs from the same pens. A total of 380 E. coli isolates were analysed by PCR and classified as ETEC when genes for adhesin factors and enterotoxins were detected. Minimum inhibitory concentrations of 13 antimicrobial agents were determined by the broth micro dilution method. Isolates were classified as resistant based on clinical breakpoints. Results. Based on logistic regression models, the odds of Non-ETEC isolates (n = 291) being pan-susceptible were significantly higher compared to ETEC isolates (n = 89), (P < 0.001, OR = 20.22, CI95% = 6.35-64.35). The odds of ETEC isolates having multidrug resistance were significantly higher compared to Non-ETEC isolates (p < 0.001, OR: 7.21, CI95%: 2.87-18.10). The odds of an isolate being resistant were significantly higher in ETEC isolates compared to Non-ETEC isolates for ampicillin (p < 0.001), apramycin (p = 0.003), sulphamethoxazole (p < 0.001) and trimethoprim (p<0.001). No overlap of resistance patterns between the three study herds was observed in the sampled ETEC isolates. In addition, there was generally good or excellent agreement when comparing resistance profiles from isolates from the same pen (pen floor and pig samples), and perfect agreement (Kappa = 1.000, SE = 0.316) was observed for ampicillin, apramycin, gentamycin, sulphamethoxazole, tetracycline and trimethoprim. Conclusions. We found that ETEC isolates were more resistant than Non-ETEC isolates. Furthermore, this study indicates that resistance testing of ETEC isolates from pen floor samples can be used as a convenient sampling method for resistance testing and in the selection of clinically relevant antimicrobial agents in the treatment of diarrhoeic pigs. The herd-level variation of resistance in ETEC isolates emphasises the importance of performing antimicrobial susceptibility testing at farm level when selecting antimicrobial agents for the treatment of E. coli-related diarrhoea.

General information
State: Published
Organisations: National Veterinary Institute, Diagnostic & Development, University of Copenhagen, Pig Research Centre
Authors: Weber, N. R. (Ekstern), Nielsen, J. P. (Ekstern), Jorsal, S. E. L. (Intern), Haugegaard, S. (Intern), Denwood, M. (Ekstern), Pedersen, K. S. (Ekstern)
Pages: 42-49
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Preventive Veterinary Medicine
Volume: 147
ISSN (Print): 0167-5877
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 1.31 SJR 1.144 CiteScore 2.26
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.2 SJR 1.249 SNIP 1.361
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.282 SNIP 1.177 CiteScore 2.1
Antimicrobial use, Resistance, Pen floor samples, Diarrhoea, ETEC, Nursery pigs

Electronic versions:
BEFO_1_s2.0_S0167587717302490_main.pdf
1_s2.0_S0167587717302490_main.pdf

DOI:
10.1016/j.prevetmed.2017.08.007

Bibliographical note
This article is published open access under a Creative Commons license.
Publication: Research - peer-review › Journal article – Annual report year: 2017
Comparison of bacterial culture and qPCR testing of rectal and pen floor samples as diagnostic approaches to detect enterotoxigenic Escherichia coli in nursery pigs

Enterotoxigenic E. coli (ETEC) are a major cause of diarrhoea in weaned pigs. The objective of this study was to evaluate the agreement at pen level among three different diagnostic approaches for the detection of ETEC in groups of nursery pigs with diarrhoea. The diagnostic approaches used were: bacterial culturing of faecal samples from three pigs (per pen) with clinical diarrhoea and subsequent testing for virulence genes in E. coli isolates; bacterial culturing of pen floor samples and subsequent testing for virulence genes in E. coli isolates; qPCR testing of pen floor samples in order to determine the quantity of F18 and F4 genes. The study was carried out in three Danish pig herds and included 31 pens with a pen-level diarrhoea prevalence of > 25%, as well as samples from 93 diarrhoeic nursery pigs from these pens. All E. coli isolates were analysed by PCR and classified as ETEC when genes for one or more adhesin factors and one or more enterotoxins were detected. Results: A total of 208 E. coli colonies from pig samples and 172 E. coli colonies from pen floor samples were isolated. Haemolytic activity was detected on blood agar plates in 111 (29.2%) of the 380 colonies that were isolated. The only adhesin factor detected in this study was F18. When comparing bacterial culture or qPCR testing of pen floor samples with detection of ETEC-positive diarrhoeic pigs by culture, agreement was found in 26 (83.9%, Kappa = 0.665) and 23 (74.2%, Kappa = 0.488) of the pens, respectively. Agreement was observed between the detection of ETEC by bacterial culture and qPCR in the same pen floor sample in 26 (83.9%, Kappa = 0.679) pens. Conclusion: We observed an acceptable agreement for the detection of ETEC-positive diarrhoeic nursery pigs in pen samples for both bacterial culture of pen floor samples and qPCR. This study showed that both bacterial culture and qPCR testing of pen floor samples can be used as a diagnostic approach for detecting groups of ETEC-positive diarrhoeic nursery pigs.

General information
State: Published
Organisations: National Veterinary Institute, Virology, Diagnostic & Development, University of Copenhagen, Pig Research Centre
Authors: Weber, N. R. (Ekstern), Nielsen, J. P. (Ekstern), Hjulsager, C. K. (Intern), Jorsal, S. E. L. (Intern), Haugegaard, S. (Ekstern), Hansen, C. F. (Ekstern), Pedersen, K. S. (Ekstern)
Pages: 61-67
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Preventive Veterinary Medicine
Volume: 143
ISSN (Print): 0167-5877
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 1.31 SJR 1.144 CiteScore 2.26
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.2 SJR 1.249 SNIP 1.361
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.282 SNIP 1.177 CiteScore 2.1
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.27 SNIP 1.407 CiteScore 2.37
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.264 SNIP 1.529 CiteScore 2.49
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.265 SNIP 1.436 CiteScore 2.45
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.194 SNIP 1.295 CiteScore 2.24
ISI indexed (2011): ISI indexed yes
Computational algorithm for lifetime exposure to antimicrobials in pigs using register data – the LEA algorithm

Accurate and detailed data on antimicrobial exposure in pig production are essential when studying the association between antimicrobial exposure and antimicrobial resistance. Due to difficulties in obtaining primary data on antimicrobial exposure in a large number of farms, there is a need for a robust and valid method to estimate the exposure using register data. An approach that estimates the antimicrobial exposure in every rearing period during the lifetime of a pig using register data was developed into a computational algorithm. In this approach data from national registers on antimicrobial purchases, movements of pigs and farm demographics registered at farm level are used. The algorithm traces batches of pigs retrospectively from slaughter to the farm(s) that housed the pigs during their finisher, weaner, and piglet period. Subsequently, the algorithm estimates the antimicrobial exposure as the number of Animal Defined Daily Doses for treatment of one kg pig in each of the rearing periods. Thus, the antimicrobial purchase data at farm level are translated into antimicrobial exposure estimates at batch level. A batch of pigs is defined here as pigs sent to slaughter at the same day from the same farm. In this study we present, validate, and optimise a computational algorithm that calculate the lifetime exposure of antimicrobials for slaughter pigs. The algorithm was evaluated by comparing the computed estimates to data on antimicrobial usage from farm records in 15 farm units. We found a good positive correlation between the two estimates. The algorithm was run for Danish slaughter pigs sent to slaughter in January to March 2015 from farms with more than 200 finishers to estimate the proportion of farms that it was applicable for. In the final process, the algorithm was successfully run for batches of pigs originating from 3,026 farms with finisher units (77% of the initial population). This number can be increased if more accurate register data can be obtained. The algorithm provides a systematic and repeatable approach to estimating the antimicrobial exposure throughout the rearing period, independent of rearing site for...
finisher batches, as a lifetime exposure measurement.

**General information**
State: Published
Organisations: National Veterinary Institute, Epidemiology, National Food Institute, Research Group for Genomic Epidemiology
Authors: Birkegård, A. C. (Intern), Dalhoff Andersen, V. (Intern), Hisham Beshara Halasa, T. (Intern), Jensen, V. F. (Intern), Toft, N. (Intern), Vigre, H. (Intern)
Pages: 173-180
Publication date: 2017
Main Research Area: Technical/natural sciences

**Publication information**
Journal: Preventive Veterinary Medicine
Volume: 146
ISSN (Print): 0167-5877
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 1.31 SJR 1.144 CiteScore 2.26
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.2 SJR 1.249 SNIP 1.361
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.282 SNIP 1.177 CiteScore 2.1
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.27 SNIP 1.407 CiteScore 2.37
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.264 SNIP 1.529 CiteScore 2.49
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.265 SNIP 1.436 CiteScore 2.45
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.194 SNIP 1.295 CiteScore 2.24
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.156 SNIP 1.284
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.032 SNIP 1.338
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.056 SNIP 1.258
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.009 SNIP 1.353
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.06 SNIP 1.277
Web of Science (2006): Indexed yes
Condensed Tannins in the Gastrointestinal Tract of Cattle after Sainfoin (Onobrychis vicifolia) Intake and Their Possible Relationship with Anthelmintic Effects

Condensed tannins' (CTs) fate along the digestive tract of ruminants may account for the variable efficacy of CTs against gastrointestinal nematodes. We analyzed CTs in the digesta of cattle fed sainfoin. With the acetone-butanol-HCl assay, the total CTs concentrations in the digesta were close to those in the diets (6.3 and 1.5% of DM in experiments 1 and 2, respectively); thus, CTs remained potentially largely undegraded/unabsorbed. With the thiolysis assay, CTs concentration was much higher in the abomasum (2.3% of DM; expt 1) compared with the rumen and intestines, along with higher mean size and prodelphinidins percentage, corroborating CTs efficacy reported only against Ostertagia ostertagi in the abomasum. In expt 2, the dietary levels of CTs were probably too low to demonstrate anthelmintic effects in the rumen.

Overall, the level of CTs accessible to thiolysis is favored under the acidic conditions of the abomasum, which seems critical for anthelmintic activity.
Conserved elements within the genome of foot-and-mouth disease virus; their influence on viral replication

Foot-and-mouth disease (FMD) is caused by a highly contagious virus infection of cloven-hoofed farm animals with high financial importance for countries, such as Denmark, which rely on a significant trade in agricultural products. At present, FMD is exotic to the cloven hoofed livestock in Denmark. However, outbreaks of FMD have previously been detected in other parts of Europe (United Kingdom) during the last decade, thus an introduction of FMD remains a continuing threat to
Several conserved elements within the genome of the foot-and-mouth disease virus (FMDV) have been identified, e.g. the IRES. Such elements can be crucial for the efficient replication of the genomic RNA. A better understanding of the influence of these elements is required to identify currently unrecognized interactions within the viruses which may be important for the development of anti-viral agents. SHAPE analysis of the entire FMDV genome (Poulsen, 2015) has identified three conserved RNA structures within the coding regions for 2B, 3C and 3D (RNA-dependent RNA polymerase) which might have an important role in virus replication. The FMDV 2A peptide, another conserved element, is responsible for the primary "cleavage" at its own C-terminus (2A/2B junction). It is believed that this "cleavage" is achieved by a protease-independent event termed ribosomal skipping or StopGo, in which the 2A peptide prevents the ribosome from linking the next amino acid to the growing polypeptide. The nature of this "cleavage" has so far not been investigated in the context of the full-length FMDV RNA within cells. The focus of this PhD thesis has been to characterize these elements and their influence on the FMDV replication. In order to fulfill the aims of this thesis a series of studies were performed and the scientific work is presented as three manuscripts.

Manuscript 1 investigated the impact of 2A modifications within the conserved C-terminal $D(V/I)E(S/T)NPG\downarrow P$ motif on FMDV protein synthesis, polyprotein processing and virus viability. Certain amino acid substitutions (E14Q, S15I, S15F and N16H) that have been shown to severely (50-70%) reduce the cleavage activity at the 2A/2B junction compared to the wt, using in vitro assays, have been found to be tolerated within infectious FMDVs. In contrast, substitutions (N16A, P17A, G18A, P19A, and P19G) that inhibit cleavage by 89-100% in vitro, reverted to the wt sequence in the rescued viruses. The 2A substitutions impaired the replication of a FMDV replicon, however surprisingly the viable 2A mutant viruses did not exhibit an attenuation of virus growth in cell culture. Expression of cDNAs encoding a truncated FMDV polyprotein, without any viral proteases showed that certain amino acid substitutions at residues E14, S15, N16 and P19 resulted in partial "cleavage" indicating that these specific residues are not essential for co-translational "cleavage". This shows that the StopGo function at the 2A/2B junction is necessary for efficient virus replication. However, maximal cleavage activity does not appear to be essential for the viability of FMDV. Manuscript 2 sought to identify which codons at each position of the coding sequence for the conserved NPG↓P motif at the 2A/2B junction would produce viable progeny viruses. This was achieved using a reverse genetics system with highly degenerate primers with all possible codons present for each of the amino acids individually within the NPG↓P motif. This generated pools of modified plasmids for each codon position from which RNA transcripts were made which were subsequently introduced into cells in culture. The rescued viruses all encoded the NPG↓P motif, confirming the importance of this amino acid sequence. However, at passage two, these four residues were found to be encoded by all possible codons (14 in total) within the rescued pools. Subsequent passages in cell culture revealed a distinct codon bias. Remarkably, this bias matches the codon bias observed in naturally occurring FMDV strains. Interestingly, the codons selected are different for P17 and P19. Residue P17 is preferentially encoded by CCU while P19 is preferentially encoded by CCC. However, a single prolyl-tRNA species recognizes both of these two codons in cattle and pigs, which are the major hosts for FMDV, and suggests a role for the RNA sequence itself. Manuscript 3 examines the influence of three conserved RNA structures within the genome of FMDV on viral protein synthesis and virus viability. Poulsen, (2015) previously identified these RNA structures within the coding regions for the FMDV 2B, 3C and 3D proteins using SHAPE probing. Interestingly, the structures had significant lower synonymous substitution rates compared to the remainder of the genome. However, introduction of synonymous substitutions which disrupted the structures but did not alter the amino acid sequence were tolerated and were retained after three passages in cell culture. The same substitutions did not impair the replication of a FMDV replicon either. This shows that the identified structures located in the coding region of 2B, 3C and 3D are not required for FMDV replication in BHK.
using pigs for experimental purposes. In addition, the immunological toolbox of pigs has grown substantially in the last decade. This development led to a boost in the use of pigs as a preclinical model for various human infections including sexually transmitted diseases (STIs) like Chlamydia trachomatis. In the current review, we discuss the use of animal models for biomedical research on the major human STIs. We summarize results obtained in the most common animal models and focus on the contributions of the pig model towards the understanding of pathogenesis and the host immune response. In addition, we present the main features of the porcine model that are particularly relevant for the study of pathogens affecting human female and male genital tracts. We also inform on the technological advancements in the porcine toolbox to facilitate new discoveries in this biologically important animal model. There is a continued need for improvements in animal modeling for biomedical research inclusive STI research. With all its advantages and the highly improved toolbox, the porcine model can play a crucial role in STI research and open the door to new exciting discoveries.

**General information**

State: Accepted/In press
Organisations: National Veterinary Institute, Adaptive Immunology, North Carolina State University, LUNAM Université, University of Saskatchewan, Université Francois Rabelais, University of Copenhagen, Oniris
Authors: Käser, T. (Ekstern), Renois, F. (Ekstern), Wilson, H. L. (Ekstern), Cnudde, T. (Ekstern), Gerdts, V. (Ekstern), Dillon, J. R. (Ekstern), Jungersen, G. (Intern), Agerholm, J. S. (Ekstern), Meurens, F. (Ekstern)
Number of pages: 58
Publication date: 2017
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Infection, Genetics and Evolution
ISSN (Print): 1567-1348
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.031 SJR 1.278 CiteScore 2.67
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.77 SJR 1.334 SNIP 1.033
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.441 SNIP 1.079 CiteScore 2.85
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.391 SNIP 1.125 CiteScore 2.99
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.563 SNIP 1.178 CiteScore 3.26
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.22 SNIP 0.989 CiteScore 2.87
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.189 SNIP 1.185 CiteScore 3.11
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.33 SNIP 1.048
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.272 SNIP 1.104
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.099 SNIP 0.895
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.188 SNIP 1.102
Scopus rating (2006): SJR 1.228 SNIP 1.181
Scopus rating (2005): SJR 1.35 SNIP 1.208
DANMAP 2016 - Use of antimicrobial agents and occurrence of antimicrobial resistance in bacteria from food animals, food and humans in Denmark

General information
State: Published
Organisations: National Food Institute, Division of Risk Assessment and Nutrition , Research Group for Genomic Epidemiology, Research Group for Microbial Food Safety, National Veterinary Institute, Bacteriology & Parasitology, Statens Seruminstitute, State Serum Institute, Statens Serum Institut
Number of pages: 130
Publication date: 2017

Publication information
Publisher: Statens Serum Institut, National Veterinary Institute, Technical University of Denmark National Food Institute, Technical University of Denmark
Original language: English
Main Research Area: Technical/natural sciences
Electronic versions: DANMAP_2016_LOW_241017.pdf
Source: PublicationPreSubmission
Source-ID: 140074257
Publication: Commissioned › Report – Annual report year: 2017

Danske metoder kan hjælpe med at bremse alt fra ebola til fugleinfluenza

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology
Authors: Kirkeby, C. T. (Intern)
Number of pages: 7
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Videnskab.dk
Volume: oktober
ISSN (Print): 1903-301X
Original language: English
Electronic versions: Danske_metoder_kan_hj_lpe_med_at_bremse_alt_fra_ebola_til_fugleinfluenza_Videnskab.pdf
Publication: Communication › Journal article – Annual report year: 2017

De-bugging and maximizing plant cytochrome P450 production in Escherichia coli with C-terminal GFP fusions
Cytochromes P450 (CYP) are attractive enzyme targets in biotechnology as they catalyze stereospecific C-hydroxylations of complex core skeletons at positions that typically are difficult to access by chemical synthesis. Membrane bound CYPs
are involved in nearly all plant pathways leading to the formation of high-value compounds. In the present study, we systematically maximize the heterologous expression of six different plant-derived CYP genes in Escherichia coli, using a workflow based on C-terminal fusions to the green fluorescent protein. The six genes can be over-expressed in both K- and B-type E. coli strains using standard growth media. Furthermore, sequences encoding a small synthetic peptide and a small bacterial membrane anchor markedly enhance the expression of all six genes. For one of the CYPs, the length of the linker region between the predicted N-terminal transmembrane segment and the soluble domain is modified, in order to verify the importance of this region for enzymatic activity. The work describes how membrane bound CYPs are optimally produced in E. coli and thus adds this plant multi-membered key enzyme family to the toolbox for bacterial cell factory design.
Design, development and experimental trial of a tailored cytotoxic T-cell vaccine against Porcine Reproductive and Respiratory Syndrome Virus-2

Porcine reproductive and respiratory syndrome virus (PRRSV) is one of the most important threats against the global swine production industry. The virus infects alveolar macrophages that leads to respiratory distress, fever, pneumonia and gives way to secondary respiratory pathogens. Infection of sows in late gestation can lead to late term abortion, early farrowing and birth of litters mixed with living, stillborn and mummified fetuses. Two species of PRRSV exist that are closely related in evolution and disease: PRRSV-1 and PRRSV-2. PRRSV has a positive sense RNA genome of about 15 kb and exhibits a high mutation rate that has led to a high degree of diversity within each species. Highly pathogenic strains evolve occasionally with large impact on animal health and production economy. Since its discovery in the late 1980s, massive efforts have been put in the development of an effective vaccine. Inspite of this, the most effective commercial vaccines available are only partly capable of protecting against a heterologous challenge. Furthermore, these vaccines are based on modified live virus that at more than one occasion have mutated back to a virulent form and have thus promoted rather that prevented viral spread. PRRSV exhibits a wide range of immunoevasive mechanisms that manipulate multiple branches of the porcine immune system. However, evidence exist that a cell-mediated immune (CMI) response is capable of clearing the virus from the organism, although this response is somewhat delayed. In the present PhD thesis, I describe the development of an innovative vaccine for the induction of a cytotoxic T-lymphocyte response against PRRSV-2. A major part of the project outline was to design a vaccine that would protect beyond genetic drift, why focus has been on identifying and selecting conserved epitopes specific for swine leukocyte antigen class I (SLA-I).

Briefly, all naturally occurring 9- and 10-mer peptides derived from 104 highly curated PRRSV-2 whole genome sequences were analyzed for their predicted binding capacities against five SLA-I alleles. Two methods for epitope prediction was applied (NetMHCpan and Position Scanning Combinatorial peptide library). The outputs of the two methods were combined and the top 2% best candidates were analyzed using the PopCover algorithm, serving to prioritize the candidates according to conservation and SLA allele coverage. Based on this, 53 peptides were purchased for in vitro verification. This was done using the assays Peptide Affinity Assay and Scintillation Proximity Assay for the determination of peptide-SLA (pSLA) binding affinity and stability, respectively. From these analyses it was decided to proceed with three of the five SLAs in combination with a total of 33 peptides/epitopes. A Classical swine fever virus (CSFV)-based virus replicon particle (VRP) was selected as vaccine platform. This VRP has the same tropism as CSFV and can thus infect dendritic cells that are the major inducers of a CMI response. On basis of this template VRP, 10 vaccine VRPs were designed for the expression of an inserted polyepitope with subsequent degradation via an uncleavable ubiquitinating, thereby leading the epitopes into the MHC-I presentation pathway. One VRP was designed as a negative control and encoded an unrelated epitope, while the remaining nine encoded polyepitopes of different combinations of the 33 PRRSV-2 epitopes. Infectivity of the VRPs and the induced polyepitope expression and degradation was verified using flow cytometry. 718
pigs of matching SLA profiles were vaccinated three times over a 10-week period with the control VRP (N=7) or the PRRSV-VRPs (N=11). After this, all pigs were inoculated with a Danish PRRSV-2 field strain and were euthanized after an additional four weeks. Seroconversion for both VRP and PRRSV was confirmed for all pigs. The induction of a CMI response was monitored using interferon-γ (IFN-γ) enzyme-linked immunospot (ELISPOT) assay pre challenge, but did unfortunately not provide any useful data. The setup was improved and post challenge ELISPOT provided evidence of a VRP-induced CMI. Viral load was measured post challenge in serum, but did not indicate any effects of vaccination. Viral load in lungs did however indicate an effect that was significant in one part of the lungs. Conclusively, the present study provides proof-of-concept that a peptide-specific CMI can be induced by vaccination with VRPs encoding conserved epitopes, along with indications of a protective effect on viral load in lungs. However, several improvements must be made to the concept before it can be subjected to field trials.

General information
State: Published
Organisations: National Veterinary Institute, Virology, Adaptive Immunology, Department of Bio and Health Informatics, Genomic Epidemiology
Authors: Welner, S. (Intern), Larsen, L. E. (Intern), Jungersen, G. (Intern), Lund, O. (Intern)
Number of pages: 178
Publication date: 2017

Publication information
Place of publication: Frederiksberg C
Publisher: Technical University of Denmark (DTU)
Original language: English
Main Research Area: Technical/natural sciences
Electronic versions:
13_06003_46_PhD_thesis_final_Simon_Welner.pdf_2774928_1_1.pdf

Detection and molecular characterization of the mosquito-borne filarial nematode Setaria tundra in Danish roe deer (Capreolus capreolus)
Setaria tundra is a mosquito-borne filarial nematode of cervids in Europe. It has recently been associated with an emerging epidemic disease causing severe morbidity and mortality in reindeer and moose in Finland. Here, we present the first report of S. tundra in six roe deer (Capreolus capreolus) collected between October 2010 and March 2014 in Denmark. The deer originated from various localities across the country: the eastern part of the Jutland peninsular and four locations on the island Zealand. With the exception of one deer, with parasites residing in a transparent cyst just under the liver capsule, worms (ranging from 2 to >20/deer) were found free in the peritoneal cavity. The worms were identified as S. tundra by morphological examination and/or molecular typing of the mitochondrial 12S rRNA and cox1 genes, which showed 99.1-99.8% identity to previously published S. tundra isolates from Europe. Roe deer are generally considered as asymptomatic carriers and their numbers in Denmark have increased significantly in recent decades. In light of climatic changes which result in warmer, more humid weather in Scandinavia greater numbers of mosquitoes and, especially, improved conditions for development of parasite larvae in the mosquito vectors are expected, which may lead to increasing prevalence of S. tundra. Monitoring of this vector-borne parasite may thus be needed in order to enhance the knowledge of factors promoting its expansion and prevalence as well as predicting disease outbreaks. (C) 2017 The Authors. Published by Elsevier Ltd on behalf of Australian Society for Parasitology.

General information
State: Published
Organisations: National Veterinary Institute, Diagnostic & Development, Production Animal and Wildlife Health Research Unit, Norwegian Veterinary Institute
Authors: Enemark, H. L. (Intern), Oksanen, A. (Ekstern), Chriél, M. (Intern), Harslund, J. L. F. (Intern), Woolsey, I. D. (Ekstern), Al-Sabi, M. N. S. (Intern)
Pages: 16-21
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: International Journal for Parasitology-parasites and Wildlife
Volume: 6
Issue number: 1
ISSN (Print): 2213-2244
Detection and quantification of *Aeromonas salmonicida* in fish tissue by real-time PCR

Furunculosis, a septicaemic infection caused by the bacterium *Aeromonas salmonicida* subsp. *salmonicida*, currently causes problems in Danish seawater rainbow trout production. Detection has mainly been achieved by bacterial culture, but more rapid and sensitive methods are needed. A previously developed real-time PCR assay targeting the plasmid encoded *aopP* gene of *A. salmonicida* was, in parallel with culturing, used for the examination of five organs of 40 fish from Danish freshwater and seawater farms. Real-time PCR showed overall a higher frequency of positives than culturing (65% of positive fish by real-time PCR compared to 30% by a culture approach). Also, no real-time PCR-negative samples were found positive by culturing. *A. salmonicida* was detected by real-time PCR, though not by culturing, in freshwater fish showing no signs of furunculosis, indicating possible presence of carrier fish. In seawater fish examined after an outbreak and antibiotics treatment, real-time PCR showed the presence of the bacterium in all examined organs (1-482 genomic units mg⁻¹). With a limit of detection of 40 target copies (1-2 genomic units) per reaction, a high reproducibility and an excellent efficiency, the present real-time PCR assay provides a sensitive tool for the detection of *A. salmonicida*. 

General information

State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Technical University of Denmark, Aarhus University
Authors: Bartkova, S. (Intern), Kokotovic, B. (Ekstern), Skall, H. F. (Ekstern), Lorenzen, N. (Ekstern), Dalsgaard, I. (Intern)
Pages: 321-242
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information

Journal: Journal of Fish Diseases
Volume: 40
Issue number: 2
ISSN (Print): 0140-7775
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.82
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.12
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 1.71
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Determinants for Treatments in Relation to Udder Health in Danish Dairy Cattle Farms

Regular cow level registrations in the Danish Cattle Database include registrations about e.g. milk yield, SCC and calvings, but also about diseases and antibiotic treatments of cows. These data could potentially be a useful source of information for the development of herd-specific udder health management programs tailored to the farmer’s preference. With tailored programs farmers may be more motivated to adopt effective management programs that can also enhance a prudent use of antibiotics.

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, University of Copenhagen, Seges Knowledge Centre for Agriculture
Authors: Gussmann, M. K. (Intern), Græsbøll, K. (Intern), Kirkeby, C. T. (Intern), Saxmose Nielsen, S. (Ekstern), Toft, N. (Intern), Farre, M. (Ekstern), Hisham Beshara Halasa, T. (Intern)
Publication date: 2017
Event: Poster session presented at SVEPM annual meeting 2017, Inverness, United Kingdom.
Main Research Area: Technical/natural sciences
Electronic versions:
SVEPM_poster_maya_inclQR_v2.pdf
Source: PublicationPreSubmission
Source-ID: 140792556
Publication: Research › Poster – Annual report year: 2017
Determinants of antimicrobial treatment for udder health in Danish dairy cattle herds

Societal pressure to limit the use of antibiotics in livestock production systems, including dairy cattle systems, is consistently increasing. To motivate farmers to reduce antibiotic usage, it is important to understand the factors that determine whether a cow will be treated with antibiotics or not. If farmers' usual practices regarding antibiotic treatments are taken into account, they may be motivated to adopt control measures that can facilitate prudent use of antibiotics and are at the same time cost-effective. In this study, we analyzed database recordings of milk yield and somatic cell count from the routine milk recording scheme, clinical registrations of mastitis and PCR results, and cow factors such as days in milk and parity in relation to antibiotic treatments for 518 dairy herds in Denmark. Farm-wise logistic regressions were used to predict antimicrobial treatment based on these factors. The resulting regression coefficients of 422 herds were further analyzed by principal component analysis and clustering to determine the driving predictors for treatment in different groups of farms. The results showed that determinants that were most important for predicting antibiotic treatments vary from one farm to another. Health indicators such as PCR or somatic cell count were most indicative for treatment on some farms, whereas other groups seemed to depend more on production factors (milk yield) or later culling of the cows. This shows that farmers behave differently and differences can be identified in register data. This information can be considered when developing cost-effective herd-specific control measures of mastitis to promote prudent use of antibiotics in Danish dairy cattle farms.
Determinants of the VP1/2A junction cleavage by the 3C protease in foot-and-mouth disease virus infected cells

The foot-and-mouth disease virus (FMDV) capsid precursor, P1-2A, is cleaved by FMDV 3C protease to yield VP0, VP3, VP1 and 2A. Cleavage of the VP1/2A junction is the slowest. Serotype O FMDVs with uncleaved VP1-2A (having a K210E substitution in VP1; at position P2 in cleavage site) have been described previously and acquired a second site substitution within the VP1 coding region of serotype A viruses with a blocked VP1/2A cleavage site (containing K210E) has now been achieved. A collection of alternative amino acid substitutions were made at this site and the properties of the mutant viruses determined. Only the presence of a positively charged residue at position P2 in the cleavage site permitted efficient cleavage of the VP1/2A junction, consistent with analyses of diverse FMDV genome sequences. Interestingly, in contrast to the serotype O virus results, no second site mutations occurred within the VP1 coding region of serotype A viruses with the blocked VP1/2A cleavage site. However, some of these viruses acquired changes in the 2C protein that is involved in enterovirus morphogenesis. These results have implications for the testing of potential antiviral agents targeting the FMDV 3C protease.
Determining T-cell specificity to understand and treat disease

Adaptive immune responses and immunopathogeneses are based on the ability of T cells to respond to specific antigens. Consequently, understanding T-cell recognition patterns in health and disease involves studying the complexity and genetic heterogeneity of the antigen recognition pathway, which includes both T-cell receptors and the antigen-presentation machinery. In this Perspective, we overview the development and use of technologies for assessing T-cell recognition in a clinical context, and discuss how knowledge of T-cell recognition pathways can be critical before, during and after disease treatment. The ability to assess T-cell-mediated immunity in individual patients during disease progression might enable the identification of patient-specific biomarkers that predict therapeutic efficacy and response. Effective strategies for the complex analysis of T-cell specificity in clinical settings are highly desirable and could complement current approaches for the monitoring of therapy responses.

Dietary cinnamaldehyde enhances acquisition of specific antibodies following helminth infection in pigs

Dietary phytonutrients such as cinnamaldehyde (CA) may contribute to immune function during pathogen infections, and CA has been reported to have positive effects on gut health when used as feed additive for livestock. Here, we investigated whether CA could enhance antibody production and specific immune responses during infection with an enteric pathogen. We examined the effect of dietary CA on plasma antibody levels in parasite-naïve pigs, and subsequently acquisition of humoral immune responses during infection with the parasitic nematode Ascaris suum. Parasite-naïve pigs fed diets supplemented with CA had higher levels of total IgA and IgG in plasma, and A. suum-infected pigs fed CA had higher levels of parasite-specific IgM and IgA in plasma 14 days post-infection. Moreover, dietary CA increased expression of genes encoding the B-cell marker CD19, sodium/glucose co-transporter1 (SLC5A1) and glucose transporter 2 (SLC2A2) in the jejunal mucosa of A. suum-infected pigs. Dietary CA induced only limited changes in the composition of the prokaryotic gut microbiota of A. suum-infected pigs, and in vitro experiments showed that CA did not directly induce proliferation or increase secretion of IgG and IgA from lymphocytes. Our results demonstrate that dietary CA can significantly enhance acquisition of specific immune responses in pigs. The underlying mechanism remains obscure, but apparently does not derive simply from direct contact between CA and host lymphocytes and appears to be independent of the gut microbiota.
Different populations of CD11b+ dendritic cells drive Th2 responses in the small intestine and colon

T-helper 2 (Th2) cell responses defend against parasites. Although dendritic cells (DCs) are vital for the induction of T-cell responses, the DC subpopulations that induce Th2 cells in the intestine are unidentified. Here we show that intestinal Th2 responses against Trichuris muris worms and Schistosoma mansoni eggs do not develop in mice with IRF-4-deficient DCs (IRF-4−/− CD11c-cre). Adoptive transfer of conventional DCs, in particular CD11b-expressing DCs from the intestine, is sufficient to prime S. mansoni-specific Th2 responses. Surprisingly, transferred IRF-4-deficient DCs also effectively prime S. mansoni-specific Th2 responses. Egg antigens do not induce the expression of IRF-4-related genes. Instead, IRF-4−/− CD11c-cre mice have fewer CD11b+ migrating DCs and fewer DCs carrying parasite antigens to the lymph nodes. Furthermore, CD11b+ CD103− DCs induce Th2 responses in the small intestine, whereas CD11b+ CD103+ DCs perform this role in the colon, revealing a specific functional heterogeneity among intestinal DCs in inducing Th2 responses.

General information

State: Published
Organisations: National Veterinary Institute, Mucosal Immunology, University of Glasgow, Lund University, University of Manchester
Authors: Mayer, J. U. (Ekstern), Demiri, M. (Ekstern), Agace, W. W. (Intern), MacDonald, A. S. (Ekstern), Svensson Frej, M. (Intern), Milling, S. W. (Ekstern)
Publication date: 2017
Main Research Area: Technical/natural sciences
Direct PCR - A rapid method for multiplexed detection of different serotypes of Salmonella in enriched pork meat samples

Salmonellosis, an infectious disease caused by Salmonella spp., is one of the most common foodborne diseases. Isolation and identification of Salmonella by conventional bacterial culture method is time consuming. In response to the demand for rapid on line or at site detection of pathogens, in this study, we developed a multiplex Direct PCR method for rapid detection of different Salmonella serotypes directly from pork meat samples without any DNA purification steps. An inhibitor-resistant Phusion Pfu DNA polymerase was used to overcome PCR inhibition. Four pairs of primers including a pair of newly designed primers targeting Salmonella spp. at subtype level were incorporated in the multiplex Direct PCR. To maximize the efficiency of the Direct PCR, the ratio between sample and dilution buffer was optimized. The sensitivity and specificity of the multiplex Direct PCR were tested using naturally contaminated pork meat samples for detecting and subtyping of Salmonella spp. Conventional bacterial culture methods were used as reference to evaluate the performance of the multiplex Direct PCR. Relative accuracy, sensitivity and specificity of 98.8%; 97.6% and 100%, respectively, were achieved by the method. Application of the multiplex Direct PCR to detect Salmonella in pork meat at slaughter reduces the time of detection from 5 to 6 days by conventional bacterial culture and serotyping methods to 14 h (including 12 h enrichment time). Furthermore, the method poses a possibility of miniaturization and integration into a point-of-need Lab-on-a-chip system for rapid online pathogen detection.
Distinct DC subsets regulate adaptive Th1 and 2 responses during Trichuris muris infection

Low- and high-dose infections with the murine large intestinal nematode *Trichuris muris* are associated with induction of adaptive Th1 and Th2 responses, respectively, in mesenteric lymph nodes (MLN). Classical dendritic cells (cDC) accumulate in the large intestinal mucosa and MLN upon *T. muris* infection, yet their role in driving adaptive responses to infection remains largely unknown. We performed low- and high-dose *T. muris* infections of mice deficient in defined cDC subsets to investigate their role in induction of adaptive immune responses. Mice lacking IRF4-dependent cDC failed to clear a high-dose infection and displayed impaired Th2 responses. Conversely, mice lacking IRF8-dependent cDC cleared a low-dose infection and displayed an impaired Th1 response while increased production of Th2 cytokines. Finally, mice lacking both IRF4- and IRF8-dependent cDC were able to generate a Th2 response and clear a low-dose infection. Collectively, these results suggest that IRF4- and IRF8-dependent cDC act antagonistically during *T. muris* infection, and demonstrate that intestinal Th2 responses can be generated towards *T. muris* in the absence of IRF4-dependent cDC.
Distinct roles for the IIId2 sub-domain in pestivirus and picornavirus internal ribosome entry sites

Viral internal ribosomes entry site (IRES) elements coordinate the recruitment of the host translation machinery to direct the initiation of viral protein synthesis. Within hepatitis C virus (HCV)-like IRES elements, the sub-domain IIId(1) is crucial for recruiting the 40S ribosomal subunit. However, some HCV-like IRES elements possess an additional sub-domain, termed IIId2, whose function remains unclear. Herein, we show that IIId2 sub-domains from divergent viruses have different functions. The IIId2 sub-domain present in Seneca valley virus (SVV), a picornavirus, is dispensable for IRES activity, while the IIId2 sub-domains of two pestiviruses, classical swine fever virus (CSFV) and border disease virus (BDV), are required for 80S ribosomes assembly and IRES activity. Unlike in SVV, the deletion of IIId2 from the CSFV and BDV IRES elements impairs initiation of translation by inhibiting the assembly of 80S ribosomes. Consequently, this negatively affects the replication of CSFV and BDV. Finally, we show that the SVV IIId2 sub-domain is required for efficient viral RNA synthesis and growth of SVV, but not for IRES function. This study sheds light on the molecular evolution of viruses by clearly demonstrating that conserved RNA structures, within distantly related RNA viruses, have acquired different roles in the virus life cycles.

General information
State: Published
Organisations: Section for Virology, Molecular Evolution, National Veterinary Institute, Virology, University of Surrey, Université Paris Descartes
Number of pages: 13
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Nucleic Acids Research
Volume: 2017
Article number: gkx991
ISSN (Print): 0305-1048
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SJR 9.025 SNIP 3.028 CiteScore 10.84
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 9.28 SJR 7.883 SNIP 2.744
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 7.358 SNIP 2.631 CiteScore 9.48
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 6.64 SNIP 2.552 CiteScore 8.74
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 6.801 SNIP 2.284 CiteScore 8.46
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 6.329 SNIP 2.407 CiteScore 8.62
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 5.976 SNIP 2.19 CiteScore 7.86
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Distribution of CNS Species on Teat Skin and in Milk Samples from Dairy Cows in Automatic Milking Systems

Coagulase-negative staphylococci (CNS) frequently colonize teat skin and are one of the most common findings cultured from milk samples of cows with subclinical intramammary infections (IMI). Several species are related to IMI, but knowledge about the epidemiology of CNS species is limited. Cows in automatic milking systems (AMS) may have increased risk for teat colonization and IMI because more than 60 cows are milked several times daily with the same milking unit. The objectives of this study are (1) to investigate patterns of CNS species in milk samples and teat skin swabs in nine AMS herds and (2) to identify the predisposing cow level risk factors for specific CNS IMI and teat colonization. In each herd, 30-40 cows with somatic cell counts > 200,000 cells/ml in the previous milk recording are randomly selected. Cows treated for mastitis during the time between milk recording and sampling are excluded. Teat skin swabs and aseptic quarter foremilk samples are taken from all quarters of all selected cows. Teat skin swabs are collected using the modified wet-dry method. Briefly, sterile swabs are rotated 360° around the teat canal orifice, first a wet swab immersed in ¼ Ringer's solution, then a dry swab. Immediately after sampling, the tips of both swabs are transferred into one tube with 2 ml of ¼ Ringer's solution. Samples are transported on ice for culturing in the laboratory. After vortexing, 0.01 mL of each quarter milk sample and 0.1 mL of each quarter teat swab are streaked simultaneously on Staphylococcus selective medium (SA Select) and calf blood agar. Colonies from quarters suspect of having CNS in milk and/or teat skin samples (cut-off five CFU) are subjected for MALDI-TOF assay for species identification. Only isolates from the right hind and left front quarters are analyzed by MALDI-TOF assay in this study. To date, preliminary results of milk and teat skin samples from 130 quarters (65 cows) are available. CNS species were identified in 86 quarters out of the total number (130), representing 69 teat skin swabs and 17 milk samples. Out of the CNS positive quarters (n= 86), 12 quarters (11 teat skin swabs and one milk sample) were harboring more than one type of the CNS species. Staphylococcus epidermidis and Staphylococcus equorum were the most frequently isolated CNS species from milk samples (7/17) and (5/17), respectively. Staphylococcus equorum, Staphylococcus haemolyticus and Staphylococcus xylosus were the most frequently isolated CNS species from teat skin swabs (56/69), (9/69), and (6/69), respectively. Staphylococcus cohnii (n= 2), Staphylococcus saprophyticus (n= 1) and Staphylococcus hominis (n= 1) were identified only in teat skin swabs while Staphylococcus simulans (n= 1) was only identified in milk samples. Staphylococcus
chromogenes was detected in both milk (n = 2) and teat skin (n = 1) samples. Data collection will be finished in April 2017. The final results will give new insights into herd specific CNS species patterns and the microbial ecology and epidemiology of common CNS species from different habitats – teat skin and milk. We hope that our findings improve the udder health, milk quality and control of mastitis caused by different CNS species in dairy herds with AMS.

**General information**

State: Published
Organisations: National Veterinary Institute, Bacteriology & Parasitology, University of Copenhagen
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Publication date: 2017
Event: Abstract from 2nd Seminar on Coagulase Negative Staphylococci, Ghent, Belgium.
Main Research Area: Technical/natural sciences
Source: PublicationPreSubmission
Source-ID: 137169561
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2017

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Diversity and functions of intestinal mononuclear phagocytes

The intestinal lamina propria (LP) contains a diverse array of mononuclear phagocyte (MNP) subsets, including conventional dendritic cells (cDC), monocytes and tissue-resident macrophages (mφ) that collectively play an essential role in mucosal homeostasis, infection and inflammation. In the current review we discuss the function of intestinal cDC and monocyte-derived MNP, highlighting how these subsets play several non-redundant roles in the regulation of intestinal immune responses. While much remains to be learnt, recent findings also underline how the various populations of MNP adapt to deal with the challenges specific to their environment. Understanding these processes should help target individual subsets for 'fine tuning' immunological responses within the intestine, a process that maybe of relevance both for the treatment of inflammatory bowel disease (IBD) and for optimized vaccine design.

**General information**

State: Published
Organisations: National Veterinary Institute, Mucosal Immunology, Lund University, University of Glasgow
Authors: Joeris, T. (Intern), Müller-Luda, K. (Ekstern), Agace, W. W. (Intern), Mowat, A. M. (Ekstern)
Pages: 845-864
Publication date: 2017
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Mucosal Immunology
Volume: 10
Issue number: 4
ISSN (Print): 1933-0219
Ratings:
- Web of Science (2018): Indexed yes
- Scopus rating (2017): CiteScore 6.63 SJR 4.314 SNIP 1.518
- Web of Science (2017): Indexed Yes
- Scopus rating (2016): CiteScore 6.36 SJR 4.464 SNIP 1.525
- Web of Science (2016): Indexed yes
- Scopus rating (2015): SJR 4.401 SNIP 1.447 CiteScore 6.53
- Web of Science (2015): Indexed yes
- Scopus rating (2014): SJR 4.597 SNIP 1.686 CiteScore 6.82
- Scopus rating (2013): SJR 4.076 SNIP 1.623 CiteScore 6.75
- ISI indexed (2013): ISI indexed yes
- Web of Science (2013): Indexed yes
- Scopus rating (2012): SJR 3.999 SNIP 1.631 CiteScore 6.69
- ISI indexed (2012): ISI indexed yes
- Web of Science (2012): Indexed yes
- Scopus rating (2011): SJR 4.534 SNIP 1.452 CiteScore 6.66
- ISI indexed (2011): ISI indexed yes
- Scopus rating (2010): SJR 4.637 SNIP 1.49
- Scopus rating (2009): SJR 2.732 SNIP 0.861
Original language: English
DOIs:
10.1038/mi.2017.22
Dødelig Haemonchus infektion hos giraffer: Nyt fra VeterinaerInstituttet

Dolphin Morbillivirus in a Fin Whale (Balaenoptera physalus) in Denmark, 2016
We studied the etiology of encephalitis in a fin whale (Balaenoptera physalus) that stranded in 2016 on the coast of Denmark. Dolphin morbillivirus (DMV) was detected in the brain and other organs. Phylogenetics showed close relation to DMV isolated from a striped dolphin (Stenella coeruleoalba) from Spain in 2012.
Draft Genome Sequence of a Sequence Type 398 Methicillin-Resistant Staphylococcus aureus Isolate from a Danish Dairy Cow with Mastitis
Livestock-associated (LA) methicillin-resistant *Staphylococcus aureus* (MRSA) strains of sequence type 398 (ST398) colonize both humans and various livestock species. In 2016, an ST398 LA-MRSA isolate (Sa52) was collected from a Danish dairy cow with mastitis, and here, we report the draft genome sequence of strain Sa52.

**General information**
- State: Published
- Organisations: National Veterinary Institute, Bacteriology & Parasitology, Statens Serum Institut
- Authors: Ronco, T. (Intern), Stegger, M. (Ekstern), Pedersen, K. (Intern)
- Number of pages: 2
- Publication date: 2017
- Main Research Area: Technical/natural sciences

**Publication information**
- Journal: Genome Announcements
- Volume: 5
- Issue number: 23
- Article number: e00492-17
- ISSN (Print): 2169-8287
- Ratings:
  - BFI (2018): BFI-level 1
  - BFI (2017): BFI-level 1
  - Scopus rating (2017): SNIP 0.407 SJR 0.553 CiteScore 1.01
  - Scopus rating (2016): CiteScore 0.41 SJR 0.583 SNIP 0.469
- Web of Science (2016): Indexed yes
- Scopus rating (2015): SJR 0.591 SNIP 0.398
- Scopus rating (2014): SJR 0.539 SNIP 0.344
- ISI indexed (2013): ISI indexed no
- Original language: English
- Electronic versions:
  - Genome_Announc_.2017_Ronco_.pdf
- DOIs:
  - 10.1128/genomeA.00492-17

**Bibliographical note**
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**Source:** FindIt
**Source-ID:** 2371261171
**Publication:** Research - peer-review › Journal article – Annual report year: 2017

**Early BCG-Denmark and Neonatal Mortality Among Infants Weighing <2500 g: A Randomized Controlled Trial**

**Background.** BCG vaccine may reduce overall mortality by increasing resistance to nontuberculosis infections. In 2 randomized trials in Guinea-Bissau of early BCG-Denmark (Statens Serum Institut) given to low-weight (LW) neonates (<2500 g at inclusion) to reduce infant mortality rates, we observed a very beneficial effect in the neonatal period. We therefore conducted the present trial to test whether early BCG-Denmark reduces neonatal mortality by 45%. We also conducted a meta-analysis of the 3 BCG-Denmark trials. Methods. In 2008–2013, we randomized LW neonates to “early BCG-Denmark” (intervention group; n = 2083) or “control” (local policy for LW and no BCG-Denmark; n = 2089) at discharge from the maternity ward or at first contact with the health center. The infants were randomized (1:1) without blinding in blocks of 24. Data was analyzed in Cox hazards models providing mortality rate ratios (MRRs). We had prespecified an analysis censoring follow-up at oral poliovirus vaccine campaigns. Results. Early administration of BCG-Denmark was associated with a nonsignificant reduction in neonatal mortality rate (MRR, 0.70; 95% confidence interval [CI], .47–1.04) and a 34% reduction (0.66; .44–1.00) when censoring for oral poliovirus vaccine campaigns. There was no reduction in mortality rate for noninfectious diseases, but a 43% reduction in infectious disease mortality rate (MRR, 0.57; 95% CI, .35–.93). A meta-analysis of 3 BCG trials showed that early BCG-Denmark reduced mortality by 38% (MRR, 0.62; 95% CI, .46–.83) within the neonatal period and 16% (0.84; .71–1.00) by age 12 months. Conclusion Early administration of BCG-Denmark in LW infants is associated with major reductions in mortality rate. It is important that all LW infants receive early BCG in areas with high neonatal mortality rates. Clinical Trials Registration. NCT00625482.

**General information**
- State: Published
- Organisations: National Veterinary Institute, Adaptive Immunology, Statens Serum Institut, INDEPTH Network
- Authors: Biering-Sørensen, S. (Ekstern), Aaby, P. (Ekstern), Lund, N. (Ekstern), Monteiro, I. (Ekstern), Jensen, K. J. (Intern), Eriksen, H. B. (Ekstern), Schaltz-Buchholzer, F. (Ekstern), Pinstrup Jørgensen, A. S. (Ekstern), Rodrigues, A. (Ekstern), Fisker, A. B. (Ekstern), Benn, C. S. (Ekstern)
Bacille Calmette-Guérin, Neonatal mortality, Heterologous immunity, Nonspecific effects
E. coli infections in poultry - what do we know and where to go.

General information
State: Published
Organisations: National Veterinary Institute, Bacteriology & Parasitology, University of Copenhagen, Knowledge Centre for Agriculture
Authors: Olsen, R. H. (Ekstern), Thøfner, I. (Ekstern), Ronco, T. (Intern), Pedersen, K. (Intern), Pors, S. E. (Ekstern), Bisgaard, M. (Ekstern), Christensen, J. P. (Ekstern), Kabell, S. (Ekstern), Christensen, H. (Ekstern)
Number of pages: 30
Publication date: 2017

Publication information
Media of output: Powerpoint
Original language: English
Publisher: University of Copenhagen
Main Research Area: Technical/natural sciences
Electronic versions: Presentation_Skt._Petersborg.pdf
Source: PublicationPreSubmission
Source-ID: 130394863
Publication: Research › Sound/Visual production (digital) – Annual report year: 2017

Editorial: Foot-and-Mouth Disease in Swine
Foot-and-mouth disease (FMD) is one of the most devastating diseases of livestock. The disease is caused by infection with a picornavirus, generically referred as FMD virus (FMDV), which is considered one of the most infectious agents affecting animals. FMD status affects national and international movement and trade of animals and animal products, and food animal trade is expected to play an important role in poverty alleviation (Perez). Applied knowledge about FMD pathogenesis and epidemiology is important in the design and implementation of effective prevention and control programs, minimizing detrimental effects of FMD outbreaks. Decision tools have been developed by applying simulation models based on characteristics of FMD pathogenesis and epidemiology. These tools are meant to be used by risk managers and risk communicators to help prioritize control options during an FMD epidemic and making the evidence available for all stakeholders. Much of the literature on FMD has focused on the pathogenesis and epidemiology of the disease in cattle. However, FMD also affects other food animal species, most notably, swine. This research topic contributes to the gain and dissemination of important knowledge on the dynamics of one of the most devastating diseases of livestock when occurring in the pig, a susceptible species for which limited information is available in the peer-reviewed literature. The ultimate objective of these original articles and reviews was to contribute preventing and mitigating the impact of FMD in swine, thus, promoting health and economic development of non-affected as well as affected countries and regions. This research topic features nine studies supplementing the state-of-the-art of the knowledge on the pathogenesis and epidemiology of FMD in swine. Three papers focus on the analysis of experimental studies, which have been designed with the objective of gaining basic knowledge on the pathogenesis of the disease. Three other papers summarize the results of field studies and review fundamental features of FMD transmission and the effectiveness of FMD vaccination in swine. The last three papers describe the design and implementation of applied epidemiology approaches to prevent or mitigate the impact of FMD epidemics in disease-free regions.

General information
State: Published
Organisations: National Veterinary Institute, University of Minnesota
Authors: Perez, A. M. (Ekstern), Willeberg, P. W. (Intern)
Publication date: 2017
Main Research Area: Technical/natural sciences
Effect of an Early Dose of Measles Vaccine on Morbidity Between 18 Weeks and 9 Months of Age: A Randomized, Controlled Trial in Guinea-Bissau

Background: Children in Guinea-Bissau receive measles vaccine (MV) at 9 months of age, but studies have shown that an additional dose before 9 months of age might have beneficial nonspecific effects. Within a randomized trial designed to examine nonspecific effects of early MV receipt on mortality, we conducted a substudy to investigate the effect of early MV receipt on morbidity. Methods: Children were randomly assigned at a ratio of 2: 1 to receive 2 doses of MV at 18 weeks and age 9 months (intervention group) or 1 dose of MV at age 9 months, in accordance with current practice (control group). Children were visited weekly from enrollment to age 9 months; the mother reported morbidity, and the field assistants examined the children. Using Cox and binomial regression models, we compared the 2 randomization groups. Results: Among the 1592 children, early measles vaccination was not associated with a higher risk of the well-known
adverse events of fever, rash, and convulsions within the first 14 days. From 15 days after randomization to age 9 months, early measles vaccination was associated with reductions in maternally reported diarrhea (hazard ratio [HR], 0.89; 95% confidence interval [CI], 0.82–0.97), vomiting (HR, 0.86; 95% CI, 0.75–0.98), and fever (HR, 0.93; 95% CI, 0.87–1.00). Conclusion. Early MV receipt was associated with reduced general morbidity in the following months, supporting that early MV receipt may improve the general health of children.
Effect of oral booster vaccination of rainbow trout against Yersinia ruckeri depends on type of primary immunization

Vaccination of rainbow trout against Enteric Redmouth Disease (ERM) caused by Yersinia ruckeri can be successfully performed by administering vaccine (a bacterin consisting of formalin killed bacteria) by immersion, bath or injection. Booster immunization is known to increase the protection of fish already primed by one of these vaccination methods. Oral vaccination of trout (administering vaccine in feed) is an even more convenient way of presenting antigen to the fish but the effect of an oral booster has not previously been described in detail. The present work describes to what extent protection may be enhanced by oral boosting following priming with different administration methods. The study confirms that vaccination by 30 s dip into a bacterin (diluted 1:10) may confer a significant protection compared to non-vaccinated fish. The immunity may be optimized by booster immunization either provided as dip (most effective), bath (less effective) or orally (least effective). Oral immunization may be used as booster after dip but applied as a single oral application it induced merely a slight and statistically non-significant response. It is noteworthy that primary oral immunization followed by an oral booster vaccination showed a trend for an even weaker response. It should be investigated if continued exposure to a low antigen concentration - as performed by two oral immunizations - may induce tolerance to the pathogen and thereby leave the fish more vulnerable.

General information
State: Accepted/In press
Organisations: National Veterinary Institute, Bacteriology & Parasitology, University of Copenhagen
Authors: Jaafar, R. M. (Ekstern), Al-Jubury, A. (Ekstern), Dalsgaard, I. (Intern), MohammadKarami, A. (Ekstern), Kania, P. W. (Ekstern), Buchmann, K. (Ekstern)
Number of pages: 21
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Fish and Shellfish Immunology
ISSN (Print): 1050-4648
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.103 SJR 1.126 CiteScore 3.37
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.36 SJR 1.128 SNIP 1.142
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.265 SNIP 1.16 CiteScore 3.19
Web of Science (2015): Indexed yes
Effect of tetracycline dose and treatment-mode on selection of resistant coliform bacteria in nursery pigs

This study describes results of a randomized clinical trial investigating the effect of oxytetracycline treatment dose and mode of administration on selection of antibiotic resistant coliform bacteria in fecal samples from nursery pigs. Nursery pigs (pigs of 4-7 weeks of age) were treated with oxytetracycline against Lawsonia intracellularis induced diarrhea in five pig herds. Each group was randomly allocated to one of five treatment groups: oral flock treatment with (i) high (20 mg/kg), (ii) medium (10 mg/kg) and (iii) low (5 mg/kg) dosage, (iv) oral-pen-wise (small group) treatment (10 mg/kg), and (v) individual intramuscular injection treatment (10 mg/kg). All groups were treated once a day for five days. In all groups, treatment caused a rise in numbers and proportion of tetracycline resistant coliform bacteria right after treatment, followed by a significant drop by the time where pigs left the nursery unit. Counts and proportion of tetracycline-resistant coliforms did not vary significantly between treatment groups, except immediately after treatment, where the highest treatment dose
resulted in the highest number of resistant coliforms. A control group treated with tiamuline did not show significant changes in number or proportion of tetracycline resistant coliforms. Selection for tetracycline-resistant coliforms was significantly correlated to selection for ampicillin- and sulfonamide-resistant, but not to cefotaxime-resistant strains. In conclusion, difference in dose of oxytetracycline and the way the drug was applied did not cause significantly different selection of tetracycline resistant coliform bacteria, under the conditions tested.

**IMPORTANCE** Antimicrobial resistance is a global threat to human health. Treatment of livestock with antimicrobials has a direct impact on this problem, and there is a need to improve the ways that we use antimicrobial in livestock production. We hypothesized that antibiotic resistance development following treatment of diarrhea in nursery pigs could be reduced by either lowering the dose of oxytetracycline or by replacing the commonly used practice of flock treatment with individual or small group treatments, since this would reduce the number of pigs treated. However, the study showed no significant difference between treatment-groups with respect to the number or proportion of tetracycline resistant coliforms selected. The most important conclusion is that under the practical field conditions, there will be no added value in terms of lowering resistance development by exchanging flock treatment with individual or small group treatment of nursery pigs. The reason for lack of effect of single animal treatment is probably that such animals share the environment with treated animals and take up resistant bacteria from the environment.

**General information**

State: Published
Organisations: Department of Applied Mathematics and Computer Science, National Veterinary Institute, Dynamical Systems, Bacteriology & Parasitology, University of Copenhagen, Odder Veterinary Practice
Authors: Græsbøll, K. (Intern), Damborg, P. (Ekstern), Mellerup, A. (Intern), Fresno, A. H. (Ekstern), Larsen, I. (Ekstern), Holm, A. (Ekstern), Nielsen, J. P. (Ekstern), Christiansen, L. E. (Intern), Angen, Ø. (Intern), Ahmed, S. (Ekstern), Folkesson, A. (Intern), Olsen, J. E. (Ekstern)
Publication date: 2017
Main Research Area: Technical/natural sciences

**Publication information**
Journal: Applied and Environmental Microbiology
Volume: 83
Issue number: 12
Article number: e00538-17
ISSN (Print): 0099-2240
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 3.99
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 4.08
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.891 SNIP 1.308 CiteScore 4.14
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.857 SNIP 1.384 CiteScore 4.02
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.899 SNIP 1.414 CiteScore 4.25
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.975 SNIP 1.429 CiteScore 4.29
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.914 SNIP 1.455 CiteScore 4.12
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Efficiency of the Clinical Veterinary Diagnostic Practices and Drug Choices for Infectious Diseases in Livestock in Bangladesh

As in most low-income countries, adequate laboratory facilities are not available in Bangladesh to assist veterinarians in diagnosing animal diseases. We aimed to determine the efficiency of veterinary diagnoses for two common ruminant diseases in Bangladesh: Peste des petits ruminants (PPR) and foot-and-mouth disease (FMD). We conducted the study from May 2009 to August 2010 in three government veterinary hospitals where veterinarians collected samples from sick livestock and recorded the presumptive diagnosis on the basis of clinical presentations. Samples were tested for PPR and FMD using real-time RT-PCR. We estimated the sensitivity, specificity, positive predictive value (PPV) and negative predictive value (NPV) of the presumptive diagnoses when compared to laboratory tests. We tested 539 goats for PPR and 340 cattle and goats for FMD. Our results indicate that the veterinarians' presumptive diagnoses were different from laboratory findings for both PPR (P < 0.05) and FMD (P < 0.05). The overall sensitivity of the presumptive clinical diagnoses was 54% (95% CI: 47–61%) while specificity was 81% (95% CI: 78–84%) compared to real-time RT-PCR tests. The kappa value obtained in our validation process for PPR (kappa: 0.25) and FMD (kappa 0.36) indicated a poor performance of the presumptive diagnoses. Most of the animals (93%) were treated with antibiotics. Our findings indicate that veterinarians can detect animals not infected with FMD or PPR but miss the true cases. The clinical competency of these veterinarians needs to be improved and access to laboratory diagnostic facilities could help veterinarians to improve the diagnostics and outcomes. The rational use of antibiotics by veterinarians in animals must be ensured.

General information

State: Published
Organisations: National Veterinary Institute, Epidemiology, University of Florida, EcoHealth Alliance, Ministry of Fisheries and Livestock, International Centre for Diarrhoeal Disease Research
Publication information
Journal: Transboundary and Emerging Diseases
Volume: 64
Issue number: 4
ISSN (Print): 1865-1674
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.87 SJR 1.147 SNIP 1.488
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.16 SJR 1.046 SNIP 0.998
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.305 SNIP 1.249 CiteScore 2.29
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.048 SNIP 1.207 CiteScore 2.23
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.975 SNIP 1.123 CiteScore 2.33
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.847 SNIP 1.178 CiteScore 2.04
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.939 SNIP 1.124 CiteScore 2.05
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.761 SNIP 0.983
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.601 SNIP 0.907
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.363 SNIP 0.707
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 0.456 SNIP 0.777
Scopus rating (2006): SJR 0.425 SNIP 0.756
Scopus rating (2005): SJR 0.394 SNIP 0.852
Scopus rating (2004): SJR 0.296 SNIP 0.571
Scopus rating (2003): SJR 0.298 SNIP 0.68
Scopus rating (2002): SJR 0.268 SNIP 0.635
Scopus rating (2001): SJR 0.33 SNIP 0.658
Scopus rating (2000): SJR 0.339 SNIP 0.602
Scopus rating (1999): SJR 0.32 SNIP 0.4
Original language: English
Clinical diagnostic practices, Presumptive diagnoses, Sensitivity, Specificity, Bangladesh, PPR, FMD
DOIs:
10.1111/tbed.12502
**Emergence of a new rhabdovirus associated with mass mortalities in eelpout (Zoarces viviparous) in the Baltic Sea**

We report the first description of a new Rhabdoviridae tentatively named eelpout rhabdovirus (EpRV genus Perhabdovirus). This virus was associated with mass mortalities in eelpout (Zoarces viviparous, Linnaeus) along the Swedish Baltic Sea coast line in 2014. Diseased fish showed signs of central nervous system infection, and brain lesions were confirmed by histology. A cytopathogenic effect was observed in cell culture, but ELISAs for the epizootic piscine viral haemorrhagic septicaemia virus (VHSV), infectious pancreas necrosis virus (IPNV), infectious haematopoietic necrosis virus (IHNV) and spring viraemia of carp virus (SVCV) were negative. Further investigations by chloroform inactivation, indirect fluorescence antibody test and electron microscopy indicated the presence of a rhabdovirus. By deep sequencing of original tissue suspension and infected cell culture supernatant, the full viral genome was assembled and we confirmed the presence of a rhabdovirus with 59.5% nucleotide similarity to the closest relative Siniperca chuatsi rhabdovirus. The full-genome sequence of this new virus, eelpout rhabdovirus (EpRV), has been deposited in GenBank under accession number KR612230. An RT-PCR based on the L-gene sequence confirmed the presence of EpRV in sick/dead eelpout, but the virus was not found in control fish. Additional investigations to characterize the pathogenicity of EpRV are planned.
Emergence of carp edema virus (CEV) and its significance to European common carp and koi Cyprinus carpio

Carp edema virus disease (CEVD), also known as koi sleepy disease, is caused by a poxvirus associated with outbreaks of clinical disease in koi and common carp Cyprinus carpio. Originally characterised in Japan in the 1970s, international trade in koi has led to the spread of CEV, although the first recognised outbreak of the disease outside of Japan was not reported until 1996 in the USA. In Europe, the disease was first recognised in 2009 and, as detection and diagnosis have improved, more EU member states have reported CEV associated with disease outbreaks. Although the structure of the CEV genome is not yet elucidated, molecular epidemiology studies have suggested distinct geographical populations of CEV infecting both koi and common carp. Detection and identification of cases of CEVD in common carp were unreliable using the original PCR primers. New primers for conventional and quantitative PCR (qPCR) have been designed that improve detection, and their sequences are provided in this paper. The qPCR primers have successfully detected CEV DNA in archive material from investigations of unexplained carp mortalities conducted > 15 yr ago. Improvement in disease management and control is possible, and the principles of biosecurity, good health management and disease surveillance, applied to koi herpesvirus disease, can be equally applied to CEVD. However, further research studies are needed to fill the knowledge gaps in the disease pathogenesis and epidemiology that, currently, prevent an accurate assessment of the likely impact of CEVD on European koi and common carp aquaculture and on wild carp stocks.
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.95 SJR 0.675 CiteScore 1.7
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.95 SJR 0.893 SNIP 0.92
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.973 SNIP 0.943 CiteScore 1.96
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.895 SNIP 0.889 CiteScore 1.86
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.831 SNIP 0.928 CiteScore 1.77
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.919 SNIP 1.092 CiteScore 2.04
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.12 SNIP 1.164 CiteScore 2.29
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.918 SNIP 0.948
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.897 SNIP 0.985
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.865 SNIP 0.995
Scopus rating (2007): SJR 0.951 SNIP 1.05
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.875 SNIP 0.966
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.909 SNIP 1.033
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.992 SNIP 1.097
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.942 SNIP 1.188
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 1.199 SNIP 1.217
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 1.35 SNIP 1.193
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.16 SNIP 1.215
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 1.193 SNIP 1.139
Original language: English
Cyprinus carpio, CEVD, Koi sleepy disease, Poxvirus, PCR, Aquaculture
DOIs:
10.3354/dao03164
Source: FindIt
Source-ID: 2373189973
**Eosinophils are key regulators of perivascular adipose tissue and vascular functionality**

Obesity impairs the relaxant capacity of adipose tissue surrounding the vasculature (PVAT) and has been implicated in resultant obesity-related hypertension and impaired glucose intolerance. Resident immune cells are thought to regulate adipocyte activity. We investigated the role of eosinophils in mediating normal PVAT function. Healthy PVAT elicits an anti-contractile effect, which was lost in mice deficient in eosinophils, mimicking the obese phenotype, and was restored upon eosinophil reconstitution. Ex vivo studies demonstrated that the loss of PVAT function was due to reduced bioavailability of adiponectin and adipocyte-derived nitric oxide, which was restored after eosinophil reconstitution. Mechanistic studies demonstrated that adiponectin and nitric oxide are released after activation of adipocyte-expressed β3 adrenoceptors by catecholamines, and identified eosinophils as a novel source of these mediators. We conclude that adipose tissue eosinophils play a key role in the regulation of normal PVAT anti-contractile function.
Epidemiological and economic consequences of purchasing livestock infected with Mycobacterium avium subsp. paratuberculosis

Paratuberculosis (PTB) is a chronic disease which may lead to reduced milk yield, lower animal welfare and death in cattle. The causative agent is Mycobacterium avium subsp. paratuberculosis (MAP). The economic consequences are particularly important incentives in the control and eradication of the infection. One strategy to control PTB in a herd is to purchase animals from farms with a low risk of MAP infection. We wanted to investigate the epidemiological and economic consequences of buying livestock from different supplier farms of low, medium or high risk, as well as farms with unknown status. We also wanted to estimate the probability of spontaneous fadeout if the farmer of an initially MAP-free herd bought a specified number of infected animals in a single year, or continually bought infected animals. This was achieved through simulation modeling, and the effects of consistently introducing one, five or ten infected animals annually into an initially infection-free herd was also modeled. Our findings show that once infected, a farm can relatively safely purchase animals from other low and medium-risk farms without experiencing an increase in the prevalence, highlighting the importance of certification programmes. Furthermore, farms free of MAP are highly susceptible and cannot purchase more than a small number of animals per year without having a high risk of being infected. The probability of spontaneous fadeout after 10 years was 82% when introducing a single infected animal into an initially MAP-free herd. When purchasing ten infected animals, this probability was 46%. The continual purchase of infected animals resulted in very low probabilities of spontaneous fadeout. We demonstrated that MAP-free farms can purchase a small number of animals, preferably from certified farms, each year and still remain free of MAP. Already infected farms have little risk of increasing the prevalence on a farm when purchasing animals from other farms.

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, Technical University of Denmark, University of Copenhagen
Epidemiology of Danish Aeromonas salmonicida subsp. salmonicida in Fish Farms Using Whole Genome Sequencing

Furunculosis, a serious infection caused by the bacterium Aeromonas salmonicida subsp. salmonicida is common in sea-reared rainbow trout production in Denmark. Developing an effective control strategy requires knowledge of the epidemiology, as well as the genomic and virulent variability of the Danish A. salmonicida subsp. salmonicida isolates. To obtain this, the genomes of 101 A. salmonicida subsp. salmonicida, including 99 Danish isolates, one Scottish strain and the type strain NCIMB 1102, were sequenced using the Illumina HiSeq platform. Isolates were de novo assembled, examined for presence of plasmids, virulence and iron acquisition proteins, genomic islands, and antibiotic resistance genes. Single Nucleotide Polymorphisms were aligned and subjected to Bayesian temporal phylogenetic and maximum likelihood tree reconstruction using the published genome of A. salmonicida subsp. salmonicida A449 as reference. Bayesian temporal phylogenetic reconstruction suggests that four major introductions of A. salmonicida subsp. salmonicida into Denmark have occurred. The introductions correlate with the freshwater and subsequent seawater expansion of rainbow trout production. Initial transmission of the bacterium could have been from seawater to freshwater or vice versa, and most minor clades include a mixture of strains from different fresh- and seawater farms. Genomic variation of A. salmonicida subsp. salmonicida mostly appeared to be associated with their plasmids and plasmid encoded virulence factors. Nine A. salmonicida subsp. salmonicida isolates harbored worldwide known antibiotic resistance genes against several antibiotics and there is an indication that 33% of the isolates contained the genomic island AsaGEI1b. These findings not only support the usefulness of whole genome sequencing for genetic studies of homogeneous bacteria in general, but provide novel information about the Danish A. salmonicida subsp. salmonicida population, with implications for vaccine development in efforts to better protect Danish rainbow trout in the future.

General information
State: Published
Organisations: National Veterinary Institute, National Food Institute, Research Group for Genomic Epidemiology, Bacteriology & Parasitology
Authors: Bartkova, S. (Intern), Leekitcharoenphon, P. (Intern), Aarestrup, F. M. (Intern), Dalsgaard, I. (Intern)
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Frontiers in Microbiology
Volume: 8
Article number: 2411
ISSN (Print): 1664-302X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.19 SJR 1.699 SNIP 1.174
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.16 SJR 1.759 SNIP 1.161
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.869 SNIP 1.193 CiteScore 4.15
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.879 SNIP 1.148 CiteScore 3.76
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.776 SNIP 0.949 CiteScore 3.56
ISI indexed (2013): ISI indexed no
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.46 SNIP 0.722 CiteScore 2.78
ISI indexed (2012): ISI indexed no
Scopus rating (2011): SJR 0.642 SNIP 0.192
Web of Science (2011): Indexed yes
Original language: English
Aeromonas salmonicida subsp. salmonicida, Furunculosis, Rainbow trout, Whole genome sequencing, SNP analysis, BEAST, Virulence factors
Electronic versions:
Epigenetic priming restores the HLA class-I antigen processing machinery expression in Merkel cell carcinoma

Merkel cell carcinoma (MCC) is a rare and aggressive, yet highly immunogenic skin cancer. The latter is due to its viral or UV-associated carcinogenesis. For tumor progression MCC has to escape the host's immuno-surveillance, e.g. by loss of HLA class-I expression. Indeed, a reduced HLA class-I expression was observed in MCC tumor tissues and MCC cell lines. This reduced HLA class-I surface expression is caused by an impaired expression of key components of the antigen processing machinery (APM), including LMP2 and LMP7 as well as TAP1 and TAP2. Notably, experimental provisions of HLA class-I binding peptides restored HLA class-I surface expression on MCC cells. Silencing of the HLA class-I APM is due to histone deacetylation as inhibition of histone deacetylases (HDACs) not only induced acetylation of histones in the respective promoter regions but also re-expression of APM components. Thus, HDAC inhibition restored HLA class-I surface expression in vitro and in a mouse xenotransplantation model. In contrast to re-induction of HLA class-I by interferons, HDAC inhibitors did not interfere with the expression of immuno-dominant viral proteins. In summary, restoration of HLA class-I expression on MCC cells by epigenetic priming is an attractive approach to enhance therapies boosting adaptive immune responses.
Estimation of the transmission dynamics of African swine fever virus within a swine house

The spread of African swine fever virus (ASFV) threatens to reach further parts of Europe. In countries with a large swine production, an outbreak of ASF may result in devastating economic consequences for the swine industry. Simulation models can assist decision makers setting up contingency plans. This creates a need for estimation of parameters. This study presents a new analysis of a previously published study. A full likelihood framework is presented including the impact of model assumptions on the estimated transmission parameters. As animals were only tested every other day, an interpretation was introduced to cover the weighted infectiousness on unobserved days for the individual animals (WIU). Based on our model and the set of assumptions, the within- and between-pen transmission parameters were estimated to $\beta_w = 1.05$ (95% CI 0.62-1.72), $\beta_b = 0.46$ (95% CI 0.17-1.00), respectively, and the WIU = 1.00 (95% CI 0-1). Furthermore, we simulated the spread of ASFV within a pig house using a modified SEIR-model to establish the time from infection of one animal until ASFV is detected in the herd. Based on a chosen detection limit of 2.55% equivalent to 10 dead pigs out of 360, the disease would be detected 13-19 days after introduction.
The hemagglutination inhibition (HI) test is the current gold standard for detecting antibodies to avian influenza virus (AIV). Enzyme-linked immunosorbent assays (ELISAs) have been explored for use in poultry and certain wild bird species because of high efficiency and lower cost. This study compared a commercial ELISA for detection of AIV subtype H5 antibodies with HI test of 572 serum samples from zoo birds. There was no significant difference between the results of the two tests when statistically compared by a McNemar $\chi^2$ test ($P = 0.86$) and assessment of $\kappa$ ($\kappa = 0.87$). With a specificity of 94.2% (95% confidence interval [CI], 0.92-0.97), a sensitivity of 93.9% (95% CI, 0.91-0.97), and an excellent correlation between the two tests, this ELISA can be recommended as an alternative to the HI test for preliminary screening of zoo bird sera for antibodies to AIV subtype H5.

General information

State: Published
Organisations: National Veterinary Institute, Virology, Diagnostic & Development, Aalborg University, Copenhagen Zoo
Authors: Jensen, T. H. (Intern), Andersen, J. H. (Ekstern), Hjulsager, C. K. (Intern), Chriél, M. (Intern), Bertelsen, M. F. (Ekstern)
Avian influenza, ELISA, H5, Hemagglutination inhibition test, Zoo birds

DOIs:
10.1638/2016-0220.1

Source: Scopus
Source-ID: 85029722141

Publication: Research - peer-review › Journal article – Annual report year: 2017
Evaluation of Strategies to Control a Potential Outbreak of Foot-and-Mouth Disease in Sweden

To minimize the potential consequences of an introduction of foot-and-mouth disease (FMD) in Europe, European Union (EU) member states are required to present a contingency plan. This study used a simulation model to study potential outbreak scenarios in Sweden and evaluate the best control strategies. The model was informed by the Swedish livestock structure using herd information from cattle, pig, and small ruminant holdings in the country. The contact structure was based on animal movement data and studies investigating the movements between farms of veterinarians, service trucks, and other farm visitors. All scenarios of outbreak control included depopulation of detected herds, 3 km protection and 10 km surveillance zones, movement tracing, and 3 days national standstill. The effect of availability of surveillance resources, i.e., number of field veterinarians per day, and timeliness of enforcement of interventions, was assessed. With the estimated currently available resources, an FMD outbreak in Sweden is expected to be controlled (i.e., last infected herd detected) within 3 weeks of detection in any evaluated scenario. The density of farms in the area where the epidemic started would have little impact on the time to control the outbreak, but spread in high density areas would require more surveillance resources, compared to areas of lower farm density. The use of vaccination did not result in a reduction in the expected number of infected herds. Preemptive depopulation was able to reduce the number of infected herds in extreme scenarios designed to test a combination of worst-case conditions of virus introduction and spread, but at the cost of doubling the number of herds culled. This likely resulted from a combination of the small outbreaks predicted by the spread model, and the high efficacy of the basic control measures evaluated, under the conditions of the Swedish livestock industry, and considering the assumed control resources available. The results indicate that the duration and extent of FMD outbreaks could be kept limited in Sweden using the EU standard control strategy and a 3 days national standstill.

Evaluation of the efficacy of an autogenous Escherichia coli vaccine in broiler breeders

In poultry production Escherichia coli autogenous vaccines are often used. However, the efficacy of autogenous E. coli vaccinations has not been evaluated experimentally in chickens after start of lay. The aim of the present study was to evaluate the protective effect of an autogenous E. coli vaccine in broiler breeders. Three groups of 28 weeks old broiler breeders (unvaccinated, vaccinated once and twice, respectively) were challenged with a homologous E. coli strain (same strain as included in the vaccine) or a heterologous challenge strain in an experimental ascending model. The clinical outcome was most pronounced in the unvaccinated group; however, the vast majority of chickens in the vaccinated groups had severe pathological manifestations similar to findings in the unvaccinated group after challenge with a homologous as well as a heterologous E. coli strain. Although significant titer rises in IgY antibodies were observed in the twice vaccinated group, antibodies did not confer significant protection in terms of pathological impact. Neither could transfer of maternal derived antibodies to offspring be demonstrated. In conclusion, with the use of the present model for ascending infection, significant protection of an autogenous E. coli vaccine against neither a homologous nor a heterologous E. coli challenge could not be documented.
Evolutionary analysis of whole-genome sequences confirms inter-farm transmission of Aleutian mink disease virus

Aleutian mink disease virus (AMDV) is a frequently encountered pathogen associated with mink farming. Previous phylogenetic analyses of AMDV have been based on shorter and more conserved parts of the genome, e.g. the partial NS1 gene. Such fragments are suitable for detection but are less useful for elucidating transmission pathways while sequencing entire viral genomes provides additional informative sites and often results in better-resolved phylogenies. We explore how whole-genome sequencing can benefit investigations of AMDV transmission by reconstructing the relationships between AMDV field samples from a Danish outbreak. We show that whole-genome phylogenies are much better resolved than those based on the partial NS1 gene sequences extracted from the same alignment. Well-resolved phylogenies contain more information about the underlying transmission trees and are useful for understanding the spread of a pathogen. In the main case investigated here, the transmission path suggested by the tree structure was supported by epidemiological data. The use of molecular clock models further improved tree resolution and provided time estimates for the viral ancestors consistent with the proposed direction of spread. It was however impossible to infer transmission pathways from the partial NS1 gene tree, since all samples from the case farms branched out from a single internal node. A sliding window analysis showed that there were no shorter genomic regions providing the same phylogenetic resolution as the entire genome. Altogether, these results suggest that phylogenetic analyses based on whole-genome sequencing taking into account sampling dates and epidemiological data is a promising set of tools for clarifying AMDV transmission.
Evolution of MHC-based technologies used for detection of antigen-responsive T cells

T cell-mediated recognition of peptide-major histocompatibility complex (pMHC) class I and II molecules is crucial for the control of intracellular pathogens and cancer, as well as for stimulation and maintenance of efficient cytotoxic responses. Such interactions may also play a role in the development of autoimmune diseases. Novel insights into this mechanism are crucial to understanding disease development and establishing new treatment strategies. MHC multimers have been used for detection of antigen-responsive T cells since the first report by Altman et al. showed that tetramerization of pMHC class I molecules provided sufficient stability to T cell receptor (TCR)-pMHC interactions, allowing detection of MHC multimer-binding T cells using flow cytometry. Since this breakthrough the scientific community has aimed for expanding the capacity of MHC multimer-based detection technologies to facilitate large-scale epitope discovery and immune monitoring in limited biological material. Screening of T cell specificity using large libraries of pMHC molecules is suitable for analyses of T cell recognition potentially at genome-wide levels rather than analyses restricted to a selection of model
antigens. Such strategies provide novel insights into the immune specificities involved in disease development and response to immunotherapy, and extend fundamental knowledge related to T cell recognition patterns and cross-recognition by TCRs. MHC multimer-based technologies have now evolved from detection of 1-2 different T cell specificities per cell sample, to include more than 1000 evaluable pMHC molecules using novel technologies. Here, we provide an overview of MHC multimer-based detection technologies developed over two decades, focusing primarily on MHC class I interactions.
Experimental Infection of Young Pigs with an Early European Strain of Porcine Epidemic Diarrhoea Virus and a Recent US Strain

Outbreaks of porcine epidemic diarrhoea (PED) were reported across Europe during the 1980s and 1990s, but only sporadic outbreaks occurred in recent years. PEDV spread for the first time into the USA in 2013 and has caused severe economic losses. Retrospectively, it was found that two different strains of PEDV have been introduced into the United States, both are closely related to strains circulating in China where a new wave of the disease occurred from 2010 onwards. Since autumn 2014, new outbreaks of PEDV have occurred in Europe. In this study, weaned piglets were inoculated with an early European isolate (Br1/87) or faecal/intestinal suspensions derived from pigs infected with a recent European strain of PEDV (from Germany) or a US strain of PEDV. No evidence for infection resulted from inoculation of pigs with the German sample that contained high levels of PEDV RNA; there were no clinical signs, excretion of viral RNA or anti-PEDV antibody production. In contrast, all the pigs in the other two groups showed evidence of infection. Mild clinical signs of disease, mainly diarrhoea, occurred in piglets inoculated with the Br1/87 and US PEDV strains. PEDV RNA was detected throughout the intestine in euthanized animals at 4 days post-inoculation. In addition, within these animals, low levels of viral RNA were detected in lungs and livers with higher levels in spleens. Serocconversion against PEDV occurred in all surviving infected animals within 10 days. PEDV RNA excretion occurred for at least 2 weeks. The US PEDV RNA was detected at low levels in serum samples on multiple days. It is apparent that current diagnostic systems can detect infection by the different virus strains.

General information
State: Published
Organisations: National Veterinary Institute, Virology
Authors: Lohse, L. (Intern), Krog, J. S. (Intern), Strandbygaard, B. (Intern), Rasmussen, T. B. (Intern), Kjær, J. (Intern), Belsham, G. (Intern), Bøtner, A. (Intern)
Pages: 1380-1386
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Transboundary and Emerging Diseases
Volume: 64
Issue number: 5
ISSN (Print): 1865-1674
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.87 SJR 1.147 SNIP 1.488
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.16 SJR 1.046 SNIP 0.998
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.305 SNIP 1.249 CiteScore 2.29
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.048 SNIP 1.207 CiteScore 2.23
Experimental Pseudomonas aeruginosa mediated rhino sinusitis in mink

The nasal and sinus cavities in children may serve as reservoirs for microorganisms that cause recurrent and chronic lung infections. This study evaluates whether the mink can be used as an animal model for studying Pseudomonas aeruginosa mediated rhino-sinusitis since there is no suitable traditional animal model for this disease. Nasal tissue samples from infected and control mink were fixed in formalin, demineralized, and embedded in paraffin. A histological examination of sections from the infected animals revealed disintegration of the respiratory epithelium lining the nasal turbinate and swelling and edema of the submucosa. The expression of mucins and sialylated glycan was examined using immunohistochemistry. MUC1, MUC2 and MUC5AC were upregulated in the inoculated animals as a much stronger staining was present in the respiratory epithelium in the infected animals compared to the controls. The goblet cells in the nasal epithelium from the infected mink showed high affinity to the Maackia amurensis lectin and anti-asialo GM1 indicating a high concentration of α2-3 sialic acid respectively βGalNAc1-4Galβ containing glycans in these mucin producing cells. The nasal cavity in the infected mink shows features of carbohydrate expression comparable to what has been described in the respiratory system after Pseudomonas aeruginosa infection in humans. It is suggested that the mink is suitable for studying Pseudomonas aeruginosa mediated rhino-sinusitis.
Experimental Vaccine Against Mink Astrovirus Infection Reduces the Incidence of Brain Lesions

General information
State: Published
Organisations: National Veterinary Institute, Pathology, Diagnostic & Development
Authors: Hansen, M. S. (Intern), Baule, C. (Ekstern), Ullman, K. (Ekstern), Jensen, T. H. (Ekstern), Larsen, G. (Ekstern), Chriél, M. (Intern)
Pages: 113-113
Publication date: 2017
Farm-level risk factors for Fasciola hepatica infection in Danish dairy cattle as evaluated by two diagnostic methods

The prevalence of bovine fasciolosis in Denmark is increasing but appropriate guidelines for control are currently lacking. In order to help develop a control strategy for liver fluke, a risk factor study of farm management factors was conducted and the utility of bulk tank milk (BTM ELISA) as a tool for diagnosis in Danish dairy cattle farms was assessed. This case-control study aimed to identify farm-level risk factors for fasciolosis in Danish dairy farms (> 50 animals slaughtered in 2013) using two diagnostic methods: recordings of liver condemnation at slaughter, and farm-level Fasciola hepatica antibody levels in BTM. A case farm was defined as having a minimum of 3 incidents of liver condemnation due to liver fluke at slaughter (in any age group) during 2013, and control farms were located within 10 km of at least one case farm and had no history of liver condemnation due to liver fluke during 2011-2013. The selected farmers were interviewed over telephone about grazing and control practices, and BTM from these farms was collected and analysed by ELISA in 2014. The final complete dataset consisting of 131 case and 63 control farms was analysed using logistic regression. Heifers grazing on wet pastures, dry cows grazing on wet pastures, herd size, breed and concurrent beef cattle production were identified as risk factors associated with being classified as a case farm. With the categorised BTM ELISA result as the response variable, heifers grazing on wet pastures, dry cows grazing on wet pastures, and purchase of cows were identified as risk factors. Within the case and control groups, 74.8 and 12.7% of farms were positive for fasciolosis on BTM ELISA, respectively. The differences are likely to be related to the detection limit of the farm-level prevalence by the BTM ELISA test, time span between slaughter data and BTM, and the relatively low sensitivity of liver inspection at slaughter.

Control of bovine fasciolosis in Denmark should target heifers and dry cows through grazing management and appropriate anthelmintic treatment, and BTM ELISA can be a useful diagnostic tool for fasciolosis in Danish dairy farms.

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, University of Copenhagen, SEGES, Danish Agriculture & Food Council, Norwegian Veterinary Institute
Authors: Takeuchi-Storm, N. (Ekstern), Denwood, M. (Ekstern), Hansen, T. V. A. (Ekstern), Halasa, T. (Intern), Rattenborg, E. (Ekstern), Boes, J. (Ekstern), Enemark, H. L. (Ekstern), Thamsborg, S. M. (Ekstern)
Number of pages: 11
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Parasites & Vectors
Volume: 10
Issue number: 1
Article number: 555
ISSN (Print): 1756-3305
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SJR 1.702 SNIP 1.295 CiteScore 3.29
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.23 SJR 1.534 SNIP 1.313
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.72 SNIP 1.396 CiteScore 3.61
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.568 SNIP 1.595 CiteScore 3.31
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.56 SNIP 1.474 CiteScore 3.52
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Farm specific transmission patterns of Fasciola hepatica in Danish dairy cattle based on different diagnostic methods and monitoring of grazing management

A recent survey based on meat inspection data showed that approximately 30% of Danish cattle farms were infected with liver flukes, leading to significant economic losses. Despite the widespread problem, up-to-date knowledge on transmission patterns, diagnostic methods and practical measures for control is still lacking. We therefore initiated a longitudinal, observational study in a few infected dairy farms to elucidate farm specific transmission patterns based on different diagnostic methods and grazing management. Two organic and two conventional dairy farms with high F. hepatica antibody levels in bulk tank milk were selected. From each farm a cohort of 40 animals from different age groups (calves, heifers, primiparous and multiparous cows) were sampled 7 times between April 2015 and January 2017. Diagnostic methods included faecal egg count by sedimentation, serum ELISA and coproantigen ELISA. Additionally, monthly bulk tank milk samples were analyzed by ELISA. The analyses are ongoing, but preliminary results indicate that F. hepatica is mainly transmitted via summer infection of snails as most animals seroconvert in late autumn without shedding of eggs. However, infection early in the grazing season due to overwintered snails has also been observed. One farm where cows are stabled have had some older cows continuing to shed F. hepatica eggs, suggesting long life span of F. hepatica, although other routes of infection cannot be ruled out. The final results will provide novel and practical information about different diagnostic tests and transmission patterns related to grazing management on farm-level.

General information
State: Published
Organisations: National Veterinary Institute, Bacteriology & Parasitology, University of Copenhagen, Norwegian Veterinary Institute
Authors: Takeuchi-Storm, N. (Ekstern), Denwood, M. (Ekstern), Petersen, H. H. (Intern), Larsen Enemark, H. (Ekstern), Thamsborg, S. M. (Ekstern)
Publication date: 2017
Event: Abstract from 26th International Conference of World Association for the Advancement of Veterinary Parasitology (WAAVP), Kuala Lumpur, Malaysia.
Main Research Area: Technical/natural sciences
Fasciola hepatica, Cattle, ELISA, Fasciolosis, Liver condemnation
Electronic versions:
WAAVP_2017_Farm_specific_transmission_patterns_of_Fasciola_hepatica_in_Danish_dairy_cattle_based_on_different_diagnostic_methods_and_monitoring_of_grazing_management.pdf
Source: PublicationPreSubmission
Source-ID: 138854797
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2017
Foderkvalitet og andre faktorer af betydning for forbruget af antibiotika på minkgårde

Antibiotikaforbruget hos mink er steget gradvist gennem det seneste årti, og forbruget på den enkelte gård påvirkes af en række faktorer. Tidligere studier har vist at forekomsten af diarre og ordination af antibiotika er influeret af foderleverandøren. Formålet med dette studie (Jensen et al. 2017) var at undersøge for eventuelle effekter af de foderparametre, som indgår i den frivillige foderkontrol, på ordination af antibiotika til mink. Studiet inkluderede alle undersøgte foderbatch fra 12 fodercentraler og tilknyttede 1472 minkgårde i perioden 2012–2014. De undersøgte foderparametre omfattede både kemiske parametre og mikrobiologiske parametre. Data blev analyseret ved multivariat variansanalyse i to modeller. I den første model var responsvariablen ordination af antibiotika på en given gård i tidsrum på 3,5 eller 7 dage fra dagen efter udfodring af den givne batch. I den anden model var responsvariablen en proportion af de gårde der var tilknyttet en given fodercentral, dvs. andelen af gårde som fik antibiotika i tilknytning til udfodring af en given batch. Analyserne korrigerede for kendte faktorer med indflydelse på antibiotikaforbruget (p < 0.0001), herunder árstids variation, tidstrends, besætningsstørrelse og udbrud af Pseudomonas aeruginosa. I alle modeller var kimtallet for fæcale coccer signifikant (p < 0.0001) relateret til ordination af antibiotika.
Forensic aspects of gene expression signatures for age determination in bruises as evaluated in an experimental porcine model

Determining the age of bruises and the force used to inflict the trauma is of crucial importance in both human and veterinary forensic pathology. In the present study, the expression of more than 50 different genes in subcutaneous fat and muscle tissue from experimental bruises in pigs was investigated. The aim was to evaluate if expression signatures of selected genes were capable of determining bruises according to age and the force of impact. Eighteen experimental pigs were anesthetized, and on each animal four blunt traumas were inflicted on the back with a low, moderate or high force. The pigs were euthanized from 1 to 10 h after infliction of the trauma and subcutaneous fat and muscle tissues were sampled. As control, subcutaneous fat and muscle tissues were sampled from two un-injured pigs. Quantitative real-time polymerase chain reaction was performed to evaluate mRNA expression of genes involved in inflammation, tissue damage and repair. Expression signatures of thirteen selected genes in subcutaneous fat but not in muscle tissue reflected the age of bruises with a precision of approximately ±2 h. Moreover, the gene expression signature in the subcutaneous fat was to some extend able to separate bruises inflicted with different forces. Expression signatures of selected genes in the subcutaneous fat will increase the precision of the age determination of bruises in pigs. Further, due to the similarity of porcine and human skin physiology and immunity, these results might also provide valuable information in human forensic science.

General information

State: Published
Organisations: National Veterinary Institute, Innate Immunology, University of Copenhagen
Authors: Barington, K. (Ekstern), Jensen, H. E. (Ekstern), Skovgaard, K. (Intern)
Pages: 151-160
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information

Journal: Forensic Science, Medicine, and Pathology
Volume: 13
Issue number: 2
ISSN (Print): 1547-769X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.865 SJR 0.695 CiteScore 1.2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.605 SNIP 0.798 CiteScore 1.05
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.736 SNIP 0.837 CiteScore 1.01
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.763 SNIP 0.931 CiteScore 1.23
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.909 SNIP 1.255 CiteScore 1.44
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.64 SNIP 1.145 CiteScore 1.5
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.037 SNIP 1.154 CiteScore 1.13
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.426 SNIP 0.685
BFI (2009): BFI-level 1
Forskellige virusstammer var årsag til udbrud af plasmacytose i danske mink (Neovison vison) i 2015

General information
State: Published
Organisations: National Veterinary Institute, Virology, Department of Bio and Health Informatics, Disease Intelligence and Molecular Evolution, Diagnostic & Development, Department of Biotechnology and Biomedicine, Kopenhagen Fur
Pages: 163-167
Publication date: 2017

Host publication information
Title of host publication: Faglig årsberetning 2016 : Kopenhagen Fur
Place of publication: Aarhus N
Publisher: Kopenhagen Fur
Main Research Area: Technical/natural sciences
Electronic versions:
DTUS.pdf
Publication: Research - peer-review › Book chapter – Annual report year: 2017

Forskere designer fleksibel strategi mod kværgsygdom

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology
Authors: Kirkeby, C. T. (Intern)
Pages: 4-4
Publication date: 2017

Publication information
Pages (from-to): 4-4
Newspaper: D T U Avisen
Volume: 2017
No.: 10
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Main Research Area: Technical/natural sciences
Electronic versions:
148708_DTUavisen_10_final_281117.pdf
Publication: Communication › Newspaper article – Annual report year: 2017

Fransk hjerteorm – en lumsk parasit

General information
State: Published
Organisations: National Veterinary Institute, Bacteriology & Parasitology
Gastrointestinal Parasites of Two Populations of Arctic Foxes (Vulpes lagopus) from Northeast Greenland
Parasitological examination of 275 faecal samples from Arctic foxes (Vulpes lagopus) collected at Zackenberg Valley and Karupelv Valley in north-east Greenland from 2006 to 2008 was conducted using sieving and microscopy. Overall, 125 (45.5%) samples contained parasite eggs of Taenia crassiceps, Taenia serialis, Toxascaris leonina, Eucoleus boehmi, Physalopteridae and Ancylostomatidae, and Strongyloides-like larvae. As long-term ecological studies are conducted at both sampling locations, the present findings constitute a baseline data set for further parasitological monitoring.
Genetic and biological characterization of a Porcine Reproductive and Respiratory Syndrome Virus 2 (PRRSV-2) causing significant clinical disease in the field

Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) is the cause of severe reproductive and respiratory disease in swine worldwide. In Denmark, both PRRSV-1 and PRRSV-2 are circulating and approximately 35% of pig herds are seropositive for PRRSV. In November 2010, a pig herd in the Northern part of Denmark experienced an infection with PRRSV-2 with clinical signs that were much more severe than normally reported from current Danish PRRSV-2 affected herds. Due to the clinical observations of reproductive failure in sows and high mortality in piglets, it was speculated that a new, more pathogenic or vaccine evading PRRSV strain had emerged in Denmark. The overall aim of the present study was to perform a genetic and biological characterization of the virus isolated from the diseased herd. Complete genome sequencing of isolates from this herd revealed that although the case strain had some unique genetic features including a deduced 3 amino acid deletion, it was in overall very similar to the other PRRS-2 viruses circulating in Denmark. In an experimental trial in growing pigs, no overt clinical signs or pathology were observed following intranasal inoculation with the new virus isolate. Virus shedding, acute phase protein responses and serological responses were comparable to those seen after experimental challenge with a Danish PRRSV-2 reference strain isolated in 1997. Vaccination with a commercial modified live PRRSV-2 vaccine had a clear reducing effect on virus shedding, magnitude, and duration of viremia and viral load in the lungs. Overall, the results indicate that the severe disease observed in the field was contributed by additional factors in combination with the PRRS virus infection.

General information
State: Published
Organisations: National Veterinary Institute, Virology, Innate Immunology, Pathology, Boehringer Ingelheim Danmark A/S, Danvet K/S, Technical University of Denmark
Authors: Kvisgaard, L. K. (Intern), Larsen, L. E. (Intern), Hjulsager, C. K. (Intern), Bøtner, A. (Intern), Rathkjen, P. H. (Ekstern), Heegaard, P. M. H. (Intern), Bisgaard, N. P. (Ekstern), Nielsen, J. (Ekstern), Hansen, M. S. (Intern)
Pages: 74-83
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Veterinary Microbiology
Volume: 211
ISSN (Print): 0378-1135
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.7 SJR 1.175 SNIP 1.241
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.363 SNIP 1.206
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.413 SNIP 1.21 CiteScore 2.56
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.291 SNIP 1.256 CiteScore 2.54
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.459 SNIP 1.471 CiteScore 3
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.441 SNIP 1.569 CiteScore 3.18
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.56 SNIP 1.729 CiteScore 3.27
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.39 SNIP 1.474
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.309 SNIP 1.466
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.164 SNIP 1.29
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.048 SNIP 1.315
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.03 SNIP 1.396
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.089 SNIP 1.259
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.873 SNIP 1.248
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.905 SNIP 1.181
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.905 SNIP 1.13
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.828 SNIP 1.051
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 0.699 SNIP 1.066
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 0.714 SNIP 1.089

Original language: English
PRRSV, PRRSV-2, Type 2, Virulence, Pigs, Experimental infection
Electronic versions:
1_s2.0_S0378113517305096_main.pdf
Genome analysis of Clostridium perfringens isolates from healthy and necrotic enteritis infected chickens and turkeys

Objective: Clostridium perfringens causes gastrointestinal diseases in both humans and domestic animals. Type A strains expressing the NetB toxin are the main cause of necrotic enteritis (NE) in chickens, which has remarkable impact on animal welfare and production economy in the international poultry industry. Three pathogenicity loci NELoc-1, -2 and -3 and a collagen adhesion gene cnaA have been found to be associated with NE in chickens, whereas the presence of these has not been investigated in diseased turkeys. The purpose was to investigate the virulence associated genome content and the genetic relationship among 30 C. perfringens isolates from both healthy and NE infected chickens and turkeys, applying whole-genome sequencing. Results: NELoc-1, -3, netB and cnaA were significantly associated with NE isolates from chickens, whereas only NELoc-2 was commonly observed in both diseased turkeys and chickens. A putative collagen adhesion gene that encodes a von Willebrand Factor (vWF) domain was identified in all diseased turkeys and designated as cnaD. The phylogenetic analysis based on single nucleotide polymorphisms showed that the isolates generally were not closely related. These results indicate that virulence factors and pathogenicity loci associated with NE in chickens are not important to the same extent in diseased turkeys except for NELoc-2. A putative collagen adhesion gene which potentially could be of importance in regard to the NE pathogenesis in turkeys was identified and need to be further investigated. Thus, the pathogenesis of NE in turkeys appears to be different from that of broiler chickens.

General information
State: Published
Organisations: National Veterinary Institute, Bacteriology & Parasitology, Diagnostic & Development, Statens Serum Institut
Authors: Ronco, T. (Intern), Stegger, M. (Ekstern), Ng, K. L. (Forskerdatabase), Lilje, B. (Ekstern), Lyhs, U. (Intern), Andersen, P. S. (Ekstern), Pedersen, K. (Intern)
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: BMC Research Notes
Volume: 10
Article number: 270
ISSN (Print): 1756-0500
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.801 SJR 0.691 CiteScore 1.54
Web of Science (2017): Indexed yes
Scopus rating (2016): CiteScore 1.29 SJR 0.662 SNIP 0.7
Web of Science (2016): Indexed yes
Scopus rating (2015): SJR 0.74 SNIP 0.757 CiteScore 1.5
Scopus rating (2014): SJR 0.669 SNIP 0.787 CiteScore 1.43
Web of Science (2014): Indexed yes
Scopus rating (2013): SJR 0.654 SNIP 0.759 CiteScore 1.55
ISI indexed (2013): ISI indexed no
Scopus rating (2012): SJR 0.616 SNIP 0.656 CiteScore 1.55
ISI indexed (2012): ISI indexed no
Web of Science (2012): Indexed yes
Scopus rating (2011): SJR 0.66 SNIP 0.652 CiteScore 1.67
ISI indexed (2011): ISI indexed no
Scopus rating (2010): SJR 0.536 SNIP 0.629
Scopus rating (2009): SJR 0.398 SNIP 0.317
Original language: English
Genome analysis, Necrotic enteritis, Poultry, Virulence factors
Electronic versions:
Ronco_et_al_2017_BMC_Research_Notes.pdf
Flavobacterium psychrophilum is a devastating bacterial pathogen of salmonids reared in freshwater worldwide. So far, serological diversity between isolates has been described but the underlying molecular factors remain unknown. By combining complete genome sequence analysis and the serotyping method proposed by Lorenzen and Olesen (1997) for a set of 34 strains, we identified key molecular determinants of the serotypes. This knowledge allowed us to develop a robust multiplex PCR-based serotyping scheme, which was applied to 244 bacterial isolates. The results revealed a striking association between PCR-serotype and fish host species and illustrate the use of this approach as a simple and cost-effective method for the determination of F. psychrophilum serogroups. PCR-based serotyping could be a useful tool in a range of applications such as disease surveillance, selection of salmonids for bacterial coldwater disease resistance and future vaccine formulation.
Genomic Sequencing of Ranaviruses Isolated from Edible Frogs (Pelophylax esculentus)

Ranaviruses were isolated from wild edible frogs (Pelophylax esculentus) during epizootics in Denmark and Italy. Phylogenomic analyses revealed that these isolates are closely related and belong to a clade of ranaviruses that includes the Andrias davidianus ranavirus (ADRV), common midwife toad ranavirus (CMTV), Testudo hermanni ranavirus (THRV), and pike-perch iridovirus (PPIV).

General information
State: Published
Organisations: National Veterinary Institute, Fish Diseases, James Cook University Queensland, University of Florida, Instituto Zooprofilattico Sperimentale delle Venezie
Authors: Ariel, E. (Ekstern), Subramaniam, K. (Ekstern), Imnoi, K. (Ekstern), Sriwanayos, P. (Ekstern), Ahasan, M. S. (Ekstern), Olesen, N. J. (Intern), Amedeo, M. (Ekstern), Toffan, A. (Ekstern), Waltzek, T. B. (Ekstern)
Pages: e01015-17
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Genome Announcements
Volume: 5
Issue number: 38
ISSN (Print): 2169-8287
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.407 SJR 0.553 CiteScore 1.01
Scopus rating (2016): CiteScore 0.41 SJR 0.583 SNIP 0.469
Web of Science (2016): Indexed yes
Scopus rating (2015): SJR 0.591 SNIP 0.398
Scopus rating (2014): SJR 0.539 SNIP 0.344
ISI indexed (2013): ISI indexed no
Original language: English
Electronic versions:
Aleutian mink disease has major economic consequences on the mink farming industry worldwide, as it causes a disease that affects both the fur quality and the health and welfare of the mink. The virus causing this disease is a single-stranded DNA virus of the genus Amdoparvovirus belonging to the family of Parvoviridae. In Denmark, infection with AMDV has largely been restricted to a region in the northern part of the country since 2001, affecting only 5% of the total Danish mink farms. However, in 2015 outbreaks of AMDV were diagnosed in all parts of the country. Initial analyses revealed that the outbreaks were caused by two different strains of AMDV that were significantly different from the circulating Danish strains. To track the source of these outbreaks, a major investigation of global AMDV strains was initiated. Samples from 13 different countries were collected and partial NS1 gene was sequenced and subjected to phylogenetic analyses. The analyses revealed that AMDV exhibited substantial genetic diversity. No clear country-wise clustering was evident, but exchange of viruses between countries was revealed. One of the Danish outbreaks was caused by a strain of AMDV that closely resembled a strain originating from Sweden. In contrast, we did not identify any potential source for the other and more widespread outbreak strain. To the authors' knowledge, this is the first major global phylogenetic study of contemporary AMDV partial NS1 sequences. The study proved that partial NS1 sequencing can be used to distinguish virus strains belonging to major clusters. The partial NS1 sequencing can therefore be a helpful tool in combination with epidemiological data, in relation to outbreak tracking. However, detailed information on farm-to-farm transmission requires full genome sequencing.
The functionality of tissue cDC is regulated, at least in part, by the signals these cells receive within their local environment. For example, we and others, have demonstrated that murine small intestinal but not colonic cDC are imprinted with an ability to generate the Vitamin A metabolite, retinoic acid, and thus an enhanced capacity to drive the generation of small intestinal homing T cells. Here we demonstrate that Glycoprotein 2 (GP2), a GPI-anchored protein previously shown to be selectively expressed by M-cells and to act as a receptor for type 1 fimbriated bacteria, is expressed by a large proportion of IRF4-dependent cDC in the small intestine but not in other tissues. While surface expression of GP2 by small intestinal CD103+CD11b+ cDC was independent of lymphocytes and MyD88 signaling, administration of broad spectrum antibiotics increased the proportion of GP2+CD103+CD11b+ cDC in the small intestine. Moreover, GP2 expressing cDC in the small intestine were dramatically reduced in the setting of intestinal inflammation. We have previously shown that mice with an IRF4 deletion in CD11c+ cells (Cd11c-cre.Irf4fl/fl mice) have reduced numbers of small intestinal CD103+CD11b+ cDC. Interestingly, we found that GP2+ CD103+CD11b+ cDC were dramatically reduced in these mice. Finally, to address the in vivo role of GP2 expression by cDC, we have generated mice with a selective deletion of GP2 in CD103+CD11b+ cDC (huLangerin-cre.gp2fl/fl mice). Results from these ongoing studies will be presented.

**GP2 is selectively expressed by small intestinal CD103+CD11b+ cDC**

The functionality of tissue cDC is regulated, at least in part, by the signals these cells receive within their local environment. For example, we and others, have demonstrated that murine small intestinal but not colonic cDC are imprinted with an ability to generate the Vitamin A metabolite, retinoic acid, and thus an enhanced capacity to drive the generation of small intestinal homing T cells. Here we demonstrate that Glycoprotein 2 (GP2), a GPI-anchored protein previously shown to be selectively expressed by M-cells and to act as a receptor for type 1 fimbriated bacteria, is expressed by a large proportion of IRF4-dependent cDC in the small intestine but not in other tissues. While surface expression of GP2 by small intestinal CD103+CD11b+ cDC was independent of lymphocytes and MyD88 signaling, administration of broad spectrum antibiotics increased the proportion of GP2+CD103+CD11b+ cDC in the small intestine. Moreover, GP2 expressing cDC in the small intestine were dramatically reduced in the setting of intestinal inflammation. We have previously shown that mice with an IRF4 deletion in CD11c+ cells (Cd11c-cre.Irf4fl/fl mice) have reduced numbers of small intestinal CD103+CD11b+ cDC. Interestingly, we found that GP2+ CD103+CD11b+ cDC were dramatically reduced in these mice. Finally, to address the in vivo role of GP2 expression by cDC, we have generated mice with a selective deletion of GP2 in CD103+CD11b+ cDC (huLangerin-cre.gp2fl/fl mice). Results from these ongoing studies will be presented.

**General information**

*State: Published*

*Organisations: National Veterinary Institute, Mucosal Immunology, Lund University, Yokohama City University*

*Authors: Müller-Luda, K. (Ekstern), Ahmadi, F. (Ekstern), Ohno, H. (Ekstern), Kotarsky, K. (Ekstern), Agace, W. W. (Intern)*
 Harmonizing methods for wildlife abundance estimation and pathogen detection in Europe—a questionnaire survey on three selected host-pathogen combinations

Background: The need for wildlife health surveillance as part of disease control in wildlife, domestic animals and humans on the global level is widely recognized. However, the objectives, methods and intensity of existing wildlife health surveillance programs vary greatly among European countries, resulting in a patchwork of data that are difficult to merge and compare. This survey aimed at evaluating the need and potential for data harmonization in wildlife health in Europe. The specific objective was to collect information on methods currently used to estimate host abundance and pathogen prevalence. Questionnaires were designed to gather detailed information for three host-pathogen combinations: (1) wild boar and Aujeszky's disease virus, (2) red fox and Echinococcus multilocularis, and (3) common vole and Francisella tularensis.

Results: We received a total of 70 responses from 19 European countries. Regarding host abundance, hunting bags are currently the most widely accessible data source for widely distributed mid-sized and larger mammals such as red fox and wild boar, but we observed large differences in hunting strategies among countries as well as among different regions within countries. For small rodents, trapping is the method of choice, but practical applications vary among study sites. Laboratory procedures are already largely harmonized but information on the sampled animals is not systematically collected.

Conclusions: The answers revealed that a large amount of information is available for the selected host-pathogen pairs and that in theory methods are already largely harmonized. However, the comparability of the data remains strongly compromised by local differences in the way, the methods are applied in practice. While these issues may easily be overcome for prevalence estimation, there is an urgent need to develop tools for the routine collection of host abundance data in a harmonized way. Wildlife health experts are encouraged to apply the harmonized APHAEA protocols in epidemiological studies in wildlife and to increase cooperation.

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, University of Bern, Erasmus Medical Center, Università degli Studi di Torino, Friedrich-Loeffler-Institute
Authors: Schulz, J. (Intern), Ryser-Degiorgis, M. (Ekstern), Kuiken, T. (Ekstern), Ferroglio, E. (Ekstern), Ulrich, R. G. (Ekstern), Conraths, F. J. (Ekstern), Gortazar, C. (Ekstern), Staubach, C. (Ekstern), Partners, A. P. (Ekstern)
Number of pages: 10
Publication date: 2017
Main Research Area: Technical/natural sciences
Histologiske forandringer efter eksperimentel infektions med plasmacytose virus


General information
State: Published
Organisations: National Veterinary Institute, Diagnostic & Development, Pathology
Authors: Jensen, T. H. (Intern), Chriél, M. (Intern), Hansen, M. S. (Intern)
Pages: 77-82
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Faglig Årsberetning
Volume: 2017
ISSN (Print): 2445-9437
Original language: English
Electronic versions:
Histologiske_forandringer_efter_eksperimentel_infektions_med_plasmacytose_virus.pdf
Links:
Horses in Denmark Are a Reservoir of Diverse Clones of Methicillin-Resistant and -Susceptible Staphylococcus aureus

Denmark is a country with a high prevalence of livestock-associated methicillin-resistant Staphylococcus aureus (MRSA) clonal complex (CC) 398 in pigs. Even though pig farming is regarded as the main source of human infection or colonization with MRSA CC398, 10-15% of the human cases appear not to be linked to pigs. Following the recent reports of MRSA CC398 in horses in other European countries and the lack of knowledge on Staphylococcus aureus carriage in this animal species, we carried out a study to investigate whether horses constitute a reservoir of MRSA CC398 in Denmark, and to gain knowledge on the frequency and genetic diversity of S. aureus in horses, including both methicillin-resistant and -susceptible S. aureus (MSSA). Nasal swabs were collected from 401 horses originating from 74 farms, either at their farms or prior to admission to veterinary clinics. Following culture on selective media, species identification by MALDI-TOF MS and MRSA confirmation by standard PCR-based methods, S. aureus and MRSA were detected in 54 (13%) and 17 (4%) horses originating from 30 (40%) and 7 (9%) farms, respectively. Based on spa typing, MSSA differed genetically from MRSA isolates. The spa type prevalent among MSSA isolates was t127 (CC1), which was detected in 12 horses from 11 farms and represents the most common S. aureus clone isolated from human bacteremia cases in Denmark. Among the 17 MRSA carriers, 10 horses from three farms carried CC398 t011 harboring the immune evasion cluster (IEC), four horses from two farms carried IEC-negative CC398 t034, and three horses from two farms carried a mecC-positive MRSA lineage previously associated with wildlife and domestic ruminants (CC130 t528). Based on whole-genome phylogenetic analysis of the 14 MRSA CC398, t011 isolates belonged to the recently identified horse-adapted clone in Europe and were closely related to human t011 isolates from three Danish equine veterinarians, whereas t034 isolates belonged to pig-adapted clones. Our study confirms that horses carry an equine-specific clone of MRSA CC398 that can be transmitted to veterinary personnel, and reveals that these animals are exposed to MRSA and MSSA clones that are likely to originate from livestock and humans, respectively.
Identification of cross-reacting T-cell epitopes in structural and non-structural proteins of swine and pandemic H1N1 influenza A virus strains in pigs

Heterologous protection against swine influenza viruses (SwIVs) of different lineages is an important concern for the pig industry. Cross-protection between 'avian-like' H1N1 and 2009 pandemic H1N1 lineages has been observed previously, indicating the involvement of cross-reacting T-cells. Here, reverse vaccinology was applied to identify cross-reacting MHC class I T-cell epitopes from two different SwIV H1 lineages in pigs. In silico prediction followed by in vitro and in vivo testing was used to identify SLA-1*0702 T-cell epitopes in heterologous SwIV-infected pigs. Following viral infection, tetramer specific T-cell populations were identified. The majority of the identified T-cell epitopes were conserved between the examined lineages, suggesting that targeting cross-reactive T-cell epitopes could be used to improve vaccines against SwIV in SLA-1*0702-positive pigs.

General information
State: Published
Organisations: National Veterinary Institute, Virology, Adaptive Immunology, Universitat Autonoma de Barcelona, Centro de Investigación en Sanidad Animal
Authors: Baratelli, M. (Ekstern), Pedersen, L. E. (Intern), Trebbien, R. (Intern), Larsen, L. E. (Intern), Jungersen, G. (Intern), Blanco, E. (Ekstern), Nielsen, J. (Intern), Montoya, M. (Ekstern)
Pages: 895-899
Publication date: 2017
Main Research Area: Technical/natural sciences
Identification of Dermacentor reticulatus Ticks Carrying Rickettsia raoultii on Migrating Jackal, Denmark

From a migrating golden jackal (Canis aureus), we retrieved 21 live male Dermacentor reticulatus ticks, a species not previously reported from wildlife in Denmark. We identified Rickettsia raoultii from 18 (86%) of the ticks. This bacterium is associated with scalp eschar and neck lymphadenopathy after tick bite syndrome among humans.

General information
State: Published
Organisations: National Veterinary Institute, Bacteriology & Parasitology, Diagnostic & Development, Pathology, Epidemiology
Authors: Schou, K. K. (Intern), Chriél, M. (Intern), Isbrand, A. (Intern), Jensen, T. K. (Intern), Bødker, R. (Intern)
Pages: 2072-2074
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Emerging Infectious Diseases (Print Edition)
Volume: 23
Issue number: 12
ISSN (Print): 1080-6040
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 4.78 SJR 3.278 SNIP 1.916
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 4.92 SJR 3.428 SNIP 2.198
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 3.101 SNIP 2.012 CiteScore 4.23
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 3.509 SNIP 2.406 CiteScore 4.59
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 3.254 SNIP 2.266 CiteScore 4.68
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 2.858 SNIP 2.131 CiteScore 4.25
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 2.785 SNIP 2.19 CiteScore 4.46
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 3.021 SNIP 2.319
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 3.168 SNIP 2.701
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 3.231 SNIP 2.277
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 2.709 SNIP 2.341
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 2.879 SNIP 2.345
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 2.816 SNIP 2.297
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 2.683 SNIP 2.562
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 2.267 SNIP 2.373
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 3.094 SNIP 2.545
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 2.346 SNIP 2.904
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.522 SNIP 2.856
Scopus rating (1999): SJR 1.71 SNIP 2.61
Original language: English
Electronic versions:
17_0919.pdf
DOIs:
10.3201/eid2312.170919

Bibliographical note
Emerging Infectious Diseases is an open access journal in the public domain. All content is freely available without charge to the user or his/her institution. In accordance with the Budapest Open Access Initiative definition of Open Access, users are allowed to read, download, copy, distribute, print, search, or link to the full texts of the articles, or use them for any other lawful purpose, without asking prior permission from the publisher or the author. Because the journal is in the public domain, its usage policy also conforms to conditions set for by Creative Commons.

General information
State: Published
Organisations: National Veterinary Institute, Innate Immunology, University of Copenhagen, Aarhus University
Improved Culture Medium (TiKa) for Mycobacterium avium Subspecies Paratuberculosis (MAP) Matches qPCR Sensitivity and Reveals Significant Proportions of Non-viable MAP in Lymphoid Tissue of Vaccinated MAP Challenged Animals

The quantitative detection of viable pathogen load is an important tool in determining the degree of infection in animals and contamination of foodstuffs. Current conventional culture methods are limited in their ability to determine these levels in Mycobacterium avium subspecies paratuberculosis (MAP) due to slow growth, clumping and low recoverability issues. The principle goal of this study was to evaluate a novel culturing process (TiKa) with unique ability to stimulate MAP growth from low sample loads and dilutions. We demonstrate it was able to stimulate a mean 29-fold increase in recoverability and an improved sensitivity of up to three logs when compared with conventional culture. Using TiKa culture, MAP clumping was minimal and produced visible colonies in half the time required by standard culture methods. Parallel quantitative evaluation of the TiKa culture approach and qPCR on MAP loads in tissue and gut mucosal samples from a MAP vaccine-challenge study, showed good correlations between colony counts (cfu) and qPCR derived genome equivalents (Geq) over a large range of loads with a 30% greater sensitivity for TiKa culture approach at low loads (two logs). Furthermore, the relative fold changes in Geq and cfu from the TiKa culture approach suggests that non-mucosal tissue loads from MAP infected animals contained a reduced proportion of non-viable MAP (mean 19-fold) which was reduced significantly further (mean 190-fold) in vaccinated “reactor” calves. This study shows TiKa culture equates well with qPCR and provides important evidence that accuracy in estimating viable MAP load using DNA tests alone may vary significantly between samples of mucosal and lymphatic origin.

General information
State: Published
Organisations: National Veterinary Institute, Adaptive Immunology, St. George’s University of London
Authors: Bull, T. J. (Ekstern), Munshil, T. (Ekstern), Melvang, H. M. (Intern), Hartmann, S. B. (Intern), Sørensen, M. R. (Intern), Garcia, J. S. (Ekstern), Lopez-Perez, P. M. (Ekstern), Hofmann, S. (Ekstern), Hapert, K. (Ekstern), Jungersen, G. (Intern)
Number of pages: 8
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Frontiers in Microbiology
Volume: 7
Article number: 2112
ISSN (Print): 1664-302X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.19 SJR 1.699 SNIP 1.174
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.16 SJR 1.759 SNIP 1.161
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.869 SNIP 1.193 CiteScore 4.15
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.879 SNIP 1.148 CiteScore 3.76
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.776 SNIP 0.949 CiteScore 3.56
ISI indexed (2013): ISI indexed no
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.46 SNIP 0.722 CiteScore 2.78
ISI indexed (2012): ISI indexed no
Scopus rating (2011): SJR 0.642 SNIP 0.192
Web of Science (2011): Indexed yes
Original language: English
Mycobacterium avium subspecies paratuberculosis, improved culture, quantification, qPCR, TiKa culture
Improving institutional memory on challenges and methods for estimation of pig herd antimicrobial exposure based on data from the Danish Veterinary Medicines Statistics Program (VetStat)

With the increasing occurrence of antimicrobial resistance, more attention has been directed towards surveillance of both human and veterinary antimicrobial use. Since the early 2000s, several research papers on Danish pig antimicrobial usage have been published, based on data from the Danish Veterinary Medicines Statistics Program (VetStat). VetStat was established in 2000, as a national database containing detailed information on purchases of veterinary medicine. This paper presents a critical set of challenges originating from static system features, which researchers must address when estimating antimicrobial exposure in Danish pig herds. Most challenges presented are followed by at least one robust solution. A set of challenges requiring awareness from the researcher, but for which no immediate solution was available, were also presented. The selection of challenges and solutions was based on a consensus by a cross-institutional group of researchers working in projects using VetStat data. No quantitative data quality evaluations were performed, as the frequency of errors and inconsistencies in a dataset will vary, depending on the period covered in the data. Instead, this paper focuses on clarifying how VetStat data may be translated to an estimation of the antimicrobial exposure at herd level, by suggesting uniform methods of extracting and editing data, in order to obtain reliable and comparable estimates on pig antimicrobial consumption for research purposes.

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, National Food Institute, Research Group for Genomic Epidemiology, University of Copenhagen
Authors: Dupont, N. H. (Ekstern), Fertner, M. (Intern), Birkegård, A. C. (Intern), Dahlhoff Andersen, V. (Intern), Nielsen, G. B. (Ekstern), Kruse, A. B. (Ekstern), de Knegt, L. V. (Intern)
Number of pages: 25
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: ArXiv
Original language: English
Electronic versions:
P_Vetstat_paper_Versao_Leo_Repository_Preparation_for_ArXiv_01_ArXiv_240517.pdf
Source: FindIt
Source-ID: 2370650759
Publication: Research - peer-review › Journal article – Annual report year: 2017

Increased Intestinal Inflammation and Digestive Dysfunction in Preterm Pigs with Severe Necrotizing Enterocolitis

The risk factors for necrotizing enterocolitis (NEC) are well known, but the factors involved in the different NEC presentations remain unclear. We hypothesized that digestive dysfunction and intestinal inflammation are mainly affected by severe NEC lesions. In 48 preterm pigs, the association between the macroscopic NEC score (range 1-6) and the expression of 48 genes related to inflammation, morphological, and digestive parameters in the distal small intestine was investigated. Only severe NEC cases (score of 5-6) were associated with the upregulation of genes involved in inflammation (CCL2, CCL3, CD14, CD163, CXCL8, HP, IL1B, IL1RN, IL6,IL10, NFKBIA, PTGS2 and TNFAIP3) compared to pigs that appeared healthy (score of 1-2) or showed mild NEC (score of 3-4). Pigs with a score of 5-6 had higher intestinal tissue IL-1β levels and a lower mucosal mass, villus height, and aminopeptidase N activity compared to pigs with a score of 1-4, and lower crypts and activities of lactase, dipeptidylpeptidase IV, and aminopeptidase A than pigs with a score of 1-2. The expression of a range of inflammation-related genes was increased only in pigs with severe NEC, concomitant with morphological changes and decreased hydrolyase activity. A severe inflammatory response and digestive dysfunction are associated mainly with severe NEC. Still, it remains difficult to separate the initial causes of NEC and the later intestinal consequences of NEC in both infants and experimental models.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, University of Copenhagen, Aarhus University
Authors: Støy, A. C. F. (Intern), Heegaard, P. M. H. (Intern), Skovgaard, K. (Intern), Bering, S. B. (Ekstern), Bjerre, M. (Ekstern), Sangild, P. T. (Ekstern)
Induction of Antigen-Specific T Cells Targeting Endogenous Retroelements During Epigenetic Treatment of Myelodysplastic Syndrome

General information
Infection experiments with novel Piscine orthoreovirus from rainbow trout (Onchorhyncus mykiss) in salmonids

A new disease in farmed rainbow trout (Onchorhyncus mykiss) was described in Norway in 2013. The disease mainly affected the heart and resembled heart and skeletal muscle inflammation (HSMI) in Atlantic salmon (Salmo salar L.). HSMI is associated with Piscine orthoreovirus (PRV), and a search for a similar virus in the diseased rainbow trout led to detection of a sequence with 85% similarity to PRV. This finding called for a targeted effort to assess the risk the new PRV-variant pose on farmed rainbow trout and Atlantic salmon by studying infection and disease pathogenesis, aiming to
provide more diagnostic knowledge. Based on the genetic relationship to PRV, the novel virus is referred to as PRV-
Oncorhynchus mykiss (PRV-Om) in contrast to PRV-Salmo salar (PRV-Ss). In experimental trials, intraperitoneally
injected PRV-Om was shown to replicate in blood in both salmonid species, but more effectively in rainbow trout. In
rainbow trout, the virus levels peaked in blood and heart of cohabitants 6 weeks post challenge, along with increased
expression of antiviral genes (Mx and viperin) in the spleen, with 80-100% of the cohabitants infected. Heart inflammation
was diagnosed in all cohabitants examined 8 weeks post challenge. In contrast, less than 50% of the Atlantic salmon
cohabitants were infected between 8 and 16 weeks post challenge and the antiviral response in these fish was very low.
From 12 weeks post challenge and onwards, mild focal myocarditis was demonstrated in a few virus-positive salmon. In
conclusion, PRV-Om infects both salmonid species, but faster transmission, more notable antiviral response and more
prominent heart pathology were observed in rainbow trout.

General information
State: Published
Organisations: National Veterinary Institute, Fish Diseases, Norwegian Veterinary Institute, Norwegian University of Life
Sciences
Authors: Hauge, H. (Ekstern), Vendramin, N. (Intern), Taksdal, T. (Ekstern), Olsen, A. B. (Ekstern), Wessel, Ø. (Ekstern),
Mikkelsen, S. S. (Intern), Alencar, A. L. F. (Intern), Olesen, N. J. (Intern), Dahle, M. K. (Ekstern)
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: P L o S One
Volume: 12
Issue number: 7
Article number: e0180293
ISSN (Print): 1932-6203
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.01 SJR 1.164 SNIP 1.111
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.11 SJR 1.236 SNIP 1.101
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.427 SNIP 1.136 CiteScore 3.32
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.559 SNIP 1.148 CiteScore 3.54
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.772 SNIP 1.153 CiteScore 3.94
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.982 SNIP 1.156 CiteScore 4.15
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 2.425 SNIP 1.233 CiteScore 4.58
ISI indexed (2011): ISI indexed no
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.705 SNIP 1.178
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 2.614 SNIP 1.046
Infection routes of Aeromonas salmonicida in rainbow trout monitored in vivo by real-time bioluminescence imaging

Recent development of imaging tools has facilitated studies of pathogen infections in vivo in real time. This trend can be exemplified by advances in bioluminescence imaging (BLI), an approach that helps to visualize dissemination of pathogens within the same animal over several time points. Here, we employ bacterial BLI for examining routes of entry and spread of Aeromonas salmonicida subsp. salmonicida in rainbow trout. A virulent Danish A. salmonicida strain was tagged with pAKgfplux1, a dual-labelled plasmid vector containing the mutated gfpmut3a gene from Aequorea victoria and the luxCDABE genes from the bacterium Photorhabdus luminescens. The resulting A. salmonicida transformant exhibited growth properties and virulence identical to the wild-type A. salmonicida, which made it suitable for an experimental infection, mimicking natural conditions. Fish were infected with pAKgfplux1 tagged A. salmonicida via immersion bath. Colonization and subsequent tissue dissemination was followed over a 24-h period using the IVIS spectrum imaging workstation. Results suggest the pathogen's colonization sites are the dorsal and pectoral fin and the gills, followed by a progression through the internal organs and an ensuing exit via the anal opening. This study provides a tool for visualizing colonization of A. salmonicida and other bacterial pathogens in fish.
Infektion med TBE-virus i Danmark 2013-2016

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, Statens Serum Institut, State Serum Institute
Authors: Ocias, L. F. (Ekstern), Petersen, A. (Ekstern), Krogfelt, K. (Ekstern), Rosenstierne, M. W. (Forskerdatabase), Fomsgaard, A. (Ekstern), Bødker, R. (Intern)
Number of pages: 2
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: E P I - Nyt
Volume: 2017
Issue number: 40
ISSN (Print): 1602-4184
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Original language: Danish
Electronic versions:
Uge_40_2017_EPI_NYT.pdf
Influence of ipilimumab on expanded tumour derived T cells from patients with metastatic melanoma

Introduction: Tumour infiltrating lymphocyte (TIL) based adoptive cell therapy (ACT) is a promising treatment for patients with advanced melanoma. Retrospective studies suggested an association between previous treatment with anti-CTLA-4 antibodies and long term survival after subsequent ACT. Thus, we hypothesized that treatment with anti-CTLA-4 antibodies can induce favourable changes to be detected in TILs. Results: Expanded T cells from Ipilimumab treated patients had a higher proportion of cells expressing CD27, intracellular CTLA-4, TIM-3 and LAG-3. In addition, broader and more frequent T cell responses against common tumour antigens were detected in patients treated with Ipilimumab as compared to anti-CTLA-4 naive patients. Materials and methods: Expanded TILs were obtained from patients with advanced melanoma who had received Ipilimumab in the previous six months, or had not received any type of anti-CTLA-4 antibody. T cell specificity and expression of phenotypic and exhaustion markers were scrutinized as well as functional properties. Conclusions: Ipilimumab may induce tumor-infiltration of T cells of a more naive phenotype expressing markers related to activation or exhaustion. Additionally, Ipilimumab may increase the frequency of T cells recognizing common tumour associated antigens.
Intramuscular DNA Vaccination of Juvenile Carp against Spring Viremia of Carp Virus Induces Full Protection and Establishes a Virus-Specific B and T Cell Response

Although spring viremia of carp virus (SVCV) can cause high mortalities in common carp, a commercial vaccine is not available for worldwide use. Here, we report a DNA vaccine based on the expression of the SVCV glycoprotein (G) which, when injected in the muscle even at a single low dose of 0.1 μg DNA/g of fish, confers up to 100% protection against a subsequent bath challenge with SVCV. Importantly, to best validate vaccine efficacy, we also optimized a reliable bath challenge model closely mimicking a natural infection, based on a prolonged exposure of carp to SVCV at 15°C. Using this optimized bath challenge, we showed a strong age-dependent susceptibility of carp to SVCV, with high susceptibility at young age (3 months) and a full resistance at 9 months. We visualized local expression of the G protein and associated early inflammatory response by immunohistochemistry and described changes in the gene expression of pro inflammatory cytokines, chemokines, and antiviral genes in the muscle of vaccinated fish. Adaptive immune responses were investigated by analyzing neutralizing titers against SVCV in the serum of vaccinated fish and the in vitro proliferation capacity of peripheral SVCV-specific T cells. We show significantly higher serum neutralizing titers and the presence of SVCV-specific T cells in the blood of vaccinated fish, which proliferated upon stimulation with SVCV. Altogether, this is the first study reporting on a protective DNA vaccine against SVCV in carp and the first to provide a detailed characterization of local innate as well as systemic adaptive immune responses elicited upon DNA vaccination that suggest a role not only of B cells but also of T cells in the protection conferred by the SVCV-G DNA vaccine.

General information

State: Published
Organisations: National Veterinary Institute, Fish Diseases, Wageningen University, Universite Paris Saclay, Veterinary Research Institute, Brno, Friedrich-Loeffler-Institute
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information

Journal: Frontiers in Immunology
Volume: 8
Article number: 1340
ISSN (Print): 1664-3224
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SJR 2.803 SNIP 1.484 CiteScore 5.62
Web of Science (2017): Indexed yes
Scopus rating (2016): CiteScore 5.37 SJR 3.034 SNIP 1.476
Web of Science (2016): Indexed yes
Scopus rating (2015): SJR 2.827 SNIP 1.277 CiteScore 5.09
Web of Science (2015): Indexed yes
Scopus rating (2014): SJR 2.389 SNIP 1.057 CiteScore 4.24
Web of Science (2014): Indexed yes
Scopus rating (2013): SJR 1.908 SNIP 0.855 CiteScore 3.55
 ISI indexed (2013): ISI indexed no
Scopus rating (2012): SJR 0.809 SNIP 0.193 CiteScore 1.38
 ISI indexed (2012): ISI indexed no
Scopus rating (2011): SJR 0.121
Web of Science (2011): Indexed yes
Original language: English
DNA vaccination, Spring viremia of carp virus, T cells, B cells, Rhabdovirus
Electronic versions:
Intrauterine inoculation of minipigs with Chlamydia trachomatis during diestrus establishes a longer lasting infection compared to vaginal inoculation during estrus

Advanced animal models, such as minipigs, are needed for the development of a globally requested human Chlamydia vaccine. Previous studies have shown that vaginal inoculation of sexually mature Göttingen minipigs with Chlamydia trachomatis resulted in an infection lasting only 3-5 days. The aim of this study was to evaluate the effect of targeting the upper porcine genital tract by transcervical and transabdominal intrauterine inoculation, compared to previously performed vaginal inoculation. Furthermore, we investigated the effect of the hormonal cycle, estrus vs. diestrus, on the establishment of a C. trachomatis infection in the minipig. Targeting the upper genital tract (transcervical inoculation) resulted in a longer lasting infection (at least 7 days) compared to vaginal inoculation (3-5 days). When comparing intrauterine inoculation during estrus and diestrus, inoculation during diestrus resulted in a longer lasting infection (at least 10 days) compared to estrus (3-5 days). Furthermore, we found a significant C. trachomatis specific IFN-γ response in pigs inoculated during estrus correlating with the accelerated clearance of infection in these pigs. These findings suggest that for implementation of an optimal model of C. trachomatis in minipigs, inoculation should bypass the cervix and preferably be performed during diestrus.
Investigations of FIBCD1: Immunohistochemical localization and immunomodulatory role upon helminth antigen stimulation in colon epithelium

Introduction: Fibrinogen C domain-containing 1 (FIBCD1) is a homotetrameric type II transmembrane protein, expressed at epithelial surfaces. FIBCD1 has a wide ligand spectrum, including chitin found in various pathogens such as helminths and fungi. Current understanding points towards a role as a pattern recognition receptor in the innate immune response. Aim: In the present study, we investigate the localization of FIBCD1 in 49 different healthy human tissues by immunohistochemistry. Further, we investigate the in vitro effects of excretory-secretory (ES) antigens from pig whipworm (Trichuris suis) on FIBCD1-transfected colon epithelial cells, and identify protein fractions in the ES-antigen that binds to FIBCD1. Results: Immunohistochemical staining shows that FIBCD1 is present at mucosal surfaces throughout the human body, with high intensity in the airways and gastrointestinal and urogenital tract. Transfection of the human colon epithelial cell line HCT116 with FIBCD1 did not result in any major genotypic differences upon stimulation with ES antigens, as determined by quantitative PCR of various pro- and anti-inflammatory genes. FIBCD1 recognizes and binds to whipworm eggshell and ES antigens. Analysis of the T. suis ES-antigen by size chromatography reveals predominant sizes of proteins ranging from 10 kDa to 200 kDa. Conclusion: FIBCD1 is present at mucosal surfaces throughout the human body, which may underline its function as a pattern recognition receptor in the innate immune system. FIBCD1 binds to ES antigens. Stimulation with ES antigens does not appear to be influenced by FIBCD1 transfection in vitro. FIBCD1 may play a role in whipworm infections in vivo.

General information
State: Published
Organisations: National Veterinary Institute, Mucosal Immunology, University of Southern Denmark, Odense University Hospital, University of Copenhagen
Authors: von Huth, S. (Ekstern), Skallerup, S. (Ekstern), Buragaite, B. (Ekstern), Schlosser, A. (Ekstern), Moeller, J. B. (Ekstern), Hammond, M. (Ekstern), Nielsen, O. (Ekstern), Marcusseen, N. (Ekstern), Svensson Frej, M. (Intern), Williams, A. R. (Ekstern), Thamsborg, S. M. (Ekstern), Sorensen, G. L. (Ekstern), Holmskov, U. (Ekstern)
Publication date: 2017
Main Research Area: Technical/natural sciences
In vivo adherence of Flavobacterium psychrophilum to mucosal external surfaces of rainbow trout (Oncorhynchus mykiss) fry

The adherence of Flavobacterium psychrophilum to surfaces of epithelial tissues has been inconclusively suggested as a mechanism, which enables the bacterium to invade the host. Hence, the present study aimed to examine the adherence of the cells of two colony phenotypes, smooth and rough, of F. psychrophilum to mucosal tissues of rainbow trout fry and to test the skin mucus as a nutrient for the growth of F. psychrophilum. Fish were immersed in water containing 10^6 CFU ml^-1 F. psychrophilum for each colony phenotype. Mucosal tissue samples from fins, gills, skin and eyes, and swab samples from spleen and kidney were taken and inoculated onto TYES agar plates. Colony phenotypes of F. psychrophilum were identified and number of colonies counted. The results showed that cells of both phenotypes initially (0 h) adhered to all mucosal surfaces, but only the rough cells were still present on tissues 1 h post-immersion. Both phenotypes showed a tissue tropism with the fin tissue being the most adhered. Furthermore, skin mucus promoted the growth of both colony phenotypes. We suggest that the growth of F. psychrophilum cells in skin mucus apparently facilitates the bacterial adherence to mucosal surfaces, and the subsequent invasion into the host.

General information

State: Published
Organisations: National Veterinary Institute, Bacteriology & Parasitology, Novia University of Applied Sciences, Åbo Akademi University
Authors: Papadopoulou, A. (Ekstern), Dalsgaard, I. (Intern), Lindén, A. (Ekstern), Wiklund, T. (Ekstern)
Pages: 1309-1320
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information

Journal: Journal of Fish Diseases
Volume: 40
Issue number: 10
ISSN (Print): 0140-7775
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.82
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.12
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 1.71
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 1.99
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 1.74
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 1.7
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.09
Irf4-dependent CD103+CD11b+ dendritic cells and the intestinal microbiome regulate monocyte and macrophage activation and intestinal peristalsis in postoperative ileus

Objective: Postoperative ileus (POI), the most frequent complication after intestinal surgery, depends on dendritic cells (DCs) and macrophages. Here, we have investigated the mechanism that activates these cells and the contribution of the intestinal microbiota for POI induction. Design: POI was induced by manipulating the intestine of mice, which selectively lack DCs, monocytes or macrophages. The disease severity in the small and large intestine was analysed by determining the distribution of orally applied fluorescein isothiocyanate isothiocyanate-dextran and by measuring the excretion time of a retrogradely inserted glass ball. The impact of the microbiota on intestinal peristalsis was evaluated after oral antibiotic treatment.

Results: We found that Cd11c-Cre+ Irf4flox/flox mice lack CD103+CD11b+ DCs, a DC subset unique to the intestine whose function is poorly understood. Their absence in the intestinal muscularis reduced pathogenic inducible nitric oxide synthase (iNOS) production by monocytes and macrophages and ameliorated POI. Pathogenic iNOS was produced in the jejunum by resident Ly6C− macrophages and infiltrating chemokine receptor 2-dependent Ly6C+ monocytes, but in the colon only by the latter demonstrating differential tolerance mechanisms along the intestinal tract. Consistently, depletion of both cell subsets reduced small intestinal POI, whereas the depletion of Ly6C+ monocytes alone was sufficient to prevent large intestinal POI. The differential role of monocytes and macrophages in small and large intestinal POI suggested a potential role of the intestinal microbiota. Indeed, antibiotic treatment reduced iNOS levels and ameliorated POI. Conclusions: Our findings reveal that CD103+CD11b+ DCs and the intestinal microbiome are a prerequisite for the activation of intestinal monocytes and macrophages for dysregulating intestinal motility in POI.

General information
State: Published
Organisations: National Veterinary Institute, Mucosal Immunology, University of Duisburg-Essen, University Hospital Essen, Weizmann Institute of Science, Lund University, Rheinische Friedrich-Wilhelms University
Pages: 2110–2120
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Gut
Volume: 66
Issue number: 12
ISSN (Print): 0017-5749
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
Isolation and molecular characterization of Clostridium perfringens from healthy Merino lambs in Patagonia region, Argentina

The presence and molecular characterization of Clostridium perfringens in healthy Merino lambs over a six-month period was investigated in this study. Overall, a high prevalence of C. perfringens was detected, even in day-old lambs. Even though the majority of the isolates were characterized as being of type A, types C and D were also isolated. Furthermore, a high genetic diversity was observed by PFGE among the type A isolates.
Karmitoxin: An amine containing polyhydroxy-polyene toxin from the marine dinoflagellate Karlodinium armiger

Marine algae from the genus Karlodinium are known to be involved in fish-killing events worldwide. Here we report for the first time the chemistry and bioactivity of a natural product from the newly described mixotrophic dinoflagellate Karlodinium armiger. Our work describes the isolation and structural characterization of a new polyhydroxy-polyene named karmitoxin. The structure elucidation work was facilitated by use of 13C enrichment and high-field 2D NMR spectroscopy, where 1H–13C long-range correlations turned out to be very informative. Karmitoxin is structurally related to amphidinols and karlotoxins; however it differs by containing the longest carbon–carbon backbone discovered for this class of compounds, as well as a primary amino group. Karmitoxin showed potent nanomolar cytotoxic activity in an RTgill-W1 cell assay as well as rapid immobilization and eventual mortality of the copepod Acartia tonsa, a natural grazer of K. armiger.
Kvægbesætninger er sårbare for indkøb af dyr med paratuberkulose

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology
Authors: Kirkeby, C. T. (Intern)
Pages: 26-27
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Dansk Veterinaertidsskrift
Volume: 2017
Issue number: 13
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
ISI indexed (2013): ISI indexed no
Laboratory examinations of transmissible spongiform encephalopathies in Denmark during 2016

The aim of this report is to give detailed information on the diagnostic examination on transmissible spongiform encephalopathies (TSE) performed in Denmark during 2016. The present annual report is the 21st on this topic published by the National Veterinary Institute, Technical University of Denmark (DTU-VET). The report is made to fulfil the demands given by the EU Commission (Regulation No 999/2001 of the European Parliament and the Council of 22 May 2001) and the Office International des Epizooties (OIE) (Manual of Diagnostic Tests and Vaccines for Terrestrial Animals, 5th edition 2008, Chapter 2.4.6 and Chapter 2.7.13) regarding diagnostic examinations. The DTU-VET is the national reference laboratory of bovine spongiform encephalopathy (BSE) and TSE/Scrapie, and therefore the results of all neuropathological examinations on BSE and Scrapie in Denmark are given in the present report as in previous years.

General information
State: Published
Organisations: National Veterinary Institute, Pathology
Authors: Jensen, T. K. (Intern)
Number of pages: 9
Publication date: 2017

Publication information
Place of publication: Frederiksberg
Publisher: National Veterinary Institute
Original language: English
Main Research Area: Technical/natural sciences
Electronic versions:
EU_RAP_2016_DTU.pdf
Publication: Research › Report – Annual report year: 2017

Leaching of viruses and other microorganisms naturally occurring in pig slurry to tile drains on a well-structured loamy field in Denmark

The amount of animal manure used in modern agriculture is increasing due to the increase in global animal production. Pig slurry is known to contain zoonotic bacteria such as E. coli, Salmonella spp. and Campylobacter spp., and viruses such as hepatitis E virus and group A rotavirus. Coliform bacteria, present in manure, have previously been shown to leach into tile drains. This poses a potential threat to aquatic environments and may also influence the quality of drinking water. As knowledge is especially scarce about the fate of viruses when applied to fields in natural settings, this project sets out to investigate the leaching potential of six different microorganisms: E. coli and Enterococcus spp. (detected by colony assay), somatic coliphages (using plaque assays), and hepatitis E virus, porcine circovirus type 2, and group A rotavirus (by real-time polymerase chain reaction). All six microorganisms leached through the soil entering the tile drains situated at 1-m depth the first day following pig slurry application. The leaching pattern of group A rotavirus differed substantially from the pattern for somatic coliphages, which are otherwise used as indicators for virus contamination. Furthermore, group A rotavirus was detected in monitoring wells at 3.5-m depth up to 2 months after pig slurry application. The detection of viral genomic material in drainage water and shallow groundwater signifies a potential hazard to human health that needs to be investigated further, as water reservoirs used for recreational use and drinking water are potentially contaminated with zoonotic pathogens.

General information
State: Published
Organisations: National Veterinary Institute, Virology, Bacteriology & Parasitology, National Food Institute, Research Group for Microbial Food Safety, University of Copenhagen, Geological Survey of Denmark and Greenland, Aarhus University
Authors: Krog, J. S. (Intern), Forslund, A. (Intern), Larsen, L. E. (Intern), Dalsgaard, A. (Ekstern), Kjaer, J. (Ekstern), Olsen, P. (Ekstern), Schultz, A. C. (Intern)
Livestock-associated methicillin-resistant Staphylococcus aureus is widespread in farmed mink (Neovison vison)

Livestock-associated methicillin-resistant Staphylococcus aureus (LA-MRSA) clonal complex (CC) 398 is widespread in the Danish pig production with around 90% of herds being positive. Since 2009, cases of CC398 LA-MRSA infections in Danish mink farmers have been observed. The objective of the study was to examine the presence of LA-MRSA in farmed mink. The investigation comprised three different sample types 1) clinical samples from carcasses submitted to the laboratory for diagnostic examination, 2) paws and pharyngeal swabs from healthy animals collected at pelting, and 3) feed samples from mink feed producers. In clinical samples, LA-MRSA was found in 34% of submissions and was most prevalent in samples from paws (33%) and pharynx (17%), followed by nasal and intestinal samples (each 13%), whereas it was never detected in perineal samples. LA-MRSA was found in healthy animals on 40% of the investigated farms, including paw samples (29%) and pharyngeal samples (16%). Twenty out of the 108 feed samples from feed producers were positive for LA-MRSA. The dominant spa-types were t034 and t011 associated to CC398, corresponding to the dominant spa-types detected in the Danish pig production, from which slaughter offal is used for mink feed. The spa-types, the high prevalence of LA-MRSA on paws and in pharynx, and its detection in feed samples, suggest feed as a possible source of LA-MRSA in mink.
Local infusion of Staphylococcus aureus into the porcine internal carotid artery as a model of sepsis-related brain abscesses - A pilot study

Brain pathology is an important aspect of human sepsis but is difficult to study in human patients. Therefore, animal models of sepsis-related brain pathology are needed. As pigs mirror multiple aspects of sepsis-related brain pathology in humans, this makes the pig a potentially suitable model. Unfortunately, models of sepsis in pigs are difficult to manage due to the accompanying massive systemic inflammatory response. To overcome these difficulties we designed a model in pigs of brain bacteremia established by local brain infusion in order to evaluate if this approach could reduce the systemic responses but still reflect the brain pathology of sepsis in humans. As a pilot study to obtain basic knowledge, we evaluated two methods of local infusion: long term infusion (60 minutes) of Staphylococcus aureus suspended in saline and, short-term infusion (10 minutes) of S. aureus embedded in autologous microthrombi. The study revealed: 1) bacteria suspended in saline as well as embedded in microthrombi can pass through the rete mirabile and thereby cause local brain bacteremia; 2) despite the high dose of S. aureus used for infusion, only mild clinical signs developed; and 3) despite the mild clinical signs, one pig had developed a brain microabscess by 48 h after infusion. The brain pathology present in this pig thereby reflected human cases of S. aureus-sepsis with microabscess formation as the predominant lesion. In addition, the abscess morphology mirrored previously observed microabscesses in experimental porcine S. aureus sepsis models.

General information
State: Published
Organisations: National Veterinary Institute, Bacteriology & Parasitology, University of Copenhagen
Authors: Astrup, L. B. (Intern), Iburg, T. M. (Intern), Agerholm, J. S. (Ekstern), Aalbæk, B. (Ekstern), Nielsen, O. L. (Ekstern), Leifsson, P. S. (Ekstern)
Long-term sex-differential effects of neonatal vitamin A supplementation on in vitro cytokine responses

High-dose vitamin A supplementation (VAS) may affect mortality to infectious diseases in a sex-differential manner. Here, we analysed the long-term immunological effects of neonatal vitamin A supplementation (NVAS) in 247 children, who had been randomly allocated to 50 000 or 25 000 IU vitamin A (15 mg and 7.5 mg retinol equivalents, respectively) or placebo
at birth. At 4-6 months of age, we assessed bacille Calmette-Guerin (BCG) scarification, and we analysed in vitro responses of TNF-α, IL-5, IL-10, IL-13 and IFN-γ in whole blood stimulations to phytohaemagglutinin (PHA), purified protein derivative (PPD), tetanus toxoid and lipopolysaccharide. There were no differences between the two doses of NVAS, and thus they were analysed combined as NVAS (any dose) v. placebo. All analyses were performed unstratified and by sex. NVAS increased the chance of having a scar after BCG vaccination in females (NVAS v. placebo: 96 v. 71 %, proportion ratio: 1.24; 95 % CI 1.09, 1.42), but not in males ($P_{\text{for interaction}}=0.012$). NVAS was associated with significant sex-differential effects on the pro- to anti-inflammatory cytokine ratios (TNF-α:IL-10) to PPD, tetanus toxoid and medium alone, which were increased in females but decreased in males. In addition, IL-17 responses tended to be increased in NVAS v. placebo recipients in males but not in females, significantly so for the PHA stimulation. The study corroborates sex-differential effects of VAS on the immune system, emphasising the importance of analysing VAS effects by sex.

**General information**

State: Published

Organisations: National Veterinary Institute, Adaptive Immunology, INDEPTH Network, Statens Serum Institut, Aarhus University Hospital, Monash University

Authors: Jensen, K. J. (Intern), Søndergaard, M. J. (Ekstern), Andersen, A. (Ekstern), Martins, C. (Ekstern), Erikstrup, C. (Ekstern), Aaby, P. (Ekstern), Flanagan, K. L. (Ekstern), Benn, C. S. (Ekstern)

Pages: 942-948

Publication date: 2017

Main Research Area: Technical/natural sciences

**Publication information**

Journal: British Journal of Nutrition

Volume: 118

Issue number: 11

ISSN (Print): 0007-1145

Ratings:

BFI (2018): BFI-level 1

Web of Science (2018): Indexed yes

BFI (2017): BFI-level 1

Scopus rating (2017): SNIP 1.555 SJR 1.756 CiteScore 3.65

Web of Science (2017): Indexed yes

BFI (2016): BFI-level 1

Scopus rating (2016): CiteScore 3.46 SJR 2.055 SNIP 1.535

Web of Science (2016): Indexed yes

BFI (2015): BFI-level 1

Scopus rating (2015): SJR 1.583 SNIP 1.442 CiteScore 3.52

Web of Science (2015): Indexed yes

BFI (2014): BFI-level 1

Scopus rating (2014): SJR 1.532 SNIP 1.273 CiteScore 3.18

Web of Science (2014): Indexed yes

BFI (2013): BFI-level 1

Scopus rating (2013): SJR 2.746 SNIP 2.479 CiteScore 3.61

ISI indexed (2013): ISI indexed yes

Web of Science (2013): Indexed yes

BFI (2012): BFI-level 1

Scopus rating (2012): SJR 2.308 SNIP 2.427 CiteScore 3.12

ISI indexed (2012): ISI indexed yes

Web of Science (2012): Indexed yes

BFI (2011): BFI-level 1

Scopus rating (2011): SJR 2.085 SNIP 1.649 CiteScore 3.13

ISI indexed (2011): ISI indexed yes

Web of Science (2011): Indexed yes

BFI (2010): BFI-level 1

Scopus rating (2010): SJR 1.236 SNIP 1.253

Web of Science (2010): Indexed yes

BFI (2009): BFI-level 1

Scopus rating (2009): SJR 0.627 SNIP 0.572
Loss of prion protein induces a primed state of type I interferon-responsive genes

The cellular prion protein (PrPC) has been extensively studied because of its pivotal role in prion diseases; however, its functions remain incompletely understood. A unique line of goats has been identified that carries a nonsense mutation that abolishes synthesis of PrPC. In these animals, the PrP-encoding mRNA is rapidly degraded. Goats without PrPC are valuable in re-addressing loss-of-function phenotypes observed in Prnp knockout mice. As PrPC has been ascribed various roles in immune cells, we analyzed transcriptomic responses to loss of PrPC in peripheral blood mononuclear cells (PBMCs) from normal goat kids (n = 8, PRNP+/+) and goat kids without PrPC (n = 8, PRNPter/ter) by mRNA sequencing. PBMCs normally express moderate levels of PrPC. The vast majority of genes were similarly expressed in the two groups. However, a curated list of 86 differentially expressed genes delineated the two genotypes. About 70% of these were classified as interferon-responsive genes. In goats without PrPC, the majority of type I interferon-responsive genes were in a primed, modestly upregulated state, with fold changes ranging from 1.4 to 3.7. Among these were ISG15, DDX58 (RIG-1), MX1, MX2, OAS1, OAS2 and DRAM1, all of which have important roles in pathogen defense, cell proliferation, apoptosis, immunomodulation and DNA damage response. Our data suggest that PrPC contributes to the fine-tuning of resting state PBMCs expression level of type I interferon-responsive genes. The molecular mechanism by which this is achieved will be an important topic for further research into PrPC physiology.

General information
State: Published
Organisations: National Veterinary Institute, Innate Immunology, Norwegian University of Life Sciences, Oslo University Hospital
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: P L o S One
Volume: 12
Issue number: 6
Article number: e0179881
Low antigen dose formulated in CAF09 adjuvant Favours a cytotoxic T-cell response following intraperitoneal immunization in Göttingen minipigs

The relationship between the antigen dose and the quality of an immune response generated upon immunization is poorly understood. However, findings show that the immune system is indeed influenced by the antigen dose; hence underlining the importance of correctly determining which dose to use in order to generate a certain type of immune response. To investigate this area further, we used Göttingen minipigs as an animal model especially due to the similar body size and
high degree of immunome similarity between humans and pigs. In this study, we show that both a humoral and a cell-mediated immune (CMI) response can be generated following intraperitoneal immunization with tetanus toxoid (TT) formulated in the CAF09 liposomal adjuvant. Importantly, a low antigen dose induced more TT-specific polyfunctional T cells, whereas antigen-specific IgG production was observed upon high-dose immunization. Independent of antigen dose, intraperitoneal administration of antigen increased the amount of TT-specific cytotoxic CD8β+ T cells within the cytokine-producing T-cell pool when compared to the non-cytokine producing T-cell compartment. Taken together, these results demonstrate that a full protein formulated in the CAF09 adjuvant and administered to pigs via the intraperitoneal route effectively generates a cytotoxic T-cell response. Moreover, we confirm the inverse relationship between the antigen dose and the induction of polyfunctional T cells in a large animal model. These findings can have implications for the design of upcoming vaccine trials aiming at establishing a cytotoxic T-cell response.

General information
State: Published
Organisations: National Veterinary Institute, Adaptive Immunology, T-cells & Cancer, University of Copenhagen, Copenhagen University Hospital
Authors: Overgaard, N. H. (Intern), Frøsig, T. M. (Intern), Jakobsen, J. T. (Intern), Buus, S. (Ekstern), Andersen, M. H. (Ekstern), Jungersen, G. (Intern)
Pages: 5629-5636
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Vaccine
Volume: 35
Issue number: 42
ISSN (Print): 0264-410X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.19 SJR 1.863 SNIP 1.124
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.33 SJR 1.985 SNIP 1.142
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.073 SNIP 1.248 CiteScore 3.45
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.105 SNIP 1.218 CiteScore 3.57
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.752 SNIP 1.115 CiteScore 3.43
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.656 SNIP 1.154 CiteScore 3.56
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.744 SNIP 1.269 CiteScore 3.86
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.663 SNIP 1.21
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.453 SNIP 1.21
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.355 SNIP 1.027
Scopus rating (2007): SJR 1.299 SNIP 1.114
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.328 SNIP 1.167
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.219 SNIP 1.068
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 1.17 SNIP 1.172
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 1.153 SNIP 1.125
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 1.277 SNIP 0.997
Scopus rating (2001): SJR 1.012 SNIP 1.03
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 0.739 SNIP 1.011
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 1 SNIP 1.244
Original language: English
Administration route, Antibody responses, Antigen dose, Cytokine production, Cytotoxic T cells, Immunization
Electronic versions:
1_s2.0_S0264410X17311556_main.pdf
DOIs:
10.1016/j.vaccine.2017.08.057

Bibliographical note
This is an open access article under the CC BY-NC-ND license.
Source: Findit
Source-ID: 2373640268
Publication: Research - peer-review › Journal article – Annual report year: 2017

Lungebetændelse hos mink med ansamlinger af mononukleære inflammationsceller

General information
State: Published
Organisations: National Veterinary Institute, Pathology, Virology, Diagnostic & Development
Authors: Hansen, M. S. (Intern), Krog, J. S. (Intern), Hjulsager, C. K. (Intern), Chriél, M. (Intern), Larsen, L. E. (Intern), Kokotovic, B. (Intern)
Pages: 113-119
Publication date: 2017

Host publication information
Title of host publication: Faglig årsberetning 2016 : Kopenhagen Fur
Place of publication: Aarhus N
Publisher: Kopenhagen Fur
Main Research Area: Technical/natural sciences
mink, non-suppurative pneumonia
Electronic versions:
DTU1.pdf
Source: PublicationPreSubmission
Source-ID: 130665236
Publication: Research - peer-review › Book chapter – Annual report year: 2017

Mårhund - risikovurdering, biologi og erfæringsgrundlag for en "best practice" i forhold til regulering

General information
State: Published
Organisations: National Veterinary Institute, Diagnostic & Development
Methods for estimating disease transmission rates: Evaluating the precision of Poisson regression and two novel methods

Precise estimates of disease transmission rates are critical for epidemiological simulation models. Most often these rates must be estimated from longitudinal field data, which are costly and time-consuming to conduct. Consequently, measures to reduce cost like increased sampling intervals or subsampling of the population are implemented. To assess the impact of such measures we implement two different SIS models to simulate disease transmission: A simple closed population model and a realistic dairy herd including population dynamics. We analyze the accuracy of different methods for estimating the transmission rate. We use data from the two simulation models and vary the sampling intervals and the size of the population sampled. We devise two new methods to determine transmission rate, and compare these to the frequently used Poisson regression method in both epidemic and endemic situations. For most tested scenarios these new methods perform similar or better than Poisson regression, especially in the case of long sampling intervals. We conclude that transmission rate estimates are easily biased, which is important to take into account when using these rates in simulation models.
Microbiota analysis of environmental slurry and its potential role as a reservoir of bovine digital dermatitis pathogens

At present, very little information exists regarding what role the environmental slurry may play as an infection reservoir and/or route of transmission for bovine digital dermatitis (DD), a disease which is a global problem in dairy herds. To investigate, if DD-related bacteria belong to the indigenous microbiota of the dairy herd environment, we used deep amplicon sequencing of the 16S RNA gene in 135 slurry samples collected from different sites in 22 dairy farms, with and without DD-infected cows. Both the general bacterial populations as well as digital dermatitis-associated Treponema were targeted in this study. The results revealed significant differences in the bacterial communities between the herds, with only 12 bacterial taxa shared across at least 80% of all the individual samples. These differences in the herd microbiota appeared to reflect mainly between-herd variation. Not surprisingly, the slurry was dominated by ubiquitous gastrointestinal bacteria, such as Ruminococcaceae and Lachnospiraceae. Despite the low relative abundance of spirochetes, which ranged from 0 to 0.6%, we were able to detect small amounts of bacterial DNA from DD-associated treponemes in the slurry. However, the DD-associated Treponema spp. were only detected in samples from herds with reported problems of DD. These data indicate that treponemes involved in the pathogenesis of DD are not part of the normal environmental microflora in dairy herds without clinical DD and, consequently, that slurry is not a primary reservoir of infection. Importance Bovine digital dermatitis (DD), a dermal disease which causes lameness in dairy cattle, is a serious problem worldwide. To control this disease, the infection reservoirs and transmission routes of DD pathogens need to be clarified. The dairy herd slurry may be a possible pathogen reservoir of DD-associated bacteria. The rationale for the present study was, therefore, to examine whether DD-associated bacteria are always present in slurry or if they are only found in DD-afflicted herds. The results strongly indicated that DD Treponema are not part of the indigenous slurry and, therefore, do not comprise an infection reservoir in healthy herds. This study applied next-generation sequencing technology to decipher the microbial compositions of environmental slurry of dairy herds with and without digital dermatitis.
We quantified the difference between the meteorological temperature recorded by the Danish Meteorological Institute (DMI) weather stations and the actual microclimatic temperatures at two or three different heights at six potential insect habitats. We then compared the impact of the hourly temperature on the extrinsic incubation period (EIP) of six pathogens. Finally, we developed a regression model, enabling us to predict the microclimatic temperatures of different habitats based on five standard meteorological parameters readily available from any meteorological institution. Microclimatic habitats were on average 3.5–5°C warmer than the DMI recorded temperatures during midday and 1–3°C cooler at midnight. The estimated EIP for five of the six microclimatic habitats was shorter than the estimates based on DMI temperatures for all pathogens studied. The microclimatic temperatures also predicted a longer season for virus development compared to DMI temperatures. Based on DMI data of hourly temperature, solar radiation, wind speed, rain and humidity, we were able...
to predict the microclimatic temperature of different habitats with an R2 of 0.87–0.96. Using only meteorological temperatures for vector-borne disease transmission models may substantially underestimate both the daily potential for virus development and the duration of the potential transmission season.

**General information**

State: Published
Organisations: National Veterinary Institute, Epidemiology, Danish Meteorological Institute
Authors: Haider, N. (Intern), Kirkeby, C. T. (Intern), Kristensen, B. (Intern), Kjær, L. J. (Intern), Havskov Sørensen, J. (Ekstern), Bedker, R. (Intern)
Publication date: 2017
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Scientific Reports
Volume: 7
Article number: 8175
ISSN (Print): 2045-2322
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.36 SJR 1.533 SNIP 1.245
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.63 SJR 1.692 SNIP 1.354
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.034 SNIP 1.597 CiteScore 5.3
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.163 SNIP 1.554 CiteScore 4.75
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.998 SNIP 1.57 CiteScore 4.06
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.531 SNIP 0.962 CiteScore 2.44
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
ISI indexed (2011): ISI indexed no
Original language: English
Entomology, Infectious diseases, Public health
Electronic versions:
Haider_et_al_2017_Scientific_Reports.pdf
DOIs:
10.1038/s41598-017-08514-9

**Bibliographical note**

This article is licensed under a Creative Commons Attribution 4.0 International License.
Publication: Research - peer-review › Journal article – Annual report year: 2017

**Microclimatic temperatures of Danish cattle farms: a better understanding of the variation in transmission potential of Schmallenberg virus**

Background: Insects inhabiting the surroundings of a cattle farm are exposed to microclimatic temperatures of the habitats surrounding the farm. Microclimatic temperatures are key drivers of the extrinsic incubation period (EIP), the speed by which an infected insect becomes infectious. The objective of this study was to quantify the variation of EIP of Schmallenberg virus among Danish cattle farms and identify possible spatial patterns of the EIPs. Methods: We quantified 21 different land cover classes within a 500 meter radius of all cattle farms in Denmark (N=22092) using CORINE land cover and regrouped them into four major land cover types: dry meadow, wet meadow, hedges, and forest. We then obtained the meteorological temperatures and other parameters (solar radiation, wind speed, humidity) near the farm from
the Danish Meteorological Institute (DMI) for the period of 2000-2016. Using recently developed microclimatic temperature prediction models for those four major land cover types, we calculated the hourly microclimatic temperatures of each farm based on their surrounding habitat types and meteorological parameters. We then modelled the daily EIP of Schmallenberg virus for each farm for each year of the period of 2000-2016 using both hourly DMI and hourly microclimatic temperatures and calculated mean EIP of 17 years for each farm. Finally, we plotted the average spatial pattern of farm level EIP for spring (May-June), summer (July-August) and autumn (September-October) in Denmark for the 17 years. Results: Of the 22082 cattle farms, we were able to predict the hourly microclimatic temperatures of 22006 farms (99.6%) - the rest of the farms had habitats either not suitable for insects resting or the microclimatic model was not able to calculate the temperature of the surrounding land covers. We found a surprisingly large between-farm variation in EIP between farms on a specific day. For example, in the year 2016, the EIP of all farms varied (5th and 95th percentiles) from 9-19 days on May 1st, 12-23 days on July 1st and 11-21 days on September 1st. The mean EIP of Schmallenberg virus [inter quartile range (IQR)] of all the cattle farms during spring, summer, and autumn for 17 years period were 16 [13-17], 15 [13-16] and 40 [38-42] days respectively, when using microclimatic temperatures. These estimated EIP values were much shorter compared to EIP estimated using DMI temperatures for the same periods of spring (29 [27-30]), summer (21 [19-24]), and autumn (56 [55-58]) days respectively. For the summer period, we observed a large area where farms with shorter EIP for Schmallenberg virus were grouped together, comprising southern Funen and associated islands, Lolland, Falster, and southern Zealand. Conclusion: Microclimatic temperature is highly important for understanding and predicting insect-borne virus transmission on Danish cattle farms. We were able to predict the daily farm level EIP of Schmallenberg virus for 17 years. We found large variation in EIP between farms and also a spatial pattern with a strong geographical trend suggesting that disease transmission may vary substantially between regions even in a small country like Denmark – and this could be useful for designing risk based surveillance for emerging and reemerging vector-borne diseases.

### MicroRNA and the innate immune response to Influenza A virus infection in pigs

Influenza A virus infections are a major public health concern. Many million cases of disease associated with influenza A virus occur every year during seasonal epidemics, and especially vulnerable populations such as the elderly, pregnant women, young children, and individuals with underlying conditions such as diabetes and patients of autoimmune diseases are at higher risk of severe complications from influenza A virus infection. However, in otherwise healthy individuals, influenza A virus infection is relatively short-lived, commonly being cleared within one to two weeks. Influenza A virus causes respiratory infection, primarily infecting the respiratory epithelial cells. In the time span from influenza A virus infection until specific antibodies and cytotoxic T lymphocytes arrive at the site of infection, innate immunity is highly important for restricting viral spread and facilitating development of a tailored adaptive immune response. Upon infection, the influenza A virus is recognized by innate viral pathogen sensors which initiate the induction of a balanced pro- and anti-inflammatory cytokine response as well as the hallmark interferon response, inducing an ‘antiviral state’ in the infected cell as well as neighboring cells. As with numerous other cellular processes, the innate host response is modulated by microRNAs, a class of short non-coding RNAs important for the regulation of translation of protein-coding gene transcripts. Comprehensive assessment of the transcriptional host response to influenza A virus infection requires the joint expression profiling of protein-coding gene and microRNA expression. Paper 1 is a review which emphasizes the importance of the pig in the study of influenza A virus infections. Pigs are themselves natural hosts for influenza A virus, and our close relationship with this species poses an ever present risk of emergence of zoonotic influenza A virus strains. The porcine response to influenza A virus infection greatly mirrors human conditions, and the pig thus represents an important animal model with great translational value for the study of human influenza A virus infection. Paper 2 presents results demonstrating the temporal dynamics of microRNA expression in circulating leukocytes from pigs after influenza A virus challenge, and emphasizes the need for control of the time parameter in suitable animal models for the evaluation of the biomarker potential of circulating microRNAs. Differential microRNA expression in circulating leukocytes peaks two weeks after challenge, suggesting that microRNAs may influence susceptibility to secondary infections. The study likewise shows that the expression profile of protein-coding genes in porcine circulating leukocytes mirrors what is seen in humans after natural or experimental influenza A virus infection. Paper 3 examines the local innate immune and microRNA response in the lungs of pigs after influenza A virus challenge. In contrast to observations in circulating leukocytes, differential microRNA expression peaks three days after challenge, suggesting that pulmonary microRNA expression may be aimed at modulating the rapid transcriptional pro-inflammatory response which peaks already one day after challenge. Paper 4 compares the local lung microRNA expression in vaccinated and unvaccinated pigs after influenza A virus challenge. Vaccinated and unvaccinated pigs displayed significantly different clinical signs, with a more severe course of disease observed in unvaccinated pigs presenting. This difference in disease severity was reflected in the pulmonary transcriptional innate host response of protein-coding genes and microRNA during infection. Target analysis of the
differentially expressed microRNA between the two groups of pigs indicated the involvement of microRNAs in host innate and adaptive immune responses, apoptosis, and lung regeneration.

**General information**
State: Published
Organisations: National Veterinary Institute, Innate Immunology, Virology
Authors: Brogaard, L. (Intern), Skovgaard, K. (Intern), Larsen, L. E. (Intern)
Number of pages: 188
Publication date: 2017

**Publication information**
Publisher: Technical University of Denmark (DTU)
Original language: English
Main Research Area: Technical/natural sciences
Electronic versions:
PhD Louise Brogaard

**Relations**
Projects:
MicroRNA and the innate immune response to influenza A virus infection in pigs
Publication: Research › Ph.D. thesis – Annual report year: 2017

Mikrobiologisk kvalitet af minkfoder

**General information**
State: Published
Organisations: National Veterinary Institute, Diagnostic & Development, Innate Immunology, Virology, Research Group for Genomic Epidemiology, Bacteriology & Parasitology, National Food Institute, Research Group for Analytical Food Chemistry, Department of Biotechnology and Biomedicine, Fungal Degradation
Authors: Lyhs, U. (Intern), Nonnemann, B. (Intern), Hjulsager, C. K. (Intern), Pedersen, K. (Intern), Chriél, M. (Intern), Frandsen, H. L. (Intern), Andersen, B. (Intern)
Pages: 111-116
Publication date: 2017
Main Research Area: Technical/natural sciences

**Publication information**
Journal: Faglig Arsberetning
Volume: 2017
ISSN (Print): 2445-9437
Original language: English
Minkfoder, Mikrobiologisk kvalitet
Electronic versions:
Mikrobiologisk_kvalitet_af_minkfoder.pdf
Links:
Source: PublicationPreSubmission
Source-ID: 146104559
Publication: Research - peer-review › Journal article – Annual report year: 2018

Mink kan også have influenza
De senere år er der i flere tilfælde fundet influenzavirus i mink med kompliceret og dødelig lungebetændelse. I Danmark rekvireres undersøgelse for influenzavirus imidlertid kun sjældent i forbindelse med diagnostiske indsendelser fra syge mink. Derfor undersøges der i reglen kun for influenzavirus, hvis der opstår mistanke om influenza ved obduktionen, eller hvis der er alvorlige langvarige
udbrud. For at kunne iværksætte foranstaltninger, der begrænser forekomsten af influenza hos mink, er det nødvendigt at kende udbredelsen af influenzavirus blandt farmede mink i Danmark. Formålet med denne undersøgelse var at gennemføre en systematisk overvågning af forekomsten af influenzavirus i lungerne fra mink indsendt til diagnostisk undersøgelse på DTU Veterinærinstituttet uanset årsag. Der blev indsamlet materiale i 2016 i perioden fra sommer til pelsning og desuden indgik mink anvendt til et minkobduktionskursus, samt vilde mink. Der blev påvist influenza A virus i mink fra otte farme. Genetiske analyser indikerede, at disse virus stammede fra både danske svin og mennesker. For at forebygge udbrud af influenza i farmede mink anbefales det, at undgå kontakt mellem mink og influenzafyge personer, samt sikre at minkfoder indeholdende biprodukter fra slagtesvin er varmebehandlet eller inaktiveret på anden vis.

**General information**
State: Published
Organisations: National Veterinary Institute, Virology, Bacteriology & Parasitology, Diagnostic & Development
Authors: Hjulsager, C. K. (Intern), Krog, J. S. (Intern), Larsen, G. (Intern), Chriél, M. (Intern), Larsen, L. E. (Intern)
Pages: 102-105
Publication date: 2017
Main Research Area: Technical/natural sciences

**Publication information**
Journal: Faglig Årsberetning
Volume: 2017
ISSN (Print): 2445-9437
Original language: English
Influenza A virus, Mink, Zoonose
Electronic versions: Mink_kan ogs have influenza.pdf
Links: https://www.kopenhagenfur.com/da/pelsdyravl/fagligt-og-forskning/faglige-aarsberetninger/
Source: PublicationPreSubmission
Source-ID: 146104619
Publication: Research - peer-review › Journal article – Annual report year: 2018

**Mitochondrial genome evolution in Alismatales: Size reduction and extensive loss of ribosomal protein genes**
The order Alismatales is a hotspot for evolution of plant mitochondrial genomes characterized by remarkable differences in genome size, substitution rates, RNA editing, retrotranscription, gene loss and intron loss. Here we have sequenced the complete mitogenomes of Zostera marina and Stratiotes aloides, which together with previously sequenced mitogenomes from Butomus and Spirodela, provide new evolutionary evidence of genome size reduction, gene loss and transfer to the nucleus. The Zostera mitogenome includes a large portion of DNA transferred from the plastome, yet it is the smallest known mitogenome from a non-parasitic plant. Using a broad sample of the Alismatales, the evolutionary history of ribosomal protein gene loss is analyzed. In Zostera almost all ribosomal protein genes are lost from the mitogenome, but only some can be found in the nucleus.

**General information**
State: Published
Organisations: National Veterinary Institute, Fish Diseases, University of Copenhagen, University of British Columbia, Cornell University
Authors: Petersen, G. (Ekstern), Cuenca, A. (Intern), Zervas, A. (Ekstern), Ross, G. T. (Ekstern), Graham, S. W. (Ekstern), Barrett, C. F. (Ekstern), Davis, J. I. (Ekstern), Seberg, O. (Ekstern)
Number of pages: 21
Publication date: 2017
Main Research Area: Technical/natural sciences

**Publication information**
Journal: PLoS One
Volume: 12
Issue number: 5
ISSN (Print): 1932-6203
Article number: e0177606
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.01 SJR 1.164 SNIP 1.111
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Modelling risk of tick exposure in southern Scandinavia using machine learning techniques, satellite imagery, and human population density maps

Vector-borne diseases such as Lyme disease and tick-borne encephalitis have become more common in recent decades and present a real health problem in many parts of Europe. Risk assessment, control, and prevention of these diseases require a better understanding of vector abundance as well as risk factors determining human exposure to ticks. There is a great need for analyses and models that can predict how vectors and their associated diseases are distributed and how this relates to high risk areas for human exposure. As a part of the ScandTick Innovation project, we surveyed ticks at approximately 30 sites (forests and meadows) in each of Denmark, southern Norway and south-eastern Sweden. At each site we measured presence/absence of ticks, and used the data obtained along with environmental satellite images to run Boosted Regression Tree machine learning algorithms to predict overall spatial distribution (probability of presence) in southern Scandinavia. Together with the predicted distribution maps, we used human density maps to determine areas with high risk of exposure to ticks. For nymphs, the predicted distribution found corresponded well with known distributions of ticks in Scandinavia, with more widespread distribution in Denmark compared to Norway and Sweden. In the Norwegian region, probability of presence was markedly higher nearer the coastline and the data shows a latitudinal boundary in the Swedish region above which probability of presence was low or close to zero. Presence of larvae was much more
clustered in the observed data, which was also reflected in the predicted distribution maps for the region. Whereas the predicted distribution of larvae was mostly even throughout Denmark, larvae were primarily around the coastlines in Norway and Sweden. When combining these distribution maps with human population density maps and accounting for area accessibility, we could assess the proportion of the population living in areas where ticks were present. Our data showed that although ticks are found in a limited proportion of the total region area (particularly for Norway and Sweden), areas with high population densities tend to overlap with these zones. Machine learning techniques allow us to predict for larger areas without having to perform extensive sampling all over the region in question, and we were able to produce models and maps with high predictive value. The results from these models help us pinpoint areas with high risk of exposure to ticks and thus potentially tick-borne diseases.

**General information**

- **State:** Published
- **Organisations:** National Veterinary Institute, Epidemiology, Bacteriology & Parasitology, University of Agder, Norwegian Institute of Public Health, Swedish University of Agricultural Sciences
- **Authors:** Kjær, L. J. (Intern), Korslund, L. (Ekstern), Kjelland, V. (Ekstern), Slettan, A. (Ekstern), Andreassen, Å. K. (Ekstern), Paulsen, K. M. (Ekstern), Christensson, M. (Ekstern), Kjellander, P. (Ekstern), Teräväinen, M. (Ekstern), Soleng, A. (Ekstern), Edgar, K. S. (Ekstern), Lindstedt, H. H. (Ekstern), Schou, K. K. (Intern), Bødker, R. (Intern)
- **Publication date:** 2017
- **Event:** Abstract from 4th Conference on Neglected Vectors and Vector-Borne Diseases, Chania, Greece.
- **Main Research Area:** Technical/natural sciences
- **Electronic versions:** Kjaer_1_oral_2.pdf
- **Source:** PublicationPreSubmission
- **Source-ID:** 137132505
- **Publication:** Research - peer-review › Conference abstract for conference – Annual report year: 2017

**Modelling spread of MRSA within a pig herd**

**General information**

- **State:** Published
- **Organisations:** National Veterinary Institute, Epidemiology, Bacteriology & Parasitology, Statens Serum Institut
- **Authors:** Sørensen, A. I. V. (Intern), Toft, N. (Intern), Espinosa-Gongora, C. (Intern), Græsbøll, K. (Intern), Boklund, A. (Intern), Larsen, J. (Ekstern), Hisham Beshara Halasa, T. (Intern)
- **Number of pages:** 1
- **Publication date:** 2017
- **Event:** Poster session presented at 2017 Annual Meeting of SVEPM 2017, 29-31 March, Inverness, Scotland, Scotland, United Kingdom.
- **Main Research Area:** Technical/natural sciences
- **Electronic versions:** S_rensen_Modelling_spread_of_MRSA_within_a_pig_herd_210317.pdf
- **Source:** PublicationPreSubmission
- **Source-ID:** 131630255
- **Publication:** Research - peer-review › Poster – Annual report year: 2017

**Modelling tick abundance using machine learning techniques and satellite imagery**

Recently, focus on tick-borne diseases has increased as diseases such as Lyme disease and tickborne encephalitis have become more widespread and represent a real health problem in many parts of Europe. Effective control and prevention of these diseases requires a better understanding of the factors affecting the vectors. There is a great need for analyses and models that can predict how vectors and their associated diseases are distributed now and possibly in the future. As a part of the ScandTick Innovation project, we surveyed and collected ticks at approximately 30 sites in each of Denmark, southern Norway and south-eastern Sweden. At each site we measured presence/absence and relative tick abundance using north- and east-facing line transect, where number of larvae, nymphs and adult females and males were counted at eight 50 m transects. We used the data obtained along with environmental satellite images to run Boosted Regression Tree machine learning algorithms to predict overall distribution (presence/absence of ticks) and relative tick abundance of nymphs and larvae in southern Scandinavia. For nymphs, the predicted abundance had a positive correlation with observed abundance and the spatial variation found corresponded well with known abundance and distributions of ticks in Scandinavia, with higher abundance and more widespread distribution in Denmark compared to Norway and Sweden. Because abundance was strongly correlated with forested habitats the risk areas were much larger in Sweden and Norway compared to Denmark. In both the Norwegian and Swedish regions, abundance was markedly higher nearer the coastline. Presence of larvae was much more clustered in the observed data, which was also reflected in the predicted abundance and distribution maps for the region. Whereas the predicted distribution of larvae was mostly even throughout Denmark, it was primarily around the coastlines in Norway and Sweden. Abundance was fairly low overall except in some fragmented patches corresponding to forested habitats in the region. Machine learning techniques allow us to predict for larger areas without having to perform extensive sampling all over the region in question. The results from these models can be used in epidemiological models and can help us determine areas under risk of disease transmission and help us
interpret human incidence data. Next step will be to analyze the collected ticks for pathogens and using the same machine learning techniques to develop prevalence maps of the ScandTick region.

**General information**

State: Published
Organisations: National Veterinary Institute, Epidemiology, Bacteriology & Parasitology, University of Agder, Norwegian Institute of Public Health, Swedish University of Agricultural Sciences
Authors: Kjær, L. J. (Intern), Korslund, L. (Ekstern), Kjelland, V. (Ekstern), Slettan, A. (Ekstern), Andreassen, Å. K. (Ekstern), Paulsen, K. M. (Ekstern), Christensson, M. (Ekstern), Kjellander, P. (Ekstern), Teräväinen, M. (Ekstern), Solem, A. (Ekstern), Edgar, K. S. (Ekstern), Lindstedt, H. H. (Ekstern), Schou, K. K. (Intern), Bødker, R. (Intern)
Publication date: 2017
Main Research Area: Technical/natural sciences

**Modulation of the Immune System by Epigenetic Therapy: A Rationale for Combined Use of DNA Methyltransferase Inhibitors and Immune Checkpoint Inhibitors**

**General information**

State: Published
Organisations: National Veterinary Institute, T-cells & Cancer
Pages: S46-S47
Publication date: 2017
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Annals of Hematology
Volume: 96
Issue number: Suppl. 1
ISSN (Print): 0939-5555
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.897 SJR 1.043 CiteScore 1.82
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.93 SJR 1.269 SNIP 0.979
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.093 SNIP 1.09 CiteScore 1.84
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.983 SNIP 0.979 CiteScore 1.72
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.93 SNIP 0.964 CiteScore 1.73
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.998 SNIP 0.976 CiteScore 1.85
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.141 SNIP 1.09 CiteScore 1.87
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Molecular diagnostics of aleutian mink disease virus: applied use of next generation sequencing and phylogenetics

Aleutian Mink Disease virus (AMDV) is a parvovirus causing Aleutian Mink Disease (AMD), often referred to as plasmacytosis. It is a systemic infection affecting mink of all ages, and is globally the most important pathogen impacting mink farming. In Denmark AMDV has since 1999 been monitored by a national control program, which is based on serological screening of all animals and encourages infected farms to stamp out. Historically there has been no consensus about which genomic region of the virus to analyse e.g. in relation to surveillance, and most previous studies in this regard, have been based either on partial or entire genes, or on pure epidemiological data. Thus, when initiating this project, little was known about AMDV’s total genomic diversity and how the virus was spread between farms.

Recent advances in the field of molecular diagnostics have made high throughput tools such as next generation sequencing cheaper and more easily available. Whole genome sequencing and advanced phylogenetic analyses have successfully been applied to describe the molecular evolution and transmission patterns for viruses such as Foot and Mouth Disease Virus (FMDV), Ebola, and avian influenza virus, however not previously for AMDV. The overall aim with this thesis was to investigate if next generation sequencing and phylogenetic analyses of full length isolates could improve our understanding of the total genomic diversity and evolution of AMDV. Additionally, we wanted to evaluate if this knowledge could contribute to the elucidation of AMDV transmission between farms and improve molecular diagnostics. During the first phase of this project a method for performing whole genome sequencing of AMDV was developed. This protocol enabled the sequencing of a large number of in vivo infectious AMDV isolates and provided the necessary dataset to act as foundation for the remaining analyses in the thesis. The first original paper (Manuscript 1) describes this protocol.

Manuscript 2 is a proof-of-concept study which demonstrated the advantage of using the whole genome sequence approach, compared to the in Denmark traditionally used partial NS1 gene sequencing, for the elucidation of transmission pathways between farms. The study was performed on samples from a small local AMDV outbreak, and clearly illustrated that the phylogenies based on partial NS1 gene sequencing were uninformative and could not be used for determining transmission pathways, even in the light of supporting epidemiological data. The whole-genome approach on the other hand, confirmed the epidemiological hypothesis about the direction of spread.

In Manuscript 3, the methodologies from Manuscript 1 and 2 were applied to generate the to-date most comprehensive phylogenetic and genetic analysis of full-length AMDV isolates, composed of more than 200 field strains. The study shed light on the diversity and evolutionary behaviour of two distinct AMDV strains, in addition to providing the first robust evolutionary rate-estimates. Altogether, the work presented in this thesis provides a contribution to the molecular diagnostics of AMDV, enables us better to understand the virus’ evolutionary behaviour in the context of mink farming, and is anticipated to be of value for more accurately tracing back in time the emergence of future outbreaks.
Morfologisk og molekylær karakterisering af en eimeriaart fra danske mink

Mortality in Danish Swine herds: Spatio-temporal clusters and risk factors
The aim of this study was to explore spatio-temporal mortality patterns in Danish swine herds from December 2013 to October 2015, and to discuss the use of mortality data for syndromic surveillance in Denmark. Although it has previously been assessed within the context of syndromic surveillance, the value of mortality data generated on a regular and mandatory basis from all swine herds remains unexplored in terms of swine surveillance in Denmark.

A total of 5010 farms were included in the analysis, corresponding to 1896 weaner herds, 1490 sow herds and 3839 finisher herds. The spatio-temporal analysis included data description for spatial, temporal, and spatio-temporal cluster analysis for three age groups: weaners (up to 30 kg), sows and finishers. Logistic regression models were used to assess the potential factors associated with finisher and weaner herds being included within multiple-herd clusters.

The spatio-temporal distribution of mortality changed over time, and suggested a general increase in mortality for the months of January and July for the three age groups. A large number of single-herd clusters (i.e. clusters with only one herd), and fewer multiple-herd clusters (i.e. clusters with at least two herds) were found. The herd size affected whether weaner herds were within multiple-herd clusters, and factors such farm type, SPF status and presence of atrophic rhinitis had an impact on finisher herds being inside vs. outside multiple-herd clusters in the univariable analysis. However, due to a strong correlation between variables, only farm type remained in the multivariable analysis for the finisher herds. The higher mortality observed for the months of January and July could be linked to infrequent updates of the data used to...
calculate mortality. The presence of single-herd clusters might indicate welfare and disease issues, while multiple-herd clusters could suggest the presence of infectious diseases within the cluster area. The impact of farm type is linked to the fact that larger farms specialize in only one age group, with high biosecurity and more specialized personnel, and subsequently a lower mortality.

Mortality data have a potential use in disease surveillance. However, detected clusters might not be due to disease, but the result of changes such as herd management practices. Further analysis to explore other spatio-temporal monitoring methods is needed before mortality data can be incorporated into a Danish disease monitoring system.

**General information**

State: Published
Organisations: National Veterinary Institute, Epidemiology, University of Southern Denmark
Authors: Lopes Antunes, A. C. (Intern), Ersbøll, A. K. (Ekstern), Bihrmann, K. (Forskerdatabase), Toft, N. (Intern)
Pages: 41-48
Publication date: 2017
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Preventive Veterinary Medicine
Volume: 145
ISSN (Print): 0167-5877
Ratings:

- BFI (2018): BFI-level 2
- Web of Science (2018): Indexed yes
- BFI (2017): BFI-level 2
- Scopus rating (2017): SNIP 1.31 SJR 1.144 CiteScore 2.26
- Web of Science (2017): Indexed yes
- BFI (2016): BFI-level 2
- Scopus rating (2016): CiteScore 2.2 SJR 1.249 SNIP 1.361
- Web of Science (2016): Indexed yes
- BFI (2015): BFI-level 2
- Scopus rating (2015): SJR 1.282 SNIP 1.177 CiteScore 2.1
- Web of Science (2015): Indexed yes
- BFI (2014): BFI-level 2
- Scopus rating (2014): SJR 1.27 SNIP 1.407 CiteScore 2.37
- Web of Science (2014): Indexed yes
- BFI (2013): BFI-level 2
- Scopus rating (2013): SJR 1.264 SNIP 1.529 CiteScore 2.49
- ISI indexed (2013): ISI indexed yes
- Web of Science (2013): Indexed yes
- BFI (2012): BFI-level 2
- Scopus rating (2012): SJR 1.265 SNIP 1.436 CiteScore 2.45
- ISI indexed (2012): ISI indexed yes
- Web of Science (2012): Indexed yes
- BFI (2011): BFI-level 2
- Scopus rating (2011): SJR 1.194 SNIP 1.295 CiteScore 2.24
- ISI indexed (2011): ISI indexed yes
- Web of Science (2011): Indexed yes
- BFI (2010): BFI-level 2
- Scopus rating (2010): SJR 1.156 SNIP 1.284
- Web of Science (2010): Indexed yes
- BFI (2009): BFI-level 2
- Scopus rating (2009): SJR 1.032 SNIP 1.338
- Web of Science (2009): Indexed yes
- BFI (2008): BFI-level 2
- Scopus rating (2008): SJR 1.056 SNIP 1.258
- Web of Science (2008): Indexed yes
- Scopus rating (2007): SJR 1.009 SNIP 1.353
MRSA i mink (Neovison vison) indsendt til diagnostik

General information
State: Published
Organisations: National Veterinary Institute, Bacteriology & Parasitology, Diagnostic & Development
Authors: Larsen, G. (Intern), Chriél, M. (Intern), Hansen, J. E. (Intern), Pedersen, K. (Intern)
Pages: 149-152
Publication date: 2017

Host publication information
Title of host publication: Faglig årsberetning 2016 : Kopenhagen Fur
Place of publication: Aarhus N
Publisher: Kopenhagen Fur
Main Research Area: Technical/natural sciences
Electronic versions:
DTU2.pdf
Publication: Research - peer-review › Book chapter – Annual report year: 2017

Mulighederne for en bedre udnyttelse af de økonomiske ressourcer til det veterinære beredskab for mund- og klovsyge

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, University of Copenhagen
Authors: Christensen, T. (Ekstern), Denver, S. (Ekstern), Boklund, A. (Intern), Halasa, T. (Intern)
Number of pages: 33
Publication date: 2017

Publication information
Publisher: Københavns Universitet
Original language: Danish
Series: IFRO udredning
Volume: 2017
Number: 22
Main Research Area: Technical/natural sciences
Electronic versions:
Multispectral polarimetric modulation spectroscopy for species and sex determination of malaria disease vectors
A multispectral polarimetric optical detection system with kHz sample rates was implemented to determine mosquito species and sex in flight. This system measures backscattered and extinguished light from mosquitoes at two wavelengths in both co- and de-polarized modes.

MuPeXI: prediction of neo-epitopes from tumor sequencing data
Personalization of immunotherapies such as cancer vaccines and adoptive T cell therapy depends on identification of patient-specific neo-epitopes that can be specifically targeted. MuPeXI, the mutant peptide extractor and informer, is a program to identify tumor-specific peptides and assess their potential to be neo-epitopes. The program input is a file with somatic mutation calls, a list of HLA types, and optionally a gene expression profile. The output is a table with all tumor-specific peptides derived from nucleotide substitutions, insertions, and deletions, along with comprehensive annotation, including HLA binding and similarity to normal peptides. The peptides are sorted according to a priority score which is intended to roughly predict immunogenicity. We applied MuPeXI to three tumors for which predicted MHC-binding peptides had been screened for T cell reactivity, and found that MuPeXI was able to prioritize immunogenic peptides with an area under the curve of 0.63. Compared to other available tools, MuPeXI provides more information and is easier to use. MuPeXI is available as stand-alone software and as a web server at http://www.cbs.dtu.dk/services/MuPeXI.
Understanding animal movements is an important factor for the development of meaningful surveillance and control programs, but also for the development of disease spread models. We analysed the Danish pig movement network using static and temporal network analysis tools to provide deeper insight in the connection between holdings dealing with pigs, such as breeding and multiplier herds, production herds, slaughterhouses or traders. Pig movements, which occurred between 1st January 2006 and 31st December 2015 in Denmark, were summarized to investigate temporal trends such as the number of active holdings, the number of registered movements and the number of pigs moved. To identify holdings and holding types with potentially higher risk for introduction or spread of diseases via pig movements, we determined loyalty patterns, annual network components and contact chains for the 24 registered holding types. The total number of active holdings as well as the number of pig movements decreased during the study period while the holding sizes increased. Around 60-90% of connections between two pig holdings were present in two consecutive years and
around one third of the connections persisted within the considered time period. Weaner herds showed the highest level of in-loyalty, whereas we observed an intermediate level of in-loyalty for all breeding sites and for production herds. Boar stations, production herds and trade herds showed a high level of out-loyalty. Production herds constituted the highest proportion of holdings in the largest strongly connected component. All production sites showed low levels of in-going contact chains and we observed a high level of out-going contact chain for breeding and multiplier herds. Except for livestock auctions, all transit sites also showed low levels of out-going contact chains. Our results reflect the pyramidal structure of the underlying network. Based on the considered disease, the time frame for the calculation of network measurements needs to be adapted. Using these adapted values for loyalty and contact chains might help to identify holdings with high potential of spreading diseases and thus limit the outbreak size or support control or eradication of the considered pathogen.

**General information**

State: Published  
Organisations: National Veterinary Institute, Epidemiology, Friedrich-Loeffler-Institute  
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Publication date: 2017  
Main Research Area: Technical/natural sciences

**Publication information**

Journal: P L o S One  
Volume: 12  
Issue number: 6  
Article number: e0179915  
ISSN (Print): 1932-6203  
Ratings:  
BFI (2018): BFI-level 1  
Web of Science (2018): Indexed yes  
BFI (2017): BFI-level 1  
Scopus rating (2017): CiteScore 3.01 SJR 1.164 SNIP 1.111  
Web of Science (2017): Indexed yes  
BFI (2016): BFI-level 1  
Scopus rating (2016): CiteScore 3.11 SJR 1.236 SNIP 1.101  
Web of Science (2016): Indexed yes  
BFI (2015): BFI-level 1  
Scopus rating (2015): SJR 1.427 SNIP 1.136 CiteScore 3.32  
Web of Science (2015): Indexed yes  
BFI (2014): BFI-level 1  
Scopus rating (2014): SJR 1.559 SNIP 1.148 CiteScore 3.54  
Web of Science (2014): Indexed yes  
BFI (2013): BFI-level 1  
Scopus rating (2013): SJR 1.772 SNIP 1.153 CiteScore 3.94  
ISI indexed (2013): ISI indexed yes  
Web of Science (2013): Indexed yes  
BFI (2012): BFI-level 1  
Scopus rating (2012): SJR 1.982 SNIP 1.156 CiteScore 4.15  
ISI indexed (2012): ISI indexed yes  
Web of Science (2012): Indexed yes  
BFI (2011): BFI-level 1  
Scopus rating (2011): SJR 2.425 SNIP 1.233 CiteScore 4.58  
ISI indexed (2011): ISI indexed no  
Web of Science (2011): Indexed yes  
BFI (2010): BFI-level 1  
Scopus rating (2010): SJR 2.705 SNIP 1.178  
Web of Science (2010): Indexed yes  
BFI (2009): BFI-level 1  
Scopus rating (2009): SJR 2.614 SNIP 1.046  
Web of Science (2009): Indexed yes
New trends in important diseases affecting the culture of fish and molluscs in the ICES area 2002-2015

The ICES Working Group on Pathology and Diseases of Marine Organisms (WGPDMO) provides annual reviews of national reports on the disease status of wild and farmed fish and molluscs in the ICES area. In 2004, the group published a first report collating this information from 1998-2002. This second report aims to provide an update on the status of the major diseases described in the original report and also to provide an overview of new diseases which have emerged since the previous report was published.

General information
State: Published
Organisations: National Veterinary Institute, Fish Diseases, National Veterinary Institute Sweden, University of Aberdeen, Virginia Institute of Marine Science, Marine Institute, Cefas, Rutgers University, Fisheries and Oceans Canada, Norwegian Veterinary Institute
Number of pages: 57
Publication date: 2017

Publication information
Publisher: International Council for the Exploration of the Sea (ICES)
ISBN (Print): 978-87-7482-201-1
Original language: English

Series: ICES Cooperative Research Report
Number: 337
ISSN: 1017-6195
Main Research Area: Technical/natural sciences
Electronic versions:
CRR_337.pdf
DOIs:
10.17895/ices.pub.2800
Source: PublicationPreSubmission
Source-ID: 142997165
Publication: Research › Report – Annual report year: 2018

No evidence of enteric viral involvement in the new neonatal porcine diarrhoea syndrome in Danish pigs

The aim of this study was to investigate whether the syndrome New Neonatal Porcine Diarrhoea Syndrome (NNPDS) is associated with a viral aetiology. Four well-managed herds experiencing neonatal diarrhoea and suspected to be affected by NNPDS were included in a case-control set up. A total of 989 piglets were clinically examined on a daily basis. Samples from diarrhoeic and non-diarrhoeic piglets at the age of three to seven days were selected for extensive virological examination using specific real time polymerase chain reactions (qPCRs) and general virus detection methods. A total of 91.7% of the animals tested positive by reverse transcription qPCR (RT-qPCR) for porcine kobuvirus 1 (PKV-1) while 9% and 3% were found to be positive for rotavirus A and porcine teschovirus (PTV), respectively. The overall prevalence of porcine astrovirus (PAstV) was 75% with 69.8% of the PAstV positive pigs infected with PAstV type 3. No animals tested positive for rotavirus C, coronavirus (TGEV, PEDV and PRCV), sapovirus, enterovirus, parechovirus, saffoldvirus, cosavirus, klassevirus or porcine circovirus type 2 (PCV2). Microarray analyses performed on a total of 18 animals were all negative, as were eight animals examined by Transmission Electron Microscopy (TEM). Using Next
Generation de novo sequencing (de novo NGS) on pools of samples from case animals within all herds, PKV-1 was detected in four herds and rotavirus A, rotavirus C and PTV were detected in one herd each. Our detailed analyses of piglets from NNPDS-affected herds demonstrated that viruses did not pose a significant contribution to NNPDS. However, further investigations are needed to investigate if a systemic virus infection plays a role in the pathogenesis of NNPDS.

General information
State: Published
Organisations: National Veterinary Institute, Virology, Section for Bacteriology, Pathology and Parasitology, Bacteriology & Parasitology, Section for Virology, Diagnostic & Development, Danish Agriculture and Food Council, Swedish University of Agricultural Sciences, Statens Serum Institut, University of Copenhagen
Number of pages: 11
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: B M C Veterinary Research
Volume: 13
Issue number: 1
Article number: 315
ISSN (Print): 1746-6148
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.108 SJR 0.934 CiteScore 2.16
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.83 SJR 0.87 SNIP 1.011
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.981 SNIP 1.009 CiteScore 1.86
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.943 SNIP 1.018 CiteScore 1.81
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.861 SNIP 0.853 CiteScore 1.85
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.779 SNIP 1.023 CiteScore 1.94
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.165 SNIP 1.447 CiteScore 2.66
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.076 SNIP 1.396
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.969 SNIP 0.985
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.529 SNIP 0.811
Scopus rating (2007): SJR 0.565 SNIP 0.877
Scopus rating (2006): SJR 0.378 SNIP 1.098
Web of Science (2006): Indexed yes
Novel Chemokine-Based Immunotoxins for Potent and Selective Targeting of Cytomegalovirus Infected Cells

Immunotoxins as antiviral therapeutics are largely unexplored but have promising prospective due to their high selectivity potential and their unparalleled efficiency. One recent example targeted the virus-encoded G protein-coupled receptor US28 as a strategy for specific and efficient treatment of human cytomegalovirus (HCMV) infections. US28 is expressed on virus-infected cells and scavenges chemokines by rapid internalization. The chemokine-based fusion-toxin protein (FTP) consisted of a variant (F49A) of CX3CL1 specifically targeting US28 linked to the catalytic domain of Pseudomonas exotoxin A (PE). Here, we systematically seek to improve F49A-FTP by modifications in its three structural domains; we generated variants with (1) altered chemokine sequence (K14A, F49L, and F49E), (2) shortened and elongated linker region, and (3) modified toxin domain. Only F49L-FTP displayed higher selectivity in its binding to US28 versus CX3CR1, the endogenous receptor for CX3CL1, but this was not matched by a more selective killing of US28-expressing cells. A longer linker and different toxin variants decreased US28 affinity and selective killing. Thereby, F49A-FTP represents the best candidate for HCMV treatment. Many viruses encode internalizing receptors suggesting that not only HCMV but also, for instance, Epstein-Barr virus and Kaposi's sarcoma-associated herpesvirus may be targeted by FTPs.

General information
State: Published
Organisations: National Veterinary Institute, University of Copenhagen, INAGEN Aps
Authors: Spiess, K. (Ekstern), Jeppesen, M. G. (Ekstern), Malmgaard-Clausen, M. (Ekstern), Krzywkowski, K. (Ekstern), Kledal, T. N. (Intern), Rosenkilde, M. M. (Ekstern)
Number of pages: 12
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Immunology Research
Volume: 2017
Article number: 4069260
ISSN (Print): 2314-8861
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.37
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.25
Scopus rating (2015): CiteScore 2.78
Web of Science (2015): Indexed yes
ISI indexed (2013): ISI indexed yes
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
ISI indexed (2011): ISI indexed yes
Scopus rating (2005): SNIP 0.354
Scopus rating (2004): SNIP 0.256
Scopus rating (2003): SNIP 0.268
Scopus rating (2002): SNIP 0.461
Scopus rating (2001): SNIP 0.415
Scopus rating (2000): SNIP 0.297
Scopus rating (1999): SNIP 0.236
Original language: English
Novel tools to assist neoepitope targeting in personalized cancer immunotherapy

Current cancer immunotherapy approaches utilize the remarkable surveillance capacity of the human immune system, which is capable of recognizing and eliminating cancer cells based on identification of tumor-associated antigens arising as a consequence of the transformation process. Among these, mutational-derived neoepitopes have proved to be powerful targets for tumor elimination and mutational load has been shown to correlate with the clinical response to treatment with checkpoint inhibitors in many different tumor types. This suggests a crucial role for neoepitope recognition in T-cell-mediated tumor eradication. Consequently, strategies to further boost neoepitope recognition, through vaccination or adoptive cell transfer, has received substantial interest. Although such strategies have enormous potential, there are also considerable challenges associated with these approaches. In the present review, we will focus on how novel technological developments can facilitate and improve feasibility and efficacy in neoepitope targeting.
Nyt virus beskrevet hos svin – Porcine circovirus type 3 (PCV3)

General information
State: Published
Organisations: National Veterinary Institute, Virology, SEGES Pig Research Center
Authors: Larsen, L. E. (Intern), Sonne Kristensen, C. (Ekstern)
Number of pages: 3
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Dansk Svineproduktion
Volume: 2017
Issue number: juli
Article number: NOTAT NR. 1721
Original language: Danish
Electronic versions:
PCV3_svin_2017_Final.pdf
Links:
http://svineproduktion.dk/publikationer/kilder/notater/2017/1721
Source: PublicationPreSubmission
Source-ID: 140842806
Publication: Communication › Journal article – Annual report year: 2017

Opportunities and challenges when pooling milk samples using ELISA
Testing large quantities of samples in order to detect one or more test-positive sample(s) is expensive and time-consuming. It is possible to optimize this process by pooling samples. Two frameworks to produce different hierarchical and non-hierarchical pooling schemes were tested and compared to standard pooling. Their efficiency and the potential savings were determined as a function of prevalence and the number of pooled samples.

The potential benefit of pooling samples is dependent upon the changes in the analytical sensitivity and specificity of the test used when diluting test-positive samples by pooling. To illustrate this, the sensitivity of antibody ELISA on pooled samples of bovine milk for Salmonella Dublin, Mycobacterium avium spp. paratuberculosis, and bovine virus diarrhea was tested. For these milk assays, the analytical sensitivity decreased rapidly with increasing pool sizes.

The efficiency of pooling is usually only measured by the number of tests performed, yet real savings depend on all the costs involved in the pooling process. These may differ between laboratories depending on the available equipment and
the salaries of the technicians, among other factors. Therefore, several cost parameters were introduced to describe the total cost and thereby calculate the total savings. In terms of overall savings, both tested schemes were potentially optimal depending on the prevalence, possible pool size, and the cost of retesting. For the pool sizes of interest in this study, the three-stage hierarchical pooling scheme was often marginally more efficient in terms of the total number of tests. However, if the price of re-pooling was high, the two-stage scheme performed better in terms of total savings. In addition, for low prevalences and the possibility of pooling a large number of samples, the two-stage non-hierarchical test may be more efficient, both in terms of number of tests and overall cost. In order to apply these results in different laboratory settings, a free Shiny WebApp was developed, to compare several pooling schemes with different cost parameters.

**General information**
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology
Authors: Græsbøll, K. (Intern), Andresen, L. O. (Intern), Hisham Beshara Halasa, T. (Intern), Toft, N. (Intern)
Pages: 93-98
Publication date: 2017
Main Research Area: Technical/natural sciences

**Publication information**
Journal: Preventive Veterinary Medicine
Volume: 139
Issue number: Part B
ISSN (Print): 0167-5877
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 1.31 SJR 1.144 CiteScore 2.26
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.2 SJR 1.249 SNIP 1.361
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.282 SNIP 1.177 CiteScore 2.1
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.27 SNIP 1.407 CiteScore 2.37
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.264 SNIP 1.529 CiteScore 2.49
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.265 SNIP 1.436 CiteScore 2.45
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.194 SNIP 1.295 CiteScore 2.24
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.156 SNIP 1.284
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.032 SNIP 1.338
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.056 SNIP 1.258
Web of Science (2008): Indexed yes
Optag af IgG i tre dage gamle minkhvalpe

Minkhvalpe fødes med et meget ufærdigt immunsystem og med lave serumkoncentrationer af cirkulerende immunoglobuliner (IgG) (antistoffer). Derfor er det vigtigt at de hurtigt efter fødslen opnår høje koncentrationer af IgG i blodet ved passiv immuniserings via moderens IgG i kolostrum (råmælk) og mælk. Dette er afgørende for hvalpenes modstandsdygtighed over for smitte (bakterier og virus) i deres nærmiljø. I dette studie undersøgte vi overførsel af IgG ved at tildele IgG oralt til tre dage gamle hvalpe. Overførsel af IgG til blodet blev vurderet efter tre timer. For at se et specifik optag af mink IgG til blodcirkulationen gav vi nogle hvalpe IgG fra svin og nogle hvalpe mink IgG. De foreløbige resultater viser, at optaget ikke er specifikt for mink IgG, idet svine IgG også optages. Dog viser resultaterne, at optaget af mink IgG er procentmæssigt større end optaget af svine IgG, hvilket indikerer, at der findes en specifik Fc-receptor for mink IgG i hvalpenes tarmvæg. Fremtidige studier vil afklare hvorvidt en øget IgG serumkoncentration er korreleret med bedre beskyttelse mod "fedtede hvalpe" syndromet.

General information
State: Published
Organisations: National Veterinary Institute, Innate Immunology, Diagnostic & Development, Kopenhagen Fur, Vordingborg Gymnasium og HF
Authors: Mathiesen, R. (Intern), Heegaard, P. M. H. (Intern), Chriél, M. (Intern), Struve, T. (Ekstern), Uttenthal, Å. (Ekstern)
Pages: 119-122
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Faglig Årsberetning
Volume: 2017
ISSN (Print): 2445-9437
Original language: English
IgG, Mink, Oral overførsel, Svin
Electronic versions:
Optag_af_IgG_i_tre_dage_gamle_minkhvalpe.pdf
Links:
Source: PublicationPreSubmission
Outbreak tracking of Aleutian mink disease virus (AMDV) using partial NS1 gene sequencing

Aleutian Mink Disease (AMD) is an infectious disease of mink (Neovison vison) and globally a major cause of economic losses in mink farming. The disease is caused by Aleutian Mink Disease Virus (AMDV) that belongs to the genus Amdoparvovirus within the Parvoviridae family. Several strains have been described with varying virulence and the severity of infection also depends on the host's genotype and immune status. Clinical signs include respiratory distress in kits and unthriftiness and low quality of the pelts. The infection can also be subclinical. Systematic control of AMDV in Danish mink farms was voluntarily initiated in 1976. Over recent decades the disease was mainly restricted to the very northern part of the country (Northern Jutland), with only sporadic outbreaks outside this region. Most of the viruses from this region have remained very closely related at the nucleotide level for decades. However, in 2015, several outbreaks of AMDV occurred at mink farms throughout Denmark, and the sources of these outbreaks were not known. Partial NS1 gene sequencing, phylogenetic analyses data were utilized along with epidemiological to determine the origin of the outbreaks. The phylogenetic analyses of partial NS1 gene sequences revealed that the outbreaks were caused by two different clusters of viruses that were clearly different from the strains found in Northern Jutland. These clusters had restricted geographical distribution, and the variation within the clusters was remarkably low. The outbreaks on Zealand were epidemiologically linked and a close sequence match was found to two virus sequences from Sweden. The other cluster of outbreaks restricted to Jutland and Funen were linked to three feed producers (FP) but secondary transmissions between farms in the same geographical area could not be excluded. This study confirmed that partial NS1 sequencing can be used in outbreak tracking to determine major viral clusters of AMDV. Using this method, two new distinct AMDV clusters with low intra-cluster sequence diversity were identified, and epidemiological data helped to reveal possible ways of viral introduction into the affected herds.

General information
State: Published
Organisations: National Veterinary Institute, Virology, Diagnostic & Development, Department of Solid Mechanics, Kopenhagen Fur
Number of pages: 9
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Virology Journal
Volume: 14
Issue number: 119
ISSN (Print): 1743-422X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
Scopus rating (2017): SNIP 0.848 SJR 1.053 CiteScore 2.43
Web of Science (2017): Indexed Yes
Scopus rating (2016): CiteScore 2.43 SJR 1.154 SNIP 0.903
Scopus rating (2015): SJR 1.196 SNIP 0.945 CiteScore 2.47
Scopus rating (2014): SJR 1.057 SNIP 0.94 CiteScore 2.27
Web of Science (2014): Indexed yes
Scopus rating (2013): SJR 1.051 SNIP 0.989 CiteScore 2.44
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
Scopus rating (2012): SJR 0.973 SNIP 0.877 CiteScore 2.37
ISI indexed (2012): ISI indexed yes
Scopus rating (2011): SJR 1.06 SNIP 0.882 CiteScore 2.65
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
Scopus rating (2010): SJR 1.088 SNIP 0.875
Web of Science (2010): Indexed yes
Scopus rating (2009): SJR 1.004 SNIP 0.793
Scopus rating (2008): SJR 0.65 SNIP 0.572
Oversvømmelser aviard influenza i vilde fugle i Danmark 2016


Der blev for første gang i Danmark påvist højpatogen aviard influenza (HPAI) virus subtype H5N8. Det første fund var i en død trolland fundet den 7. november i Stadsgraven ved Christiania, København, og var først fundet i et efterfølgende større udbrud af HPAI i vilde fugle. H5N8 HPAI blev i alt påvist i 65 døde vildefugle (1 duehøg, 1 ederfugl, 3 havørne, 1 hættetromme, 5 knopsvaner, 5 musvåger, 1 ravn, 1 sangsvane, 3 stormmåger, 9 svartbags, 4 svelmåger, 28 trollande) fordelt over hele landet i 2016. Desuden blev influenza A virus, som ikke var H5 eller H7 subtype, påvist i en stormmåge.

De øvrige 138 prøver var negative for AI virus. HPAI H5N8 blev også påvist i en høv og en troldand fundet den 7. november i Stadsgraven ved Christiania, København, og var første fund i et større udbrud af HPAI i vilde fugle. H5N8 HPAI blev i alt påvist i 65 døde vildefugle (1 duehøg, 1 ederfugl, 3 havørne, 1 hættetromme, 5 knopsvaner, 5 musvåger, 1 ravn, 1 sangsvane, 3 stormmåger, 9 svartbags, 4 svelmåger, 28 trollande) fordelt over hele landet i 2016. Desuden blev influenza A virus, som ikke var H5 eller H7 subtype, påvist i en stormmåge.

Fylogenetisk analyse af HA fra LPAI H7 prøver fra vilde fugle, der blev indsamlet i Danmark de foregående år, samt med virus fravilde fugle og fjerkræ i Europa. Fylogenetisk analyse af LPAI H5 gener fra virus påvist i 2016 viste, at disse var nært beslægtede med H5 gener fra virus på fundet i andre fuglearter, hvilket er vigtigt i forhold til at være forberedt på nye emnerne AI virus.

Ligesom de foregående år viste mange pools sig at indeholde en blanding af flere subtyper. Subtyperne H3N8, H4N6 og H6N2 er de subtyper, der oftest er påvist i vildefugle. H3N8 er den mest almindelige subtype i vildefuglen i Danmark.

Der var fjernere beslægtet med HPAI H5N8 fundet i Europa i 2014/2015 og 2016. Fylogenetisk analyse af AI virus fra HPAI H7 virus viste at disse er nært beslægtede med den humanepatogene H7N9 virus variant fra Asien, der

Bibliographical note
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Source: FindIt
Source-ID: 2371667602
Publication: Research - peer-review > Journal article – Annual report year: 2017

Citation: Overvågning af aviard influenza i vilde fugle i Danmark 2016

Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 0.641 SNIP 0.614
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.938 SNIP 0.689
Scopus rating (2005): SJR 0.398 SNIP 0.358
Original language: English

DOI: 10.1186/s12985-017-0786-5

Scopus rating (2006): SJR 0.938 SNIP 0.689
Scopus rating (2005): SJR 0.398 SNIP 0.358

Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 0.641 SNIP 0.614
Web of Science (2007): Indexed yes

DOI: 10.1186/s12985-017-0786-5

Bibliographical note
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Source: FindIt
Source-ID: 2371667602
Publication: Research - peer-review > Journal article – Annual report year: 2017

Oversvømmelser aviard influenza i vilde fugle i Danmark 2016

Oversvømmelser af fugleinfluenza, aviard influenza (AI), på EU niveau går tilbage til 2002, og Danmark er underlagt EU kommissionens bestemmelser for udformning af overvågningen, der har skiftet gennem årene i takt med indhøstede erfaringer. I 2016 blev der udført passiv oversvømmelse af døde vilde fugle, der blev fundet i naturen. Der blev testet 204 fugle. Der blev for første gang i Danmark påvist højpatogen aviard influenza (HPAI) virus subtype H5N8. Det første fund var i en død trolland fundet den 7. november i Stadsgraven ved Christiania, København, og var først fundet i et efterfølgende større udbrud af HPAI i vilde fugle. H5N8 HPAI blev i alt påvist i 65 døde vildefugle (1 duehøg, 1 ederfugl, 3 havørne, 1 hættetromme, 5 knopsvaner, 5 musvåger, 1 ravn, 1 sangsvane, 3 stormmåger, 9 svartbags, 4 svelmåger, 28 trollande) fordelt over hele landet i 2016. Desuden blev influenza A virus, som ikke var H5 eller H7 subtype, påvist i en stormmåge.

Fylogenetisk analyse af HA fra LPAI H7 prøver fra vilde fugle, der blev indsamlet i Danmark de foregående år, samt med virus fravilde fugle og fjerkræ i Europa. Fylogenetisk analyse af LPAI H5 gener fra virus påvist i 2016 viste, at disse var nært beslægtede med H5 gener fra virus på fundet i andre fuglearter, hvilket er vigtigt i forhold til at være forberedt på nye emnerne AI virus.

Ligesom de foregående år viste mange pools sig at indeholde en blanding af flere subtyper. Subtyperne H3N8, H4N6 og H6N2 er de subtyper, der oftest er påvist i vildefugle. H3N8 er den mest almindelige subtype i vildefuglen i Danmark.

Der var fjernere beslægtet med HPAI H5N8 fundet i Europa i 2014/2015 og 2016. Fylogenetisk analyse af AI virus fra HPAI H7 virus viste at disse er nært beslægtede med den humanepatogene H7N9 virus variant fra Asien, der

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Source: FindIt
Source-ID: 2371667602
Publication: Research - peer-review > Journal article – Annual report year: 2017

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Oversvømmelser af fugleinfluenza, aviard influenza (AI), på EU niveau går tilbage til 2002, og Danmark er underlagt EU kommissionens bestemmelser for udformning af overvågningen, der har skiftet gennem årene i takt med indhøstede erfaringer. I 2016 blev der udført passiv oversvømmelse af døde vilde fugle, der blev fundet i naturen. Der blev testet 204 fugle. Der blev for første gang i Danmark påvist højpatogen aviard influenza (HPAI) virus subtype H5N8. Det første fund var i en død trolland fundet den 7. november i Stadsgraven ved Christiania, København, og var først fundet i et efterfølgende større udbrud af HPAI i vilde fugle. H5N8 HPAI blev i alt påvist i 65 døde vildefugle (1 duehøg, 1 ederfugl, 3 havørne, 1 hættetromme, 5 knopsvaner, 5 musvåger, 1 ravn, 1 sangsvane, 3 stormmåger, 9 svartbags, 4 svelmåger, 28 trollande) fordelt over hele landet i 2016. Desuden blev influenza A virus, som ikke var H5 eller H7 subtype, påvist i en stormmåge.

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Ligesom de foregående år viste mange pools sig at indeholde en blanding af flere subtyper. Subtyperne H3N8, H4N6 og H6N2 er de subtyper, der oftest er påvist i vildefugle. H5N8 HPAI blev i alt påvist i 65 døde vildefugle (1 duehøg, 1 ederfugl, 3 havørne, 1 hættetromme, 5 knopsvaner, 5 musvåger, 1 ravn, 1 sangsvane, 3 stormmåger, 9 svartbags, 4 svelmåger, 28 trollande) fordelt over hele landet i 2016. Desuden blev influenza A virus, som ikke var H5 eller H7 subtype, påvist i en stormmåge.

Fylogenetisk analyse af HA fra LPAI H7 virus viste at disse er nært beslægtede med den humanepatogene H7N9 virus variant fra Asien, der

General information
State: Published
Organisations: National Veterinary Institute, Virology, University of Copenhagen
Authors: Hjulsager, C. K. (Intern), Krog, J. S. (Intern), Madsen, J. J. (Ekster), Thorup, K. (Forskerdatabase), Larsen, L. E. (Intern)
Number of pages: 40
Publication date: 2017

Publication information
Place of publication: Frederiksborg C
Publisher: Veterinarinstituttet, Danmarks Tekniske Universitet
Original language: English
Main Research Area: Technical/natural sciences
Electronic versions:
Overvågning af LPAI virus i svin - Rutinrapport 2016

Overvågning af influenza A virus i svin - Rutinrapport 2016
en ny variant af H3huN2sw, med HA der svarer til den samtidig cirkulerende H3 influenza (sæson 2015/16), hvor vi tidligere kun harpåvist H3Hu fra sæson 2004/05. Det interessante ved dette virus er, at det er en triplereassortment, hvor alle de interne gener stammer fra H1N1pdm09 subtypen, mens N2 stammer fra H3N2/H1N2 fra svin, og H3 er af human oprindelse. Da det humane H3 gen har cirkuleret i mennesker siden 1968, må det formodes, at der er stor grad af immunitet i den humane population mod denne type. Derimod må det formodes, at hele den danske svinepopulation vil være fuldt modtagelige, da prævalensen af H3 virus har været meget lav i Danmark de senere år. Tilmeld viser undersøgelser, at antistoffer dannet mod de kommercielle vacciner, der anvendes i Danmark, har meget begrænset krydsereaktion til dette virus. Resultaterne fra overvågningen er vigtige i forhold til såvel zoonotiske som veterinære aspekter ved influenza A virus infektion i svin i Danmark. Undersøgelserne har bekræftet at H1N1pdm09, som stadig må betragtes som en zoonose, nu er etableret i den danske svinepopulation, hvor den cirkulerer uafhængigt af den humane influenzavirussæson. Overvågningen har endvidere påvist adskillige nye virus reassortments, hvor gener fra H1N1pdm09 indgår. Bl.a. tyder det på, at H1N2 virus med interne gener fra H1N1pdm09 har etableret sig i den danske svine population. Der er global bevågenhed omkring svineinfluenzavirus med interne gener fra H1N1pdm09, da der i flere tilfælde er vist smitte med sådanne virus til mennesker, fx H3N2v i USA. Overvågningen har bidraget til, at vi tidligt har påvist nye virus med zoonotisk potentiale: H3hu05N2sw og H3hu16N2sw. Dette betyder, at der kan foretages en nærmere genetisk og biologisk karakterisering af dette virus, hvilket kan danne evidens-baseret baggrundsviden for risikohåndteringen, i det tilfælde at der konstateres human smitte med dette virus. Den fremtidige overvågning vil bl.a. have fokus på at undersøge, om disse virus bliver etableret i danske svin. Fra et veterinært synspunkt er det vigtigt at få fastlagt hvilke(n) subtype(r), der cirkulerer i en besætning, da valg af vaccine er afhængig af denne information. Det er derfor positivt, at der, trods et lille fald i år, over de senere år er sket en stigning i antal indsendelser til influenzapåvisning i Danmark, da det øger muligheden for at vaccinere korrekt og derved nedbringe risikoen for antibiotikakrævende sekundære infektioner. Det er positivt, at de kommende år holdes øje med, om disse virus smitter til mennesker.

General information
State: Published
Organisations: National Veterinary Institute, Virology
Authors: Krog, J. S. (Intern), Hjulsager, C. K. (Intern), Larsen, L. E. (Intern)
Number of pages: 31
Publication date: 2017
**Pathogenicity of three genetically diverse strains of PRRSV Type 1 in specific pathogen free pigs**

Studies from Eastern European countries proved that porcine reproductive and respiratory syndrome virus Type 1 (PRRSV-1) harbours high genetic diversity and that genetically divergent subtypes 2-4 circulate in this area. In the present study, we compared the pathogenicity of two different PRRSV-1 subtype 2 strains and a strain representing PRRSV-1 subtype 1. Four groups of 8-week-old specific pathogen free pigs were either infected with subtype 2 strain ILI6, subtype 2 strain or BOR59, subtype 1 strain 18794, or mock inoculated. The most pronounced clinical signs were observed in pigs infected with BOR59. Pigs from both subtype 2 strain infected groups exhibited significantly elevated mean body temperatures on DPI 2 compared to the other two groups, the difference remaining significant up to DPI 13 for the BOR59 group, only. The pigs in the latter group also displayed significantly highest levels of early viremia together with the most rapid APP response. Overall, the results indicated that BOR59 strain can be considered a highly pathogenic strain, similarly to subtype 3 strains Lena and SU1-bel, while the virulence of the other subtype 2 strain ILI6 was intermediate between BOR59 and subtype 1 strain.

**General information**

State: Published
Organisations: National Veterinary Institute, Virology, Innate Immunology, Warsaw University of Life Sciences, National Veterinary Research Institute, Parco Technologico Padano
Authors: Stadejek, T. (Ekstern), Larsen, L. E. (Intern), Podgórska, K. (Ekstern), Bøtner, A. (Intern), Botti, S. (Ekstern), Dolka, I. (Ekstern), Fabisiak, M. (Ekstern), Heegaard, P. M. H. (Intern), Hjulsager, C. K. (Intern), Huć, T. (Ekstern), Kwisgaard, L. K. (Intern), Sapierzyński, R. (Ekstern), Nielsen, J. (Ekstern)
Pages: 13-19
Publication date: 2017
Main Research Area: Technical/natural sciences
PCV2 er påvist i lymfeknuder fra børe indsendt til USK

General information
State: Published
Organisations: National Veterinary Institute, Virology, Pathology
Authors: Thorup, F. (Ekstern), Haugegaard, S. (Ekstern), Kristensen, C. S. (Ekstern), Hjulsager, C. K. (Intern), Larsen, L. E. (Intern), Jensen, T. K. (Intern)
Number of pages: 8
Publication date: 2017
Main Research Area: Technical/natural sciences
PD-1⁺ polyfunctional T cells dominate the periphery after tumor-infiltrating lymphocyte therapy for cancer

Infusion of highly heterogeneous populations of autologous tumor-infiltrating lymphocytes (TILs) can result in tumor regression of exceptional duration. Initial tumor regression has been associated with persistence of tumor-specific TILs one month after infusion, but mechanisms leading to long-lived memory responses are currently unknown. Here we studied the dynamics of bulk tumor-reactive CD8⁺ T cell populations in patients with metastatic melanoma following treatment with TILs. Experimental Design: We analyzed the function and phenotype of tumor-reactive CD8⁺ T cells contained in serial blood samples of sixteen patients treated with TILs. Results: Polyfunctional tumor-reactive CD8⁺ T cells accumulated over time in the peripheral lymphocyte pool. Combinatorial analysis of multiple surface markers (CD57, CD27, CD45RO, PD-1 and LAG-3) showed a unique differentiation pattern of polyfunctional tumor-reactive CD8⁺ T cells, with highly specific PD-1 upregulation early after infusion. The differentiation and functional status appeared largely stable for up to 1 year post-infusion. Despite some degree of clonal diversification occurring in vivo within the bulk tumor-reactive CD8⁺ T cells, further analyses showed that CD8⁺ T cells specific for defined tumor-antigens had similar differentiation status. Conclusions: We demonstrated that tumor-reactive CD8⁺ T cell subsets which persist after TIL therapy are mostly polyfunctional, display a stable partially differentiated phenotype and express high levels of PD-1. These partially differentiated PD-1⁺ polyfunctional TILs have a high capacity for persistence and may be susceptible to PD-L1/PD-L2-mediated inhibition.
Peptide-MHC-directed expansion of multifunctional antigen-responsive T cells

General information
State: Published
Organisations: Department of Electrical Engineering, Section for Immunology and Vaccinology, National Veterinary Institute, T-cells & Cancer
Authors: Rasmussen, V. M. (Intern), Marquard, A. M. (Intern), Jacobsen, S. N. (Intern), Hadrup, S. R. (Intern)
Pages: 344
Publication date: 2017
Conference: 44th Annual Meeting of the Scandinavian Society of Immunology, Stockholm, Sweden, 17/10/2017 - 17/10/2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Scandinavian Journal of Immunology
Volume: 86
Issue number: 4
Article number: D-31415
ISSN (Print): 0300-9475
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.621 SJR 0.891 CiteScore 2.11
In this review, we briefly summarize the current understanding of how fungal pathogens can persist antifungal treatment without heritable resistance mutations by forming tolerant persister cells. Fungal infections tolerant to antifungal treatment have become a major medical problem. One mechanism leading to drug recalcitrance is the formation of antifungal persister cells. These cells have wild-type genotype with the ability to survive exposure to antifungal agents due to changed membrane composition, upregulated stress response, and enhanced cell wall integrity. Knowledge of the mechanisms regulating entry and exit of the persister phenotype is limited, but it has recently been shown that the inhibition of the growth regulating TORC1 pathway induces fungal persistence. The phenotypic properties of persister cells and the involvement of the TORC1 pathway indicate that persister cells are quiescent in G0 of the cell cycle. This
knowledge leads us to suggest that the identified shared drug-tolerance mechanisms of persister and quiescent cells may serve as a foundation for developing novel treatment strategies that are independent of growth mode against systemic fungal infections.
Population genomics of the raccoon dog (Nyctereutes procyonoides) in Denmark: insights into invasion history and population development

The raccoon dog (Nyctereutes procyonoides) has a wide distribution in Europe and is a prominent example of a highly adaptable alien species. It has been recorded sporadically in Denmark since 1980 but observations since 2008 suggested that the species had established a free-ranging, self-sustaining population. To elucidate the origin and genetic patterns of Danish raccoon dogs, we studied the population genomics of 190 individuals collected in Denmark (n = 141) together with reference captive individuals from Poland (n = 21) and feral individuals from different European localities (Germany, Poland, Estonia and Finland, n = 28). We used a novel genotyping-by-sequencing approach simultaneously identifying and genotyping a large panel of single nucleotide polymorphisms (n = 4526). Overall, there was significant indication for contemporary genetic structuring of the analysed raccoon dog populations, into at least four different clusters, in spite of the existence of long distance gene flow and secondary admixture from different population sources. The Danish population was characterized by a high level of genetic admixture with neighbouring feral European ancestries and the presence of private clusters, non-retrieved in any other feral or captive populations sampled. These results suggested that the raccoon dog population in Denmark was founded by escapees from genetically unidentified Danish captive stocks, followed by a recent admixture with individuals migrating from neighbouring Germany.
Positive correlation between Aeromonas salmonicida vaccine antigen concentration and protection in vaccinated rainbow trout Oncorhynchus mykiss evaluated by a tail fin infection model

Rainbow trout, Oncorhynchus mykiss (Walbaum), are able to raise a protective immune response against Aeromonas salmonicida subsp. salmonicida (AS) following injection vaccination with commercial vaccines containing formalin-killed bacteria, but the protection is often suboptimal under Danish mariculture conditions. We elucidated whether protection can be improved by increasing the concentration of antigen (formalin-killed bacteria) in the vaccine. Rainbow trout juveniles were vaccinated by intraperitoneal (i.p.) injection with a bacterin of Aeromonas salmonicida subsp. salmonicida strain 090710-1/23 in combination with Vibrio anguillarum serotypes O1 and O2a supplemented with an oil adjuvant. Three concentrations of AS antigens were applied. Fish were subsequently challenged with the homologous bacterial strain administered by perforation of the tail fin epidermis and 60-s contact with live A. salmonicida bacteria. The infection method proved to be efficient and could differentiate efficacies of different vaccines. It was shown that protection and antibody production in exposed fish were positively correlated to the AS antigen concentration in the vaccine.
Preclinical evaluation of NF-kappa B-triggered dendritic cells expressing the viral oncogenic driver of Merkel cell carcinoma for therapeutic vaccination

**Background:** Merkel cell carcinoma (MCC) is a rare but very aggressive skin tumor that develops after integration of a truncated form of the large T-antigen (truncLT) of the Merkel cell polyomavirus (MCV) into the host's genome. Therapeutic vaccination with dendritic cells (DCs) loaded with tumor antigens is an active form of immunotherapy, which intends to direct the immune system towards tumors which express the respective vaccination antigens.

**Methods:** Cytokine-matured monocyte-derived DCs of healthy donors and MCC patients were electroporated with mRNA encoding the truncLT. To permit major histocompatibility complex (MHC) class II next to class I presentation, we used an RNA construct in which the antigen was fused to a DCLamp sequence in addition to the unmodified antigen. To further improve their immunogenicity, the DCs were additionally activated by co-transfection with the constitutively active nuclear factor (NF)-κB activator calKK. These DCs were used to stimulate autologous CD8+ T-cells or a mixture of CD4+ and CD8+ T-cells. Then the percentage of T-cells, specific for the truncLT, was quantified by interferon (IFN)γ ELISpot assays.

**Results:** Both the truncLT and its DCLamp-fusion were detected within the DCs by flow cytometry, albeit the latter required blocking of the proteasome. The transfection with calKK upregulated maturation markers and induced cytokine production. After 2-3 rounds of stimulation, the T-cells from 11 out of 13 healthy donors recognized the antigen. DCs without calKK appeared in comparison less potent in inducing such responses. When using cells derived from MCC patients, we could induce responses for 3 out of 5 patients; however, here the calKK-transfected DCs did not display their superiority.

**Conclusion:** These results show that optimized DCs are able to induce MCV-antigen-specific T-cell responses. Therapeutic vaccination with such transfected DCs could direct the immune system against MCC.

**General information**

State: Published
Organisations: National Veterinary Institute, T-cells & Cancer, Friedrich-Alexander-Universität Erlangen-Nürnberg, Universitätssklinikum Erlangen, University of Freiburg
Authors: Gerer, K. F. (Ekstern), Erdmann, M. (Ekstern), Hadrup, S. R. (Intern), Lyngaa, R. B. (Intern), Martin, L. (Ekstern), Voll, R. E. (Ekstern), Schuler-Thurner, B. (Ekstern), Schuler, G. (Ekstern), Schaft, N. (Ekstern), Hoyer, S. (Ekstern), Doerrie, J. (Ekstern)
Number of pages: 14
Pages: 451-464
Publication date: 2017
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Therapeutic Advances in Medical Oncology
Volume: 9
Issue number: 7
ISSN (Print): 1758-8340
Original language: English
Adoptive cellular immunotherapy, Dendritic cells, Large T-antigen, Merkel cell carcinoma, Polyomavirus
Electronic versions:
10.1177_1758834017712630.pdf
DOIs:
10.1177/1758834017712630
Source: FindIt
Source-ID: 2371480653
Publication: Research - peer-review › Journal article – Annual report year: 2017

Predicting tick abundance in Southern Scandinavia using machine learning techniques and satellite imagery – a part of the ScandTick Innovation project

**General information**

State: Published
Organisations: National Veterinary Institute, Epidemiology, Bacteriology & Parasitology, University of Agder, Norwegian Institute of Public Health, Swedish University of Agricultural Sciences
Authors: Kjær, L. J. (Intern), Korslund, L. (Ekstern), Kjelland, V. (Ekstern), Slettan, A. (Ekstern), Andreassen, Å. K. (Ekstern), Paulsen, K. M. (Ekstern), Christensson, M. (Ekstern), Kjellander, P. (Ekstern), Teräväinen, M. (Ekstern), Soleng, A. (Ekstern), Edgar, K. S. (Ekstern), Lindstedt, H. H. (Ekstern), Schou, K. K. (Intern), Bødker, R. (Intern)
Number of pages: 1
Publication date: 2017
Prediction and in vitro verification of potential CTL epitopes conserved among PRRSV-2 strains

Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) is the causative agent of one of the most important porcine diseases with a high impact on animal health, welfare, and production economy. PRRSV exhibits a multitude of immunoevasive strategies that, in combination with a very high mutation rate, has hampered the development of safe and broadly protective vaccines. Aiming at a vaccine inducing an effective cytotoxic T cell response, a bioinformatics approach was taken to identify conserved PRRSV-derived peptides predicted to react broadly with common swine leukocyte antigen (SLA) class I alleles. Briefly, all possible 9- and 10-mer peptides were generated from 104 complete PRRSV type 2 genomes of confirmed high quality, and peptides with high binding affinity to five common SLAs were identified combining the NetMHCpan and positional scanning combinatorial peptide libraries binding predictions. Predicted binders were prioritized according to genomic conservation and SLA coverage using the PopCover algorithm. From this, 53 peptides were acquired for further analysis. Binding affinity and stability of a subset of 101 peptide-SLA combinations were validated in vitro for 4 of the 5 SLAs. Eventually, 23% of the predicted peptide-SLA combinations showed to form complexes with a dissociation half-life ≥30 min. Additionally, combining the two prediction methods proved to be more robust across alleles than either method used alone in terms of predicted-to-observed correlations. In summary, our approach represents a finely tuned epitope prediction pipeline providing a rationally selected ensemble of peptides for future in vivo experiments with pigs expressing the included SLAs.
The aim of this study was to investigate bacterial invasiveness of the bovine endometrium during the postpartum period. Fluorescence in situ hybridization was applied to endometrial biopsies using probes for Fusobacterium necrophorum, Porphyromonas levi, Trueperella pyogenes, Escherichia coli and a probe for bacteria in general (the overall domain Bacteria) to determine their tissue localization. Holstein cows were sampled at three time points postpartum (T1: 4–12 days postpartum, T2: 24–32 days postpartum and T3: 46–54 days postpartum). At T1, cows were clinically scored as having a uterine infection based on presence of a brownish, fetid vaginal discharge or as normal if having normal lochia. An endometrial biopsy was taken from all cows at T1 (n = 57). Endometrial biopsies were taken from the same cows at T2 and T3 if allowed by the size of the cervical canal and if the cow had not been inseminated. Fifty and 39 biopsies were obtained at T2 and T3, respectively. The biopsies were evaluated for inflammation and for presence and localization of bacteria. When analyzed by the probe for the entire domain Bacteria, bacteria were found in most biopsies irrespectively of time (T1: 79.0%, T2: 82.0%, T3: 89.7%). Fusobacterium necrophorum and Porphyromonas levi were often present in
the endometrium at T1 (61.1% and 47.8%, respectively), but the prevalence decreased significantly over time. Trueperella pyogenes and Escherichia coli were less prevalent at T1 (8.8% and 10.5%, respectively) and their prevalence also decreased significantly over time. Fusobacterium necrophorum and Porphyromonas levii were often co-localized intraepithelially or in the lamina propria. Trueperella pyogenes and Escherichia coli were located only on the endometrial surface. Due to the high prevalence of tissue invasiveness, these findings emphasize the importance of Fusobacterium necrophorum and Porphyromonas levii in postpartum uterine disease of cattle and indicate that tissue invasiveness is an important aspect of the pathogenesis.
Presence of bacteria in the endometrium and placentomes of pregnant cows

Bacterial invasion of the bovine uterus during the postpartum period occurs in most cows, but the general consensus is that these bacteria are eliminated before the next pregnancy. The pregnant uterus has therefore hitherto been considered a sterile environment, but this assumption has now been challenged by recent studies in humans, which indicate that bacteria can be present in the placenta of term pregnancies without causing abortion. The aim of the present study was therefore to investigate whether bacteria are present in the uterus of pregnant cows. Specimens were taken from the intercaruncular endometrium and from placentomes of slaughtered pregnant cows (n = 43) and subjected to histology, fluorescence in situ hybridization and massive parallel sequencing. Bacteria were observed in the tissue from 90.7% (39/43) of the cows by fluorescence in situ hybridization. Fusobacterium necrophorum, Porphyromonas levii and Trueperella pyogenes were located within the endometrium, on the endometrial surface and in the caruncular stroma, but their presence was not associated with inflammation. Data from massive parallel sequencing of the 16S rRNA gene from a subset of 15 cows indicated that the most abundant bacteria were the families Porphyromonadaceae, followed by Ruminococcaceae and Lachnospiraceae. Our results indicate that the bovine uterus is not a sterile environment during pregnancy as previously assumed and that a cow can carry a pregnancy despite the presence of a few potentially pathogenic bacteria in the uterus.

General information

State: Published
Organisations: National Veterinary Institute, Pathology, University of Copenhagen, Technical University of Denmark
Authors: Karstrup, C. C. (Ekstern), Klitgaard, K. (Ekstern), Jensen, T. K. (Intern), Agerholm, J. S. (Ekstern), Pedersen, H. G. (Ekstern)
Pages: 41-47
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information

Journal: Theriogenology
Volume: 99
ISSN (Print): 0093-691X
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 1.338 SJR 0.936 CiteScore 2.27
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 1.99 SJR 0.786 SNIP 1.192
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 0.862 SNIP 1.244 CiteScore 1.86
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 0.95 SNIP 1.348 CiteScore 2.12
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.084 SNIP 1.336 CiteScore 2.07
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 2
Presence of Coxiella burnetii DNA in inflamed bovine cardiac valves

Bacterial endocarditis is a recognised disease in humans and animals. In humans, infection with Coxiella burnetii can cause endocarditis, but this has not been investigated thoroughly in animals. Endocarditis in cattle is a common post-mortem finding in abattoirs and studies have identified Trueperella pyogenes as a major cause. Despite exposure of cattle to C. burnetii, the significance of this particular bacterium for development and progression of endocarditis has not been studied in detail. Cardiac valves of cattle affected with endocarditis (n = 100) were examined by histology, fluorescence in situ hybridization (FISH) and real time quantitative polymerase chain reaction (PCR). Serum was examined for anti-C. burnetii antibodies by enzyme-linked immunosorbent assay (ELISA). Serology revealed that 70% of the cattle were positive for antibodies to C. burnetii, while PCR analysis identified 25% of endocarditis valve samples as being positive. C. burnetii was not detected by FISH, probably due to the low infection levels. Most cattle had chronic valvular vegetative endocarditis with lesions being characterised by a core of fibrous tissue covered by significant amounts of fibrin, sometimes with areas of liquefaction, and with a coagulum covering the surface. In a few cases, including the case with the highest infection level, lesions were characterized by extensive fibrosis and calcification. Histologically, bacteria other than C. burnetii were observed in most cases. The presence of C. burnetii DNA is relatively common in cattle affected with valvular endocarditis. The role of C. burnetii remains however unknown as lesions did not differ between C. burnetii infected and non-infected cattle and because T. pyogenes-like bacteria were present in the inflamed valves; a bacterium able to induce the observed lesions. Heart valves of normal cattle should be investigated to assess if C. burnetii may be present without preexisting lesions.

General information
State: Published
Organisations: National Veterinary Institute, Pathology, University of Copenhagen, Wageningen University
Authors: Agerholm, J. S. (Ekstern), Jensen, T. K. (Intern), Agger, J. F. (Ekstern), Engelsma, M. Y. (Ekstern), Roest, H. I. J. (Ekstern)
Number of pages: 7
Publication date: 2017
Main Research Area: Technical/natural sciences
Prevention of colitis-associated cancer by selective targeting of immunoproteasome subunit LMP7

Chronic inflammation is a well-known risk factor in development of intestinal tumorigenesis, although the exact mechanisms underlying development of colitis-associated cancer (CAC) still remain obscure. The activity and function of immunoproteasome has been extensively analyzed in the context of inflammation and infectious diseases. Here, we show that the proteasomal immunosubunit LMP7 plays an essential role in development of CAC. Mice devoid of LMP7 were resistant to chronic inflammation and formation of neoplasia, and developed virtually no tumors after AOM/DSS treatment. Our data reveal that LMP7 deficiency resulted in reduced expression of pro-tumorigenic chemokines CXCL1, CXCL2 and...
CXCL3 as well as adhesion molecule VCAM-1. As a consequence, an impaired recruitment and activity of tumor-infiltrating leukocytes resulting in decreased secretion of cytokines IL-6 and TNF-α was observed. Further, the deletion or pharmacological inhibition of LMP7 and consequent blockade of NF-κB abrogated the production of IL-17A, which possesses a strong carcinogenic activity in the gut. Moreover, in vivo administration of the selective LMP7 inhibitor ONX-0914 led to a marked reduction of tumor numbers in wild-type (WT) mice. Collectively, we identified the immunoproteasome as a crucial mediator of inflammation-driven neoplasia highlighting a novel potential therapeutic approach to limit colonic tumorigenesis.

General information
State: Published
Organisations: National Veterinary Institute, Mucosal Immunology, Philipps-Universität Marburg, Hannover Medical School
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Number of pages: 13
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: OncoTarget
ISSN (Print): 1949-2553
Ratings:
Web of Science (2018): Indexed yes
Web of Science (2017): Indexed yes
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.551 SNIP 1.285 CiteScore 4.96
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 3.061 SNIP 1.261 CiteScore 5.26
Scopus rating (2012): SJR 2.512 SNIP 1.065 CiteScore 6.54
ISI indexed (2011): ISI indexed no
Scopus rating (2011): SJR 1.505 SNIP 0.489 CiteScore 3.38
ISI indexed (2011): ISI indexed no
Original language: English
NF-κB, colon cancer, immunoproteasome, inflammation
Electronic versions:
14579_216643_1_PB.pdf
DOIs:
10.18632/oncotarget.14579
Links:
http://www.impactjournals.com/oncotarget/index.php?journal=oncotarget&page=article&op=view&path%5b%5d=14579
Source: FindIt
Source-ID: 2351193000
Publication: Research - peer-review › Journal article – Annual report year: 2017

Projekt skal undersøge MRSA i danske mink

General information
State: Published
Organisations: National Veterinary Institute, Bacteriology & Parasitology, Diagnostic & Development
Authors: Fertner, M. E. (Intern), Hansen, J. E. (Intern), Larsen, G. (Intern), Pedersen, K. (Intern), Chriél, M. (Intern)
Pages: 33
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Purified natural pig immunoglobulins can substitute dietary zinc in reducing piglet post weaning diarrhoea

Enteric infectious disease in weaner piglets, including postweaning diarrhoea (PWD), are usually treated and/or prevented with antibiotics and/or zinc oxide in the piglet feed. However extensive use of antibiotics and zinc oxide in intensive animal production is unwanted as it may promote microbial antibiotic resistance and pose environmental problems. Recently, in an experimental model of PWD, we observed that oral administration of purified porcine immunoglobulin G (pplG) from pooled natural pig plasma could reduce enteric infection. In the present study we were able to reproduce these results as it was observed that oral pplG accelerated clearance of faecal haemolytic bacteria in pigs challenged with E. coli in comparison with pigs not receiving pplG. This effect was observed upon feeding pplG for seven days postweaning suggesting that pplG does not have to be used prophylactically for several days preweaning. Furthermore, the effect of oral administration of pplG for seven days postweaning was equal to or better than that of dietary zinc oxide in reducing diarrhoea symptoms and in clearing faecal haemolytic bacteria for 14 days postweaning. These observations warrant future trials of dietary pplG in intensive swine production units to establish its performance as an alternative to dietary antibiotics and zinc oxide for preventing PWD.
Quantification of within-sample genetic heterogeneity from SNP-array data

Intra-tumour genetic heterogeneity (ITH) fosters drug resistance and is a critical hurdle to clinical treatment. ITH can be well-measured using multi-region sampling but this is costly and challenging to implement. There is therefore a need for tools to estimate ITH in individual samples, using standard genomic data such as SNP-arrays, that could be implemented routinely. We designed two novel scores $S$ and $R$, respectively based on the Shannon diversity index and Ripley’s $L$ statistic of spatial homogeneity, to quantify ITH in single SNP-array samples. We created in-silico and in-vitro mixtures of tumour clones, in which diversity was known for benchmarking purposes. We found significant but highly-variable associations of our scores with diversity in-silico ($p < 0.001$) and moderate associations in-vitro ($p = 0.015$ and $p = 0.085$). Our scores were also correlated to previous ITH estimates from sequencing data but heterogeneity in the fraction of tumour cells present across samples hampered accurate quantification. The prognostic potential of both scores was moderate but significantly predictive of survival in several tumour types (corrected $p = 0.03$). Our work thus shows how individual SNP-arrays reveal intra-sample clonal diversity with moderate accuracy.

General information
State: Published
Rainbow trout red mark syndrome lesion development visualized

General information
State: Published
Organisations: National Veterinary Institute, Fish Diseases, University of Copenhagen
Publication date: 2017
Event: Poster session presented at 18th International Conference on Diseases of Fish and Shellfish, Belfast, United Kingdom.
Main Research Area: Technical/natural sciences
Source: FindIt
Regionalized Development and Maintenance of the Intestinal Adaptive Immune Landscape

The intestinal immune system has the daunting task of protecting us from pathogenic insults while limiting inflammatory responses against the resident commensal microbiota and providing tolerance to food antigens. This role is particularly impressive when one considers the vast mucosal surface and changing landscape that the intestinal immune system must monitor. In this review, we highlight regional differences in the development and composition of the adaptive immune landscape of the intestine and the impact of local intrinsic and environmental factors that shape this process. To conclude, we review the evidence for a critical window of opportunity for early-life exposures that affect immune development and alter disease susceptibility later in life.

General information
State: Published
Organisations: National Veterinary Institute, Mucosal Immunology, University of Calgary
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Number of pages: 17
Pages: 532-548
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication Information
Journal: Immunity
Volume: 46
Issue number: 4
ISSN (Print): 1074-7613
Ratings:
BFI (2018): BFI-level 3
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 15.82 SJR 13.393 SNIP 4.096
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 17.17 SJR 16.957 SNIP 4.635
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 16.417 SNIP 4.024 CiteScore 15.52
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 14.618 SNIP 3.98 CiteScore 15.26
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 15.902 SNIP 3.997 CiteScore 16.16
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 17.131 SNIP 4.027 CiteScore 15.89
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 18.565 SNIP 3.763
BFI (2009): BFI-level 2
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 15.352 SNIP 3.328
Scopus rating (2007): SJR 15.893 SNIP 3.519
Reporting guidelines for diagnostic accuracy studies that use Bayesian latent class models (STARD-BLCM)

Evaluation of medical tests is usually based on comparing their results to those from a perfect reference (gold standard) procedure. The Standards for Reporting of Diagnostic Accuracy (STARD) initiative (http://www.equator-network.org/reporting-guidelines/stard/) developed reporting guidelines for studies designed to estimate the accuracy of tests when disease status is known. The original STARD statement was initially published in seven journals, while an updated version — STARD2015 — has been recently released. More than 200 biomedical journals encourage its use in their instructions to authors. An affordable, reliable, and noninvasive reference standard does not always exist as is the case for infectious diseases with a long latent period (e.g., in chronic infections such as tuberculosis). In such situations test accuracy can be estimated using latent class models that do not require knowledge of disease status (i.e., disease status is a latent variable). Statistical methods were introduced in this context by Hui and Walter and have been successfully applied since then, with the majority of the work being carried out in a Bayesian framework. While STARD provides useful reporting guidelines for diagnostic accuracy studies when a reference standard is available, it required modification and extension to address crucial aspects that are unique to latent class analysis: In the absence of a perfect reference test, the target condition must be explicitly described when performing a latent class analysis to estimate test accuracy. Latent class models, in conjunction with what the tests under evaluation actually detect (e.g., organisms or immune responses to organisms), define the latent status. Thus, a definition/interpretation of the latent disease or infection under consideration from a biological perspective is critical to communicate effectively the contextual meaning of the sensitivity and specificity estimates. A detailed description of the latent class model and its assumptions is required. A meta-analysis found that 28% of the studies that used latent class models to estimate diagnostic test accuracy failed to report any evidence that assumptions were verified or that the underlying models were of adequate fit to the data at hand. Bayesian latent class analysis requires reporting the details and justification of the prior distributions used in the primary and sensitivity analysis. This task takes on increased importance when using non-identifiable latent class models. We adapted the STARD checklist in order to fulfill the reporting requirements for diagnostic test accuracy studies that use Bayesian latent class models. The new guidelines, termed Standards for the Reporting of Diagnostic accuracy studies that use Bayesian Latent Class Models, have been recently published and are available online (https://www.equator-network.org/reporting-guidelines/stard-b lcm/). Further, a mailing list has been created and those interested can freely subscribe (http://lists.uth.gr/mailman/listinfo/lcmate). Standards for the Reporting of Diagnostic accuracy studies that use Bayesian Latent Class Models is relevant to both Bayesian and frequentist estimation methods but the focus is on the former. It should prove to be a useful tool for the sound application of latent class models in the evaluation of diagnostic tests and promote optimal reporting practices for studies that use such models.

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, University of Thessaly, University of Copenhagen, Oregon State University, University of California, McGill University, University of Sydney, University of Prince Edward Island
Authors: Kostoulas, P. (Ekstern), Nielsen, S. S. (Ekstern), Branscum, A. J. (Ekstern), Johnson, W. O. (Ekstern), Dendukuri, N. (Ekstern), Dhand, N. K. (Ekstern), Toft, N. (Intern), Gardner, I. A. (Ekstern)
Pages: 3603-3604
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Statistics in Medicine
Volume: 36
Issue number: 23
ISSN (Print): 0277-6715
Ratings:
BFI (2018): BFI-level 2
Revision of the qualification framework at the Technical University of Denmark Part 2: Applications

Using a revised Qualification Framework (QF) with four main categories: -to know, - to be, -to interact, and -to do, this paper demonstrates how to use the elements of the QF to construct Programme-Qualification Matrices. A general Programme- Qualification Matrix defines the qualifications and their respective conceptual understanding common to all engineering programmes. This is complemented by programme-specific qualification matrices with added emphasis on content and context. Redesigned educational outcomes for three bachelor programmes are presented to demonstrate the versatility of the concept.

General information

State: Published
Organisations: Department of Electrical Engineering, Biomedical Engineering, Department of Energy Conversion and Storage, Imaging and Structural Analysis, National Veterinary Institute, Adaptive Immunology
Authors: Henneberg, K. (Intern), Kuhn, L. T. (Intern), Jungersen, G. (Intern)
Risk factors associated with diarrhea in Danish commercial mink (Neovison vison) during the pre-weaning period

Pre-weaning diarrhea in mink, also known as "sticky kits", is a syndrome and outbreaks occur every year on commercial mink farms in all mink producing countries. Morbidity and mortality can be considerable on a farm with huge economic consequences for the farmer as well as compromised welfare for the mink kits. Although efforts have been taken to identify etiologic agents involved in outbreaks, the syndrome is still regarded as multifactorial and recurring problems on the same farms draw attention to management and environmental risk factors. In the pre-weaning period from May to
June 2015, a case control study was carried out on 30 Danish mink farms. Data concerning management, biosecurity, hygiene, feed consumption, antibacterial prescription and production efficiency were analyzed. The proportion of 1-year old females, farm size (total number of females), energy supply per female in the late gestation period, and dogs accessing the farm area were significantly associated with being a case farm. Case farms were prescribed almost twice the amount of antibacterials per gestational unit (female and litter) as in control farms. Farmers on case farms spent significantly more time nursing and treating the animals and experienced more females with mastitis compared to farmers on control farms. No significant differences in cleaning practices or hygienic measures between case and control farms were found and there were no differences in drinking water quality, bedding material, composition neither of color types nor in management regarding litter equalization. Results from this study showed an association between the occurrence of pre-weaning diarrhea on mink farms and parity profile, farm size and feeding intensity in the gestational period. The access of dogs to the farm area was a significant risk factor, but needs further clarification.

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, University of Copenhagen, Kopenhagen Fur
Authors: Birch, J. M. (Ekstern), Agger, J. F. (Ekstern), Dahlin, C. (Ekstern), Jensen, V. F. (Intern), Hammer, A. S. (Ekstern), Struve, T. (Ekstern), Jensen, H. E. (Ekstern)
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Acta Veterinaria Scandinavica
Volume: 59
Issue number: 1
Article number: 43
ISSN (Print): 0044-605X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.077 SJR 0.655 CiteScore 1.45
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.01 SJR 0.641 SNIP 0.826
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.644 SNIP 1.641 CiteScore 0.98
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.753 SNIP 1.21 CiteScore 1.54
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.539 SNIP 1.11 CiteScore 1.41
ISI indexed (2013): ISI indexed no
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.591 SNIP 0.789 CiteScore 1.26
ISI indexed (2012): ISI indexed no
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.664 SNIP 0.997 CiteScore 1.42
ISI indexed (2011): ISI indexed no
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.551 SNIP 1.005
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.409 SNIP 0.716
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Risk factors associated with spatio-temporal clusters of high mortality in Danish swine herds

What were our motivation and objective? Mortality data are recorded to fulfill the European Commission requirements which ensures a continuous data flow for a surveillance system. Before using these data as part of a syndromic surveillance system, it is necessary to understand why increasing changes in mortality happen. The aim of this study was to identify spatio-temporal clusters of high mortality in Danish swine herds and associated risk factors.

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, University of Southern Denmark
Authors: Lopes Antunes, A. C. (Intern), Ersbøll, A. K. (Ekstern), Bihrmann, K. (Ekstern), Toft, N. (Intern)
Publication date: 2017
Main Research Area: Technical/natural sciences
Electronic versions:
posterv2.ECVPH aclan.pdf

Risk factors associated with spatio-temporal clusters of high mortality in Danish swine herds

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, University of Southern Denmark
Authors: Lopes Antunes, A. C. (Intern), Ersbøll, A. K. (Ekstern), Bihrmann, K. (Ekstern), Toft, N. (Intern)
Number of pages: 1
Publication date: 2017
Main Research Area: Technical/natural sciences
Electronic versions:
Rotavirus type A associated diarrhea in neonatal piglets: Importance and biodynamics

Background. Rotavirus A (RVA) is a well-known cause of diarrhea in piglets, but the infection dynamics and clinical impact are not fully elucidated. The aim was to determine the significance of infection with RVA in relation to neonatal diarrhea. Material/Methods. Two commercial swine herds with neonatal diarrhea and a positive RVA diagnosis were included. Five litters from each of two herds and a total of 132 piglets were sampled. The animals were subjected to a daily clinical examination and faeces were collected daily from all piglets. The piglets were weighed at the beginning and at the end of study. The outbreak day was defined as the day where >25% of the litter showed clinical diarrhea, and for all litters this was either the 4th or 5th day of life. On outbreak day, fecal samples from all piglets in the litter were analyzed for RVA together with samples collected two days prior to outbreak day from 54 of the 132 piglets. The analyses were made by a RVA specific RT-qPCR. Virulent E. coli was ruled out by PCR as differential diagnosis in all litters by testing a pooled sample on the outbreak day. Results/Discussion. In total, 43%(57/132) of the piglets had clinical diarrhea and 66%(87/132) were positive for RVA on the outbreak day. For comparison, 89%(51/57) of the diarrheic piglets and 48%(36/75) of the non-diarrheic piglets were positive for RVA which was significantly different (P<0.001). Piglets that tested negative for RVA had a higher weight gain over the 4-day period (mean 363g vs. 278g, P<0.05) despite that the positive piglets had a significantly higher birthweight (mean 1.45kg vs. 1.27kg, P<0.05). Furthermore, 63%(34/54) of the piglets developed diarrhea within 24 hours after a positive RVA diagnosis. The results confirmed that RVA has a significant impact on incidence of diarrhea and weight gain also in E. coli negative litters.

Sampling pig farms at the abattoir in a cross-sectional study – Evaluation of a sampling method

A cross-sectional study design is relatively inexpensive, fast and easy to conduct when compared to other study designs. Careful planning is essential to obtaining a representative sample of the population, and the recommended approach is to use simple random sampling from an exhaustive list of units in the target population. This approach is rarely feasible in
practice, and other sampling procedures must often be adopted. For example, when slaughter pigs are the target population, sampling the pigs on the slaughter line may be an alternative to on-site sampling at a list of farms. However, it is difficult to sample a large number of farms from an exact predefined list, due to the logistics and workflow of an abattoir. Therefore, it is necessary to have a systematic sampling procedure and to evaluate the obtained sample with respect to the study objective. We propose a method for 1) planning, 2) conducting, and 3) evaluating the representativeness and reproducibility of a cross-sectional study when simple random sampling is not possible. We used an example of a cross-sectional study with the aim of quantifying the association of antimicrobial resistance and antimicrobial consumption in Danish slaughter pigs. It was not possible to visit farms within the designated timeframe. Therefore, it was decided to use convenience sampling at the abattoir. Our approach was carried out in three steps: 1) planning: using data from meat inspection to plan at which abattoirs and how many farms to sample; 2) conducting: sampling was carried out at five abattoirs; 3) evaluation: representativeness was evaluated by comparing sampled and non-sampled farms, and the reproducibility of the study was assessed through simulated sampling based on meat inspection data from the period where the actual data collection was carried out. In the cross-sectional study samples were taken from 681 Danish pig farms, during five weeks from February to March 2015. The evaluation showed that the sampling procedure was reproducible with results comparable to the collected sample. However, the sampling procedure favoured sampling of large farms. Furthermore, both under-sampled and over-sampled areas were found using scan statistics. In conclusion, sampling conducted at abattoirs can provide a spatially representative sample. Hence it is a possible cost-effective alternative to simple random sampling. However, it is important to assess the properties of the resulting sample so that any potential selection bias can be addressed when reporting the findings.

**General information**

State: Published
Organisations: National Veterinary Institute, Epidemiology
Authors: Birkegård, A. C. (Intern), Hisham Beshara Halasa, T. (Intern), Toft, N. (Intern)
Number of pages: 8
Pages: 83-90
Publication date: 2017
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Preventive Veterinary Medicine
Volume: 145
ISSN (Print): 0167-5877
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 1.31 SJR 1.144 CiteScore 2.26
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.2 SJR 1.249 SNIP 1.361
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.282 SNIP 1.177 CiteScore 2.1
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.27 SNIP 1.407 CiteScore 2.37
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.264 SNIP 1.529 CiteScore 2.49
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.265 SNIP 1.436 CiteScore 2.45
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.194 SNIP 1.295 CiteScore 2.24
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
Selection of Bacillus species for targeted in situ release of prebiotic galacto-rhamnogalacturonan from potato pulp in piglets

We have previously shown that galacto-rhamnogalacturonan fibers can be enzymatically extracted from potato pulp and that these fibers have potential for exerting a prebiotic effect in piglets. The spore-forming Bacillus species are widely used as probiotics in feed supplements for pigs. In this study, we evaluated the option for further functionalizing Bacillus feed supplements by selecting strains possessing the enzymes required for extraction of the potentially prebiotic fibers. We established that it would require production and secretion of pectin lyase and/or polygalacturonase but no or limited secretion of galactanase and β-galactosidase. By screening a library of 158 Bacillus species isolated from feces and soil, we demonstrated that especially strains of Bacillus amyloliquefaciens, Bacillus subtilis, and Bacillus mojavensis have the necessary enzyme profile and thus the capability to degrade polygalacturonan. Using an in vitro porcine gastrointestinal model system, we revealed that specifically strains of B. mojavensis were able to efficiently release galacto-rhamnogalacturonan from potato pulp under simulated gastrointestinal conditions. The work thus demonstrated the feasibility of producing prebiotic fibers via a feed containing Bacillus spores and potato pulp and identified candidates for future in vivo evaluation in piglets.

General information

State: Published
Organisations: Department of Biotechnology and Biomedicine, Infection Microbiology, Novo Nordisk Foundation Center for Biosustainability, Research Groups, Bacterial Signal Transduction, National Veterinary Institute, Bacteriology & Parasitology, Department of Chemical and Biochemical Engineering, Center for BioProcess Engineering, Chr. Hansen A/S
Authors: Jers, C. (Intern), Strube, M. L. (Intern), Cantor, M. D. (Ekstern), Nielsen, B. K. K. (Ekstern), Sørensen, O. B. (Ekstern), Boye, M. (Intern), Meyer, A. S. (Intern)
Pages: 3605-3615
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Semiquantitative Decision Tools for FMD Emergency Vaccination Informed by Field Observations and Simulated Outbreak Data

We present two simple, semiquantitative model-based decision tools, based on the principle of first 14 days incidence (FFI). The aim is to estimate the likelihood and the consequences, respectively, of the ultimate size of an ongoing FMD epidemic. The tools allow risk assessors to communicate timely, objectively, and efficiently to risk managers and less technically inclined stakeholders about the potential of introducing FMD suppressive emergency vaccination. To explore the FFI principle with complementary field data, we analyzed the FMD outbreaks in Argentina in 2001, with the 17 affected provinces as the units of observation. Two different vaccination strategies were applied during this extended epidemic. In a series of 5,000 Danish simulated FMD epidemics, the numbers of outbreak herds at day 14 and at the end of the epidemics were estimated under different control strategies. To simplify and optimize the presentation of the resulting data for urgent decisions to be made by the risk managers, we estimated the sensitivity, specificity, as well as the negative and positive predictive values, using a chosen day-14 outbreak number as predictor of the magnitude of the number of remaining post-day-14 outbreaks under a continued basic control strategy. Furthermore, during an ongoing outbreak, the actual cumulative number of detected infected herds at day 14 will be known exactly. Among the number of epidemics lasting >14 days out of the 5,000 simulations under the basic control scenario, we selected those with an assumed accumulated number of detected outbreaks at day 14. The distribution of the estimated number of detected outbreaks at the end of the simulated epidemics minus the number at day 14 was estimated for the epidemics lasting more than 14 days. For comparison, the same was done for identical epidemics (i.e., seeded with the same primary outbreak herds) under a suppressive vaccination scenario. The results indicate that, during the course of an FMD epidemic, simulated likelihood predictions of the remaining epidemic size and of potential benefits of alternative control strategies can be presented to risk managers and other stakeholders in objective and easily communicable ways.

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, University of Minnesota
Authors: Willeberg, P. (Intern), AlKhamis, M. (Ekstern), Boklund, A. (Intern), Perez, A. M. (Ekstern), Enøe, C. (Intern), Hisham Beshara Halasa, T. (Intern)
Number of pages: 8
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Frontiers in Veterinary Science
Volume: 4
Article number: 43
ISSN (Print): 2297-1769
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.94
Original language: English
epidemics, modeling, disease control, risk communication, Foot-and-Mouth Disease
Electronic versions:
fvets_04_00043.pdf
DOIs:
10.3389/fvets.2017.00043
Source: FindIt
Source-ID: 2356532853
Publication: Research - peer-review › Journal article – Annual report year: 2017
Separation of foot-and-mouth disease virus leader protein activities; identification of mutants that retain efficient self-processing activity but poorly induce eIF4G cleavage

Foot-and-mouth disease virus (FMDV) is a picornavirus and its RNA genome encodes a large polyprotein. The N-terminal part of this polyprotein is the Leader protein, a cysteine protease, termed Lpro. The virus causes the rapid inhibition of host cell capdependent protein synthesis within infected cells. This results from the Lpro dependent cleavage of the cellular translation initiation factor eIF4G. Lpro also releases itself from the virus capsid precursor by cleaving the L/P1 junction. Using site-directed mutagenesis of the Lpro coding sequence, we have investigated the role of 51 separate amino acid residues in the functions of this protein. These selected residues are either highly conserved or are charged and exposed on the protein surface. Using transient expression assays within BHK cells, it was found that residues around the active site (W52, L53 and A149) of Lpro and others located elsewhere (K38, K39, R44, H138 and W159) are involved in the induction of eIF4G cleavage but not in the processing of the L/P1 junction. Modified viruses, encoding such amino acid substitutions within Lpro can replicate in BHK cells but did not grow well in primary bovine thyroid cells. This study characterizes mutant viruses that are deficient in blocking host cell responses to infection (e.g. interferon induction) and can assist in the rational design of antiviral agents targeting this process and in the production of attenuated viruses.
Sequence-Based Genotyping of Expressed Swine Leukocyte Antigen Class I Alleles by Next-Generation Sequencing Reveal Novel Swine Leukocyte Antigen Class I Haplotypes and Alleles in Belgian, Danish, and Kenyan Fattening Pigs and Göttingen Minipigs

The need for typing of the swine leukocyte antigen (SLA) is increasing with the expanded use of pigs as models for human diseases and organ-transplantation experiments, their use in infection studies, and for design of veterinary vaccines. Knowledge of SLA sequences is furthermore a prerequisite for the prediction of epitope binding in pigs. The low number of known SLA class I alleles and the limited knowledge of their prevalence in different pig breeds emphasizes the need for efficient SLA typing methods. This study utilizes an SLA class I-typing method based on next-generation sequencing of barcoded PCR amplicons. The amplicons were generated with universal primers and predicted to resolve 68-88% of all known SLA class I alleles dependent on amplicon size. We analyzed the SLA profiles of 72 pigs from four different pig populations; Göttingen minipigs and Belgian, Kenyan, and Danish fattening pigs. We identified 67 alleles, nine previously described haplotypes and 15 novel haplotypes. The highest variation in SLA class I profiles was observed in the Danish pigs and the lowest among the Göttingen minipig population, which also have the highest percentage of homozygote individuals. Highlighting the fact that there are still numerous unknown SLA class I alleles to be discovered, a total of 12 novel SLA class I alleles were identified. Overall, we present new information about known and novel alleles and haplotypes and their prevalence in the tested pig populations.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Bacteriology & Parasitology, Adaptive Immunology, Technical University of Denmark, International Livestock Research Institute
Authors: Sørensen, M. R. (Intern), Ilsøe, M. (Ekstern), Strube, M. L. (Intern), Bishop, R. (Ekstern), Erbs, G. (Intern), Hartmann, S. B. (Intern), Jungersen, G. (Intern)
Publication date: 2017
Main Research Area: Technical/natural sciences
Serological evidence of hepatitis E virus infection in pigs and jaundice among pig handlers in Bangladesh

Hepatitis E virus (HEV) is the most common cause of viral hepatitis in humans. Pigs may act as a reservoir of HEV, and pig handlers were frequently identified with a higher prevalence of antibodies to HEV. The objectives of this study were to identify evidence of HEV infection in pigs and compare the history of jaundice between pig handlers and people not exposed to pigs and pork. Blood and faecal samples were collected from 100 pigs derived from three slaughterhouses in the Gazipur district of Bangladesh from January to June, 2011. We also interviewed 200 pig handlers and 250 non-exposed people who did not eat pork or handled pigs in the past 2 years. We tested the pig sera for HEV-specific antibodies using a competitive ELISA and pig faecal samples for HEV RNA using real-time RT-PCR. Of 100 pig sera, 82% (n = 82) had detectable antibody against HEV. Of the 200 pig handlers, 28% (56/200) demonstrated jaundice within the past 2 years, whereas only 17% (43/250) of controls had a history of jaundice (p < .05). Compared to non-exposed people, those who slaughtered pigs (31% versus 15%, p < .001), reared pigs (37% versus 20%, p < .001), butchered pigs (35% versus 19%, p < .001) or involved in pork transportation (35% versus 19%, p < .001) were more likely to be affected with jaundice in the preceding 2 years. In multivariate logistic regression analysis, exposure to pigs (odds ratio [OR]: 2.2, 95% CI: 1.2–3.9) and age (OR: 0.97, 95% CI: 0.95–0.99) was significantly associated with jaundice in the past 2 years. Pigs in Bangladesh demonstrated evidence of HEV infection, and a history of jaundice was significantly more frequent in pig handlers. Identifying and genotyping HEV in pigs and pig handlers may provide further evidence of the pig’s role in zoonotic HEV transmission in Bangladesh.
Simulating control of paratuberculosis in Danish dairy herds

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, University of Copenhagen
Authors: Kirkeby, C. T. (Intern), Græsbøll, K. (Intern), Nielsen, S. S. (Ekstern), Toft, N. (Intern), Hisham Beshara Halasa, T. (Intern)
Number of pages: 1
Publication date: 2017
Event: Abstract from Copenhagen Cattle 2017, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences

Simultaneous detection of antibodies to five Actinobacillus pleuropneumoniae serovars using bead-based multiplex analysis

We have developed and made a preliminary validation of a bead-based multiplexed immunoassay for simultaneous detection of porcine serum antibodies to Actinobacillus pleuropneumoniae serovars 1, 2, 6, 7, and 12. Magnetic fluorescent beads were coupled with A. pleuropneumoniae antigens and tested with a panel of serum samples from experimentally infected pigs and with serum samples from uninfected and naturally infected pigs. The multiplex assay was compared to in-house ELISAs and complement fixation (CF) tests, which have been used for decades as tools for herd classification in the Danish Specific Pathogen Free system. Assay specificities and sensitivities as well as the corresponding cutoff values were determined using receiver operating characteristic (ROC) curve analysis, and the A. pleuropneumoniae multiplex assay showed good correlation with the in-house ELISAs and CF tests with areas under ROC curves ≥ 0.988. Benefits of multiplexed assays compared to ELISAs and CF tests include reduced serum sample volumes needed for analysis, less labor, and shorter assay time.

General information
State: Published
Organisations: National Veterinary Institute, Diagnostic & Development, Innate Immunology
Authors: Berger, S. S. (Intern), Lauritsen, K. T. (Intern), Boas, U. (Intern), Lind, P. (Intern), Andresen, L. O. (Intern)
Pages: 797-804
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Veterinary Diagnostic Investigation
Volume: 29
Issue number: 6
ISSN (Print): 1040-6387
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.842 SJR 0.621 CiteScore 1.21
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.27 SJR 0.642 SNIP 0.855
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.695 SNIP 0.886 CiteScore 1.44
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.792 SNIP 0.912 CiteScore 1.36
Web of Science (2014): Indexed yes
Solid-phase PCR for rapid multiplex detection of Salmonella spp. at the subspecies level, with amplification efficiency comparable to conventional PCR

Solid-phase PCR (SP-PCR) has attracted considerable interest in different research fields since it allows parallel DNA amplification on the surface of a solid substrate. However, the applications of SP-PCR have been hampered by the low efficiency of the solid-phase amplification. In order to increase the yield of the solid-phase amplification, we studied various parameters including the length, the density, as well as the annealing position of the solid support primer. A dramatic increase in the signal-to-noise (S/N) ratio was observed when increasing the length of solid support primers from 45 to 80 bp. The density of the primer on the surface was found to be important for the S/N ratio of the SP-PCR, and the optimal S/N was obtained with a density of 1.49 × 10¹¹ molecules/mm². In addition, the use of solid support primers with a short overhang at the 5' end would help improve the S/N ratio of the SP-PCR. With optimized conditions, SP-PCR can achieve amplification efficiency comparable to conventional PCR, with a limit of detection of 1.5 copies/μl (37.5 copies/reaction). These improvements will pave the way for wider applications of SP-PCR in various fields such as clinical diagnosis, high-throughput DNA sequencing, and single-nucleotide polymorphism analysis. Graphical abstract Schematic representation of solid-phase PCR.
Spatial patterns of antimicrobial resistance genes in a cross-sectional sample of pig farms with indoor non-organic production of finishers

Antimicrobial resistance (AMR) in pig populations is a public health concern. There is a lack of information of spatial distributions of AMR genes in pig populations at large scales. The objective of the study was to describe the spatial pattern of AMR genes in faecal samples from pig farms and to test if the AMR genes were spatially randomly distributed with respect to the geographic distribution of the pig farm population at risk. Faecal samples from 687 Danish pig farms were collected in February and March 2015. DNA was extracted and the levels of seven AMR genes (ermB, ermF, sulI, sulII, tet(M), tet(O) and tet(W)) were quantified on a high-throughput real-time PCR array. Spatial differences for the levels of the AMR genes measured as relative quantities were evaluated by spatial cluster analysis and creating of risk maps using kriging analysis and kernel density estimation. Significant spatial clusters were identified for ermB, ermF, sulII and tet(W). The broad spatial trends in AMR resistance evident in the risk maps were in agreement with the results of the cluster analysis. However, they also showed that there were only small scale spatial differences in the gene levels. We conclude that the geographical location of a pig farm is not a major determinant of the presence or high levels of AMR genes assessed in this study.

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, Bacteriology & Parasitology, National Food Institute, Research Group for Genomic Epidemiology, University of Southern Denmark
Pages: 1418-1430
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Epidemiology and Infection
Volume: 145
Issue number: 7
ISSN (Print): 0950-2688
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.807 SJR 1.128 CiteScore 1.88
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.98 SJR 1.18 SNIP 0.866
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.349 SNIP 1.052 CiteScore 2.29
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.305 SNIP 1.016 CiteScore 2.19
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Sphingosine-1-Phosphate Signaling in Inflammatory Bowel Disease

An unmet medical need exists for the development of targeted therapies for the treatment of inflammatory bowel disease (IBD) with easily administered and stable oral drugs, particularly as most patients on biologics [i.e., tumor necrosis factor (TNF) inhibitors and anti-integrins] are either primary non-responders or lose responsiveness during maintenance treatment. A new class of small molecules, sphingosine-1-phosphate (S1P) receptor modulators, has recently shown efficacy in IBD. Here we provide an overview of the mechanism of action of this novel treatment principle in the context of intestinal inflammation. The remarkable impact of therapeutic modulation of the S1P/S1P receptor axis reflects the complexity of the pathogenesis of IBD and the fact that S1P receptor modulation may be a logical therapeutic approach for the future management of IBD.
Spirocerca-parasitten: En tropisk/subtropisk hundeparasit, som medfører kæftlignende svulster, er nu påvist i tre danske ræve fra Thy-området

*Spirocerca lupi* er en parasit, som tilhører familien *spiruroidea*. Parasitten forårsager sygdommen *spirocercosis*, en sygdom kendetegnet ved alvorlige kæftlignende svulster i oesophagusvægggen og aorta hos primært hunde. *Spirocerca* spp. er påvist hos danske ræve i Thy-området ved tre lejligheder, senest i 2017. Der er derfor risikofor, at hunde, som
opholder sig i området i og omkring Thy, kan blive smittet med parasitten. Alle hunderacer og hunde i alle aldre kan blive
smittet, men risiko for smitte er størst for jagthunde og sporhunde.

**General information**

State: Published
Organisations: National Veterinary Institute, Bacteriology & Parasitology, Diagnostic & Development
Authors: Petersen, H. H. (Intern), Larsen, G. (Intern), Chriél, M. (Intern)
Pages: 30-33
Publication date: 2017
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Dansk Veterinaertidsskrift
Volume: 2017
Issue number: 16
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
ISI indexed (2012): ISI indexed no
BFI (2011): BFI-level 1
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
BFI (2009): BFI-level 1
BFI (2008): BFI-level 1
Original language: English
Electronic versions:
Spirocerca_lupi_1_.pdf
Publication: Communication › Journal article – Annual report year: 2017

**Spread of avian pathogenic Escherichia coli ST117 O78:H4 in Nordic broiler production**

Escherichia coli infections known as colibacillosis constitute a considerable challenge to poultry farmers worldwide, in
terms of decreased animal welfare and production economy. Colibacillosis is caused by avian pathogenic E. coli (APEC).
APEC strains are extraintestinal pathogenic E. coli and have in general been characterized as being a genetically diverse
population. In the Nordic countries, poultry farmers depend on import of Swedish broiler breeders which are part of a
breeding pyramid. During 2014 to 2016, an increased occurrence of colibacillosis on Nordic broiler chicken farms was
reported. The aim of this study was to investigate the genetic diversity among E. coli isolates collected on poultry farms
with colibacillosis issues, using whole genome sequencing. Hundred and fourteen bacterial isolates from both broilers and
broiler breeders were whole genome sequenced. The majority of isolates were collected from poultry with colibacillosis issues,
using whole genome sequencing. Hundred and fourteen bacterial isolates from both broilers and
broiler breeders were whole genome sequenced. The majority of isolates were collected from poultry with colibacillosis on
Nordic farms. Subsequently, comparative genomic analyses were carried out. This included in silico typing (sero- and
multi-locus sequence typing), identification of virulence and resistance genes and phylogenetic analyses based on single
nucleotide polymorphisms. In general, the characterized poultry isolates constituted a genetically diverse population.
However, the phylogenetic analyses revealed a major clade of 47 closely related ST117 O78:H4 isolates. The isolates in
this clade were collected from broiler chickens and breeders with colibacillosis in multiple Nordic countries. They clustered
together with a human ST117 isolate and all carried virulence genes that previously have been associated with human
uropathogenic E. coli. The investigation revealed a lineage of ST117 O78:H4 isolates collected in different Nordic
countries from diseased broilers and breeders. The data indicate that the closely related ST117 O78:H4 strains have been
transferred vertically through the broiler breeding pyramid into distantly located farms across the Nordic countries.

**General information**

State: Published
Organisations: National Veterinary Institute, Bacteriology & Parasitology, Diagnostic & Development, State Serum Institute,
Norwegian Veterinary Institute, Finnish Food Safety Authority, University of Copenhagen
Authors: Ronco, T. (Intern), Stegger, M. (Ekstern), Olsen, R. H. (Ekstern), Sekse, C. (Ekstern), Nordstoga, A. B. (Ekstern),
Pohjanvirta, T. (Ekstern), Lilje, B. (Ekstern), Lyhs, U. (Intern), Andersen, P. S. (Ekstern), Pedersen, K. (Intern)
Number of pages: 8
STARD-BLCM: Standards for the Reporting of Diagnostic accuracy studies that use Bayesian Latent Class Models

The Standards for the Reporting of Diagnostic Accuracy (STARD) statement, which was recently updated to the STARD2015 statement, was developed to encourage complete and transparent reporting of test accuracy studies. Although STARD principles apply broadly, the checklist is limited to studies designed to evaluate the accuracy of tests when the disease status is determined from a perfect reference procedure or an imperfect one with known measures of test accuracy. However, a reference standard does not always exist, especially in the case of infectious diseases with a long latent period. In such cases, a valid alternative to classical test evaluation involves the use of latent class models that do not require a priori knowledge of disease status. Latent class models have been successfully implemented in a Bayesian framework for over 20 years. The objective of this work was to identify the STARD items that require modification and develop a modified version of STARD for studies that use Bayesian latent class analysis to estimate diagnostic test accuracy in the absence of a reference standard. Examples and elaborations for each of the modified items are provided. The new guidelines, termed STARD-BLCM (Standards for Reporting of Diagnostic accuracy studies that use Bayesian Latent Class Models), will facilitate improved quality of reporting on the design, conduct and results of diagnostic accuracy studies that use Bayesian latent class models.

General information

State: Published
Organisations: National Veterinary Institute, Epidemiology, University of Thessaly, University of Copenhagen, Oregon State University, University of California, McGill University, University of Sydney, University of Prince Edward Island
Authors: Kostoulas, P. (Ekstern), Nielsen, S. S. (Ekstern), Branscum, A. J. (Ekstern), Johnson, W. O. (Ekstern), Dendukuri, N. (Ekstern), Dhand, N. K. (Ekstern), Toft, N. (Intern), Gardner, I. A. (Ekstern)
Number of pages: 11
Pages: 37-47
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information

Journal: Preventive Veterinary Medicine
Volume: 138
ISSN (Print): 0167-5877
Ratings:
  BFI (2018): BFI-level 2
  Web of Science (2018): Indexed yes
  BFI (2017): BFI-level 2
  Scopus rating (2017): SNIP 1.31 SJR 1.144 CiteScore 2.26
  Web of Science (2017): Indexed yes
  BFI (2016): BFI-level 2
  Scopus rating (2016): CiteScore 2.2 SJR 1.249 SNIP 1.361
  Web of Science (2016): Indexed yes
  BFI (2015): BFI-level 2
  Scopus rating (2015): SJR 1.282 SNIP 1.177 CiteScore 2.1
  Web of Science (2015): Indexed yes
  BFI (2014): BFI-level 2
  Scopus rating (2014): SJR 1.27 SNIP 1.407 CiteScore 2.37
  Web of Science (2014): Indexed yes
  BFI (2013): BFI-level 2
Subtyping of swine influenza viruses using a high-throughput real time PCR platform

Introduction. Swine influenza is a respiratory disease caused by multiple subtypes of influenza A virus (IAV). The genome of IAV consists of 8 segments and subtype classification is based on the surface glycoproteins hemagglutinin (HA) and neuraminidase (NA). In Denmark, the influenza screening test and subsequent subtyping is performed by real time RT-qPCR (RT-qPCR) but several assays are needed to cover the wide range of circulating subtypes which is expensive, resource and time demanding. To mitigate these restrictions the high-throughput qPCR platform BioMark (Fluidigm) has been explored. The BioMark platform uses less sample and reagent volume compared to standard qPCR platforms and allows for up to 9,216 parallel reactions on one chip. Materials and methods. A total of 14 PCR assays specific for the different subtypes of HA and NA genes relevant for swine influenza and 6 assays specific for the internal genes of IAV were validated and optimised to run under identical reaction conditions and assembled on a dynamic array chip (Fluidigm). Results. The sensitivity and specificity of the chip was assessed by testing cell culture isolates and field samples with known subtypes (based on sequencing). The results revealed that the performance of the dynamic chip was
similar to conventional real time analysis. Discussion and conclusion. Application of the chip for subtyping of swine influenza has resulted in a significant reduction in time, cost and working hours. Thereby, it is possible to offer diagnostic services with reduced price and turnover time which will facilitate choice of vaccines and by that lead to reduction of antibiotic used.

**General information**

State: Published
Organisations: National Veterinary Institute, Virology, Innate Immunology, Friedrich Loeffler Institute
Authors: Goecke, N. B. (Intern), Krog, J. S. (Intern), Hjulsager, C. K. (Intern), Skovgaard, K. (Intern), Harder, T. (Ekstern), Larsen, L. E. (Intern)
Publication date: 2017
Event: Abstract from 9th European Symposium of Porcine Health Management (ESPHM 2017), Prague, Czech Republic.
Main Research Area: Technical/natural sciences
Source: PublicationPreSubmission
Source-ID: 140461499
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2017

**Subunit vaccine candidates against Aeromonas salmonicida in rainbow trout Oncorhynchus mykiss**

Aeromonas salmonicida subsp. salmonicida is the etiological agent of furunculosis and a major fish health problem in salmonid aquaculture worldwide. Injection vaccination with commercial mineral oil-adjuvanted bacterin vaccines has been partly successful in preventing the disease but in Danish rainbow trout (Oncorhynchus mykiss, Walbaum) aquaculture furunculosis outbreaks still occur. In this study we tested the efficacy of experimental subunit vaccines against A. salmonicida infection in rainbow trout. We utilized in silico screening of the proteome of A. salmonicida subsp. salmonicida strain A449 and identified potential protective protein antigens that were tested by in vivo challenge trial. A total of 14 proteins were recombinantly expressed in Escherichia coli and prepared in 3 different subunit vaccine combinations to immunize 3 groups of rainbow trout by intraperitoneal (i.p.) injection. The fish were exposed to virulent A. salmonicida 7 weeks after immunization. To assess the efficacy of the subunit vaccines we evaluated the immune response in fish after immunization and challenge infection by measuring the antibody levels and monitoring the survival of fish in different groups. The survival of fish at 3 weeks after challenge infection showed that all 3 groups of fish immunized with 3 different protein combinations exhibited significantly lower mortalities (17-30%) compared to the control groups (48% and 56%). The ELISA results revealed significantly elevated antibody levels in fish against several protein antigens, which in some cases were positively correlated to the survival.

**General information**

State: Published
Organisations: National Veterinary Institute, Innate Immunology, Bacteriology & Parasitology, University of Copenhagen, Evaxion Biotech
Number of pages: 15
Publication date: 2017
Main Research Area: Technical/natural sciences

**Publication information**

Journal: PLOS ONE
Volume: 12
Issue number: 2
Article number: e0171944
ISSN (Print): 1932-6203
Ratings:

BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.01 SJR 1.164 SNIP 1.111
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.11 SJR 1.236 SNIP 1.101
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.427 SNIP 1.136 CiteScore 3.32
Web of Science (2015): Indexed yes
Supplementation with Lactobacillus paracasei or Pediococcus pentosaceus does not prevent diarrhoea in neonatal pigs infected with Escherichia coli F18

Infectious diarrhea is a worldwide problem in newborns. Optimal bacterial colonisation may enhance gut maturation and protect against pathogenic bacteria after birth. We hypothesised that lactic acid bacteria (LAB) administration prevents pathogen-induced diarrhoea in formula-fed newborns. Newborn caesarean-delivered, colostrum-deprived term piglets on parenteral nutrition for the first 15 h, were used as models for sensitive newborn infants. A commercially available probiotic strain, Lactobacillus paracasei F19 (LAP, $2.6 \times 10^8$ colony-forming units (CFU)/kg per d) and a novel LAB isolate, Pediococcus pentosaceus (PEP, $1.3 \times 10^{10}$ CFU/kg per d), were administered for 5 d with or without inoculation of the porcine pathogen, Escherichia coli F18 (F18, $10^{10}$ CFU/d). This resulted in six treatment groups: Controls (n 9), LAP (n 10), PEP (n 10), F18 (n 10), F18-LAP (n 10) and F18-PEP (n 10). The pathogen challenge increased diarrhoea and density of F18 in the intestinal mucosa ($P<0.05$). LAB supplementation further increased the diarrhoea score, relative to F18 alone ($P<0.01$). Intestinal structure and permeability were similar among groups, whereas brush border enzymes were affected in variable intestinal regions with decreased activities in most cases after F18 and LAB inoculation. Bacterial density in colon mucosa increased after F18 inoculation ($P<0.05$) but was unaffected by LAB supplementation. In colon contents, acetic and butyric acids were increased by PEP ($P<0.05$). The LAB used in this study failed to reduce E. coli-induced diarrhoea in sensitive newborn pigs. In vulnerable newborns there may be a delicate balance among bacterial composition and load, diet and the host. Caution may be required when administering LAB to compromised newborns suffering from enteric infections.

General information
State: Published
Survival and infectivity of chicken ascarid eggs in soil after exposure to an egg-degrading microfungus

The microfungus Pochonia chlamydosporia has been shown to kill high numbers of chicken ascarid (Ascaridia galli and Heterakis spp.) eggs in vitro but it is not known if surviving eggs may be infective. Unembryonated ascarid eggs (predominantly A. galli) were therefore isolated from faeces and added to sterilised (S) or non-sterilised (N) soil in Petri dishes that were either treated with P. chlamydosporia (F) or left untreated (C) during incubation at 22°C for 35 days. Egg recovery was estimated before (day 0) and after (day 35) treatment. Thereafter, each of four groups of parasite-free egg-laying hens was exposed to the soil from one of the four treatments in the feed over 12 days. The hens were necropsied day 42 post first exposure. The number of surviving eggs was most substantially reduced in SF soil and SF hens had statistically lower worm burdens (both parasites) compared to SC, NC and NF hens. However, adult A. galli were primarily found in SF hens while the other groups mainly harboured immature A. galli. Accordingly, SF hens also had the highest ascarid faecal egg counts and lowest serum A. galli IgY titre. Overall, A. galli recovery increased with increasing exposure, but contrastingly resulted in a reduced risk of egg-producing adult worms, at least short-term. Eggs not destroyed by P. chlamydosporia were clearly infective to the hens. The fungus did not appear to be sufficiently effective as a biocontrol agent of ascarid eggs in natural (i.e. non-sterilised) soil unless its effect can be further optimised.

Targeting the latent cytomegalovirus reservoir with an antiviral fusion toxin protein

Reactivation of human cytomegalovirus (HCMV) in transplant recipients can cause life-threatening disease. Consequently, for transplant recipients, killing latently infected cells could have far-reaching clinical benefits. In vivo, myeloid cells and their progenitors are an important site of HCMV latency, and one viral gene expressed by latently infected myeloid cells is US28. This viral gene encodes a cell surface G protein-coupled receptor (GPCR) that binds chemokines, triggering its endocytosis. We show that the expression of US28 on the surface of latently infected cells allows monocytes and their progenitor CD34+ cells to be targeted and killed by F49A-FTP, a highly specific fusion toxin protein that binds this viral GPCR. As expected, this specific targeting of latently infected cells by F49A-FTP also robustly reduces virus reactivation in vitro. Consequently, such specific fusion toxin proteins could form the basis of a therapeutic strategy for eliminating latently infected cells before haematopoietic stem cell transplantation.
T cell recognition of breast cancer antigens

Recent studies are encouraging research of breast cancer immunogenicity to evaluate the applicability of immunotherapy as a treatment strategy. The epitope landscape in breast cancer is minimally described, thus it is necessary to identify T cell targets to develop immune mediated therapies. This project investigates four proteins commonly upregulated in breast cancer and thus probable tumor associated antigens (TAAs). Aromatase, prolactin, NEK3, and PIAS3 contribute to increase growth, survival, and motility of malignant cells. Aspiring to uncover novel epitopes for cytotoxic T cells, a reverse immunology approach is applied. Via in silico screening of the protein sequences, 415 peptides were predicted as HLA-A*0201 and HLA-B*0702 binders. Subsequent in vitro binding analysis in a MHC ELISA platform confirmed binding for 147 of the 415 predicted binders. The 147 peptides were evaluated for T cell recognition utilizing DNA barcode labeled MHC multimers to screen peripheral blood lymphocytes from breast cancer patients and healthy donor samples. Significantly more TAA specific T cell responses were detected in breast cancer patients than healthy donors for both HLA-A*0201 (P < 0.0039) and HLA-B*0702 (P < 0.001) restricted peptides. Importantly, several of the identified responses were toward peptides that were predicted as poor or intermediate affinity binders. This is indicative of the importance of inclusion these
in the search for epitopes within shared TAAs. Thus, the inspected proteins indeed contain targets for T cell reactivity. Further research will include functional testing of peptide specific T cell cultures to validate the peptides as true T cell epitopes through demonstration of intracellular processing and presentation at the cell surface.

**General information**

State: Published
Organisations: National Veterinary Institute, T-cells & Cancer, Technical University of Denmark, University Hospital Herlev
Authors: Petersen, N. V. (Intern), Andersen, S. R. (Ekstern), Andersen, R. S. (Ekstern), Straten, P. T. (Ekstern), Met, O. (Ekstern), Hadrup, S. R. (Intern)
Publication date: 2017
Main Research Area: Technical/natural sciences
Electronic versions:
2017_Scandinavian_Journal_of_Immunology_1_313.pdf
Source: FindIt
Source-ID: 2391995615
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2017

**T cell recognition of large T and small T antigen in Merkel cell polyomavirus-associated cancer**

Merkel Cell Carcinoma is an aggressive human skin cancer induced by Merkel Cell Polyomavirus (MCPyV). MCPyV is commonly found in human, but the oncogenic transformation takes place during immunosuppression. Two mutation events allow the clonal integration of the viral genome into the host genome and translation of the two viral genes large T (LTA) and small T antigen (STA). Standard treatment with chemotherapy shows poor clinical outcome instead immunotherapy offers new potential treatment strategies. The use of PD-1 checkpoint inhibitors has shown promising results (>50% response rates, RECIST). However, not all patients are able to mount an immune response. Instead adoptive transfer of MCPyV-reactive T cells is an attractive strategy for this cohort. We have previously identified T cell epitopes from the MCPyV-derived proteins LTA, STA and VP1. Here we aim to expand the knowledge about T cell epitopes by including a broader range of HLA restrictions. We analyzed 31 patients’ peripheral blood mononuclear cells through enrichment of low frequency clones, followed by revealing of T cell reactivity using combinatorial color-encoded peptide-MHC multimers. 28 T cell responses against 18 MCPyV-derived peptides were detected. Additional testing has confirmed functional T cell reactivity against one of these epitopes. We analyzed 3 patients’ tumor infiltrating lymphocytes by direct ex-vivo detection of T cell reactivity using combinatorial color-encoded peptide-MHC multimers. 5 T cell responses against 5 peptides were detected. The functional T cell response towards detected epitopes is under investigation in order to characterize them as potential T cell targets in a new therapy.

**General information**

State: Published
Organisations: National Veterinary Institute, T-cells & Cancer, University Hospital Herlev, University Hospital Essen, University of Washington
Authors: Hansen, U. K. (Intern), Lyngaa, R. B. (Intern), Straten, P. T. (Ekstern), Becker, J. C. (Ekstern), Nghiem, P. (Ekstern), Hadrup, S. R. (Intern)
Publication date: 2017
Main Research Area: Technical/natural sciences
Electronic versions:
2017_Scandinavian_Journal_of_Immunology_1_346.pdf
Source: FindIt
Source-ID: 2391995749
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2017

**The effect of color type on early wound healing in farmed mink (Neovison vison)**

Background: Individual differences of mink, including color type, are speculated to affect the course of wound healing, thereby impacting wound assessment and management on the farms, as well as the assessment of wounds in forensic cases. In this study, we examined the effect of color type on early wound healing in farmed mink. Full thickness excisional wounds (2 x 2 cm) were made on the back in 18 mink of the color types Brown, Silverblue and Blue Iris. Gross and microscopic pathology of the wounds was evaluated 2 days post-wounding together with degree of wound size reduction, presence of bacteria and blood analyses. Results: Pathological examination on day 2 showed the greatest mean wound size reduction in Brown mink (11.0%) followed by Blue Iris (7.9%) and Silverblue (1.6%). Bacteria were cultured from all wounds, and predominantly Staphylococcus species were recovered in mixed or pure culture. Histopathology from day 2 wounds showed a scab overlying necrotic wound edges, which were separated from underlying vital tissue by a demarcation zone rich in polymorphonuclear leukocytes. Fibroblasts and plump endothelial cells were more numerous in the deeper tissues. Complete blood count parameters were within normal ranges in most cases, however, the mink showed mildly to markedly decreased hematocrit and six mink of the color types Silverblue and Blue Iris showed moderately elevated numbers of circulating segmented neutrophils on day 2. There was a marked increase in concentration of serum amyloid A from day 0 to day 2 in all color types. Conclusions: We have described differences in
early wound healing between mink of the color types Brown, Silverblue and Blue Iris by use of an experimental wound model in farmed mink. The most pronounced difference pertained to the degree of wound size reduction which was greatest in Brown mink, followed by Blue Iris and Silverblue, respectively.

**General information**

State: Published
Organisations: National Veterinary Institute, Innate Immunology, Kopenhagen Fur, University of Copenhagen
Authors: Jespersen, A. (Ekstern), Jensen, H. E. (Ekstern), Agger, J. F. (Ekstern), Heegaard, P. M. H. (Intern), Damborg, P. (Ekstern), Aalbaek, B. (Ekstern), Hammer, A. S. (Ekstern)
Number of pages: 10
Publication date: 2017
Main Research Area: Technical/natural sciences

**Publication information**

Journal: BMC Veterinary Research
Volume: 13
Issue number: 1
Article number: 135
ISSN (Print): 1746-6148
Ratings:
- BFI (2018): BFI-level 1
- Web of Science (2018): Indexed yes
- BFI (2017): BFI-level 1
- Scopus rating (2017): SNIP 1.108 SJR 0.934 CiteScore 2.16
- Web of Science (2017): Indexed yes
- BFI (2016): BFI-level 1
- Scopus rating (2016): CiteScore 1.83 SJR 0.87 SNIP 1.011
- Web of Science (2016): Indexed yes
- BFI (2015): BFI-level 1
- Scopus rating (2015): SJR 0.981 SNIP 1.009 CiteScore 1.86
- Web of Science (2015): Indexed yes
- BFI (2014): BFI-level 1
- Scopus rating (2014): SJR 0.943 SNIP 1.018 CiteScore 1.81
- Web of Science (2014): Indexed yes
- BFI (2013): BFI-level 1
- Scopus rating (2013): SJR 0.861 SNIP 0.853 CiteScore 1.85
- ISI indexed (2013): ISI indexed yes
- Web of Science (2013): Indexed yes
- BFI (2012): BFI-level 1
- Scopus rating (2012): SJR 0.779 SNIP 1.023 CiteScore 1.94
- ISI indexed (2012): ISI indexed yes
- Web of Science (2012): Indexed yes
- BFI (2011): BFI-level 1
- Scopus rating (2011): SJR 1.165 SNIP 1.447 CiteScore 2.66
- ISI indexed (2011): ISI indexed no
- BFI (2010): BFI-level 1
- Scopus rating (2010): SJR 1.076 SNIP 1.396
- BFI (2009): BFI-level 1
- Scopus rating (2009): SJR 0.969 SNIP 0.985
- BFI (2008): BFI-level 1
- Scopus rating (2008): SJR 0.529 SNIP 0.811
- Scopus rating (2007): SJR 0.565 SNIP 0.877
- Scopus rating (2006): SJR 0.378 SNIP 1.098
- Web of Science (2006): Indexed yes

Original language: English
Mink, Neovison Vison, Serum amyloid a, Wound healing, Wound model

Electronic versions:
art_3A10.1186_2Fs12917_017_1052_1.pdf
The impact of a diet with fructan-rich chicory roots on Oesophagostomum dentatum worm population dynamics and host immune responses in pigs

Oesophagostomum infections in pigs persist for months. We hypothesized that feeding fructans (dried chicory roots) may improve immunity and facilitate worm expulsion. We therefore examined the effects of long-term chicory on O. dentatum population dynamics and host immune responses. Methods: Seventy-two pigs were allocated to four groups in a 2-factorial design. Group O was fed regular feed and trickle inoculated with 15 O. dentatum L3/kg/day 0-12 weeks post-infection (pi.) start. Group OC was also trickle inoculated but switched to a chicory-rich diet (12% inulin in DM) weeks 3-12 pi. Group C was uninfected but switched to chicory diet while Group Ctr remained uninfected on regular feed. Six pigs per group were necropsied 5, 9 and 12 weeks pi. for worm counts and qRT-PCR for gene expression in the gut. Faecal egg counts (FEC) and specific antibody levels were assessed regularly. Results: When group OC switched to chicory diet, FECs dropped within 3-4 days and remained very low. Worm counts were reduced 50-65% by chicory feeding (Group OC versus O; p<0.001) and was accompanied by a 2-fold higher O. dentatum-specific IgG1 response. In group O, a build-up of a typical Th2-type immune response was seen but leveled out later and worm counts remained stable. Group C had a down-regulated Th1-type response and thus an anti-inflammatory effect in colon. Conclusions: We found little evidence that chicory feeding improved host protective immunity against Oesophagostomum. It seems more likely, as previously suggested, that physico-chemical changes in caeco-colon are responsible for the observed anthelmintic effects.

The Oncopig Cancer Model: An Innovative Large Animal Translational Oncology Platform

Despite an improved understanding of cancer molecular biology, immune landscapes, and advancements in cytotoxic, biologic, and immunologic anti-cancer therapeutics, cancer remains a leading cause of death worldwide. More than 8.2 million deaths were attributed to cancer in 2012, and it is anticipated that cancer incidence will continue to rise, with 19.3 million cases expected by 2025. The development and investigation of new diagnostic modalities and innovative therapeutic tools is critical for reducing the global cancer burden. Toward this end, transitional animal models serve a crucial role in bridging the gap between fundamental diagnostic and therapeutic discoveries and human clinical trials. Such animal models offer insights into all aspects of the basic science-clinical translational cancer research continuum (screening, detection, oncogenesis, tumor biology, immunogenicity, therapeutics, and outcomes). To date, however, cancer research progress has been markedly hampered by lack of a genotypically, anatomically, and physiologically relevant large animal model. Without progressive cancer models, discoveries are hindered and cures are improbable. Herein, we describe a transgenic porcine model-the Oncopig Cancer Model (OCM)-as a next-generation large animal platform for the study of hematologic and solid tumor oncology. With mutations in key tumor suppressor and oncogenes, TP53R167H and KRASG12D, the OCM recapitulates transcriptional hallmarks of human disease while also exhibiting clinically relevant histologic and genotypic tumor phenotypes. Moreover, as obesity rates increase across the global population, cancer patients commonly present clinically with multiple comorbid conditions. Due to the effects of these comorbidities on patient management, therapeutic strategies, and clinical outcomes, an ideal animal model should develop cancer on the background of representative comorbid conditions (tumor macro- and microenvironments). As observed in clinical practice, liver cirrhosis frequently precedes development of primary liver cancer or hepatocellular carcinoma. The OCM has the capacity to develop tumors in combination with such relevant comorbidities. Furthermore, studies on the tumor microenvironment demonstrate similarities between OCM and human cancer genomic landscapes. This review highlights the potential of this and other large animal platforms as transitional models to bridge the gap...
between basic research and clinical practice.

**General information**

State: Published

Organisations: National Veterinary Institute, Adaptive Immunology, T-cells & Cancer, University of Illinois at Chicago, Albion College, University of Illinois


Publication date: 2017

Main Research Area: Technical/natural sciences

**Publication information**

Journal: Frontiers in Oncology

Volume: 7

Article number: 190

Ratings:

BFI (2018): BFI-level 1

BFI (2017): BFI-level 1

Scopus rating (2017): CiteScore 4.45

Scopus rating (2016): CiteScore 4.39

Scopus rating (2015): CiteScore 4.17

Scopus rating (2014): CiteScore 3.31

Scopus rating (2013): CiteScore 2.77

Original language: English

Cancer models, Clinical needs, Oncology, Oncopig, Pigs, Translational medicine

Electronic versions:

fonc_07_00190.pdf

DOIs:

10.3389/fonc.2017.00190

Bibliographical note

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Source: FindIt

Source-ID: 2373280588

Publication: Research - peer-review › Journal article – Annual report year: 2017

**The Pig as a Large Animal Model for Studying Anti-Tumor Immune Responses**

The immune system plays a crucial role in cancer development and progression. Cancer immunoeediting encompasses three phases: elimination, equilibrium, and escape; together, describing the complex interplay between tumor and immune cells. Specifically, the immune system both protects against cancer but also generates a selective pressure, which may lead to selection of tumor cell variants with reduced immunogenicity; thereby, increasing the risk of tumor escape. Cancer immunotherapy includes treatment strategies aimed at activating anti-tumor immune responses or inhibiting suppressive and tumor-favorable immune mechanisms. One of the promising arms of cancer immunotherapy is peptide-based therapeutic vaccines; yet, no such vaccine has been approved for use in human oncology. For many years, mouse models have provided invaluable understanding of complex immunological pathways; however, the majority of preclinical results are lost in translation from mice to humans. In particular, the success rate when translating therapeutic cancer vaccines has been extremely low; thus leaving room for improvement.

The overall aim of this Ph.D. project was to investigate the potential for the pig as a large animal model for cancer immunology research and preclinical testing of cancer immunotherapies. We hypothesized that a physiologically relevant model with high degree of homology with humans can provide a crucial link between murine studies and human patients. This may increase the success rate when translating preclinical findings in the future.

As T cells are important mediators of anti-tumor immune responses, we first developed an immunization protocol allowing the induction of a cytotoxic T lymphocyte (CTL) response and evaluation of the effect of vaccine antigen dose. Göttingen minipigs received intraperitoneal (i.p.) injections with tetanus toxoid, an exogenous model antigen, formulated in CAF09 adjuvant. We demonstrate induction of a polyfunctional CTL response upon low antigen dose immunization, while a CAF09-formulated high antigen dose generates antigen-specific IgG antibodies.

Secondly, we investigated the effect of antigen dose, when immunizing Göttingen minipigs against Indoleamine 2,3-dioxygenase (IDO), an endogenous target relevant for cancer immunotherapeutic purposes. By repeated i.p. administration of CAF09-adjuvanted IDO-derived peptides, we show a vaccine-induced break in the peripheral tolerance towards IDO and the establishment of an antigen-specific cell-mediated immune (CMI) response. When comparing the
different CAF09-formulated antigen doses, we demonstrate the induction of a CMI-dominant response upon exposure to a low endogenous peptide dose. In contrast, a mixed CMI and humoral immune response could be shown following repeated high peptide dose immunization. Together, our data underline the importance of correctly determining the first-in-human vaccine antigen dose, which may be more accurately predicted in a large animal like the pig.

Finally, we performed a T-cell focused immunological characterization of the novel transgenic Oncopig model. Following injection with an adenoviral vector Cre-recombinase (AdCre), these animals develop sarcomas at the injection site resulting from expression of two mutant transgenes: KRASG12D and TP53R167H. We demonstrate pronounced T-cell infiltration to the tumor site with a specific enrichment in both regulatory and cytotoxic subsets when compared to peripheral blood. Thus, Oncopig subcutaneous tumors can be classified as hot in accordance with the Immunoscore classification.

In an in vitro setup, we show immune-mediated specific lysis of autologous tumor cells, underlining the capacity of the Oncopig immune system to mount a cytotoxic anti-tumor response. Using the results from RNA-seq analysis, we propose a potential mechanism for in vivo inhibition of anti-tumor cytotoxicity based on elevated expression of the immunosuppressive genes IDO1, CTLA4, and PDL1 within Oncopig leiomyosarcomas. As a high rate of spontaneous regression of subcutaneous tumors occurs over time, we speculate that the anti-tumor immune responses become dominant at the later stages post AdCre injection; eventually leading to tumor elimination. Combined, our data support that the Oncopig provides a crucial platform for studying anti-tumor immune responses in a large in vivo system, although the model currently only allows preclinical testing of therapeutics against the early stages of cancer.

Retinoic acid (RA) is a vitamin A metabolite and member of the large family of retinoids that have been used in treatment of various forms of cancer and skin disorders. Also, vitamin A deficiency is associated with impaired ability to fight infections and RA has been shown to shape peripheral immune responses. However, little is known about the role of RA in the development of immune cells. We are currently investigating the role of RA signaling in thymic function. In the thymus, thymic epithelial cells (TEC) are providing the specialized microenvironment that supports T cell development and proper TEC maturation and homeostasis is required for the generation of a functional T cell pool. TEC development and differentiation is dependent on crosstalk with immune and stromal cells in the thymus and previous work of our group has suggested RA as a potential key player in this process. To study the role of RA signaling in TEC homeostasis and function in vivo we are using a transgenic mouse model where RA signaling is blocked in the TEC compartment. Thereby we could show that RA controls TEC subset composition and maturation postnatally, preferably in the cortical TEC compartment. Block of RA signaling in TEC also affects T cell development and results in reduced numbers of single positive (SP) thymocytes and naive CD8+ T cells in the periphery. These findings provide first in vivo evidence for a role of RA signaling in the adult thymus regarding TEC function and T cell development.
Transcriptional immune response in mesenteric lymph nodes in pigs with different levels of resistance to Ascaris suum

A single nucleotide polymorphism on chromosome 4 (SNP TXNIP) has been reported to be associated with roundworm (Ascaris suum) burden in pigs. The objective of the present study was to analyse the immune response to A. suum mounted by pigs with genotype AA (n = 24) and AB (n = 23) at the TXNIP locus. The pigs were repeatedly infected with A. suum from eight weeks of age until necropsy eight weeks later. An uninfected control group (AA; n = 5 and AB; n = 5) was also included. At post mortem, we collected mesenteric lymph nodes and measured the expression of 28 selected immune-related genes. Recordings of worm burdens confirmed our previous results that pigs of the AA genotype were more resistant to infection than AB pigs. We estimated the genotype difference in relative expression levels in infected and uninfected animals. No significant change in expression levels between the two genotypes due to infection was observed for any of the genes, although IL-13 approached significance (P = 0.08; Punadjusted = 0.003). Furthermore, statistical analysis testing for the effect of infection separately in each genotype showed significant up-regulation of IL-13 (P...
Transfer of maternal immunity to piglets is involved in early protection against Mycoplasma hyosynoviae infection

Mycoplasma hyosynoviae causes arthritis in pigs older than 12 weeks. The role of colostrum in protection of piglets against M. hyosynoviae infection is not clear. Our objective was therefore to investigate whether transfer of maternal immunity to piglets was involved in early protection against the infection. Experimental infections were carried out in three groups of weaners receiving different levels of M. hyosynoviae-specific colostrum components; Group NC derived from Mycoplasma free sows and possessed no specific immunity to M. hyosynoviae. Group CAb pigs, siblings of the NC group, received colostrum with M. hyosynoviae-specific antibodies immediately after birth. Group CCE pigs were born and raised by infected sows and presumably had the full set of colostrally transferred factors, including specific antibodies. When 4½ weeks old, all pigs were inoculated intranasally with M. hyosynoviae. The course of infection was measured through clinical observations of lameness, cultivation of M. hyosynoviae from tonsils, blood and synovial fluid and observation for gross pathological lesions in selected joints. Specific immune status in the pigs was evaluated through detection of antibodies by immunoblotting and measurement of M. hyosynoviae-specific T-cell proliferation. The latter analysis may possibly indicate that M. hyosynoviae infection induces a T-cell response. The CCE piglets were significantly protected against development of lameness and pathology, as well as infection with M. hyosynoviae in tonsils, blood and joints, when compared to the other two groups. Raising the CCE pigs in an infected environment until weaning, with carrier sows as mothers, apparently made them resistant to M. hyosynoviae-arthritis when challenge-infected at 4½ weeks of age. More pigs in group NC had M. hyosynoviae related pathological lesions than in group CAb, a difference that was significant for cubital joints when analysed on joint type level. This finding indicates a partially protective effect of passively transferred M. hyosynoviae-specific colostral antibodies upon development of M. hyosynoviae related pathology. Thus, the level of passive immunity transferred from sow to piglet seems to provide, at least partial, protection against development of arthritis. It cannot be ruled out that the CCE pigs, by growing up in an infected environment, have had the chance to establish an active anti-M. hyosynoviae immune response that complements the maternally transferred immune factors. Evident from this study is that the general absence of M. hyosynoviae arthritis in piglets can be ascribed mainly to their immunological status.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Section for Epidemiology, University of Prince Edward Island, University of Copenhagen, Technical University of Denmark
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Pages: 22-30
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Veterinary Immunology and Immunopathology
Volume: 183
ISSN (Print): 0165-2427
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 0.71 SJR 0.68 CiteScore 1.7
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 1.63 SJR 0.742 SNIP 0.708
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 0.862 SNIP 0.749 CiteScore 1.67
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 0.777 SNIP 0.718 CiteScore 1.6
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 0.834 SNIP 0.797 CiteScore 1.89
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 0.841 SNIP 0.913 CiteScore 2.15
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 0.859 SNIP 0.995 CiteScore 2.16
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 0.792 SNIP 0.948
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 0.784 SNIP 0.851
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 0.705 SNIP 0.87
Scopus rating (2007): SJR 0.773 SNIP 0.92
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.791 SNIP 0.999
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.681 SNIP 0.925
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.751 SNIP 0.976
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.665 SNIP 0.757
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.578 SNIP 0.92
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.628 SNIP 0.862
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 0.499 SNIP 0.792
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 0.443 SNIP 0.655

Original language: English
Mycoplasma hyosynoviae, Arthritis, Colostrum, Antibody, Pig, Lymphocyte proliferation
Electronic versions:
Transmission differentials for multiple pathogens as inferred from their prevalence in larva, nymph and adult of Ixodes ricinus (Acari: Ixodidae)

Ixodes ricinus serves as vector for a range of microorganisms capable of causing clinical illness in humans. The microorganisms occur in the same vector populations and are generally affected by the same tick-host interactions. Still, the instars have different host preferences which should manifest in different transmission patterns for various microorganisms in the tick populations, i.e., most microorganisms increase in prevalence rate from larvae to nymphs because their reservoirs are among small mammals and birds that serve as blood hosts for larvae. Other microorganisms, like Anaplasma phagocytophilum, mainly increase in prevalence rates from nymphs to adults, because their reservoirs are larger ungulates that serve as primary blood hosts for nymphs and adults. We sampled a representative sample of ticks from 12 locations on Zealand and Funen, Denmark, and investigated the differences in prevalence rate of infection in larvae, nymphs and adults for multiple pathogens. Prevalence of infection for larvae, nymphs and adults, respectively, was: 0, 1.5 and 4.5% for Borrelia burgdorferi; 0, 4.2 and 3.9% for Borrelia garinii; 0, 6.6 and 6.1% for Borrelia afzelii; 0, 0 and 0.6% for Borrelia valaisiana; 0, 3.7 and 0.8% for Borrelia spielmani; 0, 0.7 and 1.2% for Babesia divergens; 0, 0, 0.6% for Babesia venatorum; 0, 1.5 and 6.1% for A. phagocytophilum. The results were in general compatible with the hypothesis i.e., that differences in blood host for larvae and nymphs define differences in transmission of infectious agents, but other factors than differences in blood hosts between larvae and nymphs may also be important to consider.

General information
State: Published
Organisations: National Veterinary Institute, Bacteriology & Parasitology, Epidemiology, University of Copenhagen, Agence nationale de la sécurité sanitaire, alimentation, environnement et travail
Authors: Jensen, P. M. (Ekstern), Christoffersen, C. S. (Ekstern), Moutailler, S. (Ekstern), Michelet, L. (Ekstern), Schou, K. K. (Intern), Bødker, R. (Intern)
Pages: 171-182
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Experimental & Applied Acarology
Volume: 71
Issue number: 2
ISSN (Print): 0168-8162
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.13 SJR 0.745 CiteScore 1.9
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.95 SJR 0.76 SNIP 1.132
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.831 SNIP 1.17 CiteScore 1.92
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.681 SNIP 0.954 CiteScore 1.46
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.816 SNIP 1.188 CiteScore 1.85
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.822 SNIP 1.168 CiteScore 1.78
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.74 SNIP 1.201 CiteScore 1.68
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.728 SNIP 1.058
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.659 SNIP 1.069
Transmission of African swine fever virus from infected pigs by direct contact and aerosol routes

In 2014, African swine fever virus (ASFV) was introduced into the Baltic states and Poland. Since then, the disease has continued to spread within these regions, and recently, cases were reported in the Czech Republic and Romania. Currently, there is an increasing risk of ASFV introduction into Western Europe. Hence, there is an urgent need to assess current contingency plans. For this purpose, knowledge of modes of transmission and clinical outcome in pigs infected with new European ASFV strains is needed. In the present study, two experiments were conducted in pigs using an isolate of ASFV from Poland (designated here POL/2015/Podlaskie/Lindholm). In both studies, pigs were inoculated intranasally with the virus and contact pigs were exposed to the experimentally infected pigs, either directly (contact within and between pens) or by air. Pigs exposed to the virus by intranasal inoculation, by direct contact to infected animals and by aerosol developed acute disease characterized by viremia, fever and depression. Infectious virus was first detected in blood obtained from the inoculated pigs and then sequentially among the within-pen, between-pen and air-contact pigs. ASFV DNA and occasionally infectious virus was found in nasal-, oral-, and rectal swabs obtained from the pigs, and ASFV DNA was detected in air samples. No anti-ASFV antibodies were detected in sera. In conclusion, the study shows that the currently circulating strain of ASFV can be efficiently transmitted via direct contact and by aerosols. Also, the results provide quantitative transmission parameters and knowledge of infection stages in pigs infected with this ASFV.
Treatment Patterns for Mastitis in Danish Dairy Cattle Farms

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, Seges Knowledge Centre for Agriculture, University of Copenhagen
Authors: Gussmann, M. K. (Intern), Græsbøll, K. (Intern), Kirkeby, C. T. (Intern), Nielsen, S. S. (Ekstern), Toft, N. (Intern), Farre, M. (Ekstern), Hisham Beshara Halasa, T. (Intern)
Triple-reassortant influenza A virus with H3 of human seasonal origin, NA of swine origin, and internal A(H1N1) pandemic 2009 genes is established in Danish pigs

This report describes a triple-reassortant influenza A virus with a HA that resembles H3 of human seasonal influenza from 2004 to 2005, N2 from influenza A virus already established in swine, and the internal gene cassette from A(H1N1)pdm09 has spread in Danish pig herds. The virus has been detected in several Danish pig herds during the last 2-3 years and may possess a challenge for human as well as animal health.
Type I interferon is critical for the homeostasis and functional maturation of type 3 γδ T cells

Type I IFN (IFN-I) is highly expressed during viral infection and many autoimmune pathologies such as SLE and psoriasis. In addition, IFN-I is important to maintain the homeostasis of a number of different immune populations. Our aim was to identify whether IFN-I regulates type 3 γδ T (γδT3) cells. We found that IFNαβ inhibits the activation of γδT3 cells following treatment with cytokines such as IL-23 and IL-7 and abrogates their ability to produce IL-17 during viral infection. Despite this inhibitory role, γδT3 cells that are deficient in type I IFN receptor (IFNAR) signaling display anergic behavior. Such γδT3 anergy is characterized by failure to induce skin inflammation and unresponsiveness to cytokine stimuli. Moreover, IFNAR deficient mice display deregulated γδT3 homeostasis due to a neonatal maturation defect. In conclusion, our data show that tonic type I IFN signaling during neonatal and adult life is required for the full maturation and pro-inflammatory function of γδT3 cells, however acute type I IFN production during viral infection acts as a γδT3 inhibitor.
Udvikling af en sandwich-ELISA til måling af immunglobulin G i minkblod

General information
State: Published
Organisations: National Veterinary Institute, Innate Immunology, Diagnostic & Development, Kopenhagen Fur
Authors: Mathiesen, R. (Intern), Chriél, M. (Intern), Struve, T. (Ekstern), Heegaard, P. M. H. (Intern)
Pages: 159-162
Publication date: 2017

Host publication information
Title of host publication: Faglig årsberetning 2016 : Kopenhagen Fur
Place of publication: Aarhus N
Publisher: Kopenhagen Fur
Main Research Area: Technical/natural sciences
Electronic versions: DTU4_1_.pdf
Publication: Research - peer-review › Book chapter – Annual report year: 2017

Unusually High Mortality in Waterfowl Caused by Highly Pathogenic Avian Influenza A(H5N1) in Bangladesh
Mortality in ducks and geese caused by highly pathogenic avian influenza A(H5N1) infection had not been previously identified in Bangladesh. In June-July 2011, we investigated mortality in ducks, geese and chickens with suspected H5N1 infection in a north-eastern district of the country to identify the aetiologic agent and extent of the outbreak and identify possible associated human infections. We surveyed households and farms with affected poultry flocks in six villages in Netrokona district and collected cloacal and oropharyngeal swabs from sick birds and tissue samples from dead poultry. We conducted a survey in three of these villages to identify suspected human influenza-like illness cases and collected nasopharyngeal and throat swabs. We tested all swabs by real-time RT-PCR, sequenced cultured viruses, and examined tissue samples by histopathology and immunohistochemistry to detect and characterize influenza virus infection. In the six villages, among the 240 surveyed households and 11 small-scale farms, 61% (1789/2930) of chickens, 47% (4816/10184) of ducks and 73% (358/493) of geese died within 14 days preceding the investigation. Of 70 sick poultry swabbed, 80% (56/70) had detectable RNA for influenza A/H5, including 89% (49/55) of ducks, 40% (2/5) of geese and 50% (5/10) of chickens. We isolated virus from six of 25 samples; sequence analysis of the hemagglutinin and neuraminidase gene of these six isolates indicated clade 2.3.2.1a of H5N1 virus. Histopathological changes and immunohistochemistry staining of avian influenza viral antigens were recognized in the brain, pancreas and intestines of ducks and chickens. We identified ten human cases showing signs compatible with influenza-like illness; four were positive for influenza A/H3; however, none were positive for influenza A/H5. The recently introduced H5N1 clade 2.3.2.1a virus caused unusually high mortality in ducks and geese. Heightened surveillance in poultry is warranted to guide appropriate diagnostic testing and detect novel influenza strains.

General information
State: Published
Use of multiple-locus variable-number of tandem repeats analysis (MLVA) to investigate genetic diversity of Salmonella enterica subsp. enterica serovar Typhimurium isolates from human, food, and veterinary sources

Salmonella enterica subspecies enterica serovar Typhimurium is the most common zoonotic pathogen in Bulgaria. To allow efficient outbreak investigations and surveillance in the food chain, accurate and discriminatory methods for typing are needed. This study evaluated the use of multiple-locus variable-number of tandem repeats analysis (MLVA) and compared results with antimicrobial resistance (AMR) determinations for 100 S. Typhimurium strains isolated in Bulgaria during 2008-2012 (50 veterinary/food and 50 human isolates). Results showed that isolates were divided into 80 and 34 groups using MLVA and AMR, respectively. Simpson's index of diversity was determined to 0.994 ± 0.003 and 0.945 ± 0.012. The most frequently encountered MLVA profiles were 3-11-9-NA-211 (n = 5); 3-12-9-NA-211 (n = 3); 3-12-11-21-311 (n = 3); 3-17-10-NA-311 (n = 3); 2-20-9-7-212 (n = 3); and 2-23-NA-NA-111 (n = 3). No clustering of isolates related to susceptibility/resistance to antimicrobials, source of isolation, or year of isolation was observed. Some MLVA types were found in both human and veterinary/food isolates, indicating a possible route of transmission. A majority (83%) of the isolates were found to be resistant against at least one antimicrobial and 44% against ≥4 antimicrobials. Further studies are needed to verify MLVA usefulness over a longer period of time and with more isolates, including outbreak strains.

General information
State: Published
Organisations: National Veterinary Institute, Bacteriology & Parasitology, Research Group for Analytical and Predictive Microbiology, Research Group for Genomic Epidemiology, National Food Institute, National Diagnostic and Research Veterinary Medical Institute, National Center of Infectious and Parasitic Diseases Bulgaria, Bulgarian Academy of Sciences
Authors: Mateva, G. (Ekstern), Pedersen, K. (Intern), Sørensen, G. (Intern), Asseva, G. (Ekstern), Daskalov, H. (Ekstern), Petrov, P. (Ekstern), Kantardjiev, T. (Ekstern), Alexandar, I. (Ekstern), Löfström, C. (Intern)
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: MicrobiologyOpen
Volume: 7
Issue number: 1
Article number: e00528
ISSN (Print): 2045-8827
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.909 SJR 1.158 CiteScore 2.63
Web of Science (2017): Indexed yes
Scopus rating (2016): CiteScore 2.86 SJR 1.318 SNIP 0.836
Scopus rating (2015): SJR 1.212 SNIP 0.685 CiteScore 2.32
Scopus rating (2014): SJR 1.192 SNIP 1.057 CiteScore 2.19
Scopus rating (2013): SJR 0.726 SNIP 0.404 CiteScore 1.41
ISI indexed (2013): ISI indexed no
Original language: English
MLVA, Salmonella genetic diversity, antimicrobial resistance, laboratory surveillance, public health, zoonoses
Electronic versions:
Mateva_et_al_2018_MicrobiologyOpen.pdf
Koi herpesvirus (KHV) causes KHV disease (KHVD). The virus is highly contagious in carp or koi and can induce a high mortality. Latency and, in some cases, a lack of signs presents a challenge for virus detection. Appropriate immunological detection methods for anti-KHV antibodies have not yet been fully validated for KHV. Therefore, it was developed and validated an enzyme-linked immunosorbent assay (ELISA) to detect KHV antibodies. The assay was optimized with respect to plates, buffers, antigens and assay conditions. It demonstrated high diagnostic and analytical sensitivity and specificity and was particularly useful at the pond or farm levels. Considering the scale of the carp and koi industry worldwide, this assay represents an important practical tool for the indirect detection of KHV, also in the absence of clinical signs.

**General information**

**State:** Published

**Organisations:** National Veterinary Institute, Fish Diseases, Friedrich-Loeffler-Institute, Chinese Academy of Fisheries Sciences, National Veterinary Research Institute, Agence Nationale de Sécurité Sanitaire de l’Alimentation, GeneReach Biotechnology Corporation, Chinese Academy of Fishery Sciences, University of Stirling, The Hebrew University-Hadassah Medical School, Centre for Environment Fisheries and Aquaculture Science, Fish Health Service Saxony, Fish Health Service Thuringia, West Pomeranian University of Technology


**Pages:** 1511-1527

**Publication date:** 2017

**Main Research Area:** Technical/natural sciences
Validation of a serum neutralization test for detection of antibodies specific to cyprinid herpesvirus 3 in infected common and koi carp (Cyprinus carpio)

Cyprinid herpesvirus 3 (CyHV-3) is the aetiological agent of a serious infective, notifiable disease affecting common carp and varieties. In survivors, infection is generally characterized by a subclinical latency phase with restricted viral replication. The CyHV-3 genome is difficult to detect in such carrier fish that represent a potential source of dissemination if viral reactivation occurs. In this study, the analytical and diagnostic performance of an alternative serum neutralization (SN) method based on the detection of CyHV-3-specific antibodies was assessed using 151 serum or plasma samples from healthy and naturally or experimentally CyHV-3-infected carp. French CyHV-3 isolate 07/108b was neutralized efficiently by sera from carp infected with European, American and Taiwanese CyHV-3 isolates, but no neutralization was observed using sera specific to other aquatic herpesviruses. Diagnostic sensitivity, diagnostic specificity and repeatability of 95.9%, 99.0% and 99.3%, respectively, were obtained, as well as a compliance rate of 89.9% in reproducibility testing. Neutralizing antibodies were steadily detected in infected carp subjected to restrictive or permissive temperature variations over more than 25 months post-infection. The results suggest that this non-lethal diagnostic test could be used in the future to improve the epidemiological surveillance and control of CyHV-3 disease.

General information
State: Published
Organisations: Section for Virology, National Veterinary Institute, ANSES - French Agency for Food, Environmental and Occupational Health & Safety, Friedrich-Loeffler-Institute, Instituto Zooprofilattico Sperimentale delle Venezie, National Veterinary Research Institute
Authors: Cabon, J. (Ekstern), Louboutin, L. (Ekstern), Castric, J. (Ekstern), Bergmann, S. (Ekstern), Bovo, G. (Ekstern), Matras, M. (Ekstern), Haenen, O. (Ekstern), Olesen, N. J. (Intern), Morin, T. (Ekstern)
Pages: 687-701
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Fish Diseases
Volume: 40
Issue number: 5
ISSN (Print): 0140-7775
Ratings:
Vectorborne zoonoses

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, Bacteriology & Parasitology, Technical University of Denmark
Authors: Bødker, R. (Intern), Vrbová, E. (Ekstern), Schou, K. K. (Intern)
Pages: 20-21
Publication date: 2017

Host publication information
Viability Assessment of Cryptosporidium parvum Oocysts by Vital Dyes: Dry Mounts Overestimate the Number of “Ghost” Oocysts

Viability assessment of Cryptosporidium parvum oocysts is crucial for evaluation of the public health significance of this important zoonotic protozoon. Viability is commonly assessed in wet mounts after acid pretreatment and staining with fluorogenic vital dyes. However, in some studies, oocyst viability is evaluated in dry mounts after staining in suspension. Here, we evaluate the effect of acid pretreatment in nine replicate samples and compare the assessment of oocyst viability after evaluation in wet and dry mounts, respectively. Although acid pretreatment had no significant effect on the viability scores, data obtained by scoring oocysts in dry mounts resulted in ∼25% underestimation of the proportion of viable oocyst (82.5% –+ 0.9% [wet mount + acid], 57.7% –+ 2.3% [dry mount - Oacid], 76.0% –+ 1.7% [wet mount, - Oacid]), while the proportions of nonviable oocysts (DAPI+/PI+) were comparable for wet and dry mounts (9.7% –+ 0.4% [wet mount + acid], 12.1 –+ 1.5% [dry mount, - acid], 15.5% –+ 1.1% [wet mount, - acid]).

General information
State: Published
Organisations: National Veterinary Institute, Bacteriology & Parasitology, Norwegian Veterinary Institute
Authors: Petersen, H. H. (Intern), Enemark, H. L. (Ekstern)
Pages: 141-144
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Foodborne Pathogens and Disease
Volume: 15
Issue number: 3
ISSN (Print): 1535-3141
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.016 SJR 1.063 CiteScore 2.47
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.46 SJR 1.062 SNIP 1.08
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.064 SNIP 1.035 CiteScore 2.41
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.953 SNIP 1.051 CiteScore 2.16
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.184 SNIP 1.129 CiteScore 2.41
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.185 SNIP 1.144 CiteScore 2.55
ISI indexed (2012): ISI indexed yes
Viral haemorrhagic septicaemia virus (VHSV) remains viable for several days but at low levels in the water flea Moina macrocopa

Viral haemorrhagic septicaemia virus (VHSV) Genotype IVb has been isolated from amphipods belonging to the genus Diporeia, but it has yet to be established whether crustacean zooplankton act as vectors of this virus for fish species. Therefore, we evaluated the viability of infectious VHSV in the water flea Moina macrocopa. VHSV was re-isolated from replicate groups of M. macrocopa that had been immersed with 10^{8.0}, 10^{7.0}, and 10^{5.0} TCID\textsubscript{50} ml\textsuperscript{-1} of VHSV (DK-3592B, Genotype Ia). Furthermore, 40 M. macrocopa that had been immersed with 10^{8.0} TCID\textsubscript{50} ml\textsuperscript{-1} VHSV for 72 h had VHSV titers of 10^{2.7-10^{4.3}} TCID\textsubscript{50}. Thus, VHSV was clearly taken up by M. macrocopa and remained viable in this crustacean for several days. However, no mortality was observed over a 28 d period in rainbow trout Oncorhynchus mykiss that were fed VHSV-contaminated M. macrocopa for 14 d, and we found that the virus titer significantly decreased after a 4 h incubation with pyloric caecal extracts from rainbow trout, indicating that passage through the gut is likely to result in a significant decrease in viral titer. This may explain why consumption of prey containing low levels of VHSV did not result in clinical VHS.

General information
State: Published
Organisations: National Veterinary Institute, Fish Diseases, Fisheries Research Agency
Authors: Ito, T. (Ekstern), Olesen, N. J. (Intern)
Pages: 11-18
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Diseases of Aquatic Organisms
Volume: 127
Issue number: 1
ISSN (Print): 0177-5103
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.95 SJR 0.675 CiteScore 1.7
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Virus genomes reveal factors that spread and sustained the Ebola epidemic
The 2013-2016 West African epidemic caused by the Ebola virus was of unprecedented magnitude, duration and impact. Here we reconstruct the dispersal, proliferation and decline of Ebola virus throughout the region by analysing 1,610 Ebola...
virus genomes, which represent over 5% of the known cases. We test the association of geography, climate and
demography with viral movement among administrative regions, inferring a classic ‘gravity’ model, with intense dispersal
between larger and closer populations. Despite attenuation of international dispersal after border closures, cross-border
transmission had already sown the seeds for an international epidemic, rendering these measures ineffective at curbing
the epidemic. We address why the epidemic did not spread into neighbouring countries, showing that these countries were
susceptible to substantial outbreaks but at lower risk of introductions. Finally, we reveal that this large epidemic was a
heterogeneous and spatially dissociated collection of transmission clusters of varying size, duration and connectivity.
These insights will help to inform interventions in future epidemics.

General information
State: Published
Organisations: National Veterinary Institute, Virology, University of Edinburgh, Fred Hutchinson Cancer Research Center,
University of Southampton, University of Leuven, University of Oxford, Broad Institute of Harvard University and
Massachusetts Institute of Technology, U.S. Army Medical Research Institute of Infectious Diseases, Irrua Specialist
Teaching Hospital, University of Cambridge, Erasmus University Medical Centre, L. Spallanzani National Institute for
Infectious Diseases, Naval Medical Research Unit, Bernhard Nocht Institute for Tropical Medicine, Public Health England,
Liberian Institute for Biomedical Research, Institut Pasteur de Dakar, University of Sierra Leone, Kenema Government
Hospital, University of Liverpool, University of Makei, Chinese Academy of Sciences, University of Bristol, University of
Birmingham, Tulane University, Institut Pasteur, Bundeswehr Institute of Microbiology, Wellcome Trust Sanger Institute,
Centers for Disease Control and Prevention, The Scripps Research Institute, Ministry of Social Welfare, Gender and
Children's Affairs, Ministry of Health Liberia, World Health Organization, World Health Organization, Redeemer’s
University, University of Sydney, Ministry of Health and Sanitation, Ministry of Health Guinea, National Institutes of Health,
Université Gamal Abdel Nasser de Conakry, University of California, Los Angeles
Authors: Dudas, G. (Ekstern), Carvalho, L. M. (Ekstern), Bedford, T. (Ekstern), Tatem, A. J. (Ekstern), Baele, G. (Ekstern)
, Faria, N. R. (Ekstern), Park, D. J. (Ekstern), Ladner, J. T. (Ekstern), Arias Esteban, A. (Intern), Asogun, D. (Ekstern),
Bielejec, F. (Ekstern), Caddy, S. L. (Ekstern), Cotten, M. (Ekstern), D'Ambozio, J. (Ekstern), Dellicour, S. (Ekstern), Di
Caro, A. (Ekstern), Diclaro, J. W. (Ekstern), Duraffour, S. (Ekstern), Elmore, M. J. (Ekstern), Fakoli, L. S. (Ekstern), Faye,
(Okstern), Gilbert, M. L. (Ekstern), Geva, S. M. (Ekstern), Gire, S. (Ekstern), Gladden-Young, A. (Ekstern), Gnim, A.
(Okstern), Goba, A. (Ekstern), Grant, D. S. (Ekstern), Hagemans, B. L. (Ekstern), Hiscox, J. A. (Ekstern), Jah, U. (Ekstern)
, Kugelman, J. R. (Ekstern), Liu, D. (Ekstern), Lu, J. (Ekstern), Maltbeuf, C. M. (Ekstern), Mate, S. (Ekstern), Matthews, D.
A. (Ekstern), Matranga, C. B. (Ekstern), Meredith, L. W. (Ekstern), Qu, J. (Ekstern), Quick, J. (Ekstern), Pas, S. D.
(Okstern), Phan, M. V. T. (Ekstern), Polliakis, G. (Ekstern), Reusken, C. B. (Ekstern), Sanchez-Lockhart, M. (Ekstern),
Schaffner, S. F. (Ekstern), Schieffelin, J. S. (Ekstern), Sealfon, R. S. (Ekstern), Simon-Loriere, E. (Ekstern), Smits, S. L.
(Ekstern), Stoecker, K. (Ekstern), Thorne, L. (Ekstern), Tobin, E. A. (Ekstern), Vandi, M. A. (Ekstern), Watson, S.
(Ekstern), West, K. (Ekstern), Whinmer, S. (Ekstern), Wiley, M. R. (Ekstern), Winnicki, S. M. (Ekstern), Wohl, S. (Ekstern),
Wolfe, R. (Ekstern), Yozwiak, N. L. (Ekstern), Andersen, K. G. (Ekstern), Bydlen, S. O. (Ekstern), Bolay, F. (Ekstern),
Carroll, M. W. (Ekstern), Dahm, B. (Ekstern), Diolao, B. (Ekstern), Fortenay, P. (Ekstern), Fraser, C. (Ekstern), Gao, G. F.
(Ekstern), Garry, R. F. (Ekstern), Goodfellow, I. (Ekstern), Güntner, S. (Ekstern), Happi, C. T. (Ekstern), Holmes, E. C.
(Ekstern), Kargbo, B. (Ekstern), Kejia, S. (Ekstern), Kellam, P. (Ekstern), Koopmans, M. P. G. (Ekstern), Kuhn, J. H.
(Okstern), Loman, N. J. (Ekstern), Magassouba, N. (Ekstern), Naidoo, D. (Ekstern), Nichol, S. T. (Ekstern), Nyenswah, T.
(Ekstern), Palacios, G. (Ekstern), Pybus, O. G. (Ekstern), Sabeti, P. C. (Ekstern), Sall, A. (Ekstern), Stroher, U. (Ekstern),
Wurie, I. (Ekstern), Suchard, M. A. (Ekstern), Lemey, P. (Ekstern), Rambaut, A. (Ekstern)
Pages: 309-315
Publication date: 2017
Main Research Area: Technical/natural sciences

Publication information
Journal: Nature
Volume: 544
Issue number: 7650
ISSN (Print): 0028-0836
Ratings:
BFI (2018): BFI-level 3
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 14.59
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 13.33
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 14.38
Web of Science (2015): Indexed yes
Visualizing infections and immune mechanisms in zebrafish

The zebrafish has become an important model to study a wide spectrum of vertebrate biological processes. It is used within all major biological sciences and has been especially valuable within developmental biology and genetics. Within the last 20 years the amount of papers describing zebrafish as a model has increased dramatically. It is a valuable model because of several characteristics: it is a vertebrate, it has external embryological development and is fully transparent for the first 24 h post hatching, development is fast; the vertebrate organs can be identified within 48 hours (ears, eyes, brain, internal organs), embryos are simple to genetically manipulate, the genome has been mapped, thousands of transgenic lines exist and a pair of breeders are able to produce up to 300 eggs per week making it a high-throughput but low-cost model organism. Unique tools for non-invasive in vivo imaging has been developed and high quality intravital microscopy can be conducted without comparison. A transparent line has also been developed where transparency is maintained throughout the lifespan of the fish facilitating in vivo visualization of e.g. the spread of fluorescence-tagged cancer cells, immunological reactions during e.g. transplant rejections or the spread and pathogenicity of pathogens. We have, in our laboratory, used the zebrafish as a model for aquacultured fish species and their pathogens. We have 1) visualized antigen uptake in vivo following a bath in a soup containing fluorescent inactivated bacteria, 2) visualized the spread of a bacterium after either a bath or an injection in the peritoneal cavity, and 3) visualized (images + videos) the behaviour of certain immune cells, called neutrophils during a parasite disease. Using adult fish of a transgenic line with GFP-tagged neutrophils, we got an unprecedented view into the interactions between the parasites and the neutrophils.

General information
State: Published
What tools are useful for monitoring endemic diseases? A simulation study based on different time-series components.

Control and eradication programs play an important role in disease monitoring and surveillance. It is important to follow up on implemented strategies to reduce and/or eliminate a specific disease. The objectives of this study were to investigate the performance of different detection methods, including methods commonly used in biosurveillance as well as state space models, for monitoring the effect of endemic disease control and eradication programs. We simulated 16 different scenarios of changes in disease sero-prevalence, inspired by real-world data from the Danish PRRS (Porcine Reproductive and Respiratory Syndrome) monitoring program. The changes included increases, decreases and/or constant sero-prevalence levels in different combinations. Two state space models were used to model the simulated data and different monitoring methods, such as univariate process control algorithms (UPCA) and monitoring of the trend component were tested. The performance was evaluated as the proportion of iterations with an alarm for a given week. Results revealed that the different UPCA performed differently with respect to detecting increasing and decreasing changes in sero-prevalence. The trend-based methods performed well for detecting the first event but its performance was poorer in adapting to several consecutive events. The different monitoring methods had different performances in monitoring increasing and decreasing changes in disease sero-prevalence, showing that the objectives of the monitoring program should be taken into account when choosing which methods to use. The principles used in this study can also be applied in disease surveillance of (re-)emerging diseases.

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, University of Copenhagen
Authors: Lopes Antunes, A. C. (Intern), Jensen, D. (Ekstern), Hisham Beshara Halasa, T. (Intern), Toft, N. (Intern)
Pages: 5-8
Publication date: 2017

Host publication information
Title of host publication: Proceedings of the 3rd International Conference on Animal Health Surveillance - beyond animal health surveillance
Place of publication: Wellington
Publisher: New Zealand Veterinary Association
Main Research Area: Technical/natural sciences
Conference: 3rd International Conference on Animal Health Surveillance, Rotorua, New Zealand, 30/04/2017 - 30/04/2017
Surveillance, Endemic diseases, Time-series components
Source: PublicationPreSubmission
Source-ID: 131734279
Publication: Research - peer-review › Article in proceedings – Annual report year: 2017

Whole-genome sequencing of veterinary pathogens
Bacterial infections in production animals constitute a considerable burden across the globe and result in impaired animal welfare and production economy. Additionally, veterinary pathogens with zoonotic potential may cause severe infections in humans. Traditional molecular techniques based on gel-electrophoresis and single-locus sequencing has been widely used to characterize such types of veterinary pathogens. However, DNA sequencing techniques have become fast and cost effective in recent years and whole-genome sequencing data provide a much higher discriminative power and reproducibility than any of the traditional molecular techniques. In this PhD project three important veterinary pathogens (Clostridium perfringens, Escherichia coli and Staphylococcus aureus) were investigated using whole-genome sequencing. This was done in five different scientific papers which all have been published. Paper I and II In 2014, an increased mortality rate caused by Escherichia coli infections was observed among chickens (Gallus gallus domesticus) from farms in Denmark and other Nordic countries. Therefore, the genetic diversity and relatedness of 114 E. coli isolates primary associated with increased mortality in Nordic countries, was investigated using whole-genome sequencing. This was done in five different scientific papers which all have been published. Paper I and II In 2014, an increased mortality rate caused by Escherichia coli infections was observed among chickens (Gallus gallus domesticus) from farms in Denmark and other Nordic countries. Therefore, the genetic diversity and relatedness of 114 E. coli isolates primary associated with increased mortality in Nordic countries, was investigated using whole-genome sequencing. In paper I, the genome assemblies of two avian pathogenic E. coli (APEC) isolates were annotated and the draft genomes deposited in a publicly available database. In paper II, a group of 47 closely related sequence type (ST)117 O78:H4 isolates from both broiler chickens and parent birds collected across the Nordic countries, was observed. Since most Nordic poultry farmers import birds that are all part of the same breeding pyramid these results indicate that the ST117 O78:H4 isolates were transmitted vertically through this breeding pyramide. Therefore, it was concluded that vertically transmitted ST117 O78:H4 isolates were the main reason for the increased mortality rates observed in the Nordic broiler.
industry. Paper III Necrotic enteritis (NE) in chickens is primarily caused by pathogenic Clostridium perfringens strains. Studies have shown that three pathogenicity loci (NELoc-1, 2 and 3) and two virulence genes (netB and cnaA) are often carried by C. perfringens isolates collected from chickens with NE. In general, the virulence gene content have not been widely investigated in isolates from turkeys (Maleagris gallopavo) with NE. However, netB has not been found in high prevalence among isolates from diseased turkeys and prior to this study, no publications using whole-genome sequencing on NE isolates from turkeys, have been published. Here, 30 C. perfringens isolates from both healthy and NE infected chickens and turkeys were analyzed using whole-genome sequencing. The results showed that NELoc-1 and -3 and the two virulence genes netB and cnaA were significantly more associated with NE isolates from chickens compared to NE isolates from turkeys. Only NELoc-2 was associated with NE isolates from both turkeys and chickens. A putative collagen adhesion gene was discovered among all isolates from diseased turkeys and has been designated cnaD. Potentially, CnaD could be of importance in regard to the NE pathogenesis in turkeys. In general, these results suggest that the NE pathogenesis in chickens is different from that of turkeys. Paper IV and V Staphylococcus aureus is a pathogen that commonly causes mastitis in dairy cows (Bos taurus). Many different subtypes, virulence genes and pathogenicity islands have been associated with isolates from bulk tank milk (BTM) and dairy cows with clinical mastitis (CM). Prior to these studies, no Danish S. aureus isolates associated with bovine mastitis have been analyzed using whole-genome sequencing. In paper V, 157 S. aureus isolates from BTM and dairy cows with CM were whole-genome sequenced and further investigated. In general, the results showed that BTM and CM isolates were of identical genetic background. This indicates that dairy cows can be natural carriers of S. aureus subtypes that in certain cases lead to CM. A group of isolates that mostly belonged to ST151 carried three pathogenicity islands that were primarily found in this group. The prevalence of resistance genes was generally low but the first ST398 methicillin resistant S. aureus isolate from a Danish dairy cow with CM was observed. In paper IV, the assemblies from this isolate (strain Sa52) were annotated and the draft genome uploaded to a publicly available database.

General information
State: Published
Organisations: National Veterinary Institute, Bacteriology & Parasitology, National Food Institute, Research Group for Genomic Epidemiology, Statens Serum Institut
Authors: Ronco, T. (Intern), Pedersen, K. (Intern), Stegger, M. (Ekstern)
Number of pages: 111
Publication date: 2017

Publication information
Place of publication: Kgs. Lyngby
Publisher: DTU Veterinær Institutet
Original language: English
Main Research Area: Technical/natural sciences
Electronic versions:
FinalVesion_220218.pdf

Relations
Projects:
Whole-genome sequencing of veterinary pathogens
Publication: Research › Ph.D. thesis – Annual report year: 2018

Zebrafish (Danio rerio) as a model to visualize infection dynamics of Vibrio anguillarum following intraperitoneal injection and bath exposure
Vaccine development is important for sustainable fish farming and novel vaccines need to be efficacy tested before release to the market. Challenge of fish with the pathogen towards which the vaccine has been produced can be conducted either by external exposure though bathing or cohabitation, or by bypassing the mucosa through injection. The latter approach is often preferred since it is easier to control than the former. However, injection is not a very natural route of infection, and the bypass of the mucosa may result in a different efficacy profile of experimental fish compared to farmed fish, for which the vaccines are targeted. The zebrafish is by now a well established practical vertebrate model species due in part to its size and ease of maintenance and genetic manipulation. Here we use zebrafish as a model to visualize and compare the development of infection of Vibrio anguillarum on and in the fish following injection or bathing. Injection of 103 bacteria per fish resulted in approximately 50% mortality by day 4 post-injection. Similar mortality levels were reached in the other group by bathing in 1.25 × 109 bacteria for 1 min. The spreading of bacteria was followed for the first 24 h after injection/bathing by immunohistochemistry and optical projection tomography. The tissues and organs where bacteria were detected differed significantly as a result of time as well as treatment. In the bath group, bacteria were initially found on external surfaces including gut. After 24 h V. anguillarum still persisted in gut but had now also spread to the blood. In the injection group bacteria were found in the blood throughout all sampling times, as well as in the hypodermis and body cavity at most sampling times.

General information
State: Published
Organisations: National Veterinary Institute, Fish Diseases, University of Copenhagen
High throughput optimization of content-loaded nanoparticles

The present invention relates to tagged particles and the identification and characterization of particles based on their tag. In particular, the present invention relates to a method for the production of a multitude of uniquely tagged particles comprised of a range of components selected from the group consisting of carriers, cargo and surface molecules, and the identification of such particles causing a specific effect/change in a sample, such as certain tissues/cell types.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology
Authors: Hadrup, S. R. (Intern), Lyngsø, C. (Ekstern), JAKOBSEN, Søren, N. (Ekstern)
Publication date: 15 Dec 2016

Publication information
IPC: C12Q 1/68 A I
Patent number: WO2016198609
Date: 15/12/2016
Priority date: 10/06/2015
Priority number: EP20150171429
Original language: English
Main Research Area: Technical/natural sciences
Source: espacenet
Source-ID: WO2016198609
Publication: Research › Patent – Annual report year: 2016

Method for identification of tissue or organ localization of a tumour

The invention relates to a method for predicting the localization of a primary tumour, wherein said method comprises the use of genomic profile data, and wherein the method is capable of predicting the type of cancer by a classification score ranking among a variety of the possible tumour types.

General information
State: Published
Organisations: Center for Biological Sequence Analysis, Cancer Systems Biology, National Veterinary Institute, Section for Immunology and Vaccinology, Department of Bio and Health Informatics, Cancer Genomics, Department of Systems Biology
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Publication date: 23 Jun 2016

Publication information
IPC: C12Q 1/68 A I
Patent number: WO2016097251
Date: 23/06/2016
Priority date: 19/12/2014
Priority number: EP20140199179
Original language: English
A common mechanism involving the TORC1 pathway can lead to amphotericin B-persistence in biofilm and planktonic Saccharomyces cerevisiae populations

Fungal infections are an increasing clinical problem. Decreased treatment effectiveness is associated with biofilm formation and drug recalcitrance is thought to be biofilm specific. However, no systematic investigations have tested whether resistance mechanisms are shared between biofilm and planktonic populations. We performed multiplexed barcode sequencing (Bar-seq) screening of a pooled collection of gene-deletion mutants cultivated as biofilm and planktonic cells. Screening for resistance to the ergosterol-targeting fungicide amphotericin B (AmB) revealed that the two growth modes had significant overlap in AmB-persistent mutants. Mutants defective in sterol metabolism, ribosome biosynthesis, and the TORC1 and Ras pathways showed increased persistence when treated with AmB. The ras1, ras2 and tor1 mutants had a high-persister phenotype similar to wild-type biofilm and planktonic cells exposed to the TORC1 pathway inhibitor rapamycin. Inhibition of TORC1 with rapamycin also increased the proportion of persisters in Candida albicans and Candida glabrata. We propose that decreased TORC1-mediated induction of ribosome biosynthesis via Ras can lead to formation of AmB-persister cells regardless of whether the cells are in planktonic or biofilm growth mode. Identification of common pathways leading to growth mode-independent persister formation is important for developing novel strategies for treating fungal infections.

**General information**

State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, New York University, University of Copenhagen
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Number of pages: 10
Publication date: 23 Feb 2016
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Scientific Reports
Issue number: 6
Article number: 21874
ISSN (Print): 2045-2322
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.36 SJR 1.533 SNIP 1.245
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.63 SJR 1.692 SNIP 1.354
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.034 SNIP 1.597 CiteScore 5.3
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.163 SNIP 1.554 CiteScore 4.75
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.998 SNIP 1.57 CiteScore 4.06
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.928 SNIP 0.962 CiteScore 2.44
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
ISI indexed (2011): ISI indexed no
A combined prediction strategy increases identification of peptides bound with high affinity and stability to porcine MHC class I molecules SLA-1*04:01, SLA-2*04:01, and SLA-3*04:01

Affinity and stability of peptides bound by major histocompatibility complex (MHC) class I molecules are important factors in presentation of peptides to cytotoxic T lymphocytes (CTLs). In silico prediction methods of peptide-MHC binding followed by experimental analysis of peptide-MHC interactions constitute an attractive protocol to select target peptides from the vast pool of viral proteome peptides. We have earlier reported the peptide binding motif of the porcine MHC-I molecules SLA-1*04:01 and SLA-2*04:01, identified by an ELISA affinity-based positional scanning combinatorial peptide library (PSCPL) approach. Here, we report the peptide binding motif of SLA-3*04:01 and combine two prediction methods and analysis of both peptide binding affinity and stability of peptide-MHC complexes to improve rational peptide selection.

Using a peptide prediction strategy combining PSCPL binding matrices and in silico prediction algorithms (NetMHCpan), peptide ligands from a repository of 8900 peptides were predicted for binding to SLA-1*04:01, SLA-2*04:01, and SLA-3*04:01 and validated by affinity and stability assays. From the pool of predicted peptides for SLA-1*04:01, SLA-2*04:01, and SLA-3*04:01, a total of 71, 28, and 38 % were binders with affinities below 500 nM, respectively. Comparison of peptide-SLA binding affinity and complex stability showed that peptides of high affinity generally, but not always, produce complexes of high stability. In conclusion, we demonstrate how state-of-the-art prediction and in vitro immunology tools in combination can be used for accurate selection of peptides for MHC class I binding, hence providing an expansion of the field of peptide-MHC analysis also to include pigs as a livestock experimental model.
In 2007, bluetongue virus (BTV) was introduced to both Denmark (DK) and the United Kingdom (UK). For this reason, simulation models were built to predict scenarios for future incursions. The DK and UK models have a common description of within-herd dynamics, but differ greatly in their descriptions of between-herd spread, one using an explicit representation of vector dispersal, the other a transmission kernel. Here, we compare model predictions for the dynamics of bluetongue in the UK, based on the 2007 incursion and vaccination rollout in 2008. We demonstrate how an agent-based model shows greater sensitivity to the level of vaccine uptake and has lower variability compared with a kernel-based model. However, a model using a transmission kernel requires less detailed data and is often faster.
Activation of innate immune genes in caprine blood leukocytes after systemic endotoxin challenge

Sepsis is a serious health problem associated with a range of infectious diseases in animals and humans. Early events of this syndrome can be mimicked by experimental administration of lipopolysaccharides (LPS). Compared with mice, small ruminants and humans are highly sensitive to LPS, making goats valuable in inflammatory models. We performed a longitudinal study in eight Norwegian dairy goats that received LPS (0.1 μg/kg, Escherichia coli O26:B6) intravenously. A control group of five goats received corresponding volumes of sterile saline. Clinical examinations were performed continuously, and blood samples were collected throughout the trial. Characteristic signs of acute sepsis, such as sickness behavior, fever, and leukopenia were observed within 1 h of LPS administration. A high-throughput longitudinal gene expression analysis of circulating leukocytes was performed, and genes associated with the acute phase response, type I interferon signaling, LPS cascade and apoptosis, in addition to cytokines and chemokines were targeted. Pro-inflammatory genes, such as IL1B, CCL3 and IL8, were significantly up-regulated. Interestingly, increased mRNA levels of seven interferon stimulated genes (ISGs) were observed peaking at 2 h, corroborating the increasing evidence that ISGs respond immediately to bacterial endotoxins. A slower response was manifested by four extrahepatic acute phase proteins (APP) (SAA3, HP, LF and LCN2) reaching maximum levels at 5 h. We report an immediate induction of ISGs in leukocytes in response to LPS supporting a link between the interferon system and defense against bacterial infections. The extrahepatic expression of APPs suggests that leukocytes contribute to synthesis of these proteins at the beginning of a systemic inflammation. Taken together, these findings provide insights into the dynamic regulation of innate immune genes, as well as raising new questions regarding the importance of ISGs and extrahepatic APPs in leukocytes after systemic endotoxin challenge.

General Information
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Number of pages: 10
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: B M C Veterinary Research
Volume: 12
Issue number: 1
Article number: 241
ISSN (Print): 1746-6148
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.108 SJR 0.934 CiteScore 2.16
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.83 SJR 0.87 SNIP 1.011
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.981 SNIP 1.009 CiteScore 1.86
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.943 SNIP 1.018 CiteScore 1.81
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.861 SNIP 0.853 CiteScore 1.85
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.779 SNIP 1.023 CiteScore 1.94
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
Adaptive Test Schemes for Control of Paratuberculosis in Dairy Cows

Paratuberculosis is a chronic infection that in dairy cattle causes reduced milk yield, weight loss, and ultimately fatal diarrhea. Subclinical animals can excrete bacteria (Mycobacterium avium ssp. paratuberculosis, MAP) in feces and infect other animals. Farmers identify the infectious animals through a variety of test-strategies, but are challenged by the lack of perfect tests. Frequent testing increases the sensitivity but the costs of testing are a cause of concern for farmers. Here, we used a herd simulation model using milk ELISA tests to evaluate the epidemiological and economic consequences of continuously adapting the sampling interval in response to the estimated true prevalence in the herd. The key results were that the true prevalence was greatly affected by the hygiene level and to some extent by the test-frequency. Furthermore, the choice of prevalence that will be tolerated in a control scenario had a major impact on the true prevalence in the normal hygiene setting, but less so when the hygiene was poor. The net revenue is not greatly affected by the test-strategy, because of the general variation in net revenues between farms. An exception to this is the low hygiene herd, where frequent testing results in lower revenue. When we look at the probability of eradication, then it is correlated with the testing frequency and the target prevalence during the control phase. The probability of eradication is low in the low hygiene herd, and a test-and-cull strategy should probably not be the primary strategy in this herd. Based on this study we suggest that, in order to control MAP, the standard Danish dairy farm should use an adaptive strategy where a short sampling interval of three months is used when the estimated true prevalence is above 1%, and otherwise use a long sampling interval of one year.

General information
State: Published
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Number of pages: 13
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: PLoS One
Volume: 11
Issue number: 12
Article number: e0167219
ISSN (Print): 1932-6203
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1

Blood leukocyte gene expression, Endotoxemia, Extrahepatic acute phase proteins, Goat, Innate immunity, Interferon stimulated genes, Lipopolysaccharide (LPS), Systemic inflammation

Electronic versions:
art_3A10.1186_2Fs12917_016_0870_x.pdf
DOIs:
10.1186/s12917-016-0870-x
Source: FindIt
Source-ID: 2347967793
Publication: Research - peer-review › Journal article – Annual report year: 2016
Aeromonas salmonicida - Epidemiology, whole genome sequencing, detection and in vivo imaging

Aeromonas salmonicida subsp. salmonicida is a bacterial fish pathogen that is the causative agent of furunculosis, a septicemic infection responsible for great losses in aquaculture around the world. In Denmark furunculosis was first seen in freshwater in the 1950s, though currently the infection causes problems in sea reared rainbow trout (Oncorhynchus mykiss) production. Outbreaks occur repeatedly during stressful conditions such as elevated temperatures, in spite of commercial vaccines being applied. Besides seemingly lacking adequate protection, the vaccines also produce undesirable side effects. Antibiotics are therefore used as treatment, which due to the possibility of developing resistance is neither a favorable nor sustainable solution. To complicate things further, it is possible that fish can be carriers of A. salmonicida and transfer the bacterium from freshwater to the sea where they develop septicemia when exposed to stressful sea-rearing conditions and high temperatures. By use of traditional bacteriological methods, continuous investigation of bacterial diagnostics on samples from different rainbow trout farms in Denmark was done, while studying the following three aspects of the concerns regarding A. salmonicida. First, we focused on investigation of the route of
entry and initial dissemination of A. salmonicida in fish. This was done by tracing the bacterium using in vivo bioluminescence imaging. A Danish strain was transformed with a plasmid vector containing a green fluorescence protein gene and bacterial luciferase genes that served as fluorescent and bioluminescent reporters respectively. The transformed A. salmonicida was used in a series of immersion experiments where fish were followed over a 24-hour period. Results showed that probable main colonization sites of A. salmonicida were the gills and the dorsal and pectoral fins. This was followed by dissemination through internal organs. Although optimization and further immersion experiments are needed, our results indicated that this tool could be a valuable approach for visualizing A. salmonicida in fish. Focus was subsequently turned to finding a sensitive method for detecting A. salmonicida in infected and possible carrier fish. For this, a previously developed quantitative real-time polymerase chain reaction (real-time PCR) targeting the aopP gene located on A. salmonicida plasmid pAsal1 was assessed. The real-time PCR and bacterial culturing were employed for preliminary screening of A. salmonicida in 40 fish from Danish fresh- and seawater farms. A. salmonicida was detected by realtime PCR in freshwater farm fish showing no sign of disease, indicating possible presence of carrier fish. Out of five examined organs: spleen, kidney, intestine, gills and brain in each fish, A. salmonicida was most frequently detected in the spleen, brain and intestine, indicating that these three organs could play an important role in A. salmonicida infection. The real-time PCR exhibited highly sensitive detection of A. salmonicida as well as a high reproducibility and efficiency, though due to the fact that not all A. salmonicida seem to possess the target plasmid pAsal1, another sensitive detection method with a different and/or complementary target would need to be employed to be certain of avoiding false negatives. The final focal point of this thesis revolved around obtaining knowledge on genetic and virulence variation as well as epidemiology of the disease causing Danish A. salmonicida. Due to high homogeneity among the A. salmonicida subspecies population, standard molecular methods for bacterial typing cannot distinguish among A. salmonicida isolates. Whole genome sequencing was therefore applied on 99 Danish A. salmonicida isolated between years 1980 and 2014 from different geographical regions, one Scottish strain and the type strain NCIMB 1102. Sequences of the A. salmonicida were de novo assembled and then examined for presence of plasmids, virulence and iron acquisition proteins, and antibiotic resistance genes. The chromosome was also examined for single nucleotide polymorphisms that were aligned and subjected to Bayesian temporal tree reconstruction using the published genome of A. salmonicida A449 as reference. Main results revealed that there have been four major introductions of A. salmonicida into Denmark, A. salmonicida are highly homogenous with the exception of certain plasmids and virulence factors encoded on these plasmids, and nine A. salmonicida harbored several worldwide known genes encoding resistance against antibiotics. This study provided valuable information regarding the Danish disease causing A. salmonicida.
Age determination of sperm whales (Physeter macrocephalus) from the west coast of Jutland, Denmark: The 13th Danish Marine Mammal Symposium

Age determination of sperm whales (Physeter macrocephalus) by counting growth layer groups (GLG’s) in the teeth is to some extent considered to be subjective and only relative, due to: 1) Limited validation of GLG counts to "known age" of the individual; 2) Variation in methods for preparation of teeth e.g. acid (pH) and duration of etching; 3) Difference in interpretations of GLG’s between readers.1,2 Bearing in mind these challenges, the age of three sperm whales stranded in Denmark in 2012 and 2014 were determined by counts of GLG’s in the erupted teeth from the lower jaw and comparing these with the number of GLG’s obtained from rudimentary teeth in the upper jaw. Teeth were obtained from 3 adult male sperm whales; MCE 1642, stranded at Nr. Lyngby Strand, Denmark in 2012; and MCE 1644 and MCE 1645, who stranded at Henne Strand, Denmark in 2014. From each whale one non-erupted tooth from the maxilla and one erupted mandibular tooth was cut longitudinally in two half’s with a diamond blade saw and grained with sandpaper gain 800. One half of each tooth was etched in 10% acetic acid for 7 hours and the other half was etched in 15% acetic acid for 3.5 hours. The GLG’s were counted several times by two readers. Based on counting of GLG’s the average estimated ages of the three sperm whales were between 29 and 39 years. However, some deviation due to intra- and inter reader differences was observed. The number of GLG’s in the rudimentary teeth did not differ significantly from the GLG’s of the mandibular teeth. Pulp stones were seen in both erupted and non-erupted teeth from all three whales. Further studies are needed to develop the current preparation techniques to make clear and more easily readable GLG’s to obtain more accurate age determination of sperm whales.

General information
A herd- and cow-specific decision support tool for control of mastitis

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Aalborg Zoo, Danish Museum of Natural History
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Number of pages: 1
Publication date: 2016
Event: Poster session presented at 13th Danish Marine Mammal Symposium, Kastrup, Denmark.
Main Research Area: Technical/natural sciences
Electronic versions:
Poster
Source: FindIt
Source-ID: 2349217152
Publication: Research › Poster – Annual report year: 2016

Altering the balance between immune activation versus regulation in the skin to promote CD8+ T-cell activity within epithelial cancers

The Human Papilloma Virus (HPV) 16 is a high-risk HPV known to be a causative agent in numerous cancers including cervical cancer. While prophylactic vaccines exist to combat the spread of HPV16, successful therapeutic vaccines to combat established HPV16-associated disease remain elusive. The expression, in a mouse model (“E7”), of the HPV16 E7 gene in keratinocytes under the control of the K14 promoter, leads to a local immune suppressive environment, as evidenced by the lack of graft rejection when E7 skin grafts are placed on WT recipient mice. Furthermore, well healed (>30 days) E7 skin grafts are not rejected when mice are immunised with E7 peptide in combination with Quil A- or CASAC-based adjuvants. This is despite a substantial increase in E7 peptide/H-2Db pentamer staining in the blood, and marked killing of E7-peptide expressing TC-1 cells when injected i.v., confirming that CD8 T-cells respond to vaccination and differentiate into CTL capable of killing E7-expressing target cells. We hypothesised that the removal of regulatory T-cells (T-reg) might lead to E7 graft rejection in immunised mice. The co-administration of an anti-CD4-depeting antibody at the time of immunisation led to rejection of ~50% of grafts. To confirm a role for T-reg, E7-grafted T-reg-deficient Rag1/- mice received purified donor CD8 T-cells from E7-vaccinated WT mice. FACS staining of Rag1/- lymph nodes 30 days post CD8+ T-cell transfer confirmed the absence of classical CD4+FoxP3+ Treg, however the E7 grafts did not reject. As in the WT mice however, rejection could be induced through the coadministration of an anti-CD4 antibody. The data suggest that the removal of a CD4+, non T-reg cell, leads to CD8+ T-cell activity in the skin as evidenced by E7 skin graft destruction.

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Department of Applied Mathematics and Computer Science, Dynamical Systems, University of Copenhagen
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Number of pages: 1
Publication date: 2016
Event: Poster session presented at SVEPM, Elsinore, Denmark.
Main Research Area: Technical/natural sciences
Electronic versions:
Gussmann_Maya.pdf
Source: PublicationPreSubmission
Source-ID: 127804108
Publication: Research - peer-review › Poster – Annual report year: 2016

Altering the balance between immune activation versus regulation in the skin to promote CD8+ T-cell activity within epithelial cancers

The Human Papilloma Virus (HPV) 16 is a high-risk HPV known to be a causative agent in numerous cancers including cervical cancer. While prophylactic vaccines exist to combat the spread of HPV16, successful therapeutic vaccines to combat established HPV16-associated disease remain elusive. The expression, in a mouse model (“E7”), of the HPV16 E7 gene in keratinocytes under the control of the K14 promoter, leads to a local immune suppressive environment, as evidenced by the lack of graft rejection when E7 skin grafts are placed on WT recipient mice. Furthermore, well healed (>30 days) E7 skin grafts are not rejected when mice are immunised with E7 peptide in combination with Quil A- or CASAC-based adjuvants. This is despite a substantial increase in E7 peptide/H-2Db pentamer staining in the blood, and marked killing of E7-peptide expressing TC-1 cells when injected i.v., confirming that CD8 T-cells respond to vaccination and differentiate into CTL capable of killing E7-expressing target cells. We hypothesised that the removal of regulatory T-cells (T-reg) might lead to E7 graft rejection in immunised mice. The co-administration of an anti-CD4-depeting antibody at the time of immunisation led to rejection of ~50% of grafts. To confirm a role for T-reg, E7-grafted T-reg-deficient Rag1/- mice received purified donor CD8 T-cells from E7-vaccinated WT mice. FACS staining of Rag1/- lymph nodes 30 days post CD8+ T-cell transfer confirmed the absence of classical CD4+FoxP3+ Treg, however the E7 grafts did not reject. As in the WT mice however, rejection could be induced through the coadministration of an anti-CD4 antibody. The data suggest that the removal of a CD4+, non T-reg cell, leads to CD8+ T-cell activity in the skin as evidenced by E7 skin graft destruction.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, University of Queensland
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Number of pages: 1
Publication date: 2016
Main Research Area: Technical/natural sciences
Electronic versions:
Altering_the_balance_between_immune_activation_versus_regulation_in_the_skin_to_promote_CD8_AACR_abstract_Jam es_.pdf
A multiplexed immunoassay for simultaneous detection of antibodies to PRRSV, Actinobacillus pleuropneumoniae and Salmonella in pigs

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Section for Epidemiology
Authors: Berger, S. S. (Intern), Boas, U. (Intern), Lauritsen, K. T. (Intern), Lind, P. (Intern), Andresen, L. O. (Intern)
Pages: 591-591
Publication date: 2016

Host publication information
Title of host publication: Proceedings from 24th IPVS/8th ESPHM congress
Place of publication: Dublin, Ireland
Main Research Area: Technical/natural sciences
Conference: 24th International Pig Veterinary Society (IPVS) Congress, Dublin, Ireland, 07/06/2016 - 07/06/2016

A multi-subunit Chlamydia vaccine inducing neutralizing antibodies and strong IFN-γ(+) CMI responses protects against a genital infection in minipigs

Chlamydia is the most widespread sexually transmitted bacterial disease and a prophylactic vaccine is highly needed. Ideally, this vaccine is required to induce a combined response of Th1 cell-mediated immune (CMI) response in concert with neutralizing antibodies. Using a novel Götttingen minipig animal model, we evaluated the immunogenicity and efficacy of a multi-subunit vaccine formulated in the strong Th1-inducing adjuvant CAF01. We evaluated a mixture of two fusion proteins (Hirep1 and CTH93) designed to promote either neutralizing antibodies or cell-mediated immunity, respectively. Hirep1 is a novel immunogen based on the variant domain (VD) 4 region from major outer membrane protein (MOMP) serovar (Sv) D, SvE and SvF, and CTH93 is a fusion molecule of three antigens (CT043, CT414 and MOMP). Pigs were immunized twice intramuscularly with either Hirep1+CTH93/CAF01, UV-inactivated Chlamydia trachomatis SvD bacteria (UV-SvD/CAF01) or CAF01. The Hirep1+CTH93/CAF01 vaccine induced a strong CMI response against the vaccine antigens and high titers of antibodies, particularly against the VD4 region of MOMP. Sera from Hirep1+CTH93/CAF01 immunized pigs neutralized C. trachomatis SvD and SvF infectivity in vitro. Both Hirep1+CTH93/CAF01 and UV-SvD/CAF01 vaccination protected pigs against a vaginal C. trachomatis SvD infection. In conclusion, the Hirep1+CTH93/CAF01 vaccine proved highly immunogenic and equally protective as UV-SvD/CAF01 showing promise for the development of a subunit vaccine against Chlamydia.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, University of Copenhagen, Statens Serum Institut, State Serum Institute
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Number of pages: 11
Pages: 185-195
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Immunology and Cell Biology
Volume: 94
Issue number: 2
ISSN (Print): 0818-9641
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.996 SJR 2.085 CiteScore 3.45
A New Furunculosis Challenge Method for Evaluation of Vaccine Efficacy in Rainbow Trout

Experimental infection of fish for vaccine efficacy studies is associated with several limitations. Administration of live bacteria with the purpose of causing disease in fish can be performed by co-habitation, immersion or injection. We have developed a new Aeromonas salmonicida challenge method for rainbow trout and have applied it for evaluation of furunculosis vaccine efficacy. The method reveals development of systemic immunity in fish as live bacteria are introduced in the tail fin epidermis distant from the vaccine injection site (peritoneal cavity). This method seeks to mimic natural infection in fish farms where tail biting and therefore bacterial expo- sure to tail fin ulcers is widespread. By use of a multi-needle device ten epidermal perforations were introduced in the dorsal part of the tail fin of anaesthetized rainbow trout (vaccinated or naive). Subsequently 100 μL (3.4 × 108 colony-forming units (CFU) mL−1) of a 48 hour culture of Aeromonas salmonicida subsp. salmo- nicida strain 090710-1/23 was placed at the perforation site for 60 sec whereafter fish were allowed to regain consciousness in clean freshwater. Immunohistochemistry and scanning electron microscopy illustrated the spread of bacteria from the injection site. Classical furunculosis symptoms associated with a high morbidity rate were observed in control fish whereas vaccinated fish exhibited a significantly higher survival.

General information

State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Section for Bacteriology, Pathology and Parasitology, University of Copenhagen
An investigation of the microbiota in uterine flush samples and endometrial biopsies from dairy cows during the first 7 weeks postpartum

Metrotris and endometritis commonly occur in dairy cows after calving. Although numerous studies have been performed to identify the causative pathogens, a complete overview has not been done. Metagenomic studies have analyzed the bacterial populations of uterine flush samples from postpartum (pp) dairy cows, but the microbiota in the uterine luminal fluid may differ from the microbiota of the endometrium itself, and important putative pathogens may have been overlooked. In the present study, we compared the microbiota of the uterine lumen and the endometrium of healthy, metritic, and endometritic cows. Samples were collected from 68 Holstein dairy cows at 1, 4, and 7 weeks pp, and the data were analyzed by deep sequencing of the V1 and V2 hypervariable regions of the 16S ribosomal RNA gene. The results showed that Porphyromonadaceae, Fusobacteriaceae, Leptotrichiaceae, and Mycoplasmataceae may be associated with uterine disease. The microbiota of the uterine flush samples and the endometrial biopsies were correlated, but the microbiota of the biopsies was more diverse. Fusobacteriaceae and Leptotrichiaceae were not observed in the biopsies at week 7, whereas they accounted for 20% and 13%, respectively, of the bacterial populations in the flush samples. The Mycoplasmataceae family was observed in much higher quantity in the flush samples than in the biopsies of the endometritis groups at weeks 4 and 7. Our findings support the observations of previous metagenomic studies and illustrate the importance of including endometrial biopsies to obtain more detailed knowledge of the pp uterine microbiota.
An outbreak of bovine meningoencephalomyelitis with identification of Halicephalobus gingivalis

Halicephalobus gingivalis is an opportunistic parasite which is known to cause fatal meningoencephalomyelitis primarily in equines but sporadically also in humans. In April 2014, laboratory examination of the head of a young dairy calf, euthanized due to severe central nervous system symptoms, revealed the presence of granulomatous to necrotizing encephalitis and myriads of nematodes in the brain lesion. Morphologically the parasites were identified as H. gingivalis. The diagnosis was confirmed by molecular analysis of the large subunit (LSU) rRNA and the small subunit (SSU) rRNA genes, revealing genetic variations of 0.5–4.4% and 0.7–8.6%, respectively, between the H. gingivalis isolated from the Danish calf and published isolates, collected worldwide from free-living and parasitic stages of the nematode. Clinical symptoms and histological changes indicated infection with H. gingivalis from another three calves in the herd. This is the first scientific publication of H. gingivalis induced meningoencephalomyelitis in ruminants. As ante mortem diagnosis is a major challenge, the infection may easily remain undiagnosed in cattle.
A novel approach to probe host-pathogen interactions of bovine digital dermatitis, a model of a complex polymicrobial infection

Polymicrobial infections represent a great challenge for the clarification of disease etiology and the development of comprehensive diagnostic or therapeutic tools, particularly for fastidious and difficult-to-cultivate bacteria. Using bovine digital dermatitis (DD) as a disease model, we introduce a novel strategy to study the pathogenesis of complex infections. The strategy combines meta-transcriptomics with high-density peptide-microarray technology to screen for in vivo-expressed microbial genes and the host antibody response at the site of infection. Bacterial expression patterns supported the assumption that treponemes were the major DD pathogens but also indicated the active involvement of other phyla (primarily Bacteroidetes). Bacterial genes involved in chemotaxis, flagellar synthesis and protection against oxidative and acidic stress were among the major factors defining the disease. The extraordinary diversity observed in bacterial expression, antigens and host antibody responses between individual cows pointed toward microbial variability as a hallmark of DD. Persistence of infection and DD reinfection in the same individual is common; thus, high microbial diversity may undermine the host's capacity to mount an efficient immune response and maintain immunological memory towards DD. The common antigenic markers identified here using a high-density peptide microarray address this issue and may be useful for future preventive measures against DD.
A novel multiplex RT-qPCR method based on dual-labelled probes suitable for typing all known genotypes of viral hemorrhagic septicemia virus

Viral hemorrhagic septicemia (VHS) is a notifiable fish disease, whose causative agent is a rhabdovirus isolated from a wide range of fish species, not only in fresh but also in marine and brackish waters. Phylogenetic studies have identified four major genotypes, with a strong geographical relationship. In this study, we have designed and validated a new procedure – named binary multiplex RT-qPCR (bmRT-qPCR) – for simultaneous detection and typing of all four genotypes of VHSV by real-time RT-PCR based on dual-labelled probes and composed by two multiplex systems designed for European and American/Asiatic isolates, respectively, using a combination of three different fluorophores. The specificity of the procedure was assessed by including a panel of 81 VHSV isolates covering all known genotypes and subtypes of the virus, and tissue material from experimentally infected rainbow trout, resulting in a correct detection and typing of all strains. The analytical sensitivity was evaluated in a comparative assay with titration in cell culture, observing that both methods provided similar limits of detection. The proposed method can be a powerful tool for epidemiological analysis of VHSV by genotyping unknown samples within a few hours.
Anthelmintic activity of chicory (Cichorium intybus): in vitro effects on swine nematodes and relationship to sesquiterpene lactone composition

Chicory is a perennial crop that has been investigated as a forage source for outdoor-reared ruminants and pigs, and has been reported to have anthelmintic properties. Here, we investigated in vitro anthelmintic effects of forage chicory-extracts against the highly prevalent swine parasites Ascaris suum and Oesophagostomum dentatum. Methanol extracts were prepared and purified from two different cultivars of chicory (Spadona and Puna II). Marked differences were observed between the anthelmintic activity of extracts from the two cultivars. Spadona extracts had potent activity against A. suum third (L3) and fourth (L4) - stage larvae, as well as O. dentatum L4 and adults, whereas Puna II extracts had less activity against A. suum and no activity towards O. dentatum L4. Transmission-electron microscopy of A. suum L4 exposed to Spadona extracts revealed only subtle changes, perhaps indicative of a specific anthelmintic effect rather than generalized toxicity. Ultra-high liquid chromatography-mass spectrometry analysis revealed that the purified extracts were rich in sesquiterpene lactones (SL), and that the SL profile differed significantly between cultivars. This is the first report of anthelmintic activity of forage chicory towards swine nematodes. Our results indicate a significant anthelmintic effect, which may possibly be related to SL composition.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Section for Immunology and Vaccinology, University of Copenhagen
Authors: Williams, A. (Ekstern), Pena-Espinoza, M. A. (Intern), Boas, U. (Intern), Simonsen, H. T. (Intern), Enemark, H. (Intern), Thamsborg, S. M. (Ekstern)
Pages: 770-777
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Parasitology (Cambridge)
Volume: 143
Issue number: 6
ISSN (Print): 0031-1820
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 0.946 SJR 1.194 CiteScore 2.45
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): SJR 1.085 SNIP 0.927 CiteScore 2.37
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.34 SNIP 1.059 CiteScore 2.62
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.05 SNIP 1.009 CiteScore 2.3
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.157 SNIP 0.908 CiteScore 2.45
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.026 SNIP 1.004 CiteScore 2.55
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.183 SNIP 1.02 CiteScore 2.63
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
Anthelmintic activity of forage chicory (Cichorium intybus) and field efficacy of ivermectin against gastrointestinal nematodes in Danish cattle

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Norwegian Veterinary Institute, University of Copenhagen
Authors: Pena-Espinoza, M. A. (Intern), Boas, U. (Intern), Larsen Enemark, H. (Ekstern), Thamsborg, S. M. (Ekstern)
Number of pages: 152
Publication date: 2016

Publication information
Place of publication: Frederiksberg C
Publisher: National Veterinary Institute, Technical University of Denmark
Original language: English
Main Research Area: Technical/natural sciences
Electronic versions:
PhD_thesis_Miguel_Angel_Pena_Espinoza.pdf

Relations
Projects:
Anthelmintic activity of forage chicory (Cichorium intybus) and field efficacy of ivermectin against gastrointestinal nematodes in Danish cattle
Publication: Research › Ph.D. thesis – Annual report year: 2016

Anthelmintic effects of forage chicory (Cichorium intybus) against gastrointestinal nematode parasites in experimentally infected cattle
Two experiments studied the effects of dietary chicory against gastrointestinal nematodes in cattle. In Experiment (Exp.) 1, stabled calves were fed chicory silage (CHI1; n = 9) or ryegrass/clover hay (CTL1; n = 6) with balanced protein/energy
intakes between groups. After 16 days, all calves received 10 000 Ostertagia ostertagi and 66 000 Cooperia oncophora third-stage larvae (L3) [day (D) 0 post-infection (p.i.)]. In Exp. 2, calves were assigned to pure chicory (CHI2; n=10) or ryegrass/clover (CTL2; n = 10) pastures. After 7 days, animals received 20 000 O. ostertagi L3/calf (D0 p.i.) and were moved regularly preventing pasture-borne infections. Due to poor regrowth of the chicory pasture, CHI2 was supplemented with chicory silage. At D40 p.i. (Exp. 1) and D35 p.i. (Exp. 2) calves were slaughtered for worm recovery. In Exp.1, fecal egg counts (FEC) were similar between groups. However, O. ostertagi counts were significantly reduced in CHI1 by 60% (geometric mean; P < 0·01), whereas C. oncophora burdens were unaffected (P = 0·12). In Exp. 2, FEC were markedly lowered in CHI2 from D22 p.i onwards (P < 0·01). Ostertagia ostertagi adult burdens were significantly reduced in CHI2 by 66% (P < 0·001). Sesquiterpene lactones were identified only in chicory (fresh/silage). Chicory shows promise as an anti-Ostertagia feed for cattle and further studies should investigate its on-farm use.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Copenhagen
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Number of pages: 15
Pages: 1279-1293
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Parasitology (Cambridge)
Volume: 143
Issue number: 10
ISSN (Print): 0031-1820
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 0.946 SJR 1.194 CiteScore 2.45
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): SJR 1.085 SNIP 0.927 CiteScore 2.37
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.34 SNIP 1.059 CiteScore 2.62
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.05 SNIP 1.009 CiteScore 2.3
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.157 SNIP 0.908 CiteScore 2.45
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.026 SNIP 1.004 CiteScore 2.55
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.183 SNIP 1.02 CiteScore 2.63
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.13 SNIP 0.935
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 0.976 SNIP 0.943
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.086 SNIP 0.975
Antibiotic combination therapy can select for broad-spectrum multidrug resistance in *Pseudomonas aeruginosa*

Combination therapy with several antibiotics is one strategy that has been applied in order to limit the spread of antimicrobial resistance. We compared the de novo evolution of resistance during combination therapy with the β-lactam ceftazidime and the fluoroquinolone ciprofloxacin with the resistance evolved after single-drug exposure. Combination therapy selected for mutants that displayed broad-spectrum resistance, and a major resistance mechanism was mutational inactivation of the repressor gene mexR that regulates the multidrug efflux operon mexAB–oprM. Deregulation of this operon led to a broad-spectrum resistance phenotype that decreased susceptibility to the combination of drugs applied during selection as well as to unrelated antibiotic classes. Mutants isolated after single-drug exposure displayed narrow-spectrum resistance and carried mutations in the MexCD–OprJ efflux pump regulator gene nfxB conferring ciprofloxacin resistance, or in the gene encoding the non-essential penicillin-binding protein DacB conferring ceftazidime resistance. Reconstruction of resistance mutations by allelic replacement and in vitro fitness assays revealed that in contrast to single antibiotic use, combination therapy consistently selected for mutants with enhanced fitness expressing broad-spectrum resistance mechanisms.
Antigen-Encoding Bone Marrow Terminates Islet-Directed Memory CD8+ T-Cell Responses to Alleviate Islet Transplant Rejection

Islet-specific memory T cells arise early in type 1 diabetes (T1D), persist for long periods, perpetuate disease, and are rapidly reactivated by islet transplantation. As memory T cells are poorly controlled by “conventional” therapies, memory T cell-mediated attack is a substantial challenge in islet transplantation, and this will extend to application of personalized...
approaches using stem cell–derived replacement β-cells. New approaches are required to limit memory autoimmune attack of transplanted islets or replacement β-cells. Here, we show that transfer of bone marrow encoding cognate antigen directed to dendritic cells, under mild, immune-preserving conditions, inactivates established memory CD8+ T-cell populations and generates a long-lived, antigen-specific tolerogenic environment. Consequently, CD8+ memory T cell–mediated targeting of islet-expressed antigens is prevented and islet graft rejection alleviated. The immunological mechanisms of protection are mediated through deletion and induction of unresponsiveness in targeted memory T-cell populations. The data demonstrate that hematopoietic stem cell–mediated gene therapy effectively terminates antigen-specific memory T-cell responses, and this can alleviate destruction of antigen-expressing islets. This addresses a key challenge facing islet transplantation and, importantly, the clinical application of personalized β-cell replacement therapies using patient-derived stem cells.

**General information**

State: Published
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Pages: 1328-1340
Publication date: 2016
Main Research Area: Technical/natural sciences

**Publication Information**

Journal: Diabetes
Volume: 65
Issue number: 5
ISSN (Print): 0012-1797
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 1.868 SJR 4.435 CiteScore 5.89
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 6.2 SJR 4.936 SNIP 2.055
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 5.222 SNIP 2.053 CiteScore 6.33
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 4.789 SNIP 2.057 CiteScore 6.47
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 4.815 SNIP 2.155 CiteScore 7.34
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 4.708 SNIP 2.11 CiteScore 7.34
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 4.794 SNIP 2.277 CiteScore 7.6
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 5.047 SNIP 2.078
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 4.822 SNIP 2.061
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 5.367 SNIP 2.098
Scopus rating (2007): SJR 5.323 SNIP 2.099
Scopus rating (2006): SJR 5.077 SNIP 2.091
Antigen Uptake during Different Life Stages of Zebrafish (Danio rerio) Using a GFP-Tagged Yersinia ruckeri

Immersion-vaccines (bacterins) are routinely used for aquacultured rainbow trout to protect against Yersinia ruckeri (Yr). During immersion vaccination, rainbow trout take up and process the antigens, which induce protection. The zebrafish was used as a model organism to study uptake mechanisms and subsequent antigen transport in fish. A genetically modified Yr was developed to constitutively express green fluorescent protein (GFP) and was used for bacterin production. Larval, juvenile and adult transparent zebrafish (tra:nac mutant) received a bath in the bacterin for up to 30 minutes. Samples were taken after 1 min, 15 min, 30 min, 2 h, 12 h and 24 h. At each sampling point fish were used for live imaging of the uptake using a fluorescence stereomicroscope and for immunohistochemistry (IHC). In adult fish, the bacterin could be traced within 30 min in scale pockets, skin, oesophagus, intestine and fins. Within two hours post bath (pb) Yr-antigens were visible in the spleen and at 24 h in liver and kidney. Bacteria were associated with the gills, but uptake at this location was limited. Antigens were rarely detected in the blood and never in the nares. In juvenile fish uptake of the bacterin was seen in the intestine 30 min pb and in the nares 2 hpb but never in scale pockets. Antigens were detected in the spleen 12 hpb. Zebrafish larvae exhibited major Yr uptake only in the mid-intestine enterocytes 24 hpb. The different life stages of zebrafish varied with regard to uptake locations, however the gut was consistently a major uptake site. Zebrafish and rainbow trout tend to have similar uptake mechanisms following immersion or bath vaccination, which points towards zebrafish as a suitable model organism for this aquacultured species.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Copenhagen
Authors: Korbut, R. (Ekstern), Mehrdana, F. (Ekstern), Kania, P. W. (Ekstern), Larsen, M. H. (Ekstern), Frees, D. (Ekstern), Dalsgaard, I. (Intern), Jorgensen, L. V. G. (Ekstern)
Number of pages: 13
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: PLoS One
Volume: 11
Issue number: 7
Article number: e0158968
ISSN (Print): 1932-6203
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.01 SJR 1.164 SNIP 1.111
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.11 SJR 1.236 SNIP 1.101
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Anti-parasitic activity of pelleted sainfoin (Onobrychis viciifolia) against Ostertagia ostertagi and Cooperia oncophora in calves

BACKGROUND: Increasing anthelmintic-resistance in nematodes of ruminants emphasises the need for sustainable parasite control. Condensed tannin-containing legume forages such as sainfoin (Onobrychis viciifolia) have shown promising anthelmintic properties in small ruminants but this has never been explored in cattle. Therefore, our aim was to examine the efficacy of sainfoin against cattle nematodes in vivo.

METHODS: Fifteen Jersey male calves (2-4 month-old) were allocated into two groups and fed isoproteic and isoenergetic diets mainly composed of sainfoin pellets (Group SF; n = 9, three pens) or concentrate and grass-clover hay (Group CO; n = 6, two pens). After 16 days of adaptation, all animals were experimentally infected with 10,000 and 66,000 third-stage larvae of Ostertagia ostertagi and Cooperia oncophora, respectively. Egg excretion, blood parameters and bodyweights were recorded throughout the study. Worms were harvested by sieving for quantification and scanning electron microscopy (SEM) 42 days post-infection (dpi) when the calves were necropsied.

RESULTS: The number of O. ostertagi adults in the abomasum was reduced by 50% in Group SF compared with Group CO (P < 0.05). This was further reflected in higher albumin (P < 0.1) and lower pepsinogen levels (P < 0.05) in Group SF at 21 dpi, and structural damage of the worm cuticle could be visualised by SEM. Yet, the nematode egg excretion in Group SF was not significantly different from that of the controls (P > 0.05). Likewise, no statistical difference in total worm burdens of C. oncophora was found between the groups. Weight gains were lower for Group SF (P < 0.05), which may reflect lower digestibility and phosphorus levels in the SF diet, despite similar feed intake at pen-level.

CONCLUSIONS: Overall, the effect of sainfoin on abomasal nematodes corroborates results from studies with small ruminants and encourages further investigations of the use of this crop for control of cattle nematodes.
Application of Molecular Typing Results in Source Attribution Models: The Case of Multiple Locus Variable Number Tandem Repeat Analysis (MLVA) of Salmonella Isolates Obtained from Integrated Surveillance in Denmark

Salmonella is an important cause of bacterial foodborne infections in Denmark. To identify the main animal-food sources of human salmonellosis, risk managers have relied on a routine application of a microbial subtyping-based source attribution model since 1995. In 2013, multiple locus variable number tandem repeat analysis (MLVA) substituted phage typing as the subtyping method for surveillance of S. Enteritidis and S. Typhimurium isolated from animals, food, and humans in Denmark. The purpose of this study was to develop a modeling approach applying a combination of serovars, MLVA types, and antibiotic resistance profiles for the Salmonella source attribution, and assess the utility of the results for the food safety decisionmakers. Full and simplified MLVA schemes from surveillance data were tested, and model fit and consistency of results were assessed using statistical measures. We conclude that loci schemes STTR5/STTR10/STTR3 for S. Typhimurium and SE9/SE5/SE2/SE1/SE3 for S. Enteritidis can be used in microbial subtyping-based source attribution models. Based on the results, we discuss that an adjustment of the discriminatory level of the subtyping method applied often will be required to fit the purpose of the study and the available data. The issues discussed are also considered highly relevant when applying, e.g., extended multi-locus sequence typing or next-generation sequencing techniques.

General information
State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology, Research Group for Risk-Benefit, Research Group for Diagnostic Engineering, National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, State Serum Institute
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Number of pages: 18
Pages: S71-S588
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Risk Analysis
Volume: 36
Issue number: 3
ISSN (Print): 0272-4332
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.381 SJR 1.01 CiteScore 2.43
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.21 SJR 1.12 SNIP 1.485
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.334 SNIP 1.495 CiteScore 2.51
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.331 SNIP 1.588 CiteScore 2.2
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.067 SNIP 1.595 CiteScore 2.1
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.76 SNIP 1.593 CiteScore 2.12
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.735 SNIP 1.693 CiteScore 2.15
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
A Prime-Boost Vaccination Strategy in Cattle to Prevent Foot-and-Mouth Disease Using a "Single-Cycle" Alphavirus Vector and Empty Capsid Particles

Foot-and-mouth disease (FMD) remains one of the most economically important infectious diseases of production animals globally. Vaccination can successfully control this disease, however, current vaccines are imperfect. They are made using chemically inactivated FMD virus (FMDV) that is produced in large-scale mammalian cell culture under high containment conditions. Here, we have expressed the FMDV capsid protein precursor (P1-2A) of strain O1 Manisa alone or with the FMDV 3C protease (3Cpro) using a "single cycle" packaged alphavirus self-replicating RNA based on Semliki Forest virus (SFV). When the FMDV P1-2A was expressed with 3Cpro then processing of the FMDV capsid precursor protein is observed within cells and the proteins assemble into empty capsid particles. The products interact with anti-FMDV antibodies in an ELISA and bind to the integrin αvβ6 (a cellular receptor for FMDV). In cattle vaccinated with these rSFV-FMDV vectors alone, anti-FMDV antibodies were elicited but the immune response was insufficient to give protection against FMDV challenge. However, the prior vaccination with these vectors resulted in a much stronger immune response against FMDV post-challenge and the viremia observed was decreased in level and duration. In subsequent experiments, cattle were sequentially vaccinated with a rSFV-FMDV followed by recombinant FMDV empty capsid particles, or vice versa, prior to challenge. Animals given a primary vaccination with the rSFV-FMDV vector and then boosted with FMDV empty capsids showed a strong anti-FMDV antibody response prior to challenge, they were protected against disease and no FMDV RNA was detected in their sera post-challenge. Initial inoculation with empty capsids followed by the rSFV-FMDV was much less effective at combating the FMDV challenge and a large post-challenge boost to the level of anti-FMDV antibodies was observed. This prime-boost system, using reagents that can be generated outside of high-containment facilities, offers significant advantages to achieve control of FMD by vaccination.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Karolinska Institutet, The Pirbright Institute
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Number of pages: 23
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: P L o S One
Volume: 11
Issue number: 6
Article number: e0157435
Aptasensor development for detection of virus in water
Contamination of water by waterborne viruses causes serious health issues worldwide. The current virus detection methods are expensive and time-consuming and require access to well-equipped laboratories. This thesis describes the development of an impedimetric all-polymer aptasensor for detection of three types of waterborne viruses: norovirus, rotavirus and hepatitis A virus. The development of the aptasensor involved sample preparation for aptamer selection of rotavirus and hepatitis A virus, an iterative design process of the aptasensor, investigation of the surface immobilisation of aptamers and finally an impedimetric electrical characterisation of the sensor.
The sample preparation of the rotavirus was based on purification and biotinylation of the virus to meet the requirements of the aptamer selection process. The selection process, performed by an external collaborator, was based on streptavidin coated magnetic bead separation, hence the needed biotinylation. It was found that the BPH linker gave the highest yield when the biotinylated rotavirus were immobilised onto the beads.

The design of the viral aptasensor was determined by an iterative design process. The final chip design was based on a SD card design with an injection moulded PC substrate and lid. The electrodes were screen-printed PEDOT:PSS. The surface immobilisation of aptamers through UV cross-linking onto different polymer substrates was tested. As the success of this step is crucial for the aptasensor specificity and performances, the surface immobilisation was thoroughly investigated. The aptamer UV cross-linking onto PEDOT:PSS was promising. Furthermore, some passive absorption of the aptamers onto the PEDOT:PSS was found.

The impedimetric electrical characterisation of the aptasensor chip was done with different media salinity and different pH values. The impedimetric measurements of the different media salinity showed the expected behaviour with the greatest change present in the region representing the solution resistance. The pH measurements did not show any significant change of the impedance, hence the chip was stable in the measured pH range, which corresponds to the expected pH range of water samples. The stability of the aptasensor chip was tested over a 2 week period in continuous flow. It was found that the electrodes were not damaged or degraded during the time period, as a constant impedance signal was measured.

A solid foundation for the further development of the aptasensor for viral detection has been established and from this a new cheap and simple viral detection method can emerge.

A randomised clinical trial on the efficacy of oxytetracycline dose through water medication of nursery pigs on diarrhoea, faecal shedding of Lawsonia intracellularis and average daily weight gain

Oral treatment with antimicrobials is widely used in pig production for the control of gastrointestinal infections. Lawsonia intracellularis (LI) causes enteritis in pigs older than six weeks of age and is commonly treated with antimicrobials. The objective of this study was to evaluate the efficacy of three oral dosage regimens (5, 10 and 20mg/kg body weight) of oxytetracycline (OTC) in drinking water over a five-day period on diarrhoea, faecal shedding of LI and average daily weight gain (ADG). A randomised clinical trial was carried out in four Danish pig herds. In total, 539 animals from 37 batches of nursery pigs were included in the study. The dosage regimens were randomly allocated to each batch and initiated at presence of assumed LI-related diarrhoea. In general, all OTC doses used for the treatment of LI infection resulted in reduced diarrhoea and LI shedding after treatment. Treatment with a low dose of 5mg/kg OTC per kg body weight, however, tended to cause more watery faeces and resulted in higher odds of pigs shedding LI above detection level when compared to medium and high doses (with odds ratios of 5.5 and 8.4, respectively). No association was found between the dose of OTC and the ADG. In conclusion, a dose of 5mg OTC per kg body weight was adequate for reducing the high-level LI shedding associated with enteropathy, but a dose of 10mg OTC per kg body weight was necessary to obtain a maximum reduction in LI shedding.

General information
State: Published
Organisations: National Veterinary Institute, University of Copenhagen, Svinepraksis.dk
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Number of pages: 8
Pages: 52-9
Publication date: 2016
A register-based study of the antimicrobial usage in Danish veal calves and young bulls

High antimicrobial usage and multidrug resistance have been reported in veal calves in Europe. This may be attributed to a high risk of disease as veal calves are often purchased from numerous dairy herds, exposed to stress related to the transport and commingling of new animals, and fed a new ration. In this study, we used national register data to characterize the use of antimicrobials registered for large Danish veal calf and young bull producing herds in 2014. A total of 325 herds with veal calf and potentially young bull production were identified from the Danish Cattle database. According to the national Danish database on drugs for veterinary use (VetStat), a total of 537,399 Animal Daily Doses (ADD200) were registered for these 325 herds during 2014. The amount of antimicrobials registered in 2014 varied throughout the year, with the highest amounts registered in autumn and winter. Antimicrobials were registered for respiratory disorders (79%), joints/limbs/CNS disorders (17%), gastrointestinal disorders (3.7%) and other disorders (0.3%). Of the registered antimicrobials, 15% were for oral and 85% for parenteral administration. Long-acting formulations with a therapeutic effect of more than 48h covered 58% of the drugs for parenteral use. Standardized at the herd-level, as ADD200/100 calves/day, antimicrobial use distributed as median [CI95%] for starter herds (n=22): 2.14 [0.19;7.58], finisher herds (n=24): 0.48 [0.00;1.48], full-line herds (n=183): 0.78 [0.05;2.20] and herds with an inconsistent pattern of movements (n=96): 0.62 [0.00;2.24]. Full-line herds are herds, which purchase calves directly from a dairy herd and raise them to slaughter. Furthermore, we performed a risk factor analysis on the 183 herds with a full-line production. Here, we investigated, whether the number of suppliers, the number of calves purchased, the frequency of purchase, the average age at introduction, the average time in the herd and vaccination influenced the amount of antimicrobials used in the herds. The final multivariable regression analysis revealed that the number of calves introduced was positively associated with the antimicrobial use in the herd.
A sampling and metagenomic sequencing-based methodology for monitoring antimicrobial resistance in swine herds

Objectives
Reliable methods for monitoring antimicrobial resistance (AMR) in livestock and other reservoirs are essential to understand the trends, transmission and importance of agricultural resistance. Quantification of AMR is mostly done using culture-based techniques, but metagenomic read mapping shows promise for quantitative resistance monitoring.

Methods
We evaluated the ability of: (i) MIC determination for Escherichia coli; (ii) cfu counting of E. coli; (iii) cfu counting of aerobic bacteria; and (iv) metagenomic shotgun sequencing to predict expected tetracycline resistance based on known antimicrobial consumption in 10 Danish integrated slaughter pig herds. In addition, we evaluated whether fresh or manure floor samples constitute suitable proxies for intestinal sampling, using cfu counting, qPCR and metagenomic shotgun sequencing.

Results
Metagenomic read-mapping outperformed cultivation-based techniques in terms of predicting expected tetracycline resistance based on antimicrobial consumption. Our metagenomic approach had sufficient resolution to detect antimicrobial-induced changes to individual resistance gene abundances. Pen floor manure samples were found to represent rectal samples well when analysed using metagenomics, as they contain the same DNA with the exception of a few contaminating taxa that proliferate in the extraintestinal environment.

Conclusions
We present a workflow, from sampling to interpretation, showing how resistance monitoring can be carried out in swine herds using a metagenomic approach. We propose metagenomic sequencing should be part of routine livestock resistance monitoring programmes and potentially of integrated One Health monitoring in all reservoirs.

General information
State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology, National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology
Number of pages: 8
Pages: 385-392
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Antimicrobial Chemotherapy
Volume: 72
Article number: dkw415
ISSN (Print): 0305-7453
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SJR 2.419 SNIP 1.568 CiteScore 4.34
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.21 SJR 2.283 SNIP 1.521
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.259 SNIP 1.516 CiteScore 4.06
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
A simulation model for the spread of LA-MRSA within a pig herd

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Statens Serum Institut
Authors: Sørensen, A. I. V. (Intern), Boklund, A. (Intern), Toft, N. (Intern), Larsen, J. (Ekstern), Hisham Beshara Halasa, T. (Intern)
A Simulation Model to Determine Sensitivity and Timeliness of Surveillance Strategies

Animal surveillance systems need regular evaluation. We developed an easily applicable simulation model of the German wild boar population to investigate two evaluation attributes: the sensitivity and timeliness (i.e. the ability to detect a disease outbreak rapidly) of a surveillance system. Classical swine fever (CSF) was used as an example for the model. CSF is an infectious disease that may lead to massive economic losses. It can affect wild boar as well as domestic pigs, and CSF outbreaks in domestic pigs have been linked to infections in wild boar. Awareness of the CSF status in wild boar is therefore vital. Our non-epidemic simulation model is based on real data and evaluates the currently implemented German surveillance system for CSF in wild boar. The results show that active surveillance for CSF fulfils the requirements of detecting an outbreak with 95% confidence within one year after the introduction of CSF into the wild boar population. Nevertheless, there is room for improved performance and efficiency by more homogeneous (active and passive) sampling of wild boar over the year. Passive surveillance alone is not sufficient to meet the requirements for detecting the infection. Although CSF was used as example to develop the model, it may also be applied to the evaluation of other surveillance systems for viral diseases in wild boar. It is also possible to compare sensitivity and timeliness across hypothetical alternative or risk-based surveillance strategies.
A single-blinded phenobarbital-controlled trial of levetiracetam as mono-therapy in dogs with newly diagnosed epilepsy

Treatment of canine epilepsy is problematic. Few antiepileptic drugs have proven efficacy in dogs and undesirable adverse effects and pharmacoresistance are not uncommon. Consequently, the need for investigation of alternative treatment options is ongoing. The objective of this study was to investigate the efficacy and tolerability of levetiracetam as mono-therapy in dogs with idiopathic epilepsy. The study used a prospective single-blinded parallel group design. Twelve client-owned dogs were included and were randomised to treatment with levetiracetam (30 mg/kg/day or 60 mg/kg/day divided into three daily dosages) or phenobarbital (4 mg/kg/day divided twice daily). Control visits were at days 30, 60 and then every 3 months for up to 1 year. Two or more seizures within 3 months led to an increase in drug dosage (levetiracetam: 10 mg/kg/day, phenobarbital: 1 mg/kg/day). Five of six levetiracetam treated dogs and one of six phenobarbital treated dogs withdrew from the study within 2-5 months due to insufficient seizure control. In the levetiracetam treated dogs there was no significant difference in the monthly number of seizures before and after treatment, whereas in the phenobarbital treated dogs there were significantly (P = 0.013) fewer seizures after treatment. Five phenobarbital treated dogs were classified as true responders (>= 50% reduction in seizures/month) whereas none of the levetiracetam treated dogs fulfilled this criterion. Adverse effects were reported in both groups but were more frequent in the phenobarbital group. In this study levetiracetam was well tolerated but was not effective at the given doses as mono therapy in dogs with idiopathic epilepsy. (C) 2015 Elsevier Ltd. All rights reserved.
A space-time analysis of *Mycoplasma bovis*: bulk tank milk antibody screening results from all Danish dairy herds in 2013-2014

*Mycoplasma bovis* is an important pathogen causing severe disease outbreaks in cattle farms. Since 2011, there has been an apparent increase in *M. bovis* outbreaks among Danish dairy cattle herds. The dairy cattle industry performed cross-sectional antibody screening for *M. bovis* on four occasions, using the indirect BIO K 302 *M. bovis* enzyme-linked immunosorbent assay (ELISA) (Bio-X, Belgium) in bulk tank milk from all dairy herds between June 2013 and July 2014.
The objective of this study was to investigate the evolution of the spatial distribution of M. bovis in the Danish dairy herd population throughout the study period. Repeated bulk tank milk samples were used as a proxy for the herd-level diagnosis. Descriptive and spatial analyses were performed for the four screening rounds. Based on a previous diagnostic test evaluation study, the M. bovis status for each herd was determined as test-positive or test-negative using a cut-off of 50 optical density coefficient %. The spatial global clustering was evaluated through a modified K-function method, and local clusters were identified by scan statistics. The results showed that M. bovis test-positive herds had a dynamic pattern in space. The global clustering analysis showed that M. bovis test-positive herds were spatially correlated in rounds one, three and four. These findings were supported to some extent by the local clustering analysis, which found significant high- and low-risk spatial clusters in rounds one and three in the north and south of the mainland. The clusters with a high risk of observing test-positive herds did not remain between sampling rounds, indicating that M. bovis did not tend to persist upon emergence in dairy herds. In contrast, the clusters with a low risk of observing test-positive herds persisted in the same area throughout the study period.

**General information**

State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, University of Copenhagen
Number of pages: 7
Publication date: 2016
Main Research Area: Technical/natural sciences

**Publication Information**

Journal: Acta Veterinaria Scandinavica (Online)
Volume: 58
Issue number: 1
Article number: 16
ISSN (Print): 0044-605X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.077 SJR 0.655 CiteScore 1.45
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.01 SJR 0.641 SNIP 0.826
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.644 SNIP 1.641 CiteScore 0.98
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.753 SNIP 1.21 CiteScore 1.54
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.539 SNIP 1.11 CiteScore 1.41
ISI indexed (2013): ISI indexed no
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.591 SNIP 0.789 CiteScore 1.26
ISI indexed (2012): ISI indexed no
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.664 SNIP 0.997 CiteScore 1.42
ISI indexed (2011): ISI indexed no
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.551 SNIP 1.005
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.409 SNIP 0.716
Web of Science (2009): Indexed yes
Assessing the potential spread and maintenance of foot-and-mouth disease virus infection in wild ungulates: general principles and application to a specific scenario in Thrace

Foot-and-mouth disease (FMD), due to infection with serotype O virus, occurred in wild boar and within eleven outbreaks in domestic livestock in the south-east of Bulgaria, Thrace region, in 2011. Hence, the issue of the potential for the spread and maintenance of FMD virus (FMDV) infection in a population of wild ungulates became important. This assessment focused on the spread and maintenance of FMDV infection within a hypothetical wild boar and deer population in an environment, which is characterized by a climate transitional between Mediterranean and continental and variable wildlife population densities. The assessment was based on three aspects: (i) a systematic review of the literature focusing on experimental infection studies to identify the parameters describing the duration of FMDV infection in deer and wild boar, as well as observational studies assessing the occurrence of FMDV infection in wild deer and wild boar populations, (ii) prevalence survey data of wild boar and deer in Bulgaria and Turkey and (iii) an epidemiological model, simulating the host-to-host spread of FMDV infections. It is concluded, based on all three aspects, that the wildlife population in Thrace, and so wildlife populations in similar ecological settings, are probably not able to maintain FMD in the long term in the absence of FMDV infection in the domestic host population. However, limited spread of FMDV infection in time and space in the wildlife populations can occur. If there is a continued crossover of FMDV between domestic and wildlife populations or a higher population density, virus circulation may be prolonged.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, European Food Safety Authority, Helmholtz Centre for Environmental Research, Food and Agriculture Organization of the United Nations, Foot and Mouth Disease Institute, Friedrich Loeffler Institute, Colorado State University
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Number of pages: 10
Pages: 165–174
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Transboundary and Emerging Diseases
Volume: 63
Association between exposure to airborne noroviruses and gastroenteritis among wastewater workers
A three-dimensional approach to in vitro culture of immune-related cells

T lymphocytes are key players during the initiation of an adaptive immune response. The activation of these cells in vivo requires migration within the lymph nodes until they encounter antigen presenting cells (APCs) that can activate them to secrete IFN-γ which mediates downstream effector functions. The in vitro reactivation of antigen-experienced T lymphocytes and detection of IFN-γ from cell cultures can be used in a diagnostic assay to test for disease or vaccine efficacy. Practical procedures of the IFN-γ release assay (IGRA) was investigated using bovine cells and whole blood cultures was found preferable compared to PBMC cultures, partly due to the risk of losing cell subsets after purification of PBMCs.

The development of in vitro culture systems for more than 50 years ago revolutionized the biomedical world. It became possible to study cell behavior using cell lines or primary cells in culture and to measure cell activity such as IGRA, as described above. The traditional way of culturing cells are done using polystyrene (PS) plastic ware in flask-, Petri dish- or micro titer plate format. However, these artificial two dimensional (2D) surfaces on which the cells grow, has shown to interfere with cell morphology, gene expression and overall behavior and as such gives a poor reflection of in vivo cell behavior. Therefore, it is believed that by mimicking the in vivo conditions within the cultures, this would generate "closer-to-in vivo" results. For this purpose three dimensional (3D) culture setups have been developed including artificial scaffolds and extracellular matrix gels.

Optimization of IGRA was attempted using solid 3D scaffolds in various formats. The purpose of the 3D scaffolds was to facilitate T lymphocyte migration and subsequently activation due to increased chances of T lymphocyte/APC encounter. However, it turned out that the addition of this extra dimension to the cultures did not translate into increased de novo secretion of IFN-γ in these cultures. Furthermore, we often observed a non-specific effect on the level of IFN-γ when cells were cultures in 3D. This suggested that cells were sensitive to the geometry surrounding them and that this was
independent on antigen stimulation. Based on these findings and a previous discovery that the polymer PDMS, gave rise to increased differentiation of a nerve cell line in vitro, we tested the effect of PDMS on the differentiation of porcine monocytes. Monocytes are immune cells of high plasticity, and thus we speculated that they might be sensitive to culture conditions. Indeed, monocytes differentiated into monocyte-derived DC (moDCs) when cultured conventionally (2D PS) in the presence of GM-CSF and IL-4, but adopted a macrophage-like gene expression profile when cultured on PDMS. Further it was found that 3D culturing resulted in increased activation of the monocyte-derived cells.

The work in this thesis covers several aspects within primary cell culture, but central to the work is the investigation of 3D cell culture setups for improved activation/differentiation of immune cells. Conclusively, this work highlights the importance of acknowledging the effect from external factors when analyzing data generated from in vitro cultures. This being even more important when working with immune cells since these cells adopt traits and functions simply based on the nature of the culture system.

**General information**

State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Department of Micro- and Nanotechnology, Bioanalytics, BioLabChip
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Number of pages: 155
Publication date: 2016

**Publication information**

Place of publication: Frederiksberg C
Publisher: National Veterinary Institute, Technical University of Denmark
Original language: English
Main Research Area: Technical/natural sciences
Electronic versions:
PhD_thesis_Sofie_Bruun_Hartmann.pdf

**Relations**

Projects:
A three-dimensional approach to in vitro culture of immune-related cells
Publication: Research › Ph.D. thesis – Annual report year: 2016

Atlantic salmon (Salmo salar) protein hydrolysate in diets for weaning piglets – effect on growth performance, intestinal morphometry and microbiota composition
Salmon protein hydrolysates (SPH) from two different rest raw materials were evaluated in diets for weaning piglets. Four experimental diets were included in the study: a diet based on plant protein with soy protein as the main protein source (Diet PP), a diet based on fishmeal in exchange for soy protein (Diet FM) and two diets in which different SPH replaced fishmeal in the FM diet. The experimental diets were fed to piglets from the day of weaning until 32 d postweaning. In addition to the record of performance data, an intestinal sampling for mucosal morphometry and microbiota 16S rRNA gene sequencing were performed at day 11 on a subset of the animals. The duodenal villi absorption area was significantly larger in piglets receiving Diets SPH compared with Diet PP (p < 0.02). A significant positive correlation between duodenal villi height and average daily gain during the first 11 d postweaning was detected. Only small differences in intestinal microbiota community and no differences in growth performance were detected between the experimental diets. To conclude, SPH seem to be an interesting novel protein source in weanling piglets.

**General information**

State: Published
Organisations: Center for BioProcess Engineering, National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Norwegian University of Life Sciences
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Pages: 44-56
Publication date: 2016
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Archives of Animal Nutrition
Volume: 70
Issue number: 1
ISSN (Print): 1745-039X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
Awareness of rabies and response to dog bites in a Bangladesh community

Community awareness regarding rabies and treatment seeking behaviours are critical both for the prevention and control of the disease in human and animals. We conducted a study to explore people's awareness about rabies, their attitudes towards dogs and practices associated with treating dog bites in Satkhira Sadar, a south-western sub-district of Bangladesh. Of the total 3200 households (HHs) surveyed, the majority of the respondents have heard about rabies (73%) and there was a high level of awareness that dog bite is the main cause of rabies (86%), and that rabies can be prevented by vaccination (85%). However, 59% of the dog bite victims first seek treatment from traditional healers instead of visiting the hospitals, 29% received the rabies vaccine, 2% practiced proper wound washing with soap and water, while 4.8% have not taken any measures. None of the victims have received rabies immunoglobulin (RIG). Of the respondents, 5.2% reported a history of dog bite in at least one family member, and 11.8% reported a history of dog bite in domestic animals during the previous year. The HHs having a higher number of family members (OR: 1.13, 95% CI: 1.07–1.2), having a pet dog (OR: 2.1, 95% CI: 1.4–2.9) and caring or feeding a community dog (OR: 2.1, 95% CI: 1.4–2.9) showed an increased risk of getting a dog bite. Among the bite victims, 3.6% (n = 6) humans and 11.8% (n = 60) animals died. As a measure for dog population management (DPM), 56% preferred sterilization while the rest preferred killing of dogs. The current treatment seeking behaviours of the respondents should be improved through additional education and awareness programme and better availability for the provision of post-exposure prophylaxis in Bangladesh. We recommend scaling up national mass dog vaccination and DPM to reduce the burden of rabies cases and dog bites in Bangladesh.
General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Ministry of Health and Family Welfare, Chittagong Veterinary and Animal Sciences University, City University of New York
Number of pages: 9
Pages: 161-169
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Veterinary Medicine and Science
Volume: 2
Issue number: 3
ISSN (Print): 2053-1095
Ratings:
Web of Science (2018): Indexed yes
Web of Science (2016): Indexed yes
Original language: English
Awareness, Bangladesh, Dog bites, First aid measures, Post-exposure prophylaxis, Rabies
Electronic versions:
Ghosh_et_al_2016_Veterinary_Medicine_and_Science.pdf
DOI:
10.1002/vms3.30

Bibliographical note
This is an open access article under the terms of the Creative Commons Attribution-NonCommercial-NoDerivs License, which permits use and distribution in any medium, provided the original work is properly cited, the use is non-commercial and no modifications or adaptations are made.
Publication: Research - peer-review › Journal article – Annual report year: 2016

Bibliographical note
Beskrivelse af dyreværnsmæssig korrekt aflivning af dyr på EU-listen

General information
State: Published
Organisations: National Veterinary Institute, Diagnostic & Development, Pathology
Number of pages: 15
Publication date: 2016

Publication information
Place of publication: Frederiksberg C
Publisher: Veterinærinstituttet, Danmarks Tekniske Universitet
Original language: Danish
Main Research Area: Technical/natural sciences

Bibliographical note
Rapporten er ikke offentlig tilgængelig
Publication: Commissioned › Report – Annual report year: 2017

Beskrivelse af dyreværnsmæssig korrekt aflivning af dyr på EU-listen - anbefalinger

General information
State: Published
Organisations: National Veterinary Institute, Diagnostic & Development, Pathology
Number of pages: 3
Publication date: 2016

Publication information
Place of publication: Frederiksberg C
Publisher: Veterinærinstituttet, Danmarks Tekniske Universitet
Original language: Danish
Biofilm as a production platform for heterologous production of rhamnolipids by the non-pathogenic strain *Pseudomonas putida* KT2440

**Background**

Although a transition toward sustainable production of chemicals is needed, the physiochemical properties of certain biochemicals such as biosurfactants make them challenging to produce in conventional bioreactor systems. Alternative production platforms such as surface-attached biofilm populations could potentially overcome these challenges. Rhamnolipids are a group of biosurfactants highly relevant for industrial applications. However, they are mainly produced by the opportunistic pathogen *Pseudomonas aeruginosa* using hydrophobic substrates such as plant oils. As the biosynthesis is tightly regulated in *P. aeruginosa* a heterologous production of rhamnolipids in a safe organism can relieve the production from many of these limitations and alternative substrates could be used.

**Results**

In the present study, heterologous production of biosurfactants was investigated using rhamnolipids as the model compound in biofilm encased *Pseudomonas putida* KT2440. The rhlAB operon from *P. aeruginosa* was introduced into *P. putida* to produce mono-rhamnolipids. A synthetic promoter library was used in order to bypass the normal regulation of rhamnolipid synthesis and to provide varying expression levels of the rhlAB operon resulting in different levels of rhamnolipid production. Biosynthesis of rhamnolipids in *P. putida* decreased bacterial growth rate but stimulated biofilm formation by enhancing cell motility. Continuous rhamnolipid production in a biofilm was achieved using flow cell technology. Quantitative and structural investigations of the produced rhamnolipids were made by ultra performance liquid chromatography combined with high resolution mass spectrometry (HRMS) and tandem HRMS. The predominant rhamnolipid congener produced by the heterologous *P. putida* biofilm was mono-rhamnolipid with two C_{10} fatty acids.

**Conclusion**

This study shows a successful application of synthetic promoter library in *P. putida* KT2440 and a heterologous biosynthesis of rhamnolipids in biofilm encased cells without hampering biofilm capabilities. These findings expands the possibilities of cultivation setups and paves the way for employing biofilm flow systems as production platforms for biochemicals, which as a consequence of physiochemical properties are troublesome to produce in conventional fermenter setups, or for production of compounds which are inhibitory or toxic to the production organisms.

**General information**

State: Published
Organisations: Department of Systems Biology, Infection Microbiology, Metabolomics Platform, National Food Institute, Research Group for Microbial Biotechnology and Biorefining, National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology
Publication information
Journal: European Journal of Immunology
Volume: 46
Issue number: S1
ISSN (Print): 0014-2980
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.59 SJR 2.206 SNIP 0.92
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.61 SJR 2.525 SNIP 0.927
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.588 SNIP 0.965 CiteScore 3.85
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.672 SNIP 0.972 CiteScore 3.83
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 2.876 SNIP 1.05 CiteScore 4.3
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 2.989 SNIP 1.063 CiteScore 4.62
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 3.255 SNIP 1.025 CiteScore 4.69
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 3.363 SNIP 0.99
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 3.188 SNIP 1.007
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 3.435 SNIP 0.956
Scopus rating (2007): SJR 3.287 SNIP 1.003
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 3.224 SNIP 1.026
Scopus rating (2005): SJR 3.094 SNIP 1.044
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 3.01 SNIP 1.049
Scopus rating (2003): SJR 2.996 SNIP 1
Scopus rating (2002): SJR 3.105 SNIP 1.029
Scopus rating (2001): SJR 3.238 SNIP 1.077
Scopus rating (2000): SJR 3.765 SNIP 1.146
Scopus rating (1999): SJR 3.647 SNIP 1.169
Original language: English
Source: FindIt
Source-ID: 2347574413
Publication: Research - peer-review › Conference abstract in journal – Annual report year: 2016
Changes in group treatment procedures of Danish finishers and its influence on the amount of administered antimicrobials

When treating groups of pigs orally, antimicrobials can be administered through either feed or water. During the last decade, the group treatment procedure for finishers has shifted from feed to water administration. We hypothesized that farms implementing this change in treatment procedure would increase their total amount of administered antimicrobials. Based on Danish national register data, we performed a retrospective cohort study with three groups. The cohort of primary interest (Cohort Change) consisted of 50 finisher farms which changed their group treatment procedure from feed administration to water administration between 2008 and 2009. In addition, we identified 221 farms where treatment was administered through feed (Cohort Feed), and another 553 farms where treatment was administered through water (Cohort Water). Both of these groups retained their original treatment procedure throughout the study period. Cohort Change experienced a significant increase in the total amount of prescribed antimicrobials between the years. This increase might be caused by the treatment of more pigs, since antimicrobials administered through the feed are mainly administered at the pen level, while antimicrobials administered in water are mainly administered at the section level. However, we cannot exclude that a change in clinical disease has influenced the amount of prescribed antimicrobials. No change was observed in the other two cohorts. Furthermore, the difference in the amount of prescribed antimicrobials between the years was significantly different in Cohort Change when compared to both Cohort Water and Cohort Feed. Results from this study demonstrate that farms changing their procedure of group treatment from feed administration to water administration may increase their overall use of antimicrobials.

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, University of Copenhagen
Authors: Fertner, M. E. (Intern), Boklund, A. (Intern), Dupont, N. H. (Ekstern), Toft, N. (Intern)
Number of pages: 5
Pages: 89-93
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Preventive Veterinary Medicine
Volume: 126
ISSN (Print): 0167-5877
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 1.31 SJR 1.144 CiteScore 2.26
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.2 SJR 1.249 SNIP 1.361
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.282 SNIP 1.177 CiteScore 2.1
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.27 SNIP 1.407 CiteScore 2.37
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.264 SNIP 1.529 CiteScore 2.49
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.265 SNIP 1.436 CiteScore 2.45
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.194 SNIP 1.295 CiteScore 2.24
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
Characterization and differentiation of equine experimental local and early systemic inflammation by expression responses of inflammation-related genes in peripheral blood leukocytes

Local inflammation may progress into systemic inflammation. To increase our understanding of the basic immunological processes during transition of equine local inflammation into a systemic state, investigation into the equine systemic immune response to local inflammation is warranted. Therefore, the aim of this study was to investigate the innate peripheral blood leukocyte (PBL) immune response to local inflammation in horses, and to compare this response with the PBL immune response during the early phase of acute systemic inflammation. Expression of 22 selected inflammation-related genes was measured in whole blood leukocytes from 6 horses in an experimental cross-over model of lipopolysaccharide- (LPS-) induced acute synovitis (3 μg LPS intraarticularly; locally inflamed [LI] horses) and endotoxemia (1 μg LPS/kg intravenously; systemically inflamed [SI] horses). Multiple clinical and hematological/biochemical examinations were performed, and serial blood samples were analyzed by reverse transcription quantitative real-time PCR. Post-induction expression profiles of all genes were compared between study groups using principal component analysis (PCA) and hierarchical clustering. Moderate synovitis and mild systemic inflammation of approximately 24 h duration was confirmed by clinical and paraclinical observations in LI and SI horses, respectively. In the LI group, samples obtained 3-16 h post-injection showed distinct clustering in the PCA compared with baseline levels, indicating a transcriptional response to local inflammation in PBLs in this time interval. There was no clinical or hematological indication of actual systemic inflammation. There was a clear separation of all LI samples from all SI samples in two distinct clusters, indicating that expression profiles in the two study groups were different, independent of time since LPS injection. Co-regulated genes formed four clusters across study groups which were distinctly differently regulated. Only few of individual genes displayed different expression between the study groups at all times after LPS injection. Local inflammation in horses initiated an innate transcriptional response in PBLs, which differed from the transcriptional response during the early phase of systemic inflammation. This study may provide new insights into the immunobiology of PBLs during the transition of local inflammation into a systemic state.

General information
Characterization of a Novel Chimeric Swine Enteric Coronavirus from Diseased Pigs in Central Eastern Europe in 2016

During a severe outbreak of diarrhoea and vomiting in a pig herd in Central Eastern Europe, faecal samples were tested positive for porcine epidemic diarrhoea virus (PEDV) and negative for transmissible gastroenteritis virus (TGEV) using a commercial RT-qPCR assay that can detect both of these coronaviruses. However, further analyses, using other TGEV- and PEDV-specific RT-qPCR assays, provided results inconsistent with infection by either of these viruses. Sequencing of an amplicon (ca. 1.6 kb), generated by an RT-PCR specific for the PEDV S-gene, indicated a very close similarity (ca. 99% identity) to recently described chimeric viruses termed swine enteric coronaviruses (SeCoVs). These viruses (with an RNA genome of ca. 28 kb) were first identified in Italy in samples from 2009 but have not been detected there since 2012. A closely related virus was detected in archived samples in Germany from 2012, but has not been detected subsequently. Building on the initial sequence data, further amplicons were generated and over 9 kb of sequence corresponding to the 3′-terminus of the new SeCoV genome was determined. Sequence comparisons showed that the three known SeCoVs are ≥98% identical across this region and contain the S-gene and 3a sequences from PEDV within a backbone of TGEV, but the viruses are clearly distinct from each other. It is demonstrated, for the first time, that pigs from within the SeCoV-infected herd seroconverted against PEDV but tested negative in a TGEV-specific ELISA that detects antibodies against the S protein. These results indicate that SeCoV is continuing to circulate in Europe and suggest it can cause a disease that is very similar to PED. Specific detection of the chimeric SeCoVs either requires development of a new diagnostic RT-qPCR assay or the combined use of assays targeting the PEDV S-gene and another part of the TGEV genome.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, State Veterinary Institute Jihlava
Authors: Belsham, G. (Intern), Rasmussen, T. B. (Intern), Normann, P. (Intern), Vaclavek, P. (Ekstern), Strandbygaard, B. (Intern), Betner, A. (Intern)
Number of pages: 7
Pages: 595–601
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Transboundary and Emerging Diseases
Volume: 63
Issue number: 6
ISSN (Print): 1865-1674
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.87 SJR 1.147 SNIP 1.488
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.16 SJR 1.046 SNIP 0.998
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.305 SNIP 1.249 CiteScore 2.29
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.048 SNIP 1.207 CiteScore 2.23
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.975 SNIP 1.123 CiteScore 2.33
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.847 SNIP 1.178 CiteScore 2.04
Characterization of cytological changes, IgA, IgG and IL-8 levels and pH value in the vagina of prepubertal and sexually mature Ellegaard Göttingen minipigs during an estrous cycle

The pig is increasingly used as an advanced animal model of the genital tract in women and knowledge on the genital immune system is therefore needed. In this study, evaluation of vaginal smears revealed that almost no neutrophils or other leukocytes were present in the vaginal mucosa of prepubertal minipigs (n = 10). In sexually mature minipigs (n = 10), evaluated through an estrous cycle, there was an increase in number of mucosal neutrophils and other leukocytes during estrus. The level of total IgA on the vaginal mucosa increased during diestrus. The level of total IgG showed no significant changes through the cycle. The vaginal IgA level in the prepubertal minipigs was similar to the low estrus level in sexually mature minipigs, and the IgG level in prepubertal was similar to the stable level in the sexually mature minipigs.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, University of Copenhagen, Ellegaard Göttingen Minipigs A/S, CiToxLab Scantox, State Serum Institute
Authors: Lorenzen, E. (Ekstern), Agerholm, J. S. (Ekstern), Grossi, A. B. (Ekstern), Bojesen, A. M. (Ekstern), Skytte, C. (Ekstern), Erneholm, K. (Ekstern), Follmann, F. (Ekstern), Jungersen, G. (Intern)
Number of pages: 6
Pages: 57-62
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Developmental and Comparative Immunology
Volume: 59
ISSN (Print): 0145-305X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Characterization of the immune response and evaluation of the protective capacity of rSsnA against Streptococcus suis infection in pigs

The efforts made to develop vaccines against Streptococcus suis have failed because of lack of common antigens cross-reactive against different serotypes of this species. The cell wall-anchored proteins can be good vaccine candidates due to their high expression and accessibility to antibodies, among these, a cell-wall protein, DNA-nuclease (SsnA), present in most of the S. suis serotypes and clinical isolates collected from infected pigs, was selected. An experimental challenge against S. suis serotype 2 in a pig model was used to validate the efficacy of recombinant SsnA combined with aluminium hydroxide plus Quil A as adjuvants, previously tested in mice by our research group with good results. In our study, clinical characteristics, bacterial load and spread, haematological and immunological parameters and the antibody response, including the opsonophagocytosis analysis of the sera were evaluated. Moreover the composition of peripheral blood leukocyte populations was studied in infected animals. The results show that the immunization of piglets with rSsnA elicits a significant humoral antibody response. However, the antibody response is not reflected in protection of pigs that are
challenged with a virulent strain in our conventional vaccination model. Further studies are necessary to evaluate the use of rSsnA as a vaccine candidate for swine.

**General information**

State: Published
Organisations: National Veterinary Institute, Universidad de Cordoba, CICAP—Food Research Centre
Authors: Gómez-Gascón, L. (Ekstern), Cardoso-Toset, F. (Ekstern), Tarradas, C. (Ekstern), Gómez-Laguna, J. (Ekstern), Maldonado, A. (Ekstern), Nielsen, J. (Intern), Olaya-Abril, A. (Ekstern), Rodríguez-Ortega, M. J. (Ekstern), Luque, I. (Ekstern)
Number of pages: 8
Pages: 52-59
Publication date: 2016
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Comparative Immunology, Microbiology & Infectious Diseases
Volume: 47
ISSN (Print): 0147-9571
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.943 SJR 0.877 CiteScore 2.16
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.891 SNIP 0.894 CiteScore 2.05
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.064 SNIP 0.979 CiteScore 2.14
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.014 SNIP 1.001 CiteScore 2.16
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.864 SNIP 0.89 CiteScore 2.09
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.76 SNIP 1.041 CiteScore 2.12
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.731 SNIP 0.942 CiteScore 2.07
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.127 SNIP 1.556
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.821 SNIP 1.124
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 0.505 SNIP 0.809
Scopus rating (2007): SJR 0.823 SNIP 1.358
Scopus rating (2006): SJR 0.801 SNIP 1.122
Scopus rating (2005): SJR 0.655 SNIP 0.865
Scopus rating (2004): SJR 0.404 SNIP 0.603
Scopus rating (2003): SJR 0.395 SNIP 0.605
Scopus rating (2002): SJR 0.306 SNIP 0.552
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.43 SNIP 0.771
Scopus rating (2000): SJR 0.295 SNIP 0.926
Web of Science (2000): Indexed yes
Clonal neoantigens elicit T cell immunoreactivity and sensitivity to immune checkpoint blockade

As tumors grow, they acquire mutations, some of which create neoantigens that influence the response of patients to immune checkpoint inhibitors. We explored the impact of neoantigen intratumor heterogeneity (ITH) on antitumor immunity. Through integrated analysis of ITH and neoantigen burden, we demonstrate a relationship between clonal neoantigen burden and overall survival in primary lung adenocarcinomas. CD8(+) tumor-infiltrating lymphocytes reactive to clonal neoantigens were identified in early-stage non-small cell lung cancer and expressed high levels of PD-1. Sensitivity to PD-1 and CTLA-4 blockade in patients with advanced NSCLC and melanoma was enhanced in tumors enriched for clonal neoantigens. T cells recognizing clonal neoantigens were detectable in patients with durable clinical benefit. Cytotoxic chemotherapy-induced subclonal neoantigens, contributing to an increased mutational load, were enriched in certain poor responders. These data suggest that neoantigen heterogeneity may influence immune surveillance and support therapeutic developments targeting clonal neoantigens.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology
Pages: 1463-1469
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Science
Volume: 351
Issue number: 6280
ISSN (Print): 0036-8075
Ratings:
BFI (2018): BFI-level 3
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 15.85 SJR 14.142 SNIP 7.154
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 14.39 SJR 13.745 SNIP 7.547
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 12.052 SNIP 8.129 CiteScore 12.68
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 12.41 SNIP 7.809 CiteScore 12.43
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
Communicating spatial risk of tick-borne infections - Creating a ScandTick Innovation website based on surveillance data

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Section for Bacteriology, Pathology and Parasitology
Authors: Clausen, C. G. (Intern), Schou, K. K. (Intern), Kirkeby, C. (Intern), Bødker, R. (Intern)
Number of pages: 1
Publication date: 2016
Event: Poster session presented at 3rd Conference on Neglected Vectors and Vector-Borne Diseases (EurNegVec): with MC and WG Meeting of the COST Action TD1303, Zaragoza, Spain.
Main Research Area: Technical/natural sciences
Electronic versions:
Comparative Genome Analysis Provides Insights into the Pathogenicity of Flavobacterium psychrophilum

Flavobacterium psychrophilum is a fish pathogen in salmonid aquaculture worldwide that causes cold water disease (CWD) and rainbow trout fry syndrome (RTFS). Comparative genome analyses of 11 F. psychrophilum isolates representing temporally and geographically distant populations were used to describe the F. psychrophilum pan-genome and to examine virulence factors, prophages, CRISPR arrays, and genomic islands present in the genomes. Analysis of the genomic DNA sequences were complemented with selected phenotypic characteristics of the strains. The pan-genome analysis showed that F. psychrophilum could hold at least 3373 genes, while the core genome contained 1743 genes. On average, 67 new genes were detected for every new genome added to the analysis, indicating that F. psychrophilum possesses an open pan-genome. The putative virulence factors were equally distributed among isolates, independent of geographic location, year of isolation and source of isolates. Only one prophage-related sequence was found which corresponded to the previously described prophage 6H, and appeared in 5 out of 11 isolates. CRISPR array analysis revealed two different loci with dissimilar spacer content, which only matched one sequence in the database, indicating that F. psychrophilum possesses an open pan-genome. The global scale dispersion of virulence factors in the genomes and the abilities for biofilm formation, hemolytic activity and secretion of extracellular enzymes among the strains suggested that F. psychrophilum isolates have a similar mode of action on adhesion, colonization and destruction of fish tissues across large spatial and temporal scales of occurrence. Overall, the genomic characterization and phenotypic properties may provide new insights to the mechanisms of pathogenicity in F. psychrophilum.
Comparative genomics of toxigenic and non-toxigenic Staphylococcus hyicus

The most common causative agent of exudative epidermitis (EE) in pigs is Staphylococcus hyicus. S. hyicus can be grouped into toxigenic and non-toxigenic strains based on their ability to cause EE in pigs and specific virulence genes have been identified. A genome wide comparison between non-toxigenic and toxigenic strains has never been performed. In this study, we sequenced eleven toxigenic and six non-toxigenic S. hyicus strains and performed comparative genomic and phylogenetic analysis. Our analyses revealed two genomic regions encoding genes that were predominantly found in toxigenic strains and are predicted to encode for virulence determinants for EE. All toxigenic strains encoded for one of the exfoliative toxins ExhA, ExhB, ExhC, or ExhD. In addition, one of these regions encoded for an ADP-ribosyltransferase (EDIN, epidermal cell differentiation inhibitor) and a novel putative RNase toxin (polymorphic toxin) and was associated with the gene encoding ExhA. A clear differentiation between toxigenic and non-toxigenic strains based on genomic and phylogenetic analyses was not apparent. The results of this study support the observation that exfoliative toxins of S. hyicus and S. aureus are located on genetic elements such as pathogenicity islands, phages, prophages and plasmids.

General information
State: Published
Organisations: National Food Institute, Research Group for Genomic Epidemiology, National Veterinary Institute
Authors: Leekitcharoenphon, P. (Intern), Pamp, S. J. (Intern), Andresen, L. O. (Intern), Aarestrup, F. M. (Intern)
Number of pages: 7
Pages: 34-40
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Veterinary Microbiology
Volume: 185
ISSN (Print): 0378-1135
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.7 SJR 1.175 SNIP 1.241
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.363 SNIP 1.206
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.413 SNIP 1.21 CiteScore 2.56
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.291 SNIP 1.256 CiteScore 2.54
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.459 SNIP 1.471 CiteScore 3
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.441 SNIP 1.569 CiteScore 3.18
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.56 SNIP 1.729 CiteScore 3.27
Comparative Risk Analysis of Two Culicoides-Borne Diseases in Horses: Equine Encephalosis More Likely to Enter France than African Horse Sickness

African horse sickness (AHS) and equine encephalosis (EE) are Culicoides-borne viral diseases that could have the potential to spread across Europe if introduced, thus being potential threats for the European equine industry. Both share similar epidemiology, transmission patterns and geographical distribution. Using stochastic spatiotemporal models of virus entry, we assessed and compared the probabilities of both viruses entering France via two pathways: importation of live-infected animals or importation of infected vectors. Analyses were performed for three consecutive years (2010–2012). Seasonal and regional differences in virus entry probabilities were the same for both diseases. However, the probability of EE entry was much higher than the probability of AHS entry. Interestingly, the most likely entry route differed between AHS and EE: AHS has a higher probability to enter through an infected vector and EE has a higher probability to enter through an infectious host. Consequently, different effective protective measures were identified by ‘what-if’ scenarios for the two diseases. The implementation of vector protection on all animals (equine and bovine) coming from low-risk regions before their importation was the most effective in reducing the probability of AHS entry. On the other hand, the most significant reduction in the probability of EE entry was obtained by the implementation of quarantine before import for horses coming from both EU and non-EU countries. The developed models can be useful to implement risk-based surveillance.

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Wageningen University, Utrecht University
Authors: Faverjon, C. (Ekstern), Leblond, A. (Ekstern), Lecollinet, S. (Ekstern), Bødker, R. (Intern), de Koeijer, A. A. (Ekstern), Fischer, E. A. J. (Ekstern)
African horse sickness, Equine encephalosis, Culicoides, Import risk, Risk assessment, Risk of release, Quantitative risk, Risk of entry, Horses, Emerging diseases

DOIs:
10.1111/tbed.12577
Comparing algorithms performance for monitoring endemic disease: a simulation study based on the Danish PRRSV monitoring program

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, National Veterinary Institute Sweden
Authors: Lopes Antunes, A. C. (Intern), Dorea, F. (Ekstern), Hisham Beshara Halasa, T. (Intern), Toft, N. (Intern)
Number of pages: 1
Pages: 542-542
Publication date: 2016

Host publication information
Title of host publication: Book of abstracts from the 24th International Pig Veterinary Society (IPVS) Congress
Place of publication: Dublin, Ireland
Article number: PO-PW1-128
Main Research Area: Technical/natural sciences
Conference: 24th International Pig Veterinary Society (IPVS) Congress, Dublin, Ireland, 07/06/2016 - 07/06/2016
Disease monitoring, Endemic, Univariate process monitoring control algorithms
Electronic versions:
IPVS_abstract.pdf
Source: PublicationPreSubmission
Source-ID: 124137437
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2016

Comparison of innate and Th1-type host immune responses in Oesophagostomum dentatum and Trichurus suis infections in pigs
The present study investigated details of the innate and Th1/Treg type associated host immune responses in Trichurus suis and Oesophagostomum dentatum monoinfected pigs and in co-infected pigs and in vitro stimulated porcine dendritic cell cultures. Forty-eight pigs were allocated into a 2-factorial design with two groups trickle inoculated with 10 T. suis eggs/kg/day (Group T) or 20 O. dentatum L3/kg/day (O). Another group (OT) was infected with both parasites. Group C remained uninfected. Expression of innate and Th1/Treg cell associated genes in gut mucosa and associated lymph nodes was determined by qPCR at necropsy day 35 and 71. Gene expression showed suppressed/inhibited Th1 and Treg type immune reactions, in accordance with previous findings of a predominant Th2 type immune response to both nematodes. The in vitro par test examined production of TNF-α in porcine dendritic cells (DC) exposed to T. suis and/or O. dentatum excretory/secretory (E/S) products. Further, binding capacity and structure of E/S products were characterized. Glycan and lectin binding capacity were generally lower in O. dentatum E/S products compared to T. suis which may explain the earlier found weaker Th2 response to the former. Surprisingly, O. dentatum E/S products induced a significant (p < 0.0001) increase in TNF-α DC production, potentially indicating a new mode of helminth-host immune response interaction.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, University of Copenhagen, VU University Medical Centre
Conserved elements within the genome of foot-and mouth disease virus; their influence on virus replication

Objectives:
Several conserved elements within the genome of foot-and-mouth disease virus (FMDV) have been identified, e.g. the IRES. Such elements can be crucial for the efficient replication of the genomic RNA. Previously, SHAPE analysis of the entire FMDV genome (Poulsen et al., 2016 submitted) has identified a conserved RNA structure within the 3Dpol coding region (the RNA-dependent RNA polymerase) which might have an important role in virus replication.

The FMDV 2A peptide, another conserved element, is responsible for the primary “cleavage” at its own C-terminus (2A/2B junction). It is believed that this “cleavage” is achieved by ribosomal skipping, in which the 2A peptide prevents the ribosome from linking the next amino acid (aa) to the growing polypeptide. The nature of this “cleavage” has so far not been investigated in the context of the full-length FMDV RNA within cells.

Through reverse genetics, this study aims to identify how these distinct conserved elements influence the replication of FMDV RNA.

Methods:
Changes were made within the predicted 3Dpol RNA structure and the 2A peptide coding sequence which were expected to be detrimental for their function. These were:
1) Silent mutations, to disrupt the 3Dpol RNA secondary structure, were generated in a FMDV replicon containing Gaussia luciferase.
2) Sequence changes encoding selected modifications of the 2A peptide (as described by Donnelly et al., 2001) were introduced into a full-length FMDV cDNA and in a FMDV replicon cDNA containing Gaussia luciferase.

RNA transcripts were generated in vitro from the plasmids, and introduced into BHK cells by electroporation. The replication efficiency was assessed by measurement of luciferase activity or by rescue of mutant viruses. The rescued viruses derived from the 2A mutant cDNAs were passaged 3 times and the rescued RNAs were sequenced.

Results:
Initial results indicate that 3 different replicon mutants, with the disrupted 3Dpol RNA structure, had very similar RNA replication efficiencies as the wt FMDV replicon.

Furthermore, the replicon system showed that the 2A mutants were also able to undergo replication, although at a lower rate than for the wt FMDV replicon. One mutant which previously (Donnelly et al., 2001) was found not to undergo “cleavage” was still replication competent. Analysis of rescued viruses by sequencing of the third passage revealed that the 2A mutants with the lowest “cleavage” activity had reverted to the wt but some mutants with defective “cleavage” activity were viable.

Conclusions:
Initial results confirm that efficient “cleavage” at the 2A/2B junction is required for optimal replication. Rescue of viable mutant viruses with mutants previously characterized as “non-cleaving” indicates a discrepancy between in vitro and cell-based experiments.

Detrimental changes to the 3Dpol RNA structure did not change the replication efficiency in a replicon system. However these results do not eliminate a possible effect of this structure on virus replication; such analyses are in progress. Further study of these two conserved elements will provide more valuable insights into mechanisms underlying FMDV virus replication.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, University of Copenhagen
Authors: Kjær, J. (Intern), Poulsen, L. D. (Ekstern), Vinther, J. (Ekstern), Rasmussen, T. B. (Intern), Belsham, G. (Intern)
Number of pages: 2
Publication date: 2016
Event: Abstract from 19th European Study group on the molecular Biology of Picornaviruses (Europic 2016), Switzerland.
Main Research Area: Technical/natural sciences
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2016

Context-Dependent Development of Lymphoid Stroma from Adult CD34+ Adventitial Progenitors
Despite the key role of primary and secondary lymphoid organ stroma in immunity, our understanding of the heterogeneity and ontogeny of these cells remains limited. Here, we identify a functionally distinct subset of BP3-PDPN+PDGFRβ+/α+CD34+ stromal adventitial cells in both lymph nodes (LNs) and thymus that is located within the vascular niche surrounding PDPN-PDGFRβ+/α-Esam-1+ITGA7+ pericytes. CD34+ adventitial cells developed in late embryonic thymus and in postnatal LNs and in the thymus originated, along with pericytes, from a common anlage-seeding progenitor population. Using lymphoid organ re-aggregate grafts, we demonstrate that adult CD34+ adventitial cells are capable of differentiating into multiple lymphoid stroma-like subsets including pericyte-, FRC-, MRC-, and FDC-like cells, the development of which was lymphoid environment-dependent. These findings extend the current understanding of lymphoid mesenchymal cell heterogeneity and highlight a role of the CD34+ adventitia as a potential ubiquitous source of lymphoid stromal precursors in postnatal tissues.
Control of African swine fever epidemics in industrialized swine populations

African swine fever (ASF) is a notifiable infectious disease with a high impact on swine health. The disease is endemic in certain regions in the Baltic countries and has spread to Poland constituting a risk of ASF spread toward Western Europe. Therefore, as part of contingency planning, it is important to explore strategies that can effectively control an epidemic of ASF. In this study, the epidemiological and economic effects of strategies to control the spread of ASF between domestic swine herds were examined using a published model (DTU-DADS-ASF). The control strategies were the basic EU and national strategy (Basic), the basic strategy plus pre-emptive depopulation of neighboring swine herds, and intensive surveillance of herds in the control zones, including testing live or dead animals. Virus spread via wild boar was not modelled.

Under the basic control strategy, the median epidemic duration was predicted to be 21 days (5th and 95th percentiles; 1-55 days), the median number of infected herds was predicted to be 3 herds (1-8), and the total costs were predicted to be €326 million (€256–€442 million). Adding pre-emptive depopulation or intensive surveillance by testing live animals resulted in marginal improvements to the control of the epidemics. However, adding testing of dead animals in the protection and surveillance zones was predicted to be the optimal control scenario for an ASF epidemic in industrialized swine populations without contact to wild boar. This optimal scenario reduced the epidemic duration to 9 days (1–38) and the total costs to €294 million (€257–€392 million). Export losses were the driving force of the total costs of the epidemics.
African swine fever, Simulation model, Spread, Control

DOIs:
10.1016/j.vetmic.2016.11.023
Source: FindIt
Source-ID: 2349229035
Publication: Research - peer-review › Journal article – Annual report year: 2016

Coccidiose hos mink: En undervurderet sygdom?

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Bayer Animal Health Nordic
Authors: Chriél, M. (Intern), Hansen, M. S. (Intern), Petersen, H. H. (Intern), Holm, T. (Ekstern)
Pages: 38-38
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Dansk Pelsdyravl
Volume: 2016
Issue number: 4
ISSN (Print): 0011-6424
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Original language: English
Electronic versions:
Coccidier_DP_april2016.pdf
Source: PublicationPreSubmission
Source-ID: 124106631
Publication: Research › Journal article – Annual report year: 2016

Cyster af fåretinte-bændelormen påvist hos danske får

General information
State: Published
Organisations: National Veterinary Institute
Authors: Petersen, H. H. (Intern)
Pages: 42-42
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Dansk Veterinærtidsskrift
Volume: 14
ISSN (Print): 1600-2032
Ratings:
Daily Evolution of the Insect Biomass Spectrum in an Agricultural Landscape Accessed with Lidar

We present measurements of atmospheric insect fauna intercepted by a static lidar transect over arable and pastoral land over one day. We observe nearly a quarter million of events which are calibrated to optical cross section. Biomass spectra are derived from the size distribution and presented against space and time. We discuss detection limits and instrument biasing, and we relate the insect observations to relevant ecological landscape features and land use. Future directions and improvements of the technique are also outlined.

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Lund University
Authors: Brydegaard, M. (Ekstern), Gebru, A. (Ekstern), Kirkeby, C. T. (Intern), Åkesson, S. (Ekstern), Smith, H. (Ekstern)
Number of pages: 4
Publication date: 2016
Conference: 27th International Laser Radar Conference (ILRC 27), New York, United States, 05/07/2015 - 05/07/2015
Main Research Area: Technical/natural sciences

Publication information
Journal: E P J Web of Conferences
Volume: 119
Article number: 22004
ISSN (Print): 2100-014X
Ratings:
Scopus rating (2017): CiteScore 0.31 SJR 0.194 SNIP 0.233
Scopus rating (2016): CiteScore 0.28 SJR 0.2 SNIP 0.251
Scopus rating (2015): SNIP 0.219 SJR 0.201
Web of Science (2015): Indexed yes
Scopus rating (2014): SNIP 0.165 SJR 0.19
Scopus rating (2013): SNIP 0.126 SJR 0.166
ISI indexed (2013): ISI indexed no
Scopus rating (2012): SNIP 0.163 SJR 0.177
ISI indexed (2012): ISI indexed no
Scopus rating (2011): SNIP 0.201 SJR 0.155
ISI indexed (2011): ISI indexed no
Scopus rating (2010): SNIP 0.346 SJR 0.327
Original language: English
Physics and Astronomy (all)
Electronic versions:
epjconf_ilrc2016_22004.pdf
DOIs:
10.1051/epjconf/201611922004
Links:
http://www.epj-conferences.org/articles/epjconf/abs/2016/14/epjconf_ilrc2016_22004/epjconf_ilrc2016_22004.html
Source: FindIt
Source-ID: 2305483940
Publication: Research - peer-review › Conference abstract in journal – Annual report year: 2016
Delayed development of systemic immunity in preterm pigs as a model for preterm infants

Preterm neonates are highly sensitive to systemic infections in early life but little is known about systemic immune development following preterm birth. We hypothesized that preterm neonates have immature systemic immunity with distinct developmental trajectory for the first several weeks of life, relative to those born at near-term or term. Using pigs as a model, we characterized blood leukocyte subsets, antimicrobial activities and TLR-mediated cytokine production during the first weeks after preterm birth. Relative to near-term and term pigs, newborn preterm pigs had low blood leukocyte counts, poor neutrophil phagocytic rate, and limited cytokine responses to TLR1/2/5/7/9 and NOD1/2 agonists. The preterm systemic responses remained immature during the first postnatal week, but thereafter showed increased blood leukocyte numbers, NK cell proportion, neutrophil phagocytic rate and TLR2-mediated IL-6 and TNF-α production. These immune parameters remained different between preterm and near-term pigs at 2-3 weeks, even when adjusted for post-conceptional age. Our data suggest that systemic immunity follows a distinct developmental trajectory following preterm birth that may be influenced by postnatal age, complications of prematurity and environmental factors. Consequently, the immediate postnatal period may represent a window of opportunity to improve innate immunity in preterm neonates by medical, antimicrobial or dietary interventions.
Demografi hos danske ræve (Vulpes vulpes) med overvejelser af jagttrykkets betydning for aldersfordelingen

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Aalborg Zoo, Aarhus University, University of Copenhagen
Authors: Pagh, S. (Ekstern), Chriél, M. (Intern), Jensen, B. (Ekstern), Madsen, A. B. (Ekstern), Jensen, T. W. (Forskerdatabase), Hansen, M. S. (Intern)
Pages: 46-55
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Flora og Fauna
Volume: 122
Issue number: 1+2
ISSN (Print): 0015-3818
Ratings:
Web of Science (2018): Indexed yes
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Scopus rating (2000): SJR 0.472
Scopus rating (1999): SJR 0.117
Original language: English
Source: PublicationPreSubmission
Source-ID: 123798427
Publication: Research - peer-review › Journal article – Annual report year: 2016

Design, synthesis and characterization of polylysine dendrones for biomedical applications

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, University of Oslo
Authors: Mirsharghi, S. (Intern), Boas, U. (Intern), Heegaard, P. M. H. (Intern), Nyström, B. (Ekstern)
Number of pages: 126
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Place of publication: Frederiksberg C
Publisher: National Veterinary Institute, Technical University of Denmark
Original language: English
Main Research Area: Technical/natural sciences
Electronic versions:
PhD_Thesis_Sahar_Mirsharghi.pdf

Relations
Projects:
Design, synthesis and characterization of polylysine dendrones for biomedical applications
Determining the optimal number of individual samples to pool for quantification of average herd levels of antimicrobial resistance genes in Danish pig herds using high-throughput qPCR

The primary objective of this study was to determine the minimum number of individual fecal samples to pool together in order to obtain a representative sample for herd level quantification of antimicrobial resistance (AMR) genes in a Danish pig herd, using a novel high-throughput qPCR assay. The secondary objective was to assess the agreement between different methods of sample pooling. Quantification of AMR was achieved using a high-throughput qPCR method to quantify the levels of seven AMR genes (ermB, ermF, sulI, sulII, tet(M), tet(O) and tet(W)). A large variation in the levels of AMR genes was found between individual samples. As the number of samples in a pool increased, a decrease in sample variation was observed. It was concluded that the optimal pooling size is five samples, as an almost steady state in the variation was observed when pooling this number of samples. Good agreement between different pooling methods was found and the least time-consuming method of pooling, by transferring feces from each individual sample to a tube using a 10 μl inoculation loop and adding 3.5 ml of PBS, approximating a 10% solution, can therefore be used in future studies.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Section for Epidemiology, State Serum Institute
Authors: Clasen, J. (Intern), Mellerup, A. (Intern), Olsen, J. E. (Ekstern), Angen, Ø. (Ekstern), Folkesson, S. A. (Intern), Hisham Beshara Halasa, T. (Intern), Toft, N. (Intern), Birkegård, A. C. (Intern)
Number of pages: 6
Pages: 46-51
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Veterinary Microbiology
Volume: 189
ISSN (Print): 0378-1135
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.7 SJR 1.175 SNIP 1.241
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.363 SNIP 1.206
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.413 SNIP 1.21 CiteScore 2.56
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.291 SNIP 1.256 CiteScore 2.54
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.459 SNIP 1.471 CiteScore 3
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.441 SNIP 1.569 CiteScore 3.18
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.56 SNIP 1.729 CiteScore 3.27
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Development and evaluation of tailored specific real-time RT-PCR assays for detection of foot-and-mouth disease virus serotypes circulating in East Africa

Rapid, reliable and accurate diagnostic methods provide essential support to programmes that monitor and control foot-and-mouth disease (FMD). While pan-specific molecular tests for FMD virus (FMDV) detection are well established and widely used in endemic and FMD-free countries, current serotyping methods mainly rely either on antigen detection ELISAs or nucleotide sequencing approaches. This report describes the development of a panel of serotype-specific real-time RT-PCR assays (rRT-PCR) tailored to detect FMDV lineages currently circulating in East Africa. These assays target sequences within the VP1-coding region that share high intra-lineage identity, but do not cross-react with FMD viruses from other serotypes that circulate in the region. These serotype-specific assays operate with the same thermal profile as the pan-diagnostic tests making it possible to run them in parallel to produce CT values comparable to the pan-diagnostic test detecting the 3D-coding region. These assays were evaluated alongside the established pan-specific molecular test using field samples and virus isolates collected from Tanzania, Kenya and Ethiopia that had been previously characterised by nucleotide sequencing. Samples (n = 71) representing serotype A (topotype AFRICA, lineage G-I), serotype O (topotypes EA-2 and EA-4), serotype SAT 1 (topotype I (NWZ)) and serotype SAT2 (topotype IV) were correctly identified with these rRT-PCR assays. Furthermore, FMDV RNA from samples that did not contain infectious virus could still be serotyped using these assays. These serotype-specific real-time RT-PCR assays can detect and characterise FMDVs currently circulating in East Africa and hence improve disease control in this region.

General information

State: Published
Organisations: National Veterinary Institute, Section for Virology, The Pirbright Institute, Sokoine University of Agriculture, Tanzania Veterinary Laboratory Agency
Authors: Bachanek-Bankowska, K. (Ekstern), Mero, H. R. (Ekstern), Wadsworth, J. (Ekstern), Mioulet, V. (Ekstern), Sallu, R. (Ekstern), Belsham, G. (Intern), Kasanga, C. J. (Ekstern), Knowles, N. J. (Ekstern), King, D. P. (Ekstern)
Number of pages: 7
Pages: 114-120
Development of a novel real-time qPCR assay for the dual detection of canine and phocine distemper virus

In a commercial diagnostic setting streamlining and optimization is an important factor when the goal is to provide high quality diagnostic results while remaining competitive. In the PCR diagnostics unit at DTU National Veterinary Institute part of this optimization programme is to replace conventional PCR assays with real-time PCR assays to obtain a uniform assay palette. The present work describes the development of a novel real-time RT-qPCR assay for the dual detection of canine and phocine distemper virus. The assay is relevant for the future detection of outbreaks of canine distemper virus in e.g. farmed mink and wildlife and phocine distemper in seals.

A set of primers and dual labelled probe was designed based on an alignment of distemper sequences in GenBank from various species and in-house sequences from recent outbreaks in Danish farmed mink. The assay amplifies a segment of 151 bp in the Phosphoprotein (P) gene of the distemper virus genome. The dynamic range and PCR efficiency (E) was experimentally determined using 10-fold dilutions of a specially designed distemper DNA-oligo in addition to extracted RNA from clinical samples.

E of the real-time assay was shown to range between 0.95 and 1.05 when using both clinical samples and the distemper DNA-oligo. Comparing the real-time RT-PCR assay to a currently used conventional assay showed that the real-time assay detects a 102-fold further dilution of a clinical sample. Tests of distemper positive clinical samples from a wide range of different species performed in parallel with the conventional PCR assay revealed that whereas both assays detect canine and phocine distemper virus, only the conventional assay could detect the dolphin distemper variant. Furthermore it was shown that the Taqman assay does not amplify influenza, a common differential diagnosis in mink and seals.

Further testing is needed to determine the effects of PCR inhibitors in clinical samples. In addition, an elaborate panel of potential differential diagnostic agents must be tested in order to determine the assay specificity.

General information
State: Published
Organisations: National Veterinary Institute
Authors: Nielsen, L. B. (Intern), Hjulsager, C. K. (Intern), Larsen, H. (Intern)
Number of pages: 1
Publication date: 2016
Main Research Area: Technical/natural sciences
Electronic versions:
Poster_abstract.pdf
Source: PublicationPreSubmission
Source-ID: 127353865
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2016

Development of a novel real-time qPCR assay for the dual detection of canine and phocine distemper virus

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E of the real-time assay was shown to range between 0.95 and 1.05 when using both clinical samples and the distemper DNA-oligo. Comparing the real-time RT-PCR assay to a currently used conventional assay showed that the real-time assay detects a 102-fold further dilution of a clinical sample. Tests of distemper positive clinical samples from a wide range of different species performed in parallel with the conventional PCR assay revealed that whereas both assays detect canine and phocine distemper virus, only the conventional assay could detect the dolphin distemper variant. Furthermore it was shown that the Taqman assay does not amplify influenza, a common differential diagnosis in mink and seals.

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detect canine and phocine distemper virus, only the conventional assay could detect the dolphin distemper variant. Furthermore it was shown that the Taqman assay does not amplify influenza, a common differential diagnosis in mink and seals. Further testing is needed to determine the effects of PCR inhibitors in clinical samples. In addition, an elaborate panel of potential differential diagnostic agents must be tested in order to determine the assay specificity.

**General information**
State: Published
Organisations: National Veterinary Institute
Authors: Nielsen, L. B. (Intern), Hjulsager, C. K. (Intern), Larsen, H. (Intern)
Number of pages: 1
Publication date: 2016
Main Research Area: Technical/natural sciences
Electronic versions:
Poster_1.pdf
Publication: Research - peer-review › Poster – Annual report year: 2016

**Development of a sandwich ELISA for quantification of immunoglobulin G in mink blood**

A major concern amongst the Danish mink farmers is the incidence of the syndrome pre-weaning diarrhea. The syndrome causes major management issues and decreases the welfare of the mink and increases mortality in the pre-weaning period. The etiology of the syndrome is considered multifactorial as a specific cause is not fully established or understood. Adding to an increased risk of developing pre-weaning diarrhea is the fact that the mink kits are born with very low levels of circulating immunoglobulins. Rapid achievement of high levels of immunoglobulins in the bloodstream is essential for the kits early immunity and thus their resistance against pathogenic agents found in the environment.

This study describes a sandwich ELISA for quantification of the concentration of total immunoglobulin G in mink blood. The ELISA was validated with serum samples from females (n=8) and their kits (litters of 4-12). Preliminary results show that the IgG concentration among kits from the same litter was similar, while litter to litter variation was high.

**General information**
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Kopenhagen Fur
Authors: Mathiesen, R. (Intern), Chriél, M. (Intern), Struve, T. (Ekstern), Heegaard, P. M. H. (Intern)
Number of pages: 5
Publication date: 2016
Event: Abstract from 11th IFASA congress (International Fur Animal Scientific Association), Helsinki, Finland.
Main Research Area: Technical/natural sciences
Diagnostic evaluation of assays for detection of antibodies against porcine epidemic diarrhea virus (PEDV) in pigs exposed to different PEDV strains

Porcine epidemic diarrhea virus (PEDV) has caused economic losses in the Americas, Asia and Europe in recent years. Reliable serological assays are essential for epidemiological studies and vaccine evaluation. The objective of this study was to compare the ability of five enzyme-linked immunosorbent assays (ELISAs) to detect antibodies against different PEDV strains in pig serum. A total of 732 serum samples from North American or European pigs were tested. Samples included experimental samples from pigs infected with classical (G1a PEDV) or variant genogroup 1 PEDV (G1b PEDV), pandemic genogroup 2 PEDV (G2b PEDV) or non-infected controls. Field samples from herds with confirmed or unknown PEDV exposure were also used. Three indirect ELISAs based on G2b antigens (ELISAs 1, 2 and 3), a competitive ELISA based on the G2b antigen (ELISA 4) and a competitive ELISA based on the G1a antigen (ELISA 5) were compared.

Overall, the tests had a moderate agreement (κ = 0.61). G1a PEDV infected pigs were earliest detected by ELISA 3, G1b PEDV infected pigs were earliest detected by ELISAs 4 and 5 and the performance of all tests was similar for the G2b PEDV group. ELISA 1 showed the overall lowest detection on experimentally and field derived samples. Diagnostic sensitivity and specificity with a 95% probability interval were estimated to be 68.2% (62.1–74.4%) and 97.5% (95.2–99.0%) for ELISA 1, 73.7% (71.5–79.6%) and 98.4% (96.6–99.5%) for ELISA 2, 86.2% (81.1–90.6%) and 91.6% (87.7–94.8%) for ELISA 3, 78.3% (72.8–83.5%) and 99.7% (98.2–100%) for ELISA 4, and 93.5% (90.3–96.0%) and 91.2% (83.8–97.9%) for ELISA 5. Differences in detection among assays seem to be more related to intrinsic factors of an assay than to the PEDV antigen used.

General information
State: Published
Organisations: National Veterinary Institute, University of Edinburgh, Iowa State University, Innovative Diagnostics IDvet
Authors: Gerber, P. F. (Ekstern), Lelli, D. (Ekstern), Zhang, J. (Ekstern), Strandbygaard, B. (Intern), Moreno, A. (Ekstern), Lavazza, A. (Ekstern), Perulli, S. (Ekstern), Betner, A. (Intern), Comtet, L. (Ekstern), Roche, M. (Ekstern), Pourquier, P. (Ekstern), Wang, C. (Ekstern), Opriessnig, T. (Ekstern)
Pages: 87-94
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Preventive Veterinary Medicine
Volume: 135
ISSN (Print): 0167-5877
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 1.31 SJR 1.144 CiteScore 2.26
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.2 SJR 1.249 SNIP 1.361
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.282 SNIP 1.177 CiteScore 2.1
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.27 SNIP 1.407 CiteScore 2.37
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.264 SNIP 1.529 CiteScore 2.49
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.265 SNIP 1.436 CiteScore 2.45
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
Different capabilities of five ELISAs for detection of antibodies against PEDV in pigs exposed to geographically different strains

**General information**

State: Published
Organisations: National Veterinary Institute, University of Edinburgh, Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia, Iowa State University, Innovative Diagnostics IDvet
Authors: Gerber, P. (Ekstern), Lelli, D. (Ekstern), Zhang, J. (Ekstern), Strandbygaard, B. (Intern), Perulli, S. (Ekstern), Betner, A. (Intern), Comte, L. (Ekstern), Roche, M. (Ekstern), Pourquier, P. (Ekstern), Opriessnig, T. (Ekstern)
Publication date: 2016
Event: Poster session presented at 8th European Symposium of Porcine Health Management, Dublin, Ireland.
Main Research Area: Technical/natural sciences
Antibodies, Diagnostic test, PEDV
Electronic versions: Gerber_et_al.pdf
Source: PublicationPreSubmission
Source-ID: 125249085
Publication: Research - peer-review › Poster – Annual report year: 2016

Differential Analysis of the Nasal Microbiome of Pig Carriers or Non-Carriers of Staphylococcus aureus

Staphylococcus aureus is presently regarded as an emerging zoonotic agent due to the spread of specific methicillin-resistant S. aureus (MRSA) clones in pig farms. Studying the microbiota can be useful for the identification of bacteria that antagonize such opportunistic veterinary and zoonotic pathogen in animal carriers. The aim of this study was to determine whether the nasal microbiome of pig S. aureus carriers differs from that of non-carriers. The V3-V5 region of the 16S rRNA gene was sequenced from nasal swabs of 44 S. aureus carriers and 56 non-carriers using the 454 GS FLX titanium system. Carriers and non-carriers were selected on the basis of quantitative longitudinal data on S. aureus carriage in 600 pigs sampled at 20 Danish herds included in two previous studies in Denmark. Raw sequences were analysed with the BION meta package and the resulting abundance matrix was analysed using the DESeq2 package in R to identify operational taxonomic units (OTUs) with differential abundance between S. aureus carriers and non-carriers. Twenty OTUs were significantly associated to non-carriers, including species with known probiotic potential and antimicrobial effect such as lactic acid-producing isolates described among Leuconostoc spp. and some members of the Lachnospiraceae family, which is known for butyrate production. Further 5 OTUs were significantly associated to carriage, including known pathogenic bacteria such as Pasteurella multocida and Klebsiella spp. Our results show that the nasal microbiome of pigs that are not colonized with S. aureus harbours several species/taxa that are significantly less abundant in pig carriers, suggesting that the nasal microbiota may play a role in the individual predisposition to S. aureus nasal carriage in pigs. Further research is warranted to isolate these bacteria and assess their possible antagonistic effect on S. aureus for the pursuit of new strategies to control MRSA in pig farming.

**General information**

State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Danish Genome Institute, University of Copenhagen
Authors: Espinosa-Gongora, C. (Intern), Larsen, N. (Ekstern), Schonning, K. (Ekstern), Fredholm, M. (Ekstern), Guardabassi, L. (Ekstern)
Number of pages: 13
Publication date: 2016
Main Research Area: Technical/natural sciences

**Publication information**

Journal: P L o S One
Volume: 11
Issue number: 8
Article number: e0160331
ISSN (Print): 1932-6203
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.01 SJR 1.164 SNIP 1.111
Web of Science (2017): Indexed yes
OBJECTIVE: Chemotherapy-induced intestinal toxicity is a common adverse effect of cancer treatment. We hypothesized that a milk diet containing bovine colostrum (BC) would reduce intestinal toxicity in doxorubicin-treated piglets. METHODS: Study 1 investigated intestinal parameters nine days after a single dose of doxorubicin (1×75mg/m) in piglets fed bovine milk enriched with whey protein (BM). In Study 2, responses to doxorubicin treatment were investigated in piglets receiving either seven BC feedings per day (Only-BC, n=13), four BC feedings (High-BC, n=13), two BC feedings (Low-BC, n=14) or no BC (only BM, n=13). RESULTS: Doxorubicin treatment induced clinical signs of intestinal toxicity with diarrhea and weight loss, relative to controls (P<0.05). White blood cells, hexose absorptive function, plasma citrulline, weights of intestine, colon, and spleen were reduced, while gut permeability and plasma C-reactive protein (CRP) levels were increased (all P<0.05). Limited or no effects were observed for digestive enzymes, pro-inflammatory cytokines or tight-junction proteins in the intestine. Increasing BC supplementation to doxorubicin-treated piglets (Study 2) had no consistent effects on plasma CRP and citrulline levels, intestinal morphology, digestive enzymes, permeability, or proinflammatory cytokines. However, Only-BC pigs had lower diarrhea severity towards the end of the experiment (P<0.05 versus BM) and across the BC groups, intestinal toxicity was reduced (P<0.01). CONCLUSIONS: Doxorubicin-treated piglets are relevant for studying chemotherapy-induced gut toxicity. Colostrum supplementation had limited effects on doxorubicin-induced toxicity in milk-fed piglets suggesting that colostrum and a bovine milk diet enriched with whey protein provided similar chemotherapy protection of the developing intestine.
Draft Genome Sequences of Two Avian Pathogenic *Escherichia coli* Strains of Clinical Importance, E44 and E51

Avian pathogenic *Escherichia coli* strains have remarkable impacts on animal welfare and the production economy in the poultry industry worldwide. Here, we present the draft genomes of two isolates from chickens (E44 and E51) obtained from field outbreaks and subsequently investigated for their potential for use in autogenous vaccines for broiler breeders.

**General information**

State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Statens Serum Institut, South China University of Technology, University of Copenhagen
Authors: Ronco, T. (Intern), Stegger, M. (Ekstern), Andersen, P. S. (Ekstern), Pedersen, K. (Intern), Li, L. (Ekstern), Thøfner, I. C. N. (Ekstern), Olsen, R. H. (Ekstern)
Pages: 2
Publication date: 2016
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Genome Announcements
Volume: 4
Issue number: 4
Article number: e00768-16
ISSN (Print): 2169-8287
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.407 SJR 0.553 CiteScore 1.01
Scopus rating (2016): CiteScore 0.41 SJR 0.583 SNIP 0.469
Web of Science (2016): Indexed yes
Scopus rating (2015): SJR 0.591 SNIP 0.398
Scopus rating (2014): SJR 0.539 SNIP 0.344
ISI indexed (2013): ISI indexed no
Original language: English
Electronic versions:
Genome_Announc._2016_Ronco_.pdf
DOIs:
10.1128/genomeA.00768-16

**Bibliographical note**

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Source: FindIt
Source-ID: 2307096009
Publication: Research - peer-review › Journal article – Annual report year: 2016

**DTU Veterinærinstituttet udbyder tests til påvisning af antistoffer mod PRRSV og Actinobacillus pleuropneumoniae i spyt fra svin**

**General information**

State: Published
Organisations: National Veterinary Institute
Authors: Lauritsen, K. T. (Intern)
Pages: 40-40
Publication date: 2016
Main Research Area: Technical/natural sciences

**Publication information**
Dynamic changes of histone H3 marks during Caenorhabditis elegans lifecycle revealed by middle-down proteomics

We applied a middle-down proteomics strategy for large scale protein analysis during in vivo development of Caenorhabditis elegans. We characterized post-translational modifications (PTMs) on histone H3 N-terminal tails at eight time points during the C. elegans lifecycle, including embryo, larval stages (L1 to L4), dauer and L1/L4 post dauer. Histones were analyzed by our optimized middle-down protein sequencing platform using high mass accuracy tandem mass spectrometry. This allows quantification of intact histone tails and detailed characterization of distinct histone tails carrying co-occurring PTMs. We measured temporally distinct combinatorial PTM profiles during C. elegans development. We show that the doubly modified form H3K23me3K27me3, which is rare or non-existent in mammals, is the most abundant PTM in all stages of C. elegans lifecycle. The abundance of H3K23me3 increased during development and it was mutually exclusive of the active marks H3K18ac, R26me1 and R40me1, suggesting a role for H3K23me3 in silent chromatin. We observed distinct PTM profiles for normal L1 larvae and for L1-post dauer larvae, or L4 and L4 post-dauer, suggesting that histone PTMs mediate an epigenetic memory that is transmitted during dauer formation. Collectively, our data describe the dynamics of histone H3 combinatorial code during C. elegans lifecycle and demonstrate the feasibility of using middle-down proteomics to study in vivo development of multicellular organisms. This article is protected by copyright. All rights reserved.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, University of Copenhagen
Authors: Sidoli, S. (Ekstern), Vandamme, J. (Intern), Elisabetta Salcini, A. (Ekstern), Jensen, O. N. (Ekstern)
Number of pages: 13
Pages: 459-464
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Proteomics
Volume: 16
Issue number: 3
ISSN (Print): 1615-9853
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.774 SJR 1.435 CiteScore 3.42
Dynamic generalized linear models for monitoring endemic diseases: moving beyond univariate process monitoring control algorithms

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, University of Copenhagen
Early enteral feeding reduces sepsis response and neuroinflammation in a pig model of neonatal bloodstream infection

General information
State: Published
Organisations: National Veterinary Institute, Innate Immunology, University of Copenhagen
Authors: Brunse, A. (Ekstern), Worsoe, P. (Ekstern), Pors, S. E. (Ekstern), Skovgaard, K. (Intern), Sangild, P. T. (Ekstern)
Number of pages: 1
Pages: 1497-1497
Publication date: 2016
Conference: 6th congress of the european academy of paediatric societies (EAPS), Geneva, Switzerland, 21/10/2016 - 21/10/2016
Main Research Area: Technical/natural sciences

Publication information
Journal: European Journal of Pediatrics
Volume: 175
Issue number: 11
ISSN (Print): 0340-6199
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.051 SJR 0.992 CiteScore 2.11
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.908 SNIP 1.002 CiteScore 1.83
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.855 SNIP 1.134 CiteScore 1.74
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.824 SNIP 1.163 CiteScore 1.9
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.867 SNIP 1.341 CiteScore 2.1
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.792 SNIP 1.295 CiteScore 2.01
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.804 SNIP 1.189 CiteScore 2.02
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.704 SNIP 1.065
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.73 SNIP 1.006
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.688 SNIP 0.833
Scopus rating (2007): SJR 0.549 SNIP 0.818
Scopus rating (2006): SJR 0.579 SNIP 0.896
Early warning of diarrhea and pen fouling in growing pigs using sensor-based monitoring

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, University of Copenhagen
Authors: Jensen, D. B. (Ekstern), Toft, N. (Intern), Kristensen, A. R. (Ekstern)
Pages: 153-153
Publication date: 2016

Host publication information
Title of host publication: 24th International Pig Veterinary Society Congress - abstracts book
Place of publication: Dublin, Ireland
Publisher: Royal Dublin Society
Article number: O-HHM3-011
Main Research Area: Technical/natural sciences
Conference: 24th International Pig Veterinary Society (IPVS) Congress, Dublin, Ireland, 07/06/2016 - 07/06/2016
Electronic versions:
Book of abstracts
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2016

Economic analysis of activities to prevent foot and mouth disease in Denmark
The latest foot and mouth disease (FMD) epidemic in Denmark dates back to 1982-1983. Hence, Denmark has not experienced an FMD outbreak in more than 30 years. Still this disease poses a serious threat either as a risk of introduction and spread in Denmark or as a risk of a ban on Danish export of pigs, pork, cattle, beef and milk products due to an outbreak in another country within the EU. It is estimated that a middle sized outbreak of FMD would cost around € 1 billion. It is evident that even though the probability of introducing FMD is very low the consequences are devastating for the agricultural sector and society because the expected costs are so enormous. Therefore, the industry and the public authority have implemented a number of mitigating and preventive activities. The costs of FMD and swine fever related activities in Denmark in 2013 were estimated to be approximately € 32 million. The purpose of the present study is to estimate how changes in resources allocated to the FMD related activities may affect the costs of an FMD outbreak. Nine alternative scenarios describing changes in the contingency plan were formulated by a group of experts from the livestock industry, universities and public authorities. A modified version of Davis Animal Disease Simulation model (DADS version 0.05) was used to estimate costs of FMD outbreaks in each of these alternative scenarios. The modified and updated version by the technical university of Denmark (DTU) is called DTU-DADS. The model simulations indicate that some changes in risk-reducing activities may significantly affect expected costs of an outbreak while other changes have no effect. Our results suggest that increased efforts in terms of efficiently restricting low-risk contacts between farms, such as non-professional visitors and trucks, might reduce the size and costs of an FMD outbreak. In addition, simulations indicate that current resources allocated to depopulation and surveillance could – but only to some extent – be reduced without affecting the size and costs of an outbreak.

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology
Authors: Denver, S. (Ekstern), Alban, L. (Intern), Boklund, A. (Intern), Hisham Beshara Halasa, T. (Intern), Houe, H. (Ekstern), Mortensen, S. (Ekstern), Rattenborg, E. (Ekstern), Tamstorf, T. (Ekstern), Zobbe, H. (Ekstern), Christensen, T. (Ekstern)
Number of pages: 5
Pages: 479-483
Publication date: 2016

Host publication information
Effect of Bacteriophages on the Growth of Flavobacterium psychrophilum and Development of Phage-Resistant Strains

The controlling effect of single and multiple phages on the density of Flavobacterium psychrophilum at different initial multiplicity of infection (MOI) was assessed in batch cultures to explore the potential for phage-based treatment of this important fish pathogen. A high initial phage concentration (MOI = 0.3–4) was crucial for efficient viral lysis, resulting in a 104–105-fold reduction of phage-sensitive cells (both single phages and phage cocktails), which was maintained throughout the incubation (>10 days). Following cell lysis, regrowth of phage-resistant strains was examined and resistant strains were isolated for further characterization. The application of a mathematical model allowed simulation of phage-host interactions and resistance development, confirming indications from strain isolations that phage-sensitive strains dominated the regrowing population (>99.8 %) at low MOI and phage-resistant strains (>87.8 %) dominated at high MOI. A cross-infectivity test covering 68 isolated strains and 22 phages resulted in 23 different host susceptibility patterns, with 20 of the isolates being resistant to all the applied phages. Eleven isolated strains with different susceptibility patterns had lower growth rates (0.093 to 0.31 h⁻¹) than the host strain (0.33 h⁻¹), while 10 of 14 examined strains had lost the ability to take up specific substrates as shown by BIOLOG profiles. Despite increased selection for phage resistance at high MOI, the results emphasize that high initial MOI is essential for fast and effective control of F. psychrophilum infection and suggest that the small populations of resistant clones had reduced competitive abilities relative to the sensitive ancestral strain.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Copenhagen
Authors: Christiansen, R. H. (Intern), Madsen, L. (Intern), Dalsgaard, I. (Intern), Castillo, D. (Ekstern), Kalatzis, P. G. (Ekstern), Middelboe, M. (Ekstern)
Pages: 845-859
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Microbial Ecology
Volume: 71
ISSN (Print): 0095-3628
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.112 SJR 1.272 CiteScore 3.54
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.55 SJR 1.325 SNIP 1.108
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.348 SNIP 1.015 CiteScore 3.13
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.329 SNIP 1.15 CiteScore 3.08
BFI (2013): BFI-level 2
Effekten af stegetid og -temperatur på kvaliteten af spiseolier

General information
State: Published
Organisations: National Food Institute, Research Group for Bioactives – Analysis and Application, National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Division of Risk Assessment and Nutrition, Technical University of Denmark
Authors: Jacobsen, C. (Intern), Holmer, I. (Intern), Simony Jensen, J. (Ekstern), Stampe Madsen, S. (Ekstern), Lund-Larsen, M. (Ekstern), Mejborn, H. (Intern)
Number of pages: 42
Publication date: 2016

Publication information
Place of publication: Søborg
Publisher: DTU Fødevareinstituttet, Danmarks Tekniske Universitet
ISBN (Electronic): 978-87-93109-76-6
Original language: Danish
Main Research Area: Technical/natural sciences

Electronic versions:
Efficacy of ivermectin against gastrointestinal nematodes of cattle in Denmark evaluated by different methods for analysis of faecal egg count reduction

The efficacy of ivermectin (IVM) against gastrointestinal nematodes in Danish cattle was assessed by faecal egg count reduction test (FECRT). Six cattle farms with history of clinical parasitism and avermectin use were included. On the day of treatment (Day 0), 20 naturally infected calves per farm (total n = 120) were stratified by initial faecal egg counts (FEC) and randomly allocated to a treatment group dosed with 0.2 mg IVM kg\(^{-1}\) body weight s.c. (IVM; n = 10) or an untreated control group (CTL; n = 10). Individual FEC were obtained at Day 0 and Day 14 post-treatment and pooled faeces by group were cultured to isolate L3 for detection of Ostertagia ostertagi and Cooperia oncophora by qPCR. Treatment efficacies were analysed using the recommended WAAVP method and two open-source statistical procedures based on Bayesian modelling: ‘eggCounts’ and ‘Bayescount’. A simulation study evaluated the performance of the different procedures to correctly identify FEC reduction percentages of simulated bovine FEC data representing the observed real data. In the FECRT, reduced IVM efficacy was detected in three farms by all procedures using data from treated animals only, and in one farm according to the procedures including data from treated and untreated cattle. Post-treatment, O. ostertagi and C. oncophora L3 were detected by qPCR in faeces of treated animals from one and three herds with declared reduced IVM efficacy, respectively. Based on the simulation study, all methods showed a reduced performance when FEC aggregation increased post-treatment and suggested that a treatment group of 10 animals is insufficient for the FECRT in cattle. This is the first report of reduced anthelmintic efficacy in Danish cattle and warrants the implementation of larger surveys. Advantages and caveats regarding the use of Bayesian modelling and the relevance of including untreated cattle in the FECRT are discussed.

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, University of Copenhagen, Technical University of Denmark
Pages: 241-370
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: International Journal for Parasitology: Drugs and Drug Resistance
Volume: 6
Issue number: 3
ISSN (Print): 2211-3207
Ratings:
Web of Science (2018): Indexed yes
Scopus rating (2017): SNIP 1.318 SJR 1.556 CiteScore 3.81
Web of Science (2017): Indexed Yes
Scopus rating (2016): CiteScore 4.87 SJR 1.836 SNIP 1.489
Web of Science (2016): Indexed yes
Scopus rating (2015): SJR 1.688 SNIP 1.283 CiteScore 4.09
Web of Science (2015): Indexed yes
Scopus rating (2014): SJR 1.142 SNIP 1.243 CiteScore 3.49
Scopus rating (2013): SJR 1.252 SNIP 1.191 CiteScore 2.67
Scopus rating (2012): SJR 0.638 SNIP 0.433 CiteScore 1.75
Original language: English
Electronic versions:
1_s2.0_S2211320716300604_main.pdf
1_s2.0_S2211320716300604_main.pdf
DOIs:
10.1016/j.jipddr.2016.10.004
Publication: Research - peer-review › Journal article – Annual report year: 2016

Engineering a CTL-Tailored Replicon RNA Vaccine against PRRSV
The development of vaccines against porcine reproductive and respiratory syndrome virus (PRRSV) has been hampered by the high mutation rate and the multiple immunoevasive strategies of the virus. With the overall aim of designing a broad coverage vaccine that induces an effective CTL response against PRRSV, we have used a bioinformatics approach to identify common PRRSV type 2 epitopes predicted to react broadly with
predominant swine MHC (SLA) alleles. All possible 9- and 10-mer peptides derived from 104 wild-type strains were analyzed in silico for their predicted binding affinity to 3 common SLA class I alleles and ranked according to genomic conservation and SLA binding coverage. Of the 53 top-ranked peptides, 33 were verified in vitro as high affinity binders. Polypeptide gene cassettes of these peptides, flanked by an upstream ubiquitin sequence and a downstream FLAG tag, were cloned into a classical swine fever virus (CSFV)-derived replicon vector. Virus replicon particles (VRP) were rescued by transfection of a complementing cell line with replicon RNA. Polypeptide expression and subsequent proteasomal degradation was confirmed indirectly by increased FLAG-tagged protein detection in the presence of a proteasome inhibitor.

Finally, a vaccination-challenge experiment using 18 SLA-matched pigs is currently being conducted until July 2016 in which a test group and a control group are being vaccinated twice with VRPs expressing PRRSV epitopes and non-sense control epitopes, respectively, before challenged with live wild type PRRSV. The induced epitope specific cell-mediated immune responses are being monitored by ELISPOT, flow cytometry and cytotoxicity assays, and the degree of protection against infection will be characterized by qPCR and antibody analysis. The results will be available for IVIS. This study exemplifies how bioinformatics epitope prediction, recombinant SLA molecules and RNA virus replicon design can be used to engineer a replicating non-propagating vaccine tailored to deliver conserved and immunogenic CTL epitopes.

Epidemiological cut-off values for Flavobacterium psychrophilum MIC data generated by a standard test protocol
Epidemiological cut-off values were developed for application to antibiotic susceptibility data for Flavobacterium psychrophilum generated by standard CLSI test protocols. The MIC values for ten antibiotic agents against Flavobacterium psychrophilum were determined in two laboratories. For five antibiotics, the data sets were of sufficient quality and quantity to allow the setting of valid epidemiological cut-off values. For these agents, the cut-off values, calculated by the application of the statistically based normalized resistance interpretation method, were ≤16 mg L-1 for erythromycin, ≤0.025 mg L-1 for florfenicol, ≤0.025 mg L-1 for oxolinic acid (OXO), ≤0.125 mg L-1 for oxytetracycline and ≤20 (1/19) mg L-1 for trimethoprim/sulphamethoxazole. For ampicillin and amoxicillin, the majority of putative wild-type observations were ‘off scale’, and therefore, statistically valid cut-off values could not be calculated. For ormetoprim/sulphadimethoxine, the data were excessively diverse and a valid cut-off could not be determined. For flumequine, the putative wild-type data were extremely skewed, and for enrofloxacin, there was inadequate separation in the MIC values for putative wild-type and non-wild-type strains. It is argued that the adoption of OXO as a class representative for the quinolone group would be a valid method of determining susceptibilities to these agents.
Estimating sensitivity and specificity of a PCR for boot socks to detect Campylobacter in broiler primary production using Bayesian latent class analysis

The present study compares three different assays for sample collection and detection of Campylobacter spp. in broiler flocks, based on (i) the collection of faecal samples from intestinal organs (caecum), (ii) individual faecal droppings collected from the bedding and (iii) faecal material collected by socks placed on the outside of a pair of boots (boot socks) and used for walking around in the flock. The two first methods are examined for Campylobacter using a culture method (ISO-10272-2:2006), while the boot socks are tested using PCR. The PCR-assay is a genus specific multiplex PCR with primers targeting 16S rDNA in Campylobacter and primers targeting Yersinia ruckerii. Sixty-seven broiler flocks from Austria and 83 broiler flocks from Denmark were included in this prospective study and 89 of these were found to be positive in at least one method (AT: 49 samples, DK: 40 samples) whereas 61 of these were negative in all assays. In Austria samples for the three assays were collected simultaneously, which facilitates a direct comparison of the diagnostic test performance. In Denmark, however, boot socks and faecal droppings were collected three days before slaughter while
caecum samples were collected at slaughter. The results were evaluated in the absence of a gold standard using a
Bayesian latent class model. Austrian results showed higher sensitivity for PCR detection in sock samples (0.98; Bayesian
credible interval (BCI) [0.93-1]) than for culture of faecal droppings (0.86; BCI [0.76-0.91]) or caecal samples (0.92; BCI
[0.85-0.97]). The potential impact of Campylobacter introduction within the final three days before slaughter was observed
in Denmark, where four flocks were tested negative three days before slaughter, but were detected positive at the
slaughterhouse. Therefore the model results for the PCR sensitivity (0.88; BCI [0.83-0.97]) and cultural ISO-method in
faecal samples (0.84; BCI [0.76-0.92]) are lower than for caecal samples (0.93; BCI [0.85-0.98]). In our study, PCR
detection on boot sock samples is more sensitive than conventional culture. In view of the advantage of rapid results
before slaughter and low costs for sampling, especially in combination with existing Salmonella surveillance systems (just
another pair of boot socks needed), this method-matrix combination could be a valuable surveillance tool in the broiler
primary production.

**General information**

State: Published
Organisations: National Veterinary Institute, Austrian Agency for Health and Food Safety
Authors: Matt, M. (Ekstern), Nordentoft, S. (Intern), Ian, K. (Ekstern), Thomas, P. (Ekstern), Heimo, L. (Ekstern), Sandra,
J. (Ekstern), Stüger, H. P. (Ekstern)
Pages: 51-57
Publication date: 2016
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Preventive Veterinary Medicine
Volume: 128
ISSN (Print): 0167-5877
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 1.31 SJR 1.144 CiteScore 2.26
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.2 SJR 1.249 SNIP 1.361
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.282 SNIP 1.177 CiteScore 2.1
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.27 SNIP 1.407 CiteScore 2.37
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.264 SNIP 1.529 CiteScore 2.49
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.265 SNIP 1.436 CiteScore 2.45
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.194 SNIP 1.295 CiteScore 2.24
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.156 SNIP 1.284
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.032 SNIP 1.338
Web of Science (2009): Indexed yes
Evaluating prediction strategies for identification of T cell responsive mutation-derived neoepitopes in cancer

Increasing evidences point to an important role of mutation-derived antigens in immune recognition of cancer. Current strategies for prediction of immunogenic neoepitopes results in large personalized peptide libraries, but only a minority (< 1%) elicit T cell responses at detectable levels. Neoepitopes are of potential valuable as predictors of response to therapy and targets for personalized immunotherapeutic approached. Consequently, there is an unmet need to understand the rules identifying immunogenic neoepitopes. Both tumor mutation mapping via exome sequencing and mass-spectrometry-based elution for MHC class I presented peptides has been applied in different studies, combined with RNA sequencing to determine the expression level of relevant transcripts. Additionally, neoepitopes may be defined based on either autologeous tumor cell lines or snapfrozen tumor material. We present here a study in which all the above mentioned strategies are assessed in three melanoma patients. Predicted large peptide libraries matching the HLA expression of the patients was identified and selected based on any of the strategies given above. This resulted in a total of ~3000 peptides for the three patients. We investigated the T cell recognition of these personalized peptide libraries using a new technology based on DNA-barcode labeled MHC multimers to detect multiple, potentially > 1000, different neoepitope specific T cell populations in a single sample. Through this unbiased comparison, we evaluate selection strategies for prediction of immunogenic cancer-associated neoepitopes, and identify rules for precise prediction. Precise prediction is essential for future application of neoepitopes both as predictors of responses to therapy and immunotherapeutic targets.
Evaluating prediction strategies for identification of T cell responsive mutation-derived neoepitopes in cancer

Increasing evidences point to an important role of mutation-derived antigens in immune recognition of cancer. Current strategies for prediction of immunogenic neoepitopes results in large personalized peptide libraries, but only a minority (<1%) elicit T cell responses at detectable levels. Neoepitopes are of potential valuable as predictors of response to therapy and targets for personalized immunotherapeutic approached. Consequently, there is an unmet need to understand the rules identifying immunogenic neoepitopes. Both tumor mutation mapping via exome sequencing and mass-spectrometry-based elution for MHC class I presented peptides has been applied in different studies, combined with RNA sequencing to determine the expression level of relevant transcripts. Additionally, neoepitopes may be defined based on either autologuous tumor cell lines or snapfrozen tumor material. We present here a study in which all the above mentioned strategies are assessed in three melanoma patients. Predicted large peptide libraries matching the HLA expression of the patients was identified and selected based on any of the strategies given above. This resulted in a total of ~3000 peptides for the three patients. We investigated the T cell recognition of these personalized peptide libraries using a new technology based on DNA-barcode labeled MHC multimers to detect multiple, potentially >1000, different neoepitope specific T cell populations in a single sample. Through this unbiased comparison, we evaluate selection strategies for prediction of immunogenic cancer-associated neoepitopes, and identify rules for precise prediction. Precise prediction is essential for future application of neoepitopes both as predictors of responses to therapy and immunotherapeutic targets.

General Information
State: Published
Organisations: National Veterinary Institute, Virology, Department of Bio and Health Informatics, Cancer Genomics, Immunoinformatics and Machine Learning, T-cells & Cancer, Philochem AG, Technical University of Denmark, University Hospital Herlev
Pages: 862-862
Publication date: 2016
Conference: ICI 2016 International Congress of Immunology, Melbourne, Australia, 21/08/2016 - 21/08/2016
Main Research Area: Technical/natural sciences

Publication Information
Journal: European Journal of Immunology
Volume: 46
Issue number: Suppl. 1
ISSN (Print): 0014-2980
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.59 SJR 2.206 SNIP 0.92
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.61 SJR 2.525 SNIP 0.927
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.588 SNIP 0.965 CiteScore 3.85
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.672 SNIP 0.972 CiteScore 3.83
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 2.876 SNIP 1.05 CiteScore 4.3
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 2.989 SNIP 1.063 CiteScore 4.62
Evaluation of temporal surveillance system sensitivity and freedom from bovine viral diarrhea in Danish dairy herds using scenario tree modelling

The temporal sensitivity of the surveillance system (TemSSe) for Bovine Viral Diarrhea (BVD) in Danish dairy herds was evaluated. Currently, the Danish antibody blocking ELISA is used to test quarterly bulk tank milk (BTM). To optimize the surveillance system as an early warning system, we considered the possibility of using the SVANOVIR ELISA, as this test has been shown to detect BVD-positive herds earlier than the blocking ELISA in BTM tests. Information from data (2010) and outputs from two published stochastic models were fed into a stochastic scenario tree to estimate the TemSSe. For that purpose we considered: the risk of BVD introduction into the dairy population, the ELISA used and the high risk period (HRP) from BVD introduction to testing (at 90 or 365 days). The effect of introducing one persistently infected (PI) calf or one transiently infected (TI) milking cow into 1 (or 8) dairy herd(s) was investigated. Additionally we estimated the confidence in low (PLow) herd prevalence (}
Evidence for a dual function of monocyte-derived mononuclear phagocytes during chronic intestinal inflammation
Mononuclear phagocytes derived from tissue-infiltrating monocytes play diverse roles in immunity, ranging from pathogen killing to immune regulation. We and others showed that, upon recruitment to the intestinal mucosa, the differentiation of Ly6Chi monocytes into phagocytes with anti- versus pro-inflammatory phenotypes can be shaped by the steady state versus inflammatory local tissue environment. However the in vivo functions of these monocyte-derived phagocytes (MDP) remain poorly understood. Using the T cell transfer colitis model, we now show that MDP represent more than 85% of the total antigen presenting cells pool in the inflamed intestinal mucosa. However, surprisingly, mice deficient for the chemokine receptor CCR2, which exhibit highly decreased amounts of intestinal MDP, develop an intestinal pathology similar to their wild type littersmates. Preliminary experiments using the anti-CD40 colitis model suggest a dual and time-restricted contribution of MDP during the development and healing phases of the disease.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology
Expanding specificity of class I restricted CD8⁺ T cells for viral epitopes following multiple inoculations of swine with a human adenovirus vectored foot-and-mouth disease virus (FMDV) vaccine

The immune response to the highly acute foot-and-mouth disease virus (FMDV) is routinely reported as a measure of serum antibody. However, a critical effector function of immune responses combating viral infection of mammals is the cytotoxic T lymphocyte (CTL) response mediated by virus specific CD8 expressing T cells. This immune mechanism arrests viral spread by killing virus infected cells before new, mature virus can develop. We have previously shown that infection of swine by FMDV results in a measurable CTL response and have correlated CTL killing of virus-infected cells with specific class I major histocompatibility complex (MHC) tetramer staining. We also showed that a modified replication defective human adenovirus 5 vector expressing the FMDV structural proteins (Ad5-FMDV-T vaccine) targets the induction of a CD8(+) CTL response with a minimal humoral response. In this report, we show that the specificity of the CD8(+) T cell response to Ad5-FMDV-T varies between cohorts of genetically identical animals. Further, we demonstrate epitope specificity of CD8(+) T cells expands following multiple immunizations with this vaccine.

General information
State: Published
Organisations: Department of Systems Biology, Center for Biological Sequence Analysis, National Veterinary Institute, Section for Immunology and Vaccinology, Technical University of Denmark, Agricultural Research Service, University of Vermont, University of Copenhagen
Authors: Pedersen, L. E. (Ekstern), Patch, J. R. (Ekstern), Kenney, M. (Ekstern), Glabman, R. A. (Ekstern), Nielsen, M. (Intern), Jungersen, G. (Intern), Buus, S. (Ekstern), Golde, W. T. (Ekstern)
Number of pages: 9
Pages: 59-67
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Veterinary Immunology and Immunopathology
Volume: 181
ISSN (Print): 0165-2427
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 0.71 SJR 0.68 CiteScore 1.7
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 1.63 SJR 0.742 SNIP 0.708
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 0.862 SNIP 0.749 CiteScore 1.67
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 0.777 SNIP 0.718 CiteScore 1.6
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 0.834 SNIP 0.797 CiteScore 1.89
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 0.841 SNIP 0.913 CiteScore 2.15
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Experimental infection of piglets with an early European strain of PED virus and a recent US PEDV strain

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Lohse, L. (Intern), Krog, J. S. (Intern), Strandbygaard, B. (Intern), Rasmussen, T. B. (Intern), Kjær, J. (Intern), Belsham, G. (Intern), Bøtner, A. (Intern)
Publication date: 2016
Event: Poster session presented at 8th European Symposium of Porcine Health Management, Dublin, Ireland.
Main Research Area: Technical/natural sciences
Electronic versions:
Poster_IPVS2016_PED.pdf
Source: PublicationPreSubmission
Source-ID: 125249116
Publication: Research - peer-review › Poster – Annual report year: 2016

Experimental pig-to-pig transmission study with a recent European African Swine Fever virus isolate

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Section for Virology
Experimental Treatment of Ebola Virus Disease with TKM-130803: A Single-Arm Phase 2 Clinical Trial

BACKGROUND:
TKM-130803, a small interfering RNA lipid nanoparticle product, has been developed for the treatment of Ebola virus disease (EVD), but its efficacy and safety in humans has not been evaluated.

METHODS AND FINDINGS:
In this single-arm phase 2 trial, adults with laboratory-confirmed EVD received 0.3 mg/kg of TKM-130803 by intravenous infusion once daily for up to 7 d. On days when trial enrolment capacity was reached, patients were enrolled into a concurrent observational cohort. The primary outcome was survival to day 14 after admission, excluding patients who died within 48 h of admission. After 14 adults with EVD had received TKM-130803, the pre-specified futility boundary was reached, indicating a probability of survival to day 14 of ≤0.55, and enrolment was stopped. Pre-treatment geometric mean Ebola virus load in the 14 TKM-130803 recipients was 2.24 × 10^9 RNA copies/ml plasma (95% CI 7.52 × 10^8, 6.66 × 10^9). Two of the TKM-130803 recipients died within 48 h of admission and were therefore excluded from the primary outcome analysis. Of the remaining 12 TKM-130803 recipients, nine died and three survived. The probability that a TKM-130803 recipient who survived for 48 h will subsequently survive to day 14 was estimated to be 0.27 (95% CI 0.06, 0.58). TKM-130803 infusions were well tolerated, with 56 doses administered and only one possible infusion-related reaction observed. Three patients were enrolled in the observational cohort, of whom two died.

CONCLUSIONS:
Administration of TKM-130803 at a dose of 0.3 mg/kg/d by intravenous infusion to adult patients with severe EVD was not shown to improve survival when compared to historic controls.

TRIAL REGISTRATION:
Pan African Clinical Trials Registry PACTR201501000997429.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Number of pages: 19
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: PLOS Medicine
Volume: 13
Issue number: 4
Article number: e1001997
ISSN (Print): 1549-1277
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 3.163 SJR 5.914 CiteScore 8.59
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Explanation and Elaboration Document for the STROBE-Vet Statement: Strengthening the Reporting of Observational Studies in Epidemiology - Veterinary Extension

The STROBE (Strengthening the Reporting of Observational Studies in Epidemiology) statement was first published in 2007 and again in 2014. The purpose of the original STROBE was to provide guidance for authors, reviewers and editors to improve the comprehensiveness of reporting; however, STROBE has a unique focus on observational studies. Although much of the guidance provided by the original STROBE document is directly applicable, it was deemed useful to map those statements to veterinary concepts, provide veterinary examples and highlight unique aspects of reporting in veterinary observational studies. Here, we present the examples and explanations for the checklist items included in the STROBE-Vet Statement. Thus, this is a companion document to the STROBE-Vet Statement Methods and process document, which describes the checklist and how it was developed.

General information
State: Published
Organisations: National Veterinary Institute, National Food Institute, Research Group for Genomic Epidemiology
Pages: 662-698
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Zoonoses and Public Health
Volume: 63
Extraction and analysis of signatures from the Gene Expression Omnibus by the crowd

Gene expression data are accumulating exponentially in public repositories. Reanalysis and integration of themed collections from these studies may provide new insights, but requires further human curation. Here we report a crowdsourcing project to annotate and reanalyse a large number of gene expression profiles from Gene Expression Omnibus (GEO). Through a massive open online course on Coursera, over 70 participants from over 25 countries identify and annotate 2,460 single-gene perturbation signatures, 839 disease versus normal signatures, and 906 drug perturbation signatures. All these signatures are unique and are manually validated for quality. Global analysis of these signatures confirms known associations and identifies novel associations between genes, diseases and drugs. The manually curated signatures are used as a training set to develop classifiers for extracting similar signatures from the entire GEO repository. We develop a web portal to serve these signatures for query, download and visualization.

General information

State: Published
Organisations: National Veterinary Institute, Section for Virology

Number of pages: 11
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information

Journal: Nature Communications
Volume: 7
Article number: 12846
ISSN (Print): 2041-1723
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 12.41 SJR 6.582 SNIP 2.912
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 11.8 SJR 6.414 SNIP 2.855
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 6.287 SNIP 2.86 CiteScore 11.23
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 6.41 SNIP 3.034 CiteScore 10.77
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 6.206 SNIP 2.797 CiteScore 9.85
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
Scopus rating (2012): SJR 5.866 SNIP 2.829 CiteScore 8.32
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
Scopus rating (2011): SJR 3.137 SNIP 1.825 CiteScore 4.44
ISI indexed (2011): ISI indexed no
Factors associated with usage of antimicrobials in commercial mink (Neovison vison) production in Denmark

The American mink (Neovison vison) is used for commercial fur production in Denmark. In recent years, antimicrobial prescription for Danish mink has been increasing. In this study, the patterns and trends in antimicrobial use in mink were described and a multi-variable variance analysis was carried out with the objective of identifying risk factors for antimicrobial use on herd level. The study was based on register data for 2007-2012. Information on antimicrobial use was obtained from the national database VetStat, monitoring all medicinal products used for animals on prescription level. Data on microbiological feed quality was obtained from the Voluntary Feed Control under the Mink producers Organization, and data on herd size and the relation between farm and feed producer was obtained from the registers at Kopenhagen Fur, based on yearly reporting from the mink producers. Descriptive analysis showed a clear significant effect of season on antimicrobial use, with a peak in "treatment proportions", TP (defined daily doses per kg biomass-days) in May, around the time of whelping, and a high level in the following months. In autumn, a minor peak in antimicrobial use occurred throughout the study period. From 2007 to 2011, a 102% increase in annual antimicrobial TP was noted; on herd level, the increase was associated with an increasing frequency of prescription, and a decrease in the amounts prescribed in months with prescription. A binomial model showed that on herd level, the annual number of months with antimicrobial prescription was significantly (p<0.01) affected by feed producer, veterinarian, disease (specific laboratory diagnosis) infection, herd size and year, with an interaction between feed producer and year. A log-normal model showed that in months with antimicrobial use, the TP on herd level was significantly (p<0.001) affected by year, month (season), feed producer, feed quality score, veterinarian, herd size and laboratory confirmed diagnosis of specific infections; additionally the interaction terms year×feed producer and herd size×month were significant (p<0.001). In conclusion, antimicrobial use on herd level was significantly associated with the microbiological food quality, the feed producer, and the veterinarian. The prescription patterns varied significantly between veterinarians, and some veterinarians were associated with both larger and more frequent prescriptions of antimicrobials at herd level. Herd size is associated with different prescription patterns. Finally, infection with Pseudomonas aeruginosa, astrovirus, influenza virus and Salmonella spp. was associated with an increase in antimicrobial use.

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Department of Applied Mathematics and Computer Science, Statistics and Data Analysis, Kopenhagen Fur
Authors: Jensen, V. F. (Intern), Sommer, H. M. (Intern), Struve, T. (Ekstern), Clausen, J. (Ekstern), Chriél, M. (Intern)
Pages: 170-182
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Preventive Veterinary Medicine
Volume: 126
ISSN (Print): 0167-5877
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 1.31 SJR 1.144 CiteScore 2.26
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.2 SJR 1.249 SNIP 1.361
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.282 SNIP 1.177 CiteScore 2.1
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Fava bean feed reduces sensitivity of PCV2-PCR on oral fluids

General information
Findings from the surveillance of avian influenza in wild birds and poultry in Denmark

Avian influenza (AI) is a highly contagious disease that can affect all bird species. The clinical signs include respiratory disease, lethargy, drop in egg production, neurological signs, hemorrhages in shanks, swollen wattles, combs and eyes, and mortality. The severity of disease depends on the virus strain and species of bird, and varies from a subclinical to a highly pathogenic form with up to 100% mortality within 48 hours. AI is of high economic importance for the poultry production worldwide. Elimination of the disease is a common goal, and in EU, the disease is mainly controlled by surveillance and stamping out procedures.

First characterization of avian influenza viruses from Greenland 2014

In late February 2014, unusually high numbers of wild birds, thick-billed murre (Uria lomvia), were found dead at the coast of South Greenland. To investigate the cause of death, 45 birds were submitted for laboratory examinations in Denmark. Avian influenza viruses (AIVs) with subtypes H11N2 and low pathogenic (LP) H5N1 were detected in some of the birds. Characterization of the viruses by full-genome sequencing revealed that all the gene segments belonged to the North American lineage of AIVs.

The seemingly sparse and mixed subtype occurrence of LP AIVs in these birds, in addition to an emaciated appearance of birds, suggests that the murre die-off was not due to infection with AIV, but could be the mere cause of sparse food availability or stormy weather. Here we present the first characterization of AIVs isolated in Greenland, and our results support the idea that wild birds in Greenland may be involved in the movement of AIV between North America and Europe.
First evidence of infectious hematopoietic necrosis virus (IHNV) in the Netherlands

In spring 2008, infectious hematopoietic necrosis virus (IHNV) was detected for the first time in the Netherlands. The virus was isolated from rainbow trout, Oncorhynchus mykiss (Walbaum), from a put-and-take fishery with angling ponds. IHNV is the causative agent of a serious fish disease, infectious hematopoietic necrosis (IHN). From 2008 to 2011, we diagnosed eight IHNV infections in rainbow trout originating from six put-and-take fisheries (symptomatic and asymptomatic fish), and four IHNV infections from three rainbow trout farms (of which two were co-infected by infectious pancreatic necrosis virus, IPNV), at water temperatures between 5 and 15 °C. At least one farm delivered trout to four of these eight IHNV-positive farms. Mortalities related to IHNV were mostly <40%, but increased to nearly 100% in case of IHNV and IPNV co-infection. Subsequent phylogenetic analysis revealed that these 12 isolates clustered into two different monophyletic groups within the European IHNV genogroup E. One of these two groups indicates a virus-introduction event by a German trout import, whereas the second group indicates that IHNV was already (several years) in the Netherlands before its discovery in 2008.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Wageningen University & Research, Friedrich Loeffler Institute, Netherlands Food and Consumer Product Safety Authority
Number of pages: 9
Pages: 971-979
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Fish Diseases
Volume: 39
Issue number: 8
ISSN (Print): 0140-7775
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.82
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.12
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 1.71
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 1.99
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 1.74
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 1.7
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
First international collaborative study to evaluate rabies antibody detection method for use in monitoring the effectiveness of oral vaccination programmes in fox and raccoon dog in Europe

The most effective and sustainable method to control and eliminate rabies in wildlife is the oral rabies vaccination (ORV) of target species, namely foxes and raccoon dogs in Europe. According to WHO and OIE, the effectiveness of oral vaccination campaigns should be regularly assessed via disease surveillance and ORV antibody monitoring. Rabies antibodies are generally screened for in field animal cadavers, whose body fluids are often of poor quality. Therefore, the use of alternative methods such as the enzyme-linked immunosorbent assay (ELISA) has been proposed to improve reliability of serological results obtained on wildlife samples. We undertook an international collaborative study to determine if the commercial BioPro ELISA Rabies Ab kit is a reliable and reproducible tool for rabies serological testing. Our results reveal that the overall specificity evaluated on naïve samples reached 96.7%, and the coefficients of concordance obtained for fox and raccoon dog samples were 97.2% and 97.5%, respectively. The overall agreement values obtained for the four marketed oral vaccines used in Europe were all equal to or greater than 95%. The coefficients of concordance obtained by laboratories ranged from 87.2% to 100%. The results of this collaborative study show good robustness and reproducibility of the BioPro ELISA Rabies Ab kit.

General information
State: Published
Organisations: National Veterinary Institute
Pages: 77-85
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Virological Methods
Volume: 238
ISSN (Print): 0166-0934
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.817 SJR 0.858 CiteScore 1.82
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.873 SNIP 0.729 CiteScore 1.78
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.87 SNIP 0.802 CiteScore 1.68
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.898 SNIP 0.933 CiteScore 1.87
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.866 SNIP 0.9 CiteScore 1.99
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.873 SNIP 0.929 CiteScore 2.08
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.908 SNIP 0.987 CiteScore 2.23
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.91 SNIP 1.001
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.973 SNIP 1.059
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.926 SNIP 1.072
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 0.963 SNIP 1.025
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.886 SNIP 1.073
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.873 SNIP 1.021
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.723 SNIP 1.079
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.759 SNIP 1.012
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.714 SNIP 1.058
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.755 SNIP 0.948
Scopus rating (2000): SJR 0.628 SNIP 0.899
Scopus rating (1999): SJR 0.635 SNIP 0.836
Original language: English
ELISA, collaborative study, oral vaccination campaigns, rabies, rabies antibodies
DOIs:
10.1016/j.jviromet.2016.10.006
Source: FindIt
Source-ID: 2347626002
Publication: Research - peer-review › Journal article – Annual report year: 2016
Foot-and-mouth disease virus capsid proteins; analysis of protein processing, assembly and utility as vaccines

Foot-and-mouth disease (FMD) remains one of the most economically important infectious diseases of production animals globally. The infection is caused by foot-and-mouth disease virus (FMDV), a member of the picornavirus family. The positive sense RNA genome of the virus includes a single, large, open reading frame that encodes a polyprotein. The intact polyprotein is never observed as it is processed, both during and after translation, to 15 different mature proteins plus a variety of precursors. The FMDV capsid protein precursor, P1-2A, is cleaved by the virus encoded 3C protease (3Cpro) to generate VP0, VP3, VP1 and the peptide 2A. Sixty copies of each of the capsid proteins “self-assemble” into empty capsid particles or with the RNA genome into infectious viruses. These particles normally lack 2A but it is possible to construct and isolate mutant FMDVs in which the cleavage of the VP1/2A junction is greatly inhibited, leading to the production of “self-tagged” virus particles that retain the 2A peptide. Interestingly, such mutant viruses acquire “second site” changes elsewhere within VP1.

Recent studies have shown that reducing the expression level of the 3Cpro relative to the P1-2A capsid precursor enhances the yield of processed capsid proteins and their assembly into empty capsid particles within mammalian cells. Such particles can potentially form the basis of a vaccine but they may only have the same properties as the current inactivated vaccines. We have expressed the FMDV P1-2A alone or with FMDV 3Cpro using a “single cycle” alphavirus vector based on Semliki Forest virus (SFV). Cattle vaccinated with these rSFV-FMDV vectors alone, produced anti-FMDV antibodies but the immune response was insufficient to give protection against FMDV challenge. However, vaccination with these vectors primed a much stronger immune response against FMDV post-challenge. In subsequent experiments, cattle were sequentially vaccinated with a rSFV-FMDV followed by recombinant FMDV empty capsid particles, or vice versa, prior to challenge. Animals given a primary vaccination with the rSFV-FMDV vector and then boosted with FMDV empty capsids showed a strong anti-FMDV antibody response prior to challenge; they were protected against disease and no FMDV RNA was detected in their sera post-challenge. Initial inoculation with empty capsids followed by the rSFV-FMDV was much less effective at combating the FMDV challenge. This prime-boost system, using reagents that can be generated outside of high-containment facilities, offers significant advantages to achieve control of FMD by vaccination.
Functional analysis of replication determinants in classical swine fever virus

The ability to efficiently produce new viral progeny is an essential process in the viral life cycle. Virus replication is a complex process involving viral proteins, interactions within the viral genome and assistance from host proteins. Identification of replication determinants of important human and animal pathogens should facilitate finding new approaches for efficient disease control. The principal aim of this thesis is to characterise determinants involved in the replication of classical swine fever virus (CSFV). Classical swine fever is a highly contagious virus disease of domestic pigs and wild boar with great socio-economic importance for countries, like Denmark, that have a significant trade in agricultural production. CSFV has, like other RNA viruses, a high mutation rate allowing the virus to adapt to changes in selection pressure. Hence obtaining a more thorough knowledge of sequence variation during virus replication is crucial for the design of effective vaccines and for diagnostic purposes. This thesis is comprised of four parts: An overview consisting of a general introduction (part 1) and a discussion (part 4) which provides a review of CSFV biology with an emphasis on the viral life cycle and structural RNA elements important for virus replication. This establishes at theoretical background and provides perspectives for the work performed during this Ph.D., which is outlined in part 2 that summarises the project aims and findings. These findings are described in-depth in part 3 comprising the three manuscripts included in the thesis. Manuscript 1 has focused on adaptations that occurred in the CSFV genome following introduction of mutations into the internal ribosome entry site (IRES) and after serial passaging in cell culture and when tested in vivo. Sequence adaptations occurred in the coding regions for NS2 and NS5B that restored the coding sequence to that of the parental field strain. When rescued viruses, containing mutant IRES elements, were introduced into pigs no induction of clinical disease could be observed and only limited levels of viral RNA were detected. In contrast, inoculation with the parental virus caused similar clinical symptoms as that observed with the parental field strain. Analysing the adaptation of the viruses throughout the entire viral genome during virus replication allowed a more comprehensive understanding of the virus properties beyond what can be explained by knowing just the consensus sequence. Manuscript 2 examines replication determinants by analysing a sequence motif in the coding region of NS5B which has the possibility to form long-range RNA-RNA interactions. When synonymous mutations were introduced into this motif in a CSFV replicon (a self-replicating but non-infectious genome) reduced RNA replication was observed compared to a wild type replicon. However, this effect was not observed in the context of the infectious virus. Interestingly, an adaptive silent mutation in a conserved part of the structural CSFV protein E1 occurred upon virus passaging in cell culture. Knowledge of these sequence variations and putative long-range interactions will provide valuable insights into mechanisms underlying virus translation and replication. In manuscript 3, a selection marker has been inserted into a CSFV-based replicon making it suitable for screening of antiviral drugs that block virus translation or RNA replication. The neomycin phosphotransferase coding sequence was chosen as a selection marker which confers resistance to neomycin. The neomycin-selectable replicon was demonstrated to be functional and designed with the aim of facilitating the maintenance of replicons by selection within mammalian cells. This might prove to be useful for the maintenance and expression of specific viral antigens in an efficient manner in order to produce more effective and safer prototype vaccine candidates.
Generation and transcriptional programming of intestinal dendritic cells: essential role of retinoic acid

Retinoic acid (RA), a vitamin A metabolite, regulates adaptive immunity in the intestines, with well-characterized effects on IgA responses, Treg induction, and gut trafficking of T- and B-effector cells. It also controls the generation of conventional dendritic cell (cDC) precursors in the bone marrow and regulates cDC subset representation, but its roles in the specialization of intestinal cDC subsets are understudied. Here we show that RA acts cell intrinsically in developing gut-tropic pre-mucosal dendritic cell (pre-μDC) to effect the differentiation and drive the specialization of intestinal CD103+CD11b- (cDC1) and of CD103+CD11b+ (cDC2). Systemic deficiency or DC-restricted antagonism of RA signaling resulted in altered phenotypes of intestinal cDC1 and cDC2, and reduced numbers of cDC2. Effects of dietary deficiency were most apparent in the proximal small intestine and were rapidly reversed by reintroducing vitamin A. In cultures of pre-μDC with Flt3L and granulocyte-macrophage colony-stimulating factor (GM-CSF), RA induced cDC with characteristic phenotypes of intestinal cDC1 and cDC2 by controlling subset-defining cell surface receptors, regulating subset-specific transcriptional programs, and suppressing proinflammatory nuclear factor-κB-dependent gene expression. Thus, RA is required for transcriptional programming and maturation of intestinal cDC, and with GM-CSF and Flt3L provides a minimal environment for in vitro generation of intestinal cDC1- and cDC2-like cDC from specialized precursors.
Genetic characterization of Australian Mycoplasma bovis isolates through whole genome sequencing analysis

Mycoplasma bovis is a major pathogen in cattle causing mastitis, arthritis and pneumonia. First isolated in Australian cattle in 1970, M. bovis has persisted causing serious disease in infected herds. To date, genetic analysis of Australian M. bovis isolates has not been performed. With whole genome sequencing (WGS) becoming a common tool for genetic characterization, this method was utilized to determine the degree of genetic diversity among Australian M. bovis isolates collected over a nine year period (2006–2015) from various geographical locations, anatomical sites, and from clinically affected and non-clinical carrier animals. Eighty-two M. bovis isolates underwent WGS from which single nucleotide polymorphism (SNP) analysis, comparative genomics and analysis of virulence genes was completed. SNP analysis identified a single M. bovis strain circulating throughout Australia with marked genomic similarity. Comparative genomics suggested minimal variation in gene content between isolates from clinical and carrier animals, and between isolates recovered from different anatomical sites. A total of 50 virulence genes from the virulence factors database (VFDB) were identified as highly similar in the Australian isolates, while the presence of variable surface lipoprotein (vsp) genes was greatly reduced compared to reference strain M. bovis PG45. These results highlight that, while the introduction of multiple M. bovis strains has been prevented, elimination of the current strain has not been successful. The persistence of this strain may be due to the significant role that carrier animals play in harboring the pathogen. The similarity of clinical and non-clinical isolates suggests host and environmental factors play a significant role in determining host pathogen outcomes.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Sydney
Authors: Parker, A. M. (Ekstern), Shukla, A. (Intern), House, J. K. (Ekstern), Hazelton, M. S. (Ekstern), Bosward, K. L. (Ekstern), Kokotovic, B. (Intern), Sheehy, P. A. (Ekstern)
Number of pages: 8
Pages: 118-125
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Veterinary Microbiology
Volume: 196
ISSN (Print): 0378-1135
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.7 SJR 1.175 SNIP 1.241
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.363 SNIP 1.206
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.413 SNIP 1.21 CiteScore 2.56
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.291 SNIP 1.256 CiteScore 2.54
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.459 SNIP 1.471 CiteScore 3
 ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.441 SNIP 1.569 CiteScore 3.18
 ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.56 SNIP 1.729 CiteScore 3.27
 ISI indexed (2011): ISI indexed yes
Genome-wide Purification of Extrachromosomal Circular DNA from Eukaryotic Cells

Extrachromosomal circular DNAs (eccDNAs) are common genetic elements in Saccharomyces cerevisiae and are reported in other eukaryotes as well. EccDNAs contribute to genetic variation among somatic cells in multicellular organisms and to evolution of unicellular eukaryotes. Sensitive methods for detecting eccDNA are needed to clarify how these elements affect genome stability and how environmental and biological factors induce their formation in eukaryotic cells. This video presents a sensitive eccDNA-purification method called Circle-Seq. The method encompasses column purification of circular DNA, removal of remaining linear chromosomal DNA, rolling-circle amplification of eccDNA, deep sequencing, and mapping. Extensive exonuclease treatment was required for sufficient linear chromosomal DNA degradation. The rolling-circle amplification step by φ29 polymerase enriched for circular DNA over linear DNA. Validation of the Circle-Seq method on three S. cerevisiae CEN.PK populations of 10(10) cells detected hundreds of eccDNA profiles in sizes larger than 1 kilobase. Repeated findings of ASP3-1, COS111, CUP1, RSC30, HXT6, HXT7 genes on circular DNA in both S288c and CEN.PK suggests that DNA circularization is conserved between strains at these loci. In sum, the Circle-Seq method has broad applicability for genome-scale screening for eccDNA in eukaryotes as well as for detecting specific eccDNA types.

General Information

State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Copenhagen, Princeton University, Group Health Research Institute, Calico Life Sciences LLC.
Authors: Møller, H. D. (Ekstern), Bojsen, R. K. (Intern), Tachibana, C. (Ekstern), Parsons, L. (Ekstern), Botstein, D. (Ekstern), Regenberg, B. (Ekstern)
Number of pages: 8
Publication date: 2016
Main Research Area: Technical/natural sciences
Genomic characterization of avian pathogenic escherichia coli isolates from nordic broiler production reveals a major st117 O78:H4 lineage

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Statens Serum Institute, Norwegian Veterinary Institute, Statens Serum Institut, University of Copenhagen, Finnish Food Safety Authority
Authors: Ronco, T. (Intern), Stegger, M. (Ekstern), Olsen, R. H. (Ekstern), Lilje, B. (Ekstern), Pohjanvirta, T. (Ekstern), Sekse, C. (Ekstern), Bang Nordstoga, A. (Ekstern), Andersen, P. S. (Ekstern), Pedersen, K. (Intern)
Pages: 67-67
Publication date: 2016

Host publication information
Title of host publication: The Danish Microbiological Society Annual Congress 2016 : Programme & Abstracts
Place of publication: Copenhagen
Publisher: American Society for Microbiology
Article number: P50
Main Research Area: Technical/natural sciences
Conference: Danish Microbiological Society Annual Congress 2016, Copenhagen, Denmark, 14/11/2016 - 14/11/2016
Electronic versions:
Programme & Abstracts book
Publication: Research - peer-review » Conference abstract in proceedings – Annual report year: 2016

Genomic Sequence of a Ranavirus Isolated from Short-Finned Eel (Anguilla australis)
The short-finned eel ranavirus (SERV) was isolated from short-finned eel imported to Italy from New Zealand. Phylogenomic analyses revealed that SERV is a unique member of the genus Ranavirus, family Iridoviridae, branching at
the base of the tree near other fish ranaviruses.

**Genome Sequencing of Ranaviruses Isolated from Turbot (Scophthalmus maximus) and Atlantic Cod (Gadus morhua)**

Ranaviruses have been isolated from Atlantic cod (Gadus morhua) and turbot (Scophthalmus maximus) in Denmark. Phylogenomic analyses revealed that these two ranaviruses are nearly identical and form a distinct clade at the base of the ranavirus tree branching off near other fish ranaviruses.
Gut, immunity and brain development is immature in preterm pigs and responsive to different milk diets

General information
State: Published
Organisations: National Veterinary Institute, Innate Immunology, University of Copenhagen
Authors: Ryom, K. (Ekstern), Andersen, A. D. (Ekstern), Nguyen, D. N. (Ekstern), Bergström, A. (Ekstern), Skovgaard, K. (Intern), Thymann, T. (Ekstern), Sangild, P. T. (Ekstern), Bering, S. B. (Ekstern)
Number of pages: 2
Pages: 1517-1518
Publication date: 2016
Conference: 6th congress of the european academy of paediatric societies (EAPS), Geneva, Switzerland, 21/10/2016 - 21/10/2016
Main Research Area: Technical/natural sciences

Publication information
Journal: European Journal of Pediatrics
Volume: 175
Issue number: 11
ISSN (Print): 0340-6199
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.051 SJR 0.992 CiteScore 2.11
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.908 SNIP 1.002 CiteScore 1.83
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.855 SNIP 1.134 CiteScore 1.74
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.824 SNIP 1.163 CiteScore 1.9
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.867 SNIP 1.341 CiteScore 2.1
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.792 SNIP 1.295 CiteScore 2.01
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.804 SNIP 1.189 CiteScore 2.02
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.704 SNIP 1.065
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.73 SNIP 1.006
BFI (2008): BFI-level 1
Hepatic expression of inflammatory genes and microRNAs in pigs with high "cholesteryl ester transfer protein" (CETP) activity

Human obesity and obesity-related diseases (ORD) are growing health problems worldwide and represent a major public health challenge. Most of these diseases are complex conditions, influenced by many genes (including microRNAs) and environmental factors. Many metabolic perturbations are associated with obesity; e.g., low levels of high-density lipoproteins (HDL) are high risk factors of cardiovascular events. A number of genetic, lifestyle, and environmental factors have been shown to contribute to the lowering of HDL-cholesterol. One of these factors is cholesteryl ester transfer protein (CETP) promoting the redistribution of cholesteryl esters, triglycerides, and phospholipids between plasma proteins. Moreover, obesity and ORD are often linked with chronic low-grade inflammation leading to insulin resistance and endothelial and microvascular dysfunctions. The aim of this study was to detect differences in the hepatic expression of genes involved in low-grade inflammation and of obesity- and cholesterol-related microRNAs in two mixed breed populations of pigs (Yorkshire-Göttingen minipig, YM and Duroc-Göttingen minipig, DM) including males and females, with extreme phenotypes for CETP activity levels (designated as CETP-high and CETP-low, respectively). Furthermore, breed and gender differences were also investigated. We found significant difference (P <0.05) in hepatic expression levels of several mRNAs and microRNAs between the CETP-high and -low groups (C5, IL1RN, IL18, and miR-223-5p); between the two mixed breeds (IL1RAP and miR-140-5p); and between gender (APOA1, IL1RN, and FBLN1). Furthermore, when taking breed into account we show that the transcriptional levels of TNF, miR20a, miR33b, and miR130a differed between the two CETP groups. We conclude that increased CETP activity is accompanied by a modest differential hepatic expression of several microRNAs and inflammatory-related genes. Furthermore, our study demonstrates that when modeling the analysis of expression data, it is important to take gender- and breed-specific effects into account.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, University of Copenhagen
Authors: Cirera, S. (Ekstern), Tørsleff, B. C. J. (Ekstern), Ritz, C. (Ekstern), Fredholm, M. (Ekstern), Heegaard, P. M. H. (Intern), Skovgaard, K. (Intern)
Number of pages: 8
Pages: 503-510
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Mammalian Genome
Volume: 27
Issue number: 9
ISSN (Print): 0938-8990
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.68 SJR 1.647 CiteScore 2.63
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 1.42 SNIP 0.682 CiteScore 2.27
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.101 SNIP 0.757 CiteScore 2.74
High diversity of picornaviruses in rats from different continents revealed by deep sequencing

Outbreaks of zoonotic diseases in humans and livestock are not uncommon, and an important component in containment of such emerging viral diseases is rapid and reliable diagnostics. Such methods are often PCR-based and hence require the availability of sequence data from the pathogen. Rattus norvegicus (R. norvegicus) is a known reservoir for important zoonotic pathogens. Transmission may be direct via contact with the animal, for example, through exposure to its faecal matter, or indirectly mediated by arthropod vectors. Here we investigated the viral content in rat faecal matter (n=29) collected from two continents by analyzing 2.2 billion next-generation sequencing reads derived from both DNA and RNA. Among other virus families, we found sequences from members of the Picornaviridae to be abundant in the microbiome of all the samples. Here we describe the diversity of the picornavirus-like contigs including near-full-length genomes closely related to the Boone cardiovirus and Theiler's encephalomyelitis virus. From this study, we conclude that picornaviruses within R. norvegicus are more diverse than previously recognized. The virome of R. norvegicus should be investigated further to assess the full potential for zoonotic virus transmission.
High-fat but not sucrose intake is essential for induction of dyslipidemia and non-alcoholic steatohepatitis in guinea pigs

Background Non-alcoholic fatty liver disease (NAFLD) and dyslipidemia are closely related. Diet plays an important role in the progression of these diseases, but the role of specific dietary components is not completely understood. Therefore, we investigated the role of dietary sucrose and fat/cholesterol on the development of dyslipidemia and NAFLD. Methods Seventy female guinea pigs were block-randomized (based on weight) into five groups and fed a normal chow diet (control: 4 % fat), a very high-sucrose diet (vHS: 4 % fat, 25 % sucrose), a high-fat diet (HF: 20 % fat, 0.35 % cholesterol), a high-fat/high-sucrose diet (HFHS: 20 % fat, 15 % sucrose, 0.35 % cholesterol) or a high-fat/very high-sucrose diet (HFvHS: 20 % fat, 25 % sucrose, 0.35 % cholesterol) for 16 and 25 weeks. Results All three high-fat diets induced dyslipidemia with increased concentrations of plasma cholesterol (p < 0.0001), LDL-C (p < 0.0001) and VLDL-C (p < 0.05) compared to control and vHS. Contrary to this, plasma triglycerides were increased in control and vHS compared to high-fat fed animals (p < 0.01), while circulating levels of free fatty acids were even between groups. Histological evaluation of liver sections revealed non-alcoholic steatohepatitis (NASH) with progressive inflammation and bridging fibrosis in high-fat fed animals. Accordingly, hepatic triglycerides (p < 0.05) and cholesterol (p < 0.0001) was increased alongside elevated levels of alanine and aspartate aminotransferase (p < 0.01) compared to control and vHS. Conclusion Collectively, our results suggest that intake of fat and cholesterol, but not sucrose, are the main factors driving the development and progression of dyslipidemia and NAFLD/NASH.
High-throughput discovery of T cell epitopes in type 1 diabetes using DNA barcode labelled peptide-MHC multimers

Type 1 diabetes (T1D) is characterized by a CD8⁺ lymphocyte-mediated selective destruction of the insulin-producing β-cells causing clinical diabetes. Several autoantigens including glutamic acid decarboxylase 65kDa (GAD65), insulin, protein tyrosine phosphatase (IA-2) and zinc transporter 8 (ZnT8) have been identified based on reactivity in sera from T1D individuals. Here we investigate if post-translational deamination of arginine in the form of citrullination plays a role in
T cell recognition of T1D autoantigens. Citrullination may lead to generation of neo-epitopes, which has been described as T cell targets in other autoimmune diseases. We used netMHC prediction algorithm to identify 764 epitopes from Insulin, GAD65, IA-2 and ZnT8 restricted to HLA-A2, A24, B8 and B15. Among these 91 peptide sequences were susceptible for citrullination. We evaluate the MHC-affinity of both the citrullinated and non-citrullinated library, to identity potential neo-epitopes and to understand the impact of citrullination on MHC affinity. In parallel we will analyse peripheral blood lymphocytes from 50 T1D patients for immune reactivity against the full library. The large library screen will be conducted applying a novel technology where the selection of MHC-multimer binding T cells is followed by amplification and sequencing of MHC multimer-associated DNA barcodes revealing their recognition. This technique enables simultaneous detection of >1000 specificities. Identifying post translational modifications capable of eliciting autoreactive T cell responses in T1D patients is highly relevant for understanding the underlying mechanisms leading to T1D.
Horse-adapted MRSA CC398 t011 clone in Denmark

General information
State: Published
Organisations: National Veterinary Institute, Bacteriology & Parasitology, Statens Serum Institut, Højgård Hestehospital, Ross University School of Veterinary Medicine, University of Copenhagen
Authors: Islam, M. Z. (Ekstern), Espinosa-Gongora, C. (Intern), Damborg, P. (Ekstern), Sieber, R. N. (Ekstern), Munk, R. (Ekstern), Husted, L. (Ekstern), Skov, R. (Ekstern), Moodley, A. (Ekstern), Larsen, J. (Ekstern), Guardabassi, L. (Ekstern)
Number of pages: 1
Publication date: 2016
Event: Poster session presented at 17th International Symposium on Staphylococci and Staphylococcal Infections, Seoul, Korea, Republic of.
Main Research Area: Technical/natural sciences

How to pool fecal samples in a cross-sectional study of antimicrobial resistance genes in Danish pig herds

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology
Authors: Birkegård, A. C. (Intern)
Pages: 99-104
Publication date: 2016

Host publication information
Title of host publication: Book of presentations of the 3rd CPH Pig seminar : Up to date with pig research
Publisher: Copenhagen University
Main Research Area: Technical/natural sciences
Conference: 3rd CPH Pig seminar, Copenhagen, Denmark, 03/02/2016 - 03/02/2016
Electronic versions:
Publication: Research - peer-review » Conference abstract in proceedings – Annual report year: 2016
Identification of common bacterial antigenic markers from bovine digital dermatitis lesions using meta-transcriptomics in combination with high-density peptide-microarrays

Bovine digital dermatitis (DD) is the most important infectious cause of lameness in dairy cattle, and a major contributing factor to welfare problems and economic losses in the dairy cattle industry worldwide. DD is a disease that involves chronic dermal inflammatory processes and destruction of collagenous and connective tissues. Multiple Treponema species, many of which are not-yet-cultivable, are strongly implicated in disease progression. Despite the economic and welfare importance of this disease, no effective vaccine is available; and there is presently very little knowledge concerning efficacious immunoprophylactic antigens against DD.

It is highly likely that DD-associated treponemes possess considerable antigenic variation, as cows exhibit a variable humoral response against different isolates of Treponema. Hence, combinations of antigens from multiple Treponema species should be used for the development of disease prevention measures. As treponemes from DD lesions are extremely difficult to culture, identification of these antigens is challenging. To circumvent this problem, we studied the in situ gene expression patterns of the microbiome in DD-affected skin lesions and the host antibody response directed at the site of infection. By metatranscriptomics we measured the in situ genome-wide transcriptome of the bacterial population in DD-affected skin lesions from 21 dairy cows. From the transcriptome data, we identified a panel of Treponema genes that were highly expressed in multiple animals, and we monitored the host immune response to these target genes using high-density peptide microarrays. By this approach, we identified a small group of antigenic proteins, which were expressed in the majority of the samples, and demonstrated antigenicity when screened against sera from infected animal. Future studies will show if these proteins represent candidates for the development of novel biomarkers or vaccines.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology, and Parasitology, Center for Biological Sequence Analysis, Department of Bio and Health Informatics, Immunoinformatics and Machine Learning, Metagenomics, Schafer-N, Technical University of Denmark
Number of pages: 1
Publication date: 2016
Main Research Area: Technical/natural sciences
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2016

IL-18Rα-deficient CD4+ T cells induce intestinal inflammation in the CD45RBhi transfer model of colitis despite impaired innate responsiveness

IL-18 has been implicated in inflammatory bowel disease (IBD), however its role in the regulation of intestinal CD4+ T-cell function remains unclear. Here we show that murine intestinal CD4+ T cells express high levels of IL-18Rα and provide evidence that IL-18Rα expression is induced on these cells subsequent to their entry into the intestinal mucosa. Using the CD45RBhi T-cell transfer colitis model, we show that IL-18Rα is expressed on IFN-γ+, IL-17+ and IL-17+/IFN-γ+ effector CD4+ T cells in the inflamed colonic lamina propria (cLP) and mesenteric lymph node (MLN) and is required for the optimal generation and/or maintenance of IFN-γ-producing cells in the cLP. In the steady state and during colitis, TCR-independent cytokine-induced IFN-γ and IL-17 production by intestinal CD4+ T cells was largely IL-18Rα-dependent. Despite these findings however, IL-18Rα-deficient CD4+ T cells induced comparable intestinal pathology to WT CD4+ T cells. These findings suggest that IL-18-dependent cytokine induced activation of CD4+ T cells is not critical for the development of T-cell-mediated colitis.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Lund University
Authors: Holmkvist, P. (Ekstern), Pool, L. (Intern), Hägerbrand, K. (Ekstern), Agace, W. W. (Intern), Rivollier, A. M. C. (Intern)
Pages: 1371-1382
Publication date: 2016
Main Research Area: Technical/natural sciences
Publication information
Journal: European Journal of Immunology
Volume: 46
Issue number: 6
ISSN (Print): 0014-2980
Ratings: BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Immune Mechanisms in Myelodysplastic Syndrome

Myelodysplastic syndrome (MDS) is a spectrum of diseases, characterized by debilitating cytopenias and a propensity of developing acute myeloid leukemia. Comprehensive sequencing efforts have revealed a range of mutations characteristic,
but not specific, of MDS. Epidemiologically, autoimmune diseases are common in patients with MDS, fueling hypotheses of common etiological mechanisms. Both innate and adaptive immune pathways are overly active in the hematopoietic niche of MDS. Although supportive care, growth factors, and hypomethylating agents are the mainstay of MDS treatment, some patients—especially younger low-risk patients with HLA-DR15 tissue type—demonstrate impressive response rates after immunosuppressive therapy. This is in contrast to higher-risk MDS patients, where several immune activating treatments, such as immune checkpoint inhibitors, are in the pipeline. Thus, the dual role of immune mechanisms in MDS is challenging, and rigorous translational studies are needed to establish the value of immune manipulation as a treatment of MDS.

**General information**

**State:** Published

**Organisations:** National Veterinary Institute, Section for Immunology and Vaccinology, University of Copenhagen, Van Andel Research Institute

**Authors:** Glenthøj, A. (Ekstern), Ørskov, A. D. (Ekstern), Hansen, J. W. (Ekstern), Hadrup, S. R. (Intern), O'Connell, C. (Ekstern), Grønbæk, K. (Ekstern)

**Publication date:** 2016

**Main Research Area:** Technical/natural sciences

**Publication information**

**Journal:** International Journal of Molecular Sciences

**Volume:** 17

**Issue number:** 6

**Article number:** 944

**ISSN (Print):** 1661-6596

**Ratings:**

- BFI (2018): BFI-level 1
- Web of Science (2018): Indexed yes
- BFI (2017): BFI-level 1
- Scopus rating (2017): SNIP 1.124 SJR 1.26 CiteScore 3.86
- Web of Science (2017): Indexed Yes
- BFI (2016): BFI-level 1
- Scopus rating (2016): CiteScore 3.73 SJR 1.235 SNIP 1.15
- Web of Science (2016): Indexed yes
- BFI (2015): BFI-level 1
- Scopus rating (2015): SJR 1.157 SNIP 1.118 CiteScore 3.37
- Web of Science (2015): Indexed yes
- BFI (2014): BFI-level 1
- Scopus rating (2014): SJR 0.991 SNIP 1.143 CiteScore 3.06
- BFI (2013): BFI-level 1
- Scopus rating (2013): SJR 0.769 SNIP 1.103 CiteScore 2.83
- ISI indexed (2013): ISI indexed yes
- Web of Science (2013): Indexed yes
- BFI (2012): BFI-level 1
- Scopus rating (2012): SJR 0.77 SNIP 1.195 CiteScore 2.86
- ISI indexed (2012): ISI indexed yes
- BFI (2011): BFI-level 1
- Scopus rating (2011): SJR 0.787 SNIP 1.172 CiteScore 2.95
- ISI indexed (2011): ISI indexed yes
- BFI (2010): BFI-level 1
- Scopus rating (2010): SJR 0.659 SNIP 0.905
- BFI (2009): BFI-level 1
- Scopus rating (2009): SJR 0.358 SNIP 0.63
- BFI (2008): BFI-level 1
- Scopus rating (2008): SJR 0.305 SNIP 0.395
- Scopus rating (2007): SJR 0.262 SNIP 0.434
- Scopus rating (2006): SJR 0.357 SNIP 0.559
- Scopus rating (2005): SJR 0.617 SNIP 0.782
- Scopus rating (2004): SJR 0.66 SNIP 0.796
Immunity raised by recent European subtype 1 PRRSV strains allows better replication of East European subtype 3 PRRSV strain Lena than that raised by an older strain

Stable spatial distribution of porcine reproductive and respiratory syndrome (PRRSV)-1 subtypes in Europe is accompanied by a strong population immunity induced by local PRRSV strains. In the present study, it was examined if the immunity induced by three West European subtype 1 PRRSV strains (2007 isolate 07V063 and 2013 isolates 13V091 and 13V117) offers protection against the highly virulent East European subtype 3 PRRSV strain Lena. The number of fever days was greater ($p < 0.05$) in the control group (7.6 ± 1.7 days) compared to the immune groups (07V063-immune: 4.0 ± 1.2 days, 13V091-immune: 4.6 ± 1.1 days, 13V117-immune: 4.0 ± 2.9 days). In all groups, protection was characterized by reduction ($p < 0.05$) of AUC values of nasal shedding (control: 14.6, 07V063-immune: 3.4, 13V091-immune: 8.9, 13V117-immune: 8.0) and viremia (control: 28.1, 07V063-immune: 5.4, 13V091-immune: 9.0, 13V117-immune: 8.3). Reduction of respiratory disease, nasal shedding (mean AUC and mean peak values) and viremia (mean AUC and mean peak values) was more pronounced in 07V063-immune ($p < 0.05$) than in 13V091-immune and 13V117-immune animals. Inoculation with subtype 1 PRRSV strains caused priming of the Lena-specific virus neutralization antibody response. Upon challenge with Lena, we observed a very strong serological booster effect for neutralizing antibodies against strains used for the first inoculation. Our results indicate that inoculation with subtype 1 PRRSV strains can partially protect against antigenically divergent subtype 3 strains. The lower protection level elicited by recently isolated subtype 1 PRRSV strains may impair the outcome of the spatial expansion of subtype 3 strains from East Europe to West Europe.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Ghent University
Authors: Trus, I. (Ekstern), Frydas, I. S. (Ekstern), Reddy, V. R. A. P. (Ekstern), Bonckaert, C. (Ekstern), Li, Y. (Ekstern), Kvisgaard, L. K. (Intern), Larsen, L. E. (Intern), Nauwynck, H. J. (Ekstern)
Number of pages: 9
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Veterinary Research
Volume: 47
Issue number: 1
Article number: 15
ISSN (Print): 0928-4249
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 1.139 SJR 1.266
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): SJR 1.44 SNIP 1.303
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.537 SNIP 1.153 CiteScore 2.66
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.453 SNIP 1.423 CiteScore 2.46
Plants containing condensed tannins (CT) may have potential to control gastrointestinal nematodes (GIN) of cattle. The aim was to investigate the anthelmintic activities of four flavan-3-ols, two galloyl derivatives and 14 purified CT fractions, and to define which structural features of CT determine the anti-parasitic effects against the main cattle nematodes. We used in vitro tests targeting L1 larvae (feeding inhibition assay) and adults (motility assay) of Ostertagia ostertagi and Cooperia oncophora. In the larval feeding inhibition assay, O. ostertagi L1 were significantly more susceptible to all CT fractions than C. oncophora L1. The mean degree of polymerization of CT (i.e. average size) was the most important structural parameter: large CT reduced larval feeding more than small CT. The flavan-3-ols of prodelphinidin (PD)-type tannins had a stronger negative influence on parasite activity than the stereochemistry, i.e. cis- vs trans-configurations, or the presence of a gallate group. In contrast, for C. oncophora high reductions in the motility of larvae and adult worms were strongly related with a higher percentage of PDs within the CT fractions while there was no effect of size. Overall, the size and the percentage of PDs within CT seemed to be the most important parameters that influence anti-parasitic
Impact Of Mutation-derived Antigens In Immune Recognition Of Hematological Malignancies, Specifically Myeloid Dysplastic Syndromes (MDS)

Mutation-derived neoepitopes have been suggested as a major component for immune recognition of solid tumors with a high mutational load, e.g. Melanoma and Non-Small-Cell Lung Cancer (NSCLC). Myelodysplastic syndromes (MDS) are a heterogeneous group of myeloid neoplasms characterized by increasing bone marrow failure due to clonal expansion of immature dysplastic cells in the bone marrow. Compared to Melanoma and NSCLC, these dysplastic cells carry low numbers of point mutations, but high levels of frameshifts, indels, splice variations or epigenetic changes. All of which may contribute to the generation of tumor-specific neoepitopes.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Department of Systems Biology, Center for Biological Sequence Analysis, Cancer Systems Biology, Technical University of Denmark, Georg-Speyer-Haus
Number of pages: 1
Pages: 66-66
Publication date: 2016
Conference: 21st Congress of the European Hematology Association, Copenhagen, Denmark, 09/06/2016 - 09/06/2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Haematologica
Volume: 101
Issue number: S1
Article number: P237
ISSN (Print): 0390-6078
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.658 SJR 3.063 CiteScore 4.28
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 2.821 SNIP 1.703 CiteScore 4.1
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.959 SNIP 1.793 CiteScore 4.22
BFI (2014): BFI-level 1
Improving productivity in growing pigs by combining specific and non-specific monitoring

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Section for Virology, SEGES Pig Research Center, University of Copenhagen, Svinevet Pig Practise
Number of pages: 1
Publication date: 2016
Event: Poster session presented at 24th International Pig Veterinary Society (IPVS) Congress, Dublin, Ireland.
Main Research Area: Technical/natural sciences
Electronic versions:
IPVS2016_340.pdf
Source: PublicationPreSubmission
Source-ID: 124140967
Publication: Research - peer-review › Poster – Annual report year: 2016

Improving productivity in growing pigs by combining specific and non-specific monitoring

General information
State: Published
Influence of soil structure on contaminant leaching from injected slurry

Animal manure application to agricultural land provides beneficial organic matter and nutrients but can spread harmful contaminants to the environment. Contamination of fresh produce, surface water and shallow groundwater with the manure-borne pollutants can be a critical concern. Leaching and persistence of nitrogen, microorganisms (bacteriophage, E. coli, and Enterococcus) and a group of steroid hormone (estrogens) were investigated after injection of swine slurry into either intact (structured) or disturbed (homogeneous repacked) soil. The slurry was injected into hexaplicate soil columns at a rate of 50 t ha(-1) and followed with four irrigation events: 3.5-h period at 10 mm h(-1) after 1, 2, 3, and 4 weeks. The disturbed columns delayed the leaching of a conservative tracer and microorganisms in the first irrigation event compared to the intact columns due to the effect of disturbed macropore flow paths. The slurry constituents that ended up in or near the macropore flow paths of the intact soil were presumably washed out relatively quickly in the first event. For the last three events the intact soil leached fewer microorganisms than the disturbed soil due to the bypassing effect of water through the macropore flow path in the intact soil. Estrogen leached from the intact soil in the first event only, but for the disturbed soil it was detected in the leachates of last two events also. Leaching from the later events was attributed to higher colloid transport from the disturbed soils. In contrast, NO3-N leaching from the intact soil was higher for all events except the first event, probably due to a lower nitrification rate in the disturbed soil. A week after the last irrigation event, the redistribution of all slurry constituents except NO3-N in most of the sections of the soil column was higher for the disturbed soil. Total recovery of E. coli was significantly higher from the disturbed soil and total leaching of mineral nitrogen was significantly lower from the disturbed soil. Results demonstrate how manure-borne constituents injected into undisturbed soil columns respond more as expected in the field, in terms of leaching and persistence, than do the same constituents injected into typically constructed columns of disturbed soil.
Inter-laboratory study to characterize the detection of serum antibodies against porcine epidemic diarrhoea virus

Porcine epidemic diarrhoea virus (PEDV) has caused extensive economic losses to pig producers in many countries. It was recently introduced, for the first time, into North America and outbreaks have occurred again in multiple countries within Europe as well. To assess the properties of various diagnostic assays for the detection of PEDV infection, multiple panels of porcine sera have been shared and tested for the presence of antibodies against PEDV in an inter-laboratory ring trial. Different laboratories have used a variety of “in house” ELISAs and also one commercial assay. The sensitivity and specificity of each assay has been estimated using a Bayesian analysis applied to the ring trial results obtained with the different assays in the absence of a gold standard. Although different characteristics were found, it can be concluded that each of the assays used can detect infection of pigs at a herd level by either the early European strains of PEDV or the recently circulating strains (INDEL and non-INDEL). However, not all the assays seem suitable for demonstrating freedom from disease in a country. The results from individual animals, especially when the infection has occurred within an experimental situation, show more variation.

General information
International ring trials for adoption and validation of real-time RT-PCR protocols for sub-typing European swine influenza viruses

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Reid, S. M. (Ekstern), Russell, C. (Ekstern), Williamson, S. (Ekstern), Simon, G. (Ekstern), Loeffen, W. (Ekstern), Larsen, L. E. (Intern), Zohari, S. (Ekstern), Chiapponi, C. (Ekstern), Harder, T. (Ekstern), Gorin, S. (Ekstern), Queguiner, S. (Ekstern), Krog, J. S. (Intern), Foni, E. (Ekstern), Brookes, S. (Ekstern), Brown, I. (Ekstern)
Pages: 600-600
Publication date: 2016

Introduction of replacement gilts to PRRS-positive sow herds

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, SEGES Pig Research Center
Authors: Hoelstad, B. E. (Intern), Larsen, L. E. (Intern), Hjulsager, C. K. (Intern), Kristensen, C. (Ekstern)
Pages: 568-568
Publication date: 2016
Introduktion af polte i PRRSV-besætninger: Notat nr. 1609

I dette veterinære speciale blev det vist, at polte, der var vaccineret mod PRRS-virus (PRRSV), ikke udskilt virus ved første løbning. Studiet fandt en tendens til en sammenhæng mellem brug af karantæne og det, at poltene var beskyttet af antistoffer mod PRRSV.

Studiet inkluderede 69 besætninger positive for PRRSV. Der blev taget 5 blodprøver fra løbeklare polte i hver besætning, og et spørgeskema vedrørende polterekrutteringsstrategi, vaccinationsstrategi m.m. blev udfyldt.

Blodprøverne blev analyseret for PRRSV ved RT-qPCR, ELISA og IPT.

Studiet viste, at poltene fra de deltagende besætninger ikke havde PRRSV i blodet (var viræmiske) ved første løbning, og at der var en lille del, som ikke havde dannet antistoffer mod PRRSV trods vaccination. Sidstnævnte kunne tyde på et svigt i vaccinationsproceduren i besætningerne. Desuden var det meget få besætninger, der reelt havde en optimal karantæne. En optimal karantæne blev defineret som en stald, der ikke delte luftområde med øvrige staldafsnit, havde separat indgang og kørte alt ind/alt ud. På trods af at poltene ikke var viræmiske ved løbning, fører studiet ikke til ændringer i anbefalinger i anbefalingerne vedrørende introduktion af polte i PRRS-positive besætninger.

Anbefalingerne er derfor stadig at immunisere poltene og så sætte dem i karantæne i minimum 8 uger og allerhelst 12.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Hoelstad, B. E. (Intern), Sonne Kristensen, C. (Ekstern), Qvist Pawlowski, M. (Ekstern), Hjulsager, C. K. (Intern), Kvisgaard, L. K. (Intern), Lauritsen, K. T. (Intern), Larsen, L. E. (Intern)
Number of pages: 4
Publication date: 2016

Investigating the Role of Surface Materials and Three Dimensional Architecture on In Vitro Differentiation of Porcine Monocyte-Derived Dendritic Cells

In vitro generation of dendritic-like cells through differentiation of peripheral blood monocytes is typically done using two-dimensional polystyrene culture plates. In the process of optimising cell culture techniques, engineers have developed fluidic micro-devices usually manufactured in materials other than polystyrene and applying three-dimensional structures more similar to the in vivo environment. Polydimethylsiloxane (PDMS) is an often used polymer for lab-on-a-chip devices but not much is known about the effect of changing the culture surface material from polystyrene to PDMS. In the present study the differentiation of porcine monocytes to monocyte-derived dendritic cells (moDCs) was investigated using CD172apos pig blood monocytes stimulated with GM-CSF and IL-4. Monocytes were cultured on surfaces made of two- and three-dimensional polystyrene as well as two- and three-dimensional PDMS and carbonised three-dimensional PDMS. Cells cultured conventionally (on two-dimensional polystyrene) differentiated into moDCs as expected.

Interestingly, gene expression of a wide range of cytokines, chemokines, and pattern recognition receptors was influenced by culture surface material and architecture. Distinct clustering of cells, based on similar expression patterns of 46 genes of interest, was seen for cells isolated from two- and three-dimensional polystyrene as well as two- and three-dimensional PDMS. Changing the material from polystyrene to PDMS resulted in cells with expression patterns usually associated with macrophage expression (upregulation of CD163 and downregulation of CD1a, FLT3, LAMP3 and BATF3). However, this was purely based on gene expression level, and no functional assays were included in this study which would be necessary in order to classify the cells as being macrophages. When changing to three-dimensional culture the cells became increasingly activated in terms of IL6, IL8, IL10 and CCR5 gene expression. Further stimulation with LPS resulted in a slight increase in the expression of maturation markers (SLA-DRB1, CD86 and CD40) as well as cytokines (IL6, IL8, IL10 and IL23A) but the influence of the surfaces was unchanged. These findings highlights future challenges of combining and comparing data generated from microfluidic cell culture-devices made using alternative materials to data generated using conventional polystyrene plates used by most laboratories today.
Pseudomonas putida as a microbial cell factory

The extensive use of fossil fuels has a severe influence on the environment. In order to reduce the dependency on these limited resources and to protect the environment substantial effort is being made to implement renewable resources. One part of this transition is to develop methods for sustainable production of chemicals, which can be achieved by microbial cell factories. The work presented in this PhD thesis elucidates the application of Pseudomonas putida as a microbial cell factory for production of the biosurfactant rhamnolipid. The rhamnolipid production was achieved by heterologous expression of the rhlAB operon from Pseudomonas aeruginosa using a synthetic promoter library in P. putida. Since rhamnolipid production is associated with difficulties in conventional bioreactors we have used biofilm encased P. putida to circumvent these problems. We show that biofilm can be used as a production platform for continuous production of rhamnolipids. A method for quantitative and qualitative analysis of the produced rhamnolipids was developed based on ultra performance liquid chromatography combined with high resolution mass spectrometry. This enabled detection of low levels of rhamnolipids. The applicability of glycerol as a substrate was also investigated. Since glycerol is a poor substrate adaptive evolution was made in order to improve the capabilities of P. putida to proliferate on glycerol. The evolved lineages all had significantly increased growth rate, enhanced cell density and reduced lag phase. The genomic alterations were identified by genome sequencing and revealed parallel evolution. Glycerol was also shown to be able to support biofilm growth and as a result of this it can be used as an alternative substrate for producing biochemicals in conventional and biofilm reactors. The use of biofilm as a production platform and the usage of glycerol as a feedstock show the potential of using microbial cell factories in the transition toward sustainable production of chemicals. Particularly, the applicability of biofilm as a production platform can emerge as a promising alternative for producing toxic biochemicals and for producing biochemicals which are difficult to cope in conventional bioreactors.

IRF8 dependent classical dendritic cells are essential for intestinal T cell homeostasis

The role of dendritic cells (DCs) in intestinal immune homeostasis remains incompletely defined. Here we show that mice lacking IRF8 dependent DCs have reduced numbers of T cells in the small intestine (SI), but not large intestine (LI), including an almost complete absence of SI CD8ab+ and CD4+CD8aa+ T cells; the latter requiring b8 integrin expression by migratory IRF8 dependent CD103+CD11b+ DCs. SI homing receptor induction was impaired during T cell priming in mesenteric lymph nodes (MLN), which correlated with a reduction in aldehyde dehydrogenase activity by SI derived MLN DCs, and inefficient T cell localization to the SI. Finally, mice with a DC deletion in IRF8 lacked intestinal T helper 1 (Th1) cells, and failed to support Th1 cell differentiation in MLN and mount Th1 responses to Trichuris muris infection. Collectively these results highlight multiple non-redundant roles for IRF8 dependent DCs in the maintenance of intestinal T cell homeostasis.
IRF8-dependent DCs play a key role in the regulation of CD8 T cell responses to epithelial-derived antigen in the steady state but not in inflammation

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Lund University, Ghent University
Authors: Joeris, T. (Intern), Casado, G. C. (Ekstern), Holmkvist, P. (Ekstern), Luda, K. (Ekstern), Tavernier, S. (Ekstern), Lambrecht, B. N. (Ekstern), Agace, W. W. (Intern)
Number of pages: 1
Pages: 787-787
Publication date: 2016
Conference: ICI 2016 International Congress of Immunology, Melbourne, Australia, 21/08/2016 - 21/08/2016
Main Research Area: Technical/natural sciences

Publication information
Journal: European Journal of Immunology
Volume: 46
Issue number: S1
ISSN (Print): 0014-2980
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.59 SJR 2.206 SNIP 0.92
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.61 SJR 2.525 SNIP 0.927
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.588 SNIP 0.965 CiteScore 3.85
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.672 SNIP 0.972 CiteScore 3.83
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 2.876 SNIP 1.05 CiteScore 4.3
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 2.989 SNIP 1.063 CiteScore 4.62
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 3.255 SNIP 1.025 CiteScore 4.69
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 3.363 SNIP 0.99
IRF8-dependent DCs play a key role in the regulation of CD8 T cell responses to epithelial-derived antigen in the steady state but not in inflammation

Along the process of epithelial self-renewal, antigens derived from apoptotic intestinal epithelial cells (IECs) are taken up by antigen presenting cells (APCs), transported to gut-draining lymph nodes and cross-presented to CD8 T cells. In steady state, rapid tolerization of CD8 T cells reactive towards epithelial-derived antigens is crucial to maintain tissue homeostasis. Since IRF8-dependent dendritic cells (IRF8-DCs) have superior cross-presenting capabilities, we aimed to investigate their role in this process. IFABP-tOva mice, expressing the model-antigen Ovalbumin (Ova) in IECs, were used as recipients to set up chimeras using either CD11c-cre.Irf8fl/fl bone marrow, which cannot generate IRF8-DCs, or cre-negative Irf8fl/fl control bone marrow. Whereas transfer of Ova-specific CD8 T cells (OT-I cells) to control chimeras resulted in their rapid tolerization, OT-I cells transferred to CD11c-cre.Irf8fl/fl chimeras spontaneously developed into cytotoxic effector T cells (CTLs), causing epithelial destruction and intestinal inflammation. However, when the adjuvant R848 was applied in addition to OT-I transfer, inflammation was triggered in both, CD11c-cre.Irf8fl/fl and control chimeras. This demonstrates that IRF8-DCs are crucial for the rapid tolerization of CD8 T cells reactive towards epithelial-derived antigen in steady state, but are not essential for the induction of CTLs in an inflammatory setting such as found in infection.
towards epithelial-associated, pathogen-derived antigens. Currently, little is known about the regulation of CD8 T cells by intestinal APCs in these two different contexts. Since IRF8-dependent dendritic cells (IRF8-DCs) have superior cross-presenting capabilities, we aimed to investigate their role in this process. IFABP-tOva mice, expressing the model-antigen Ovalbumin (Ova) in IECs, were used as recipients to set up chimeras using either CD11c-cre.Irf8<sup>fl/fl</sup> bone marrow, which cannot generate IRF8-DCs, or crenegative Irf8<sup>fl/fl</sup> control bone marrow. Whereas transfer of Ova-specific CD8 T cells (OT-I cells) to steady state control chimeras resulted in their rapid tolerization, OT-I cells transferred to CD11c-cre.Irf8<sup>fl/fl</sup> chimeras spontaneously developed into CTLs, causing epithelial destruction and intestinal inflammation. However, when the TLR7-ligand R848 was applied as an inflammatory trigger mimicking viral infection in addition to OT-I transfer, expansion of CTLs occurred at similar rates in both, CD11c-cre.Irf8<sup>fl/fl</sup> and control chimeras. Taken together, this demonstrates that IRF8-DCs are crucial for the rapid tolerization of CD8 T cells reactive towards epithelial-derived antigen in steady state, but are not essential for the induction of CTLs in an inflammatory setting such as found in infection.
Interferon regulatory factor-8 (IRF8) has been proposed to be essential for development of monocytes, plasmacytoid dendritic cells (pDCs) and type 1 conventional dendritic cells (cDC1s) and remains highly expressed in differentiated DCs. Transcription factors that are required to maintain the identity of terminally differentiated cells are designated "terminal selectors." Using BM chimeras, conditional Irf8(fl/fl) mice and various promotors to target Cre recombinase to different stages of monocyte and DC development, we have identified IRF8 as a terminal selector of the cDC1 lineage controlling survival. In monocytes, IRF8 was necessary during early but not late development. Complete or late deletion of IRF8 had no effect on pDC development or survival but altered their phenotype and gene-expression profile leading to increased T cell stimulatory function but decreased type 1 interferon production. Thus, IRF8 differentially controls the survival and function of terminally differentiated monocytes, cDC1s, and pDCs.
IRF8 Transcription-Factor-Dependent Classical Dendritic Cells Are Essential for Intestinal T Cell Homeostasis

The role of dendritic cells (DCs) in intestinal immune homeostasis remains incompletely defined. Here we show that mice lacking IRF8 transcription-factor-dependent DCs had reduced numbers of T cells in the small intestine (SI), but not large intestine (LI), including an almost complete absence of SI CD8αβ+ and CD4+CD8αα+ T cells; the latter requiring β8 integrin expression by migratory IRF8 dependent CD103+CD11b- DCs. SI homing receptor induction was impaired during T cell priming in mesenteric lymph nodes (MLN), which correlated with a reduction in aldehyde dehydrogenase activity by SI-derived MLN DCs, and inefficient T cell localization to the SI. These mice also lacked intestinal T helper 1 (Th1) cells, and failed to support Th1 cell differentiation in MLN and mount Th1 cell responses to Trichuris muris infection. Collectively these results highlight multiple non-redundant roles for IRF8 dependent DCs in the maintenance of intestinal T cell homeostasis.

General information

State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Lund University, University of Copenhagen, University of Manchester, Oslo University Hospital, Inflammatin Research Center (IRC)

DOI: 10.1016/j.immuni.2016.08.013
Source: Findit
Source-ID: 2343507744
Publication: Research - peer-review › Journal article – Annual report year: 2016
Laboratory Examination of Transmissible Spongiform Encephalopathies in Denmark during 2015

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology
Authors: Jensen, T. K. (Intern)
Number of pages: 7
Publication date: 2016

Publication information
Place of publication: Frederiksberg C
Publisher: National Veterinary Institute, Technical University of Denmark
Original language: English
Main Research Area: Technical/natural sciences
Electronic versions:
EU_TSE_RAP_2015_DTU_31_03_2016.pdf

Bibliographical note
Annual Report
Source: PublicationPreSubmission
Source-ID: 123046341
Publication: Research › Report – Annual report year: 2016

Lammelser af bagparten hos mink forårsaget af knoglemarvsbetaendelse i ryghvirvlerne

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Copenhagen
Authors: Larsen, G. (Intern), Nonnemann, B. (Intern), Buelund, L. E. (Ekstern), Holm, E. (Intern), Jensen, T. K. (Intern), Chriél, M. (Intern)
Pages: 115-117
Publication date: 2016

Host publication information
Title of host publication: Faglig årsberetning 2015 : Kopenhagen Fur
Place of publication: Aarhus N
Publisher: Kopenhagen Fur
Main Research Area: Technical/natural sciences
Electronic versions:
Faglig_årsberetning_2015.pdf
Source: PublicationPreSubmission
Source-ID: 123345075
Publication: Research › Report chapter – Annual report year: 2016

Large-scale detection of antigen-specific T cells using peptide-MHC-I multimers labeled with DNA barcodes
Identification of the peptides recognized by individual T cells is important for understanding and treating immune-related diseases. Current cytometry-based approaches are limited to the simultaneous screening of 10-100 distinct T-cell specificities in one sample. Here we use peptide-major histocompatibility complex (MHC) multimers labeled with individual DNA barcodes to screen >1,000 peptide specificities in a single sample, and detect low-frequency CD8 T cells specific for virus- or cancer-restricted antigens. When analyzing T-cell recognition of shared melanoma antigens before and after adoptive cell therapy in melanoma patients, we observe a greater number of melanoma-specific T-cell populations compared with cytometry-based approaches. Furthermore, we detect neoepitope-specific T cells in tumor-infiltrating lymphocytes and peripheral blood from patients with non-small cell lung cancer. Barcode-labeled pMHC multimers enable the combination of functional T-cell analysis with large-scale epitope recognition profiling for the characterization of T-cell recognition in various diseases, including in small clinical samples.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Department of Systems Biology, Center for Biological Sequence Analysis, Cancer Systems Biology, University of Copenhagen, UCL Cancer Institute, The Francis Crick Institute
Late regulation of immune genes and microRNAs in circulating leukocytes in a pig model of influenza A (H1N2) infection

MicroRNAs (miRNAs) are a class of short regulatory RNA molecules which are implicated in modulating gene expression. Levels of circulating, cell-associated miRNAs in response to influenza A virus (IAV) infection has received limited attention so far. To further understand the temporal dynamics and biological implications of miRNA regulation in circulating leukocytes, we collected blood samples before and after (1, 3, and 14 days) IAV challenge of pigs. Differential expression of miRNAs and innate immune factor mRNA transcripts was analysed using RT-qPCR. A total of 20 miRNAs were regulated after IAV challenge, with the highest number of regulated miRNAs seen on day 14 after infection at which time the infection was cleared. Targets of the regulated miRNAs included genes involved in apoptosis and cell cycle regulation. Significant regulation of both miRNAs and mRNA transcripts at 14 days after challenge points to a protracted effect of IAV infection, potentially affecting the host’s ability to respond to secondary infections. In conclusion, experimental IAV infection of pigs demonstrated the dynamic nature of miRNA and mRNA regulation in circulating leukocytes during and after infection, and revealed the need for further investigation of the potential immunosuppressing effect of miRNA and innate immune signaling after IAV infection.
Levels of MRSA on pigs and environmental samples

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology
Authors: Hansen, J. E. (Intern)
Pages: 87-91
Publication date: 2016

Host publication information
Title of host publication: Book of presentations of the 3rd CPH Pig seminar: Up to date with pig research
Publisher: Copenhagen University
Main Research Area: Technical/natural sciences
Conference: 3rd CPH Pig seminar, Copenhagen, Denmark, 03/02/2016 - 03/02/2016
Electronic versions:
Source: PublicationPreSubmission
Source-ID: 125887365
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2016

Limited effects of preterm birth and the first enteral nutrition on cerebellum morphology and gene expression in piglets

Preterm pigs show many signs of immaturity that are characteristic of preterm infants. In preterm infants, the cerebellum grows particularly rapid and hypoplasia and cellular lesions are associated with motor dysfunction and cognitive deficits. We hypothesized that functional brain delays observed in preterm pigs would be paralleled by both structural and molecular differences in the cerebellum relative to term born piglets. Cerebella were collected from term (n = 56) and preterm (90% gestation, n = 112) pigs at 0, 5, and 26 days after birth for stereological volume estimations, large-scale qPCR gene expression analyses (selected neurodevelopmental genes) and western blot protein expression analysis (Sonic Hedgehog pathway). Memory and learning was tested using a T-maze, documenting that preterm pigs showed delayed learning. Preterm pigs also showed reduced volume of both white and gray matter at all three ages but the proportion of white matter increased postnatally, relative to term pigs. Early initiation of enteral nutrition had limited structural or molecular effects. The Sonic Hedgehog pathway was unaffected by preterm birth. Few differences in expression of the selected genes were found, except consistently higher mRNA levels of Midkine, p75, and Neurotrophic factor 3 in the preterm cerebellum postnatally, probably reflecting an adaptive response to preterm birth. Pig cerebellar development appears more affected by postconceptional age than by environmental factors at birth or postnatally. Compensatory mechanisms following preterm birth may include faster white matter growth and increased expression of selected genes for neurotrophic factors and regulation of angiogenesis. While the pig cerebellum is immature in 90% gestation preterm pigs, it appears relatively mature and resilient toward environmental factors.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, University of Copenhagen, Bispebjerg-Frederiksberg Hospitals, Academic Medical Center, Rigshospitalet
Livestock-associated MRSA CC398 survival in manure

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology
Authors: Hansen, J. E. (Intern), Astrup, L. B. (Intern), Pedersen, K. (Intern)
Number of pages: 1
Publication date: 2016
Event: Abstract from 17th International Symposium on Staphylococci and Staphylococcal Infections, Seoul, Korea, Republic of.
Main Research Area: Technical/natural sciences
Electronic versions: trykt_abstract.pdf
Source: PublicationPreSubmission
Source-ID: 125884991
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2016

Livestock-associated MRSA CC398 survival in manure

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology
Authors: Hansen, J. E. (Intern), Astrup, L. B. (Intern), Pedersen, K. (Intern)
Livestock-associated MRSA in the Danish cattle production

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Section for Epidemiology, SEGES Cattle, Statens Serum Institut
Authors: Hansen, J. E. (Intern), Pedersen, K. (Intern), Fertner, M. E. (Intern), Læssøe Martin, H. (Ekstern), Rhod Larsen, A. (Ekstern), Toft, N. (Intern)
Number of pages: 1
Publication date: 2016
Event: Poster session presented at 17th International Symposium on Staphylococci and Staphylococcal Infections, Seoul, Korea, Republic of.
Main Research Area: Technical/natural sciences
Electronic versions:
Cattle_poster_2_ISSSI2016..pdf
Publication: Research - peer-review › Poster – Annual report year: 2016

Low transfusion transmission of hepatitis E among 25,637 single-donation, nucleic acid-tested blood donors

BACKGROUND: Hepatitis E virus genotype-3 (HEV-gt-3) causes autochthonous infections in western countries, with a primary reservoir in animals, especially pigs. HEV transfusion transmission has been reported, and HEV-gt-3 prevalence is high in some European countries. The prevalence of HEV RNA was investigated among Danish blood donors, and the prevalence of HEV transfusion-transmitted infection (TTI) was investigated among recipients. STUDY DESIGN AND METHODS: Samples from 25,637 consenting donors collected during 1 month in 2015 were screened retrospectively using an individual-donation HEV RNA nucleic acid test with a 95% detection probability of 7.9 IU/mL. HEV-positive samples were quantified by real-time polymerase chain reaction and genotyped. Transmission was evaluated among recipients of HEV RNA-positive blood components. Phylogenetic analyses compared HEV sequences from blood donors, symptomatic patients, and swine. RESULTS: Eleven donations (0.04%) were confirmed as positive for HEV RNA (median HEV RNA level, 13 IU/mL). Two donations were successfully genotyped as HEV-gt-3. Only one donor had a travel history outside Europe. Nine of 11 donors were male, but the gender ratio was nonsignificant compared with the total donor population. Seven available recipients tested negative for HEV RNA and anti-HEV immunoglobulin M in follow-up samples. One recipient was HEV RNA-negative but anti-HEV immunoglobulin G-positive. HEV TTI was considered unlikely, but a transfusion-induced secondary immune response could not be excluded. Phylogenetic analysis showed relatively large sequence differences between HEV from donors, symptomatic patients, and swine. CONCLUSIONS: Despite an HEV RNA prevalence of 0.04% in Danish blood donations, all HEV-positive donations carried low viral loads, and no evidence of TTI was found.

General information
State: Published
Organisations: National Veterinary Institute, Copenhagen University Hospital, Odense University Hospital, Næstved Hospital, Aalborg University, Sanquin Research and Diagnostic Service, Statens Serum Institut, Aarhus University
Pages: 2225-2232
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Transfusion
Volume: 56
Issue number: 9
ISSN (Print): 0041-1132
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
Macrophage and dendritic cell subsets in IBD: ALDH+ cells are reduced in colon tissue of patients with ulcerative colitis regardless of inflammation

Disruption of the homeostatic balance of intestinal dendritic cells (DCs) and macrophages (MQs) may contribute to inflammatory bowel disease. We characterized DC and MQ populations, including their ability to produce retinoic acid, in clinical material encompassing Crohn’s ileitis, Crohn’s colitis and ulcerative colitis (UC) as well as mesenteric lymph nodes (MLNs) draining these sites. Increased CD14+DRint MQs characterized inflamed intestinal mucosa while total CD141+ or CD1c+ DCs numbers were unchanged. However, CD103+ DCs, including CD141+CD103+ and CD1c+CD103+ DCs, were reduced in inflamed intestine. In MLNs, two CD14+ DC populations were identified: CD11cintHLADRhi and CD11chi HLADRint cells. A marked increase of CD11cintHLADRintDC, particularly DRintCD1c+ DCs, characterized MLNs draining inflamed intestine. The fraction of DC and MQ populations expressing aldehyde dehydrogenase (ALDH) activity, reflecting retinoic acid synthesis, in UC colon, both in active disease and remission, were reduced compared to controls and inflamed Crohn’s colon. In contrast, no difference in the frequency of ALDH+ cells among blood precursors was detected between UC patients and non-inflamed controls. This suggests that ALDH activity in myeloid cells in the colon of UC patients, regardless of whether the disease is active or in remission, is influenced by the intestinal environment.

General information

State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Aarhus University Hospital, Sahlgrenska University Hospital, Skåne University Hospital, Lund University, University of Gothenburg
Authors: Magnusson, M. K. (Ekstern), Brynjólfsson, S. F. (Ekstern), Dige, A. (Ekstern), Uhren-Hansson, H. (Ekstern), Börjesson, L. G. (Ekstern), Bengtsson, J. L. (Ekstern), Gudjonsson, S. (Ekstern), Öhman, L. (Ekstern), Agnholt, J.
The raccoon dog (Nyctereutes procyonoides) is an omnivorous carnivore from East Asia, which has been introduced in Europe. It has recently established a free-ranging population in Denmark. The dietary habits of this non-native species were examined and compared to the diet of native badger (Meles meles) and red fox (Vulpes vulpes). The raccoon dog diet was determined from undigested remains in the stomach. The examined raccoon dogs primarily originated from road kills, hunting and culling. Individuals that were caught in baited traps were excluded from the analysis. A total of 244 free-ranging raccoon dogs were collected in 2008-2014. Only 129 of these were included in the analysis based on the cause of death. The diet of raccoon dogs comprised small mammals (56% frequency of occurrence (FO) and carcasses/unidentified materials (57% FO); invertebrates (86% FO); birds (46% FO); fruits/berries (34% FO) and amphibians (44% FO). The importance of amphibians and fruits/berries varied according to seasonal availability, peaking during spring-summer and summer-autumn, respectively. The raccoon dogs’ food niche was wider than the food niche of badgers and red fox (Levin’s standard index: 0.68, 0.37 and 0.30, respectively). Percentage food overlap between raccoon dog and badger was higher (70%) than food overlap with red fox (45%). The study suggests that birds’ eggs and nestlings is a rare food for raccoon dogs as also observed in most other European dietary studies of raccoon dogs. To determine whether the impact of raccoon dog is a threat to populations of birds, amphibians and other prey, studies on the prey populations in relation to the predation pressure of other non-native, native mammalian and avian predators are needed.
Methods and Processes of Developing the Strengthening the Reporting of Observational Studies in Epidemiology - Veterinary (STROBE-Vet) Statement

The reporting of observational studies in veterinary research presents many challenges that often are not adequately addressed in published reporting guidelines. A consensus meeting of experts was organized to develop an extension of the STROBE statement to address observational studies in veterinary medicine with respect to animal health, animal production, animal welfare and food safety outcomes. The consensus meeting was held 11-13 May 2014 in Mississauga, Ontario, Canada. Seventeen experts from North America, Europe and Australia attended the meeting. The experts were epidemiologists and biostatisticians, many of whom hold or have held editorial positions with relevant journals. Prior to the meeting, 19 experts completed a survey about whether they felt any of the 22 items of the STROBE statement should be modified and whether items should be added to address unique issues related to observational studies in animal species with health, production, welfare or food safety outcomes. At the meeting, the participants were provided with the survey responses and relevant literature concerning the reporting of veterinary observational studies. During the meeting, each STROBE item was discussed to determine whether or not re-wording was recommended, and whether additions were warranted. Anonymous voting was used to determine whether there was consensus for each item change or addition. The consensus was that six items needed no modifications or additions. Modifications or additions were made to the STROBE items numbered as follows: 1 (title and abstract), 3 (objectives), 5 (setting), 6 (participants), 7 (variables), 8 (data sources/measurement), 9 (bias), 10 (study size), 12 (statistical methods), 13 (participants), 14 (descriptive data), 15 (outcome data), 16 (main results), 17 (other analyses), 19 (limitations) and 22 (funding). Published literature was not always available to support modification to, or inclusion of, an item. The methods and processes used in the development of this statement were similar to those used for other extensions of the STROBE statement. The use of this extension to the STROBE statement should improve the reporting of observational studies in veterinary research related to animal health, production, welfare or food safety outcomes by recognizing the unique features of observational studies involving food-producing and companion animals, products of animal origin, aquaculture and wildlife.
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 1.074 SJR 1.248 CiteScore 2.59
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.3 SJR 1.119 SNIP 0.988
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.263 SNIP 1.095 CiteScore 2.27
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.036 SNIP 0.955 CiteScore 1.97
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 0.948 SNIP 1.041 CiteScore 2.24
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.052 SNIP 1.223 CiteScore 2.35
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 0.924 SNIP 1.137 CiteScore 2.05
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 0.869 SNIP 1.135
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 0.791 SNIP 1.164
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 0.611 SNIP 0.873
Scopus rating (2007): SJR 0.712 SNIP 1.077
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.66 SNIP 0.922
Scopus rating (2005): SJR 0.711 SNIP 0.912
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.598 SNIP 0.968
Scopus rating (2003): SJR 0.359 SNIP 0.578
Scopus rating (2002): SJR 0.395 SNIP 0.673
Scopus rating (2001): SJR 0.378 SNIP 0.671
Scopus rating (2000): SJR 0.315 SNIP 0.699
Scopus rating (1999): SJR 0.329 SNIP 0.621
Original language: English
Reporting guidelines, animal, observational study, veterinary
Electronic versions:
Sargeant_et_al_2016_Zoonoses_and_Public_Health.pdf
DOIs:
10.1111/zph.12314
Source: FindIt
Source-ID: 2349192644
Publication: Research - peer-review › Journal article – Annual report year: 2016
Methods and Processes of Developing the Strengthening the Reporting of Observational Studies in Epidemiology—Veterinary (STROBE-Vet) Statement

Reporting of observational studies in veterinary research presents challenges that often are not addressed in published reporting guidelines. Our objective was to develop an extension of the STROBE (Strengthening the Reporting of Observational Studies in Epidemiology) statement that addresses unique reporting requirements for observational studies in veterinary medicine related to health, production, welfare, and food safety. We conducted a consensus meeting with 17 experts in Mississauga, Canada. Experts completed a premeeting survey about whether items in the STROBE statement should be modified or added to address unique issues related to observational studies in animal species with health, production, welfare, or food safety outcomes. During the meeting, each STROBE item was discussed to determine whether or not rewording was recommended, and whether additions were warranted. Anonymous voting was used to determine consensus. Six items required no modifications or additions. Modifications or additions were made to the STROBE items 1 (title and abstract), 3 (objectives), 5 (setting), 6 (participants), 7 (variables), 8 (data sources and measurement), 9 (bias), 10 (study size), 12 (statistical methods), 13 (participants), 14 (descriptive data), 15 (outcome data), 16 (main results), 17 (other analyses), 19 (limitations), and 22 (funding). The methods and processes used were similar to those used for other extensions of the STROBE statement. The use of this STROBE statement extension should improve reporting of observational studies in veterinary research by recognizing unique features of observational studies involving food-producing and companion animals, products of animal origin, aquaculture, and wildlife.

General information
State: Published
Organisations: National Veterinary Institute, National Food Institute, Research Group for Genomic Epidemiology, University of Guelph, Iowa State University, University of Prince Edward Island, Cornell University, University of Bern, University of Southern Denmark, University of Copenhagen, University of London, U.S. Food and Drug Administration, University of Saskatchewan, University of Sydney
Number of pages: 9
Pages: 2211-2219
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Food Protection
Volume: 79
Issue number: 12
ISSN (Print): 0362-028x
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.823 SJR 0.761 CiteScore 1.63
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.68 SJR 0.769 SNIP 0.811
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.954 SNIP 1.024 CiteScore 2.03
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.914 SNIP 0.953 CiteScore 1.94
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.101 SNIP 1.09 CiteScore 2.11
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.083 SNIP 0.981 CiteScore 2.03
Microclimate temperature play a vital role for vector borne disease transmission in the cool scandinavian climate

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Technical University of Denmark
Authors: Haider, N. (Intern), Kristensen, B. (Ekstern), Kirkeby, C. T. (Intern), Toft, N. (Intern), Bødker, R. (Intern)
Pages: 70-71
Publication date: 2016

Host publication information
Title of host publication: 3rd Conference on Neglected Vectors and Vector-Borne Diseases (EurNegVec): with MC and WG Meeting of the COST Action TD1303 : Abstract book
Place of publication: ZARAGOZA
Publisher: European Science Foundation
Main Research Area: Technical/natural sciences
Microclimatic temperature play a vital role for vector borne disease transmission in the cool Scandinavian climates

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology
Authors: Haider, N. (Intern), Kristensen, B. (Intern), Kirkeby, C. (Intern), Toft, N. (Intern), Bødker, R. (Intern)
Pages: 69-70
Publication date: 2016

Milk diets influence doxorubicin-induced intestinal toxicity in piglets
Chemotherapy-induced gastrointestinal (GI) toxicity is a common adverse effect of cancer treatment. We used preweaned piglets as models to test our hypothesis that the immunomodulatory and GI trophic effects of bovine colostrum would reduce the severity of GI complications associated with doxorubicin (DOX) treatment. Five-day-old pigs were administered DOX (1 × 100 mg/m²) or an equivalent volume of saline (SAL) and either fed formula (DOX-Form, n = 9, or SAL-Form, n = 7) or bovine colostrum (DOX-Colos, n = 9, or SAL-Colos, n = 7). Pigs were euthanized 5 days after initiation of chemotherapy to assess markers of small intestinal function and inflammation. All DOX-treated animals developed diarrhea, growth deficits, and leukopenia. However, the intestines of DOX-Colos pigs had lower intestinal permeability, longer intestinal villi with higher activities of brush border enzymes, and lower tissue IL-8 levels compared with DOX-Form (all P <0.05). DOX-Form pigs, but not DOX-Colos pigs, had significantly higher plasma C-reactive protein, compared with SAL-Form. Plasma citrulline was not affected by DOX treatment or diet. Thus a single dose of DOX induces intestinal toxicity in preweaned pigs and may lead to a systemic inflammatory response. The toxicity is affected by type of enteral nutrition with more pronounced GI toxicity when formula is fed compared with bovine colostrum. The results indicate that bovine colostrum may be a beneficial supplementary diet for children subjected to chemotherapy and subsequent intestinal toxicity.
Minimal short-term effect of dietary 2'-fucosyllactose on bacterial colonisation, intestinal function and necrotising enterocolitis in preterm pigs

Human milk decreases the risk of necrotising enterocolitis (NEC), a severe gastrointestinal disease that occurs in 5–10 % of preterm infants. The prebiotic and immune-modulatory effects of milk oligosaccharides may contribute to this protection.
Preterm pigs were used to test whether infant formula enriched with α1,2-fucosyllactose (2'-FL, the most abundant oligosaccharide in human milk) would benefit gut microbial colonisation and NEC resistance after preterm birth. Caesarean-delivered preterm pigs were fed formula (Controls, n 17) or formula with 5 g/l 2'-FL (2'-FL, n 16) for 5 d; eight 2'-FL pigs (50 %) and twelve Controls (71 %) developed NEC, with no difference in lesion scores (P=0·35); 2'-FL pigs tended to have less anaerobic bacteria in caecal contents (P=0·22), but no difference in gut microbiota between groups were observed by fluorescence in situ hybridisation and 454 pyrosequencing. Abundant α1,2-fucose was detected in the intestine with no difference between groups, and intestinal structure (villus height, permeability) and digestive function (hexose absorption, brush border enzyme activities) were not affected by 2'-FL. Formula enrichment with 2'-FL does not affect gut microbiology, digestive function or NEC sensitivity in pigs within the first few days after preterm birth. Milk 2'-FL may not be critical in the immediate postnatal period of preterm neonates when gut colonisation and intestinal immunity are still immature.

General information
State: Published
Organisations: National Veterinary Institute, University of Copenhagen, Boston College
Authors: Cilieborg, M. S. (Intern), Bering, S. B. (Ekstern), Østergaard, M. V. (Ekstern), Jensen, M. L. (Ekstern), Krych, Ł. (Ekstern), Newburg, D. S. (Ekstern), Sangild, P. T. (Ekstern)
Number of pages: 8
Pages: 834-841
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: British Journal of Nutrition
Volume: 116
Issue number: 5
ISSN (Print): 0007-1145
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.555 SJR 1.756 CiteScore 3.65
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.46 SJR 2.055 SNIP 1.535
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.583 SNIP 1.442 CiteScore 3.52
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.532 SNIP 1.273 CiteScore 3.18
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 2.746 SNIP 2.479 CiteScore 3.61
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 2.308 SNIP 2.427 CiteScore 3.12
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 2.085 SNIP 1.649 CiteScore 3.13
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.236 SNIP 1.253
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.627 SNIP 0.572
Modeling the growth dynamics of multiple Escherichia coli strains in the pig intestine following intramuscular ampicillin treatment

Background: This study evaluated how dosing regimen for intramuscularly-administered ampicillin, composition of Escherichia coli strains with regard to ampicillin susceptibility, and excretion of bacteria from the intestine affected the level of resistance among Escherichia coli strains in the intestine of nursery pigs. It also examined the dynamics of the composition of bacterial strains during and after the treatment. The growth responses of strains to ampicillin concentrations were determined using in vitro growth curves. Using these results as input data, growth predictions were generated using a mathematical model to simulate the competitive growth of E. coli strains in a pig intestine under specified plasma concentration profiles of ampicillin.

Results: In vitro growth results demonstrated that the resistant strains did not carry a fitness cost for their resistance, and that the most susceptible strains were more affected by increasing concentrations of antibiotics that the rest of the strains. The modeling revealed that short treatment duration resulted in lower levels of resistance and that dosing frequency did not substantially influence the growth of resistant strains. Resistance levels were found to be sensitive to the number of competing strains, and this effect was enhanced by longer duration of treatment. High excretion of bacteria from the intestine favored resistant strains over sensitive strains, but at the same time it resulted in a faster return to pre-treatment levels after the treatment ended. When the duration of high excretion was set to be limited to the treatment time (i.e. the treatment was assumed to result in a cure of diarrhea) resistant strains required longer time to reach the previous level.

Conclusion: No fitness cost was found to be associated with ampicillin resistance in E. coli. Besides dosing factors, epidemiological factors (such as number of competing strains and bacterial excretion) influenced resistance development and need to be considered further in relation to optimal treatment strategies. The modeling approach used in the study is generic, and could be used for prediction of the effect of treatment with other drugs and other administration routes for effect on resistance development in the intestine of pigs.

General information
Modelling severe Staphylococcus aureus sepsis in conscious pigs: are implications for animal welfare justified?

A porcine model of haematogenous Staphylococcus aureus sepsis has previously been established in our research group. In these studies, pigs developed severe sepsis including liver dysfunction during a 48 h study period. As pigs were awake during the study, animal welfare was challenged by the severity of induced disease, which in some cases necessitated humane euthanasia. A pilot study was therefore performed in order to establish the sufficient inoculum concentration and application protocol needed to produce signs of liver dysfunction within limits of our pre-defined humane endpoints. Four pigs received $1 \times 10^8$ cfu/kg BW of S. aureus, and two controls were sham inoculated with saline. A fixed infusion rate of 3 mL/min was used, while the inoculum concentration, i.e., the dose volume, was changed between the pigs. The following dose volumes were used: 10 mL (n = 1), 20 mL (n = 2), and 30 mL (n = 1), corresponding to infusion durations of 3.33, 6.66, and 10 min at dose rates of $3 \times 10^7$, $1.5 \times 10^7$, and $1 \times 10^7$ cfu/min/kg BW, respectively. Blood samples were drawn for complete blood count, clinical chemistry, and inflammatory markers before and every 6 h after inoculation. Prior to euthanasia, a galactose elimination capacity test was performed to assess liver function. Pigs were euthanised 48 h post inoculation for necropsy and histopathological evaluation. While infusion times of 6.66 min, and higher, did not induce liver dysfunction (n = 3), the infusion time of 3.33 min (n = 1) caused alterations in parameters similar to what had been seen in our previous studies, i.e., increasing bilirubin and aspartate aminotransferase, as well as histopathological occurrence of intravascular fibrin split products in the liver. This pig was however euthanised after 30 h, according to humane endpoints. A usable balance between scientific purpose and animal welfare could not be achieved, and we therefore find it hard to justify further use of this conscious porcine sepsis model. In order to make a model of translational relevance for human sepsis, we suggest that future model versions should use long-term anaesthesia.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, University of Copenhagen
Number of pages: 10
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: BMC Research Notes
Volume: 9
Issue number: 1
Article number: 99
ISSN (Print): 1756-0500
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.801 SJR 0.691 CiteScore 1.54
Web of Science (2017): Indexed yes
Scopus rating (2016): CiteScore 1.29 SJR 0.662 SNIP 0.7
Web of Science (2016): Indexed yes
Models to Estimate Lactation Curves of Milk Yield and Somatic Cell Count in Dairy Cows at the Herd Level for the Use in Simulations and Predictive Models

Typically, central milk recording data from dairy herds are recorded less than monthly. Over-fitting early in lactation periods is a challenge, which we explored in different ways by reducing the number of parameters needed to describe the milk yield and somatic cell count of individual cows. Furthermore, we investigated how the parameters of lactation models correlate between parities and from dam to offspring. The aim of the study was to provide simple and robust models for cow level milk yield and somatic cell count for fitting to sparse data to parameterize herd- and cow-specific simulation of dairy herds. Data from 610 Danish Holstein herds were used to determine parity traits in milk production regarding milk yield and somatic cell count of individual cows. Parity was stratified in first, second, and third and higher for milk, and first to sixth and higher for somatic cell count. Fitting of herd level parameters allowed for cow level lactation curves with three, two, or one parameters per lactation. Correlations of milk yield and somatic cell count were estimated between lactations and between dam and offspring. The shape of the lactation curves varied markedly between farms. The correlation between lactations for milk yield and somatic cell count was 0.2–0.6 and significant on more than 95% of farms. The variation in the daily milk yield was observed to be a source of variation to the somatic cell count, and the total somatic cell count was less correlated with the milk production than somatic cells per milliliter. A positive correlation was found between relative levels of the total somatic cell count and the milk yield. The variation of lactation and somatic cell count curves between farms highlights the importance of a herd level approach. The one-parameter per cow model using a herd level curve allows for estimating the cow production level from first the recording in the parity, while a two-parameter model requires more recordings for a credible estimate, but may more precisely predict persistence, and given the independence of parameters, these can be easily drawn for use in simulation models. We also conclude that using total somatic cell count may stabilize models, and therefore, the dilution factor is of importance in Danish Holstein.

General information
State: Published
Organisations: Department of Applied Mathematics and Computer Science, National Veterinary Institute, Section for Epidemiology, Dynamical Systems, University of Copenhagen
Authors: Græsbøll, K. (Intern), Kirkeby, C. T. (Intern), Nielsen, S. S. (Ekstern), Hisham Beshara Halasa, T. (Intern), Toft, N. (Intern), Christiansen, L. E. (Intern)
Number of pages: 10
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Frontiers in Veterinary Science
Volume: 3
Article number: 115
ISSN (Print): 2297-1769
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Molecular tracing of viral diseases in aquaculture

General information
State: Published
Organisations: Section for Virology, National Veterinary Institute
Authors: Mikkelsen, S. S. (Intern), Bigarre, L. (Ekstern), Jensen, B. B. (Ekstern), Kristoffersen, A. B. (Ekstern), Jansen, P. A. (Ekstern), Panzarin, V. (Ekstern), Bayliss, S. C. (Ekstern), Avarre, J. C. (Ekstern), Olesen, N. J. (Intern)
Number of pages: 6
Pages: 46-51
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Bulletin of the European Association of Fish Pathologists
Volume: 36
Issue number: 1
ISSN (Print): 0108-0288
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 0.5 SJR 0.268 SNIP 0.404
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 0.49 SJR 0.222 SNIP 0.41
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.265 SNIP 0.48 CiteScore 0.64
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.345 SNIP 0.435 CiteScore 0.68
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.384 SNIP 0.428 CiteScore 0.62
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.257 SNIP 0.491 CiteScore 0.47
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.246 SNIP 0.47 CiteScore 0.41
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.349 SNIP 0.531
BFI (2009): BFI-level 1
Monitoring diseases based on register data: Methods and application in the Danish swine production

The spread of diseases is one of the most important threats to animal production and public health. Disease spread causes considerable economic losses for the agricultural sector and constitutes trade-limiting factors, as transmission to countries free from disease should be avoided. Monitoring and surveillance systems are critical for the timely and effective control of infectious diseases. The ability of a system to detect changes in the disease burden depends on the choice of data source. Many factors can lead to inconsistent data collection among populations and it is therefore important to assess the quality of data before use in disease monitoring and surveillance. Over the past decade, several studies have focused on using statistical control methods to detect outbreaks of (re-)emerging diseases in the context of syndromic surveillance – both in human and veterinary medicine – in an attempt to supplement traditional sentinel surveillance. However, it may not be possible to generalize the performance of these methods to the context of other countries (where data have different characteristics), or to the context of endemic diseases. Lower incidence rates are normally expected for endemic diseases compared to highly infectious (re-emerging) diseases, due to control measures such as vaccination or health management programs. Furthermore, the data collected differ from those obtained from traditional surveillance (generally related to incidence monitoring), due to its focus on the endemic scenario, with less frequently sampled data. This reflects the added complexity of monitoring endemic diseases, as disease burden is affected not only by the incidence, but also by the duration and recovery rate. The aim of this thesis was to evaluate existing register data related to veterinary health, as a tool for monitoring swine diseases in Denmark. This included: i) describing and evaluating the quality of data (regarding the potential for disease monitoring and surveillance) in Danish databases related to swine health; ii) assessing the feasibility of studying changes in data records over time to detect changes that might indicate disease spread between swine herds; iii) evaluating the performance of different time-series methods for the monitoring and surveillance of endemic diseases, as well as assessing the impact of noise in the data on the results when using these methods. Some of the work presented was focused on endemic diseases, using Porcine Reproductive and Respiratory Syndrome (PRRS) as example. Interviews were conducted with relevant stakeholders in order to assess the data quality of seven databases: the Central Husbandry Register (CHR), the swine movement database (SMD), the national Danish database of drugs for veterinary use (VetStat), laboratory diagnostic data from the National Veterinary Institute – Technical University of Denmark (DTU-Vet lab) and the Pig Research Centre - SEGES (VSP-SEGES lab), the Specific Pathogen Free System (SPF System) and the Meat Inspection database. The guidelines from the European Centre for Disease Prevention and Control (ECDC) for monitoring data quality and surveillance systems were used. The findings showed that limitations included delayed transfer of data to databases and incomplete representation of Danish swine herds. Laboratory submission data for testing PRRS were used to study temporal changes in data records, due to the large amount of diagnostic data available. The laboratory data proved to be useful for monitoring temporal patterns of disease occurrence. The fact that some Danish swine herds are tested monthly allows for changes in disease prevalence and incidence to be monitored, which is an example of sentinel surveillance. However, for other herds, the frequency of testing (i.e., the representativeness of the data) depends on factors such as the herd status, farmer compliance, the value of the animal, commercial purposes and ongoing control and eradication programs. This limitation did not apply to the mortality data, which is available for all Danish swine herds on a monthly basis. However, observed changes might be due to disease occurrence, or as a result of changes in herd management or a lack of accuracy in the calculation of mortality. Several scenarios representative of changes in endemic disease sero-prevalence programs were simulated to test the
performance of different monitoring methods. These included univariate process control algorithms applied directly to the simulated data, as well as using the forecast errors and trend-based methods. The performance of these methods was evaluated based on the sensitivity and time taken to detect changes, which showed that some methods were more efficient than others for specific patterns. Therefore, choosing a single temporal monitoring method is challenging, and the objectives of the monitoring program and the differing performance of the methods in detecting a specific pattern should be taken into account. Changes in the noise of the data had an impact on the univariate process control algorithms, while the trend-based methods provided a consistent approach to monitoring changes in disease or sero-prevalence. The findings of this thesis may serve as a basis for the improvement of monitoring swine diseases in Denmark. Although the available databases have the potential for use in disease monitoring and surveillance of swine herds in Denmark, improvements are needed for accurate and real-time implementation. Further research relating to the improvement of data quality, as well as combining different data sources for monitoring endemic diseases in Denmark is needed.

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology
Authors: Lopes Antunes, A. C. (Intern), Toft, N. (Intern), Hisham Beshara Halasa, T. (Intern)
Number of pages: 44
Publication date: 2016

Publication information
Place of publication: Frederiksberg C
Publisher: National Veterinary Institute, Technical University of Denmark
Original language: English
Main Research Area: Technical/natural sciences
Electronic versions: ACLAN_thesis UPLOAD.pdf

Relations
Projects:
Monitoring diseases based on register data: Methods and application in the Danish swine production
Source: Publication PreSubmission
Source-ID: 131791093
Publication: Research › Ph.D. thesis – Annual report year: 2017

Monitoring endemic livestock diseases using laboratory diagnostic data: A simulation study to evaluate the performance of univariate process monitoring control algorithms
Surveillance systems are critical for accurate, timely monitoring and effective disease control. In this study, we investigated the performance of univariate process monitoring control algorithms in detecting changes in seroprevalence for endemic diseases. We also assessed the effect of sample size (number of sentinel herds tested in the surveillance system) on the performance of the algorithms.

Three univariate process monitoring control algorithms were compared: Shewart p Chart 1 (PSHEW), Cumulative Sum 2 (CUSUM) and Exponentially Weighted Moving Average 3 (EWMA). Increases in seroprevalence were simulated from 0.10 to 0.15 and 0.20 over 4, 8, 24, 52 and 104 weeks. Each epidemic scenario was run with 2000 iterations. The cumulative sensitivity 4 (CumSe) and timeliness were used to evaluate the algorithms’ performance with a 1% false alarm rate. Using these performance evaluation criteria, it was possible to assess the accuracy and timeliness of the surveillance system working in real-time.

The results showed that EWMA and PSHEW had higher CumSe (when compared with the CUSUM) from week 1 until the end of the period for all simulated scenarios. Changes in seroprevalence from 0.10 to 0.20 were more easily detected (higher CumSe) than changes from 0.10 to 0.15 for all three algorithms. Similar results were found with EWMA and PSHEW, based on the median time to detection. Changes in the seroprevalence were detected later with CUSUM, compared to EWMA and PSHEW for the different scenarios. Increasing the sample size 10 fold halved the time to detection (CumSe = 1), whereas increasing the sample size 100 fold reduced the time to detection by a factor of 6.

This study investigated the performance of three univariate process monitoring control algorithms in monitoring endemic diseases. It was shown that automated systems based on these detection methods identified changes in seroprevalence at different times. Increasing the number of tested herds would lead to faster detection. However, the practical implications of increasing the sample size (such as the costs associated with the disease) should also be taken into account.

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, National Veterinary Institute Sweden
Authors: Lopes Antunes, A. C. (Intern), Dorea, F. (Ekstern), Hisham Beshara Halasa, T. (Intern), Toft, N. (Intern)
Pages: 15-20
Multi-stage subunit vaccine development against Mycobacterium paratuberculosis and Johne's disease in ruminants

Mycobacterium avium subsb. paratuberculosis (Map) is the causal agent of paratuberculosis or Johne's disease (JD) in ruminants. JD mainly affects the small intestine and the GALT, but is otherwise a typical mycobacterial disease with granulomatous inflammation and slow Map replication in macrophages. The disease progression is very slow with neonatal animals being the most susceptible to infection, but without development of detectable IFN-γ responses for
months after infection and rarely with clinical disease before the second or third year of life. Available whole cell vaccines against paratuberculosis provide only partial protection and interfere with diagnostic tests for JD and surveillance for bovine TB. In contrast, recombinant subunit vaccines can be designed to be used without compromising control of bTB and Map.

Taking advantage of data from mouse TB studies, and early Map vaccination- and field-studies we developed a vaccine with a single recombinant fusion protein comprising four acute-stage antigens (Ags) and one latent-stage Ag formulated in adjuvant (FET-vaccine). In post-exposure vaccination of calves and goats with necropsy 8-12 months post inoculation, we determined that vaccination at an immunocompetent age 4 months after neonatal inoculation provided better protection than early vaccination at the time of inoculation. In pre-exposure vaccination of young calves 2-11 weeks of age followed by high-dose Map challenge, the observed protection was variable, without any correlation with age and less protective than animals vaccinated with killed whole-cell Map vaccine. Short-term studies with killing 9 weeks post challenge failed to show any protective effect of vaccination, while some animals were protected in longer studies with killing 28 weeks post inoculation. Collectively, these results indicate that induction of protective cell-mediated immunity to Map is more dependent on immunocompetence at time of vaccination than early vaccination, and that vaccine efficacy can only reliably be evaluated in long-term studies.

It is a common perception that vaccines against mycobacterial infections should induce Th1 responses, characterized by Ag-specific IFN-γ and possibly polyfunctional CD4+ T cells, to provide sustained protection. This is in line with our early observations of a reduced IFN-γ response to vaccination in neonates compared to the better protected older calves, but in vaccination-challenge studies protection was not associated with level of FET-specific IFN-γ production, and Map-specific IFN-γ production appeared as a surrogate of disease with an inverse relationship to level of Map in tissues at slaughter. Polyfunctional T cells were induced by FET vaccination, but could not be sustained during the long-term infection although FET- and Map-specific IFN-γ levels increased throughout the study period.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology
Authors: Jungersen, G. (Intern)
Number of pages: 1
Publication date: 2016
Event: Abstract from BSI/NVVI Annual Congress 2016, Liverpool, United Kingdom.
Main Research Area: Technical/natural sciences
Electronic versions:
Jungersen_Abstract_Friday_One_HealthTB_vaccines.pdf
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2016

Multistain models predict sequential multidrug treatment strategies to result in less antimicrobial resistance than combination treatment

Background: Combination treatment is increasingly used to fight infections caused by bacteria resistant to two or more antimicrobials. While multiple studies have evaluated treatment strategies to minimize the emergence of resistant strains for single antimicrobial treatment, fewer studies have considered combination treatments. The current study modeled bacterial growth in the intestine of pigs after intramuscular combination treatment (i.e. using two antibiotics simultaneously) and sequential treatments (i.e. alternating between two antibiotics) in order to identify the factors that favor the sensitive fraction of the commensal flora. Growth parameters for competing bacterial strains were estimated from the combined in vitro pharmacodynamic effect of two antimicrobials using the relationship between concentration and net bacterial growth rate. Predictions of in vivo bacterial growth were generated by a mathematical model of the competitive growth of multiple strains of Escherichia coli. Results: Simulation studies showed that sequential use of tetracycline and ampicillin reduced the level of double resistance, when compared to the combination treatment. The effect of the cycling frequency (how frequently antibiotics are alternated in a sequential treatment) of the two drugs was dependent upon the order in which the two drugs were used. Conclusion: Sequential treatment was more effective in preventing the growth of resistant strains when compared to the combination treatment. The cycling frequency did not play a role in suppressing the growth of resistant strains, but the specific order of the two antimicrobials did. Predictions made from the study could be used to redesign multidrug treatment strategies not only for intramuscular treatment in pigs, but also for other dosing routes.

General information
State: Published
Organisations: Department of Applied Mathematics and Computer Science, Dynamical Systems, National Veterinary Institute, Section for Epidemiology, University of Copenhagen, University of Glasgow
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Number of pages: 10
Publication date: 2016
Main Research Area: Technical/natural sciences
Publication information
Journal: B M C Microbiology
Volume: 16
Natural Pig Plasma Immunoglobulins Have Anti-Bacterial Effects: Potential for Use as Feed Supplement for Treatment of Intestinal Infections in Pigs

There is an increasing demand for non-antibiotics solutions to control infectious disease in intensive pig production. Here, one such alternative, namely pig antibodies purified from slaughterhouse blood was investigated in order to elucidate its potential usability to control post-weaning diarrhoea (PWD), which is one of the top indications for antibiotics usage in the pig production. A very cost-efficient and rapid one-step expanded bed adsorption (EBA) chromatography procedure was used to purify pig immunoglobulin G from slaughterhouse pig plasma (more than 100 litres), resulting in >85% pure pig IgG (pplG). The pplG thus comprised natural pig immunoglobulins and was subsequently shown to contain activity towards four pig-relevant bacterial strains (three different types of Escherichia coli and one type of Salmonella enterica) but not towards a fish pathogen (Yersinia ruckeri), and was demonstrated to inhibit the binding of the four pig relevant bacteria to a pig intestinal cell line (IPEC-J2). Finally it was demonstrated in an in vivo weaning piglet model for intestinal colonization with an E. coli F4+ challenge strain that pplG given in the feed significantly reduced shedding of the challenge strain, reduced the proportion of the bacterial family Enterobacteriaceae, increased the proportion of families Enterococccaeae and Streptococccaeae and generally increased ileal microbiota diversity. Conclusively, our data support the idea that natural IgG directly purified from pig plasma and given as a feed supplement can be used in modern swine production as an efficient and cost-effective means for reducing both occurrence of PWD and antibiotics usage and with a potential for the prevention and treatment of other intestinal infectious diseases even if the causative agent might not be known.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Section for Bacteriology, Pathology and Parasitology, Upfront Chromatography A/S
Authors: Hedegaard, C. J. (Intern), Strube, M. L. (Intern), Hansen, M. B. (Ekstern), Lindved, B. K. (Ekstern), Lihme, A. (Ekstern), Boye, M. (Intern), Heegaard, P. M. H. (Intern)
Number of pages: 14
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: P L o S One
Volume: 11
Issue number: 1
Article number: e0147373
ISSN (Print): 1932-6203
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.01 SJR 1.164 SNIP 1.111
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.11 SJR 1.236 SNIP 1.101
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.427 SNIP 1.136 CiteScore 3.32
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.559 SNIP 1.148 CiteScore 3.54
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.772 SNIP 1.153 CiteScore 3.94
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.982 SNIP 1.156 CiteScore 4.15
Necropsy Findings of 11 White-Beaked Dolphins (Lagenorhynchus albirostris) Stranded in Denmark During 2008-2014

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Aarhus University Hospital, Fisheries and Maritime Museum, Marine Mammal Atlas of Denmark, Aalborg University
Authors: Alstrup, A. K. O. (Ekstern), Jensen, L. F. (Ekstern), Hansen, M. S. (Intern), Kinze, C. C. (Ekstern), Hammer, T. (Ekstern)
Number of pages: 8
Pages: 292-299
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Aquatic Mammals
Volume: 42
Issue number: 3
ISSN (Print): 0167-5427
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.618 SJR 0.474 CiteScore 0.83
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.446 SNIP 0.602 CiteScore 0.86
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.453 SNIP 0.429 CiteScore 0.77
BFI (2014): BFI-level 1
Recognition of neoantigens that are formed as a consequence of DNA damage is likely to form a major driving force behind the clinical activity of cancer immunotherapies such as T-cell checkpoint blockade and adoptive T-cell therapy. Therefore, strategies to selectively enhance T-cell reactivity against genetically defined neoantigens are currently under development. In mouse models, T-cell pressure can sculpt the antigenicity of tumours, resulting in the emergence of tumours that lack defined mutant antigens. However, whether the T-cell-recognized neoantigen repertoire in human cancers is constant over time is unclear. Here we analyse the stability of neoantigen-specific T-cell responses and the antigens they recognize in two patients with stage IV melanoma treated by adoptive T-cell transfer. The T-cell-recognized neoantigens can be selectively lost from the tumour cell population, either by overall reduced expression of the genes or loss of the mutant alleles. Notably, loss of expression of T-cell-recognized neoantigens was accompanied by development of neoantigen-specific T-cell reactivity in tumour-infiltrating lymphocytes. These data demonstrate the dynamic interactions between cancer cells and T cells, which suggest that T cells mediate neoantigen immunoediting, and indicate that the therapeutic induction of broad neoantigen-specific T-cell responses should be used to avoid tumour resistance.
Next-generation detection of antigen-responsive T cells using DNA barcode-labeled peptide-major histocompatibility complex I multimers

Identification of antigenic peptides recognized by T cells is important for understanding and treating immune related diseases. Current cytometry-based approaches are limited to simultaneous screening of T cell reactivity towards 10-100 distinct peptide specificities, which poorly match the large diversity of T cell recognition in humans. Consequently it has been impossible to comprehensively analyze T cell responsiveness in cancer, infectious and autoimmune diseases. We present and validate a novel technology that enables parallel detection of numerous different peptide-MHC responsive T cells in a single sample using >1000 different peptide-MHC multimers labeled with individual DNA barcodes. After isolation of MHC multimer binding T cells their recognition are revealed by amplification and sequencing of the MHC multimer-associated DNA barcodes. The relative frequency of the sequenced DNA barcodes originating from a given peptide-MHC motif relates to the size of the antigen-responsive T cell population. We have demonstrated the use of large panels of >1000 DNA barcoded MHC multimers for detection of rare T cell populations of virus and cancer-restricted origin in various
tissues and compared with combinatorial encoding of fluorescent-labeled MHC multimers. Finally, we have demonstrated that this technology can be applied for multiplex T cell detection both in limited biological samples, such as uncultured tumor material, and for simultaneous assessment of target recognition and functional capability of T cells. This technology enables true high-throughput detection of antigen-responsive T cells and will advance our understanding of immune recognition from model antigens to genomewide immune assessments on a personalized basis.

**General information**

State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Department of Systems Biology, Center for Biological Sequence Analysis, Copenhagen University Hospital, Immudex
Number of pages: 1
Pages: 8-8
Publication date: 2016
Conference: ICI 2016 International Congress of Immunology, Melbourne, Australia, 21/08/2016 - 21/08/2016
Main Research Area: Technical/natural sciences

**Publication information**

Journal: European Journal of Immunology
Volume: 46
Issue number: S1
Article number: 1831
ISSN (Print): 0014-2980
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.59 SJR 2.206 SNIP 0.92
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.61 SJR 2.525 SNIP 0.927
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.588 SNIP 0.965 CiteScore 3.85
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.672 SNIP 0.972 CiteScore 3.83
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 2.876 SNIP 1.05 CiteScore 4.3
ISSI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 2.989 SNIP 1.063 CiteScore 4.62
ISSI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 3.255 SNIP 1.025 CiteScore 4.69
ISSI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 3.363 SNIP 0.99
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 3.188 SNIP 1.007
Web of Science (2009): Indexed yes
Next-generation detection of antigen-responsive T cells using DNA barcode-labeled peptide-major histocompatibility complex I multimers

Identification of antigenic peptides recognized by T cells is important for understanding and treating immune-related diseases. Current cytometry-based approaches are limited to simultaneous screening of T cell reactivity towards 10-100 distinct peptide specificities, which poorly match the large diversity of T cell recognition in humans. Consequently, it has been impossible to comprehensively analyze T cell responsiveness in cancer, infectious, and autoimmune diseases. We present and validate a novel technology that enables parallel detection of numerous different peptide-MHC responsive T cells in a single sample using >1000 different peptide-MHC multimers labeled with individual DNA barcodes. After isolation of MHC multimer binding T cells, their recognition are revealed by amplification and sequencing of the MHC multimer-associated DNA barcodes. The relative frequency of the sequenced DNA barcodes originating from a given peptide-MHC motif relates to the size of the antigen-responsive T cell population. We have demonstrated the use of large panels of >1000 DNA barcoded MHC multimers for detection of rare T cell populations of virus and cancer-restricted origin in various tissues and compared with combinatorial encoding of fluorescent-labeled MHC multimers. Finally, we have demonstrated that this technology can be applied for multiplex T cell detection both in limited biological samples, such as uncultured tumor material, and for simultaneous assessment of target recognition and functional capability of T cells. This technology enables true high-throughput detection of antigen-responsive T cells and will advance our understanding of immune recognition from model antigens to genomewide immune assessments on a personalized basis.
Norovirus Polymerase Fidelity Contributes to Viral Transmission In Vivo
Intrahost genetic diversity and replication error rates are intricately linked to RNA virus pathogenesis, with alterations in viral polymerase fidelity typically leading to attenuation during infections in vivo. We have previously shown that norovirus intrahost genetic diversity also influences viral pathogenesis using the murine norovirus model, as increasing viral mutation frequency using a mutagenic nucleoside resulted in clearance of a persistent infection in mice. Given the role of replication fidelity and genetic diversity in pathogenesis, we have now investigated whether polymerase fidelity can also impact virus transmission between susceptible hosts. We have identified a high-fidelity norovirus RNA-dependent RNA polymerase mutant (I391L) which displays delayed replication kinetics in vivo but not in cell culture. The I391L polymerase mutant also exhibited lower transmission rates between susceptible hosts than the wild-type virus and, most notably, another replication defective mutant that has wild-type levels of polymerase fidelity. These results provide the first experimental evidence that norovirus polymerase fidelity contributes to virus transmission between hosts and that maintaining diversity is important for the establishment of infection. This work supports the hypothesis that the reduced polymerase fidelity of the pandemic GII.4 human norovirus isolates may contribute to their global dominance.
Novel Adjuvants and Immunomodulators for Veterinary Vaccines

Adjuvants are crucial for efficacy of vaccines, especially subunit and recombinant vaccines. Rational vaccine design, including knowledge-based and molecularly defined adjuvants tailored for directing and potentiating specific types of host immune responses towards the antigens included in the vaccine is becoming a reality with our increased understanding of innate and adaptive immune activation. This will allow future vaccines to induce immune reactivity having adequate specificity as well as protective and recallable immune effector mechanisms in appropriate body compartments, including mucosal surfaces. Here we describe these new developments and, when possible, relate new immunological knowledge to the many years of experience with traditional, empirical adjuvants. Finally, some protocols are given for production of emulsion (oil-based) and liposome-based adjuvant/antigen formulations.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Technical University of Denmark
Authors: Heegaard, P. M. H. (Intern), Fang, Y. (Ekstern), Jungersen, G. (Intern)
Number of pages: 20
Pages: 63-82
Publication date: 2016

Host publication information
Title of host publication: Vaccine Technologies for Veterinary Viral Diseases : Methods and Protocols
Place of publication: New York
Publisher: Springer Science+Business Media
Editor: Brun, A.
Chapter: 5
Series: Methods in Molecular Biology
Volume: 1349
ISSN: 1064-3745
Main Research Area: Technical/natural sciences
Adjuvant, Immunomodulator, Innate immune system, Protective immune responses, Vaccination
DOIs:
10.1007/978-1-4939-3008-1_5
Source: FindIt
Source-ID: 2286910841
Publication: Research - peer-review › Book chapter – Annual report year: 2016

Novel regulators of CD8+ T-cell functions in the skin

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, University of Queensland
Authors: Bridge, J. A. (Ekstern), Overgaard, N. H. (Intern), Cruz, J. L. G. (Ekstern), Veitch, M. (Ekstern), Frazer, I. H. (Ekstern), Steptoe, R. (Ekstern), Wells, J. W. (Ekstern)
Number of pages: 1
Publication date: 2016
Event: Abstract from 10th Asia-Pacific Dermatology Conference, Melbourne, Australia.
Main Research Area: Technical/natural sciences
Electronic versions:
Abstract_ASDR_Jennifer_Bridge_2016.pdf
Source: PublicationPreSubmission
Source-ID: 127762034
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2016

Observations of movement dynamics of flying insects using high resolution lidar

Insects are fundamental to ecosystem functioning and biodiversity, yet the study of insect movement, dispersal and activity patterns remains a challenge. Here we present results from a novel high resolution laser-radar (lidar) system for quantifying flying insect abundance recorded during one summer night in Sweden. We compare lidar recordings with data from a light trap deployed alongside the lidar. A total of 22808 insect were recorded, and the relative temporal quantities measured matched the quantities recorded with the light trap within a radius of 5m. Lidar records showed that small insects (wing size <2.5mm2 in cross-section) moved across the field and clustered near the light trap around 22:00 local time, while larger insects (wing size >2.5mm2 in cross-section) were most abundant near the lidar beam before 22:00 and then moved towards the light trap between 22:00 and 23:30. We could distinguish three insect clusters based on morphology and found that two contained insects predominantly recorded above the field in the evening, whereas the third
was formed by insects near the forest at around 21:30. Together our results demonstrate the capability of lidar for distinguishing different types of insect during flight and quantifying their movements.

**General information**

State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Lund University
Authors: Kirkeby, C. T. (Intern), Wellenreuther, M. (Ekstern), Brydegaard, M. (Ekstern)
Number of pages: 11
Publication date: 2016
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Scientific Reports
Volume: 6
Article number: 29083
ISSN (Print): 2045-2322
Ratings:
- BFI (2018): BFI-level 1
- Web of Science (2018): Indexed yes
- BFI (2017): BFI-level 1
- Scopus rating (2017): CiteScore 4.36 SJR 1.533 SNIP 1.245
- Web of Science (2017): Indexed yes
- BFI (2016): BFI-level 1
- Scopus rating (2016): CiteScore 4.63 SJR 1.692 SNIP 1.354
- Web of Science (2016): Indexed yes
- BFI (2015): BFI-level 1
- Scopus rating (2015): SJR 2.034 SNIP 1.597 CiteScore 5.3
- Web of Science (2015): Indexed yes
- BFI (2014): BFI-level 1
- Scopus rating (2014): SJR 2.163 SNIP 1.554 CiteScore 4.75
- Web of Science (2014): Indexed yes
- BFI (2013): BFI-level 1
- Scopus rating (2013): SJR 1.998 SNIP 1.57 CiteScore 4.06
- ISI indexed (2013): ISI indexed yes
- Web of Science (2013): Indexed yes
- BFI (2012): BFI-level 1
- Scopus rating (2012): SJR 1.531 SNIP 0.962 CiteScore 2.44
- ISI indexed (2012): ISI indexed yes
- Web of Science (2012): Indexed yes
- ISI indexed (2011): ISI indexed no

Original language: English
Electronic versions:
- srep29083.pdf
- DOIs: 10.1038/srep29083

Publication: Research - peer-review › Journal article – Annual report year: 2016

**Occurrence of Swine Enteric Coronavirus (SeCoV) infection during 2016 within Central Eastern Europe**

**General information**

State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Bøtner, A. (Intern), Rasmussen, T. B. (Intern), Strandbygaard, B. (Intern), Belsham, G. (Intern)
Pages: 103-103
Publication date: 2016

**Host publication information**

Title of host publication: EPIZONE 10th annual meeting : Programme & abstracts
Place of publication: Madrid, Spain
Main Research Area: Technical/natural sciences
Oil adjuvant elevates protection of rainbow trout (Oncorhynchus my-kiss) following injection vaccination against Yersinia ruckeri

Enteric redmouth disease (ERM) caused by the fish pathogen Yersinia ruckeri is a major threat to freshwater production of rainbow trout throughout all life stages. Injection vaccination of rainbow trout against Y. ruckeri infection has been shown to confer better protection compared to the traditionally applied immersion vaccination. It may be hypothesized, based on experience from other vaccines, that adjuvants may increase the protective level of ERM injection vaccines even more. Controlled comparative vaccination studies conducted to investigate effects of the oil adjuvant Montanide™ ISA 763 A VG when added to an experimental Y. ruckeri bacterin (containing both biotype 1 and 2 of serotype O1). A total of 1000 fish with mean weight 19 g was divided into five different groups (in duplicated tanks 2 • 100 fish per group) 1) non-vaccinated control fish (NonVac), 2) fish injected with a commercial vaccine (AquaVac® Relera™) (ComVac), 3) fish injected with an experimental vaccine (ExpVac), 4) fish injected with an experimental vaccine + adjuvant (ExpVacAdj) and 5) fish injected with adjuvant alone (Adj). Injection of the experimental vaccine (both adjuvanted and non-adjuvanted) induced a significantly higher antibody (IgM) level, increased occurrence of IgM+ cells in spleen tissue and significant up-regulation of several immune genes. Additional experiments using a higher challenge dosage suggested an immune enhancing effect of the adjuvant as the challenge produced 100% mortality in the NonVac group, 60% mortality in both of ComVac and Adj groups and only 13 and 2.5% mortalities in the ExpVac and the ExpVacAdj groups, respectively.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Copenhagen
Authors: Jaafar, R. M. (Ekstern), Chetri, J. K. (Ekstern), Dalsgaard, I. (Intern), Al-Jubury, A. (Ekstern), Kania, P. W. (Ekstern), Skov, J. (Ekstern), Buchmann, K. (Ekstern)
Number of pages: 2
Pages: 65-66
Publication date: 2016
Conference: 2nd International Conference of Fish & Shellfish Immunology, Maine, United States, 26/06/2016 - 26/06/2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Fish and Shellfish Immunology
Volume: 53
Article number: O-022
ISSN (Print): 1050-4648
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.103 SJR 1.126 CiteScore 3.37
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.36 SJR 1.128 SNIP 1.142
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.265 SNIP 1.16 CiteScore 3.19
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.14 SNIP 1.098 CiteScore 2.92
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.997 SNIP 1.138 CiteScore 3.11
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Oekologisk fiskeopdræt kræver robuste fisk

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology
Authors: Andersen, N. G. (Intern), Madsen, L. (Intern)
Pages: 15-15
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Oekologi & Erhverv
Volume: 36
Issue number: 597
ISSN (Print): 1904-1586
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no

Scopus rating (2012): SJR 1.156 SNIP 1.169 CiteScore 3.02
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.209 SNIP 1.262 CiteScore 3.52
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.143 SNIP 1.06
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.979 SNIP 1.104
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 0.962 SNIP 1.061
Scopus rating (2007): SJR 0.864 SNIP 1.371
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.964 SNIP 1.303
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.808 SNIP 0.854
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.858 SNIP 1.141
Scopus rating (2003): SJR 0.707 SNIP 1.114
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.756 SNIP 1.3
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.673 SNIP 0.966
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.125 SNIP 1.088
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 1.122 SNIP 1.054
Original language: English
Rainbow trout, Yersinia ruckeri, Vaccination, Adjuvant
DOIs:
10.1016/j.fsi.2016.03.065
Source: FindIt
Source-ID: 2306257612
Publication: Research - peer-review › Conference abstract in journal – Annual report year: 2016
Optimised surveillance for paratuberculosis

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Section for Immunology and Vaccinology, University of Copenhagen
Authors: Kirkeby, C. T. (Intern), Græsbøll, K. (Intern), Nielsen, S. S. (Ekstern), Hisham Beshara Halasa, T. (Intern), Toft, N. (Intern), Jungersen, G. (Intern)
Number of pages: 1
Publication date: 2016
Event: Poster session presented at 13th International Colloquium on Paratuberculosis, Nantes, France.
Main Research Area: Technical/natural sciences

Bibliographical note
Poster for ICP 2016
Source: PublicationPreSubmission
Source-ID: 124272979
Publication: Research - peer-review › Poster – Annual report year: 2016

Oral fluid ELISAs for detection of antibodies against Actinobacillus pleuropneumoniae serotypes 2, 6 and 12

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Technical University of Denmark
Authors: Lauritsen, K. T. (Intern), Sørensen, N. (Ekstern), Lind, P. (Intern)
Number of pages: 1
Publication date: 2016

Host publication information
Title of host publication: Proceedings from 24th IPVS/8th ESPHM congress
Place of publication: Dublin, Ireland
Main Research Area: Technical/natural sciences
Conference: 24th International Pig Veterinary Society (IPVS) Congress, Dublin, Ireland, 07/06/2016 - 07/06/2016
Electronic versions: Spyt_abstract_det_trykte.JPG
Source: PublicationPreSubmission
Source-ID: 127551930
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2016

Oral fluid samples for the monitoring of PRRSV status and dynamics

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Danvet K/S, Boehringer Ingelheim AH
Authors: Holmgren, S. (Ekstern), Kvisgaard, L. K. (Intern), Bak, H. (Ekstern), Larsen, L. E. (Intern)
Pages: 578-578
Publication date: 2016

Host publication information
Title of host publication: 24th International Pig Veterinary Society Congress - abstracts book
Place of publication: Dublin, Ireland
Outbreaks of Aleutian mink disease in farmed mink (Neovison vison) in Denmark: molecular characterization by partial NS1 gene sequencing

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Department of Systems Biology, Center for Biological Sequence Analysis, Molecular Evolution, Department of Bio and Health Informatics, Kopenhagen Fur
Pages: 85-87
Publication date: 2016

Host publication information
Title of host publication: Proceedings of the XIth International Scientific Congress in Fur Animal Production
Place of publication: Helsinki, Finland
Publisher: Libris
Editors: Mäki-Tanila, A., Valaja, J., Mononen, J., Sironen, T., Vapalahti, O.
Series: Scientifur
Volume: 40
Number: 3/4
ISSN: 2445-6292
Main Research Area: Technical/natural sciences
Electronic versions:
IFASA2016_Vol.40_1_.pdf
Links:
Publication: Research › Conference abstract in proceedings – Annual report year: 2016

Overførsel af Aleutian Mink Disease Virus med lopper

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Section for Virology, KSL Consulting ApS, Kopenhagen Diagnostics, Aalborg University
Authors: Hartby, C. M. (Intern), Hammer Jensen, T. (Ekstern), Søholt Larsen, K. (Ekstern), Hansen, M. S. (Intern), Chriél, M. (Intern), Larsen, L. E. (Intern), Struve, T. (Ekstern), Hjulsager, C. K. (Intern)
Pages: 91-94
Publication date: 2016

Host publication information
Title of host publication: Faglig årsberetning 2015 : Kopenhagen Fur
Place of publication: Aarhus N
Publisher: Kopenhagen Fur
Main Research Area: Technical/natural sciences
Electronic versions:
Faglig_rsberetning_2015.pdf
Publication: Research › Report chapter – Annual report year: 2016

Overvågning af aviær influenza i vilde fugle i Danmark 2015

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, University of Copenhagen
Overweight and the feline gut microbiome - a pilot study

Compared with lean humans, the gut microbiota is altered in the obese. Whether these changes are due to an obesogenic diet, and whether the microbiota contributes to adiposity is currently discussed. In the cat population, where obesity is also prevalent, gut microbiome changes associated with obesity have not been studied. Consequently, the aim of this study was to compare the gut microbiota of lean cats, with that of overweight and obese cats. Seventy-seven rescue-shelter cats housed for ≥3 consecutive days were included in the study. Faecal samples were obtained by rectal swab and, when available, by a paired litter box sample. Body condition was assessed using a 9-point scoring system. DNA was extracted, and the 16S rRNA gene was amplified with a high-throughput quantitative real-time PCR chip. Overweight and obese cats had a significantly different gut microbiota compared to lean cats (p < 0.05), but this finding could not be linked to differences in specific bacterial groups. The rectal samples obtained higher DNA concentration than litter box samples (p < 0.0001). In conclusion, overweight and obese cats seem to have an altered gut microbiome as compared to lean cats.

Overvågning af influenza A virus i svin - Slutrapport 2015

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Krog, J. S. (Intern), Hjulsager, C. K. (Intern), Larsen, L. E. (Intern)
Number of pages: 29
Publication date: 2016

Overweight and the feline gut microbiome - a pilot study

Compared with lean humans, the gut microbiota is altered in the obese. Whether these changes are due to an obesogenic diet, and whether the microbiota contributes to adiposity is currently discussed. In the cat population, where obesity is also prevalent, gut microbiome changes associated with obesity have not been studied. Consequently, the aim of this study was to compare the gut microbiota of lean cats, with that of overweight and obese cats. Seventy-seven rescue-shelter cats housed for ≥3 consecutive days were included in the study. Faecal samples were obtained by rectal swab and, when available, by a paired litter box sample. Body condition was assessed using a 9-point scoring system. DNA was extracted, and the 16S rRNA gene was amplified with a high-throughput quantitative real-time PCR chip. Overweight and obese cats had a significantly different gut microbiota compared to lean cats (p < 0.05), but this finding could not be linked to differences in specific bacterial groups. The rectal samples obtained higher DNA concentration than litter box samples (p < 0.0001). In conclusion, overweight and obese cats seem to have an altered gut microbiome as compared to lean cats.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Copenhagen
Authors: Kieler, I. N. (Ekstern), Melbak, L. (Intern), Hansen, L. L. (Ekstern), Hermann-Bank, M. L. (Intern), Bjornvad, C. R. (Ekstern)
Number of pages: 7
Pages: 478-484
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Animal Physiology and Animal Nutrition
Volume: 100
Issue number: 3
ISSN (Print): 0931-2439
Ratings:
Partially differentiated polyfunctional T cells dominate the periphery after tumor-infiltrating lymphocytes therapy for cancer

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, University Hospital Herlev, Cardiff University, University of Warwick
Authors: Donia, M. (Ekstern), Westerlin Kjeldsen, J. (Ekstern), Andersen, R. (Ekstern), Wulff Westergaard, M. C. (Ekstern), Bianchin, V. (Ekstern), Legut, M. (Ekstern), Dolton, G. (Ekstern), Szomolay, B. (Ekstern), Ott, S. (Ekstern), Lyngaa, R. B. (Intern), Hadrup, S. R. (Intern), Kelvin Sewell, A. (Ekstern), Marie Svane, I. (Ekstern)
Pages: 19-19
Publication date: 2016

Intestinal, Gut microbiota, Cats, Obesity, qPCR

DOIs:
10.1111/jpn.12409

Source: FindIt
Source-ID: 2286856652
Publication: Research - peer-review › Journal article – Annual report year: 2015
Passive immunisation, an old idea revisited: Basic principles and application to modern animal production systems

Immunisation by administration of antibodies (immunoglobulins) has been known for more than one hundred years as a very efficient means of obtaining immediate, short-lived protection against infection and/or against the disease-causing effects of toxins from microbial pathogens and from other sources. Thus, due to its rapid action, passive immunisation is
often used to treat disease caused by infection and/or toxin exposure. However immunoglobulins may also be administered prior to exposure to infection and/or toxin, although they will not provide long-lasting protection as is seen with active immunisation (vaccination) in which an immunological memory is established by controlled exposure of the host to the pathogen in question. With multi-factorial infectious diseases in production animals, especially those that have proven hard to control by vaccination, the potential of passive immunisation remains big. This review highlights a number of examples on the use of passive immunisation for the control of infectious disease in the modern production of a range of animals, including pigs, cattle, sheep, goat, poultry and fish. Special emphasis is given on the enablement of passive immunisation strategies in these production systems through low cost and ease of use as well as on the sources, composition and purity of immunoglobulin preparations used and their benefits as compared to current measures, including vaccination (also comprising maternal vaccination), antibiotics and feed additives such as spray-dried plasma. It is concluded that provided highly efficient, relatively low-price immunoglobulin products are available, passive immunisation has a clear role in the modern animal production sector as a means of controlling infectious diseases, importantly with a very low risk of causing development of bacterial resistance, thus constituting a real and widely applicable alternative to antibiotics.
Peptide Vaccination Against Cancer Testis Antigens in Combination With Azacitidine for Patients With Myelodysplastic Syndrome and Acute Myeloid Leukemia: an ongoing phase I study

Myelodysplastic Syndrome (MDS) is a clonal disorder and characterized by increasing bone marrow failure due to accumulation of genetic and epigenetic changes in hematopoietic stem cells. Patients with high-risk disease have a poor prognosis and a high risk of progression to Acute Myeloid Leukemia (AML). The dysplastic cells harbor chromosomal breakage, point mutations and promoter hyper-methylation of tumor suppressor genes. For most patients, who are not eligible for bone marrow transplantation, hypomethylating agents, such as azacitidine (AZA), are currently the only treatment option. The demand for more effective therapies in this patient group is huge. Though the mechanism of AZA is not fully elucidated re-expression of tumor suppressor genes can serve as a mechanism for growth arrest. In addition, there is accumulating evidence for an up-regulation of cancer testis antigens (CTA), which could lead to increased immune recognition of tumor cells and immune-mediated tumor cell killing. CTA’s are known to be immunogenic and are only expressed at immunoprivileged sites and on malignant cells, making them attractive as targets for therapeutic cancer vaccination.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, University Hospital Herlev
Authors: Holmberg, S. (Ekstern), Ortved Gang, A. (Ekstern), Svane, I. (Ekstern), Høgh Dufva, I. (Ekstern), Hadrup, S. R. (Intern)
Number of pages: 2
Pages: 771-772
Publication date: 2016
Conference: 21st Congress of the European Hematology Association, Copenhagen, Denmark, 09/06/2016 - 09/06/2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Haematologica
Volume: 101
Issue number: S1
Phylogeny of the Viral Hemorrhagic Septicemia Virus in European Aquaculture

One of the most valuable aquaculture fish in Europe is the rainbow trout, Oncorhynchus mykiss, but the profitability of trout production is threatened by a highly lethal infectious disease, viral hemorrhagic septicemia (VHS), caused by the VHS virus (VHSV). For the past few decades, the subgenogroup Ia of VHSV has been the main cause of VHS outbreaks in European freshwater-farmed rainbow trout. Little is currently known, however, about the phylogenetic radiation of this Ia lineage into subordinate Ia clades and their subsequent geographical spread routes. We investigated this topic using the largest Ia-isolate dataset ever compiled, comprising 651 complete G gene sequences: 209 GenBank Ia isolates and 442 Ia isolates from this study. The sequences come from 11 European countries and cover the period 1971-2015. Based on
this dataset, we documented the extensive spread of the la population and the strong mixing of la isolates, assumed to be the result of the Europe-wide trout trade. For example, the la lineage underwent a radiation into nine la clades, most of which are difficult to allocate to a specific geographic distribution. Furthermore, we found indications for two rapid, large-scale population growth events, and identified three polytomies among the la clades, both of which possibly indicate a rapid radiation. However, only about 4% of la haplotypes (out of 398) occur in more than one European country. This apparently conflicting finding regarding the Europe-wide spread and mixing of la isolates can be explained by the high mutation rate of VHSV. Accordingly, the mean period of occurrence of a single la haplotype was less than a full year, and we found a substitution rate of up to $7.813 \times 10^{-4}$ nucleotides per site per year. Finally, we documented significant differences between Germany and Denmark regarding their VHS epidemiology, apparently due to those countries’ individual handling of VHS.
Pooling of faecal samples for quantitative virus diagnostics by real-time PCR

General information
State: Published
Organisations: National Veterinary Institute, Virology, Section for Virology
Authors: Hartby, C. M. (Intern), Andersen, M. R. (Intern), Kvisgaard, L. K. (Intern), Chriél, M. (Intern), Larsen, L. E. (Intern), Hjulsager, C. K. (Intern)
Pages: 27-30
Publication date: 2016

Host publication information
Title of host publication: Proceedings of the XIth International Scientific Congress in Fur Animal Production
Place of publication: Helsinki, Finland
Publisher: Libris
Editors: Mäki-Tanila, A., Valaja, J., Mononen, J., Sironen, T., Vapalahti, O.
Series: Scientifur
Volume: 40
Number: 3/4
ISSN: 2445-6292
Main Research Area: Technical/natural sciences
Electronic versions:
IFASA2016_Vol.40_1_.pdf
Links:
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2016

Potential bacterial core species associated with digital dermatitis in cattle herds identified by molecular profiling of interdigital skin samples

Although treponemes are consistently identified in tissue from bovine digital dermatitis (DD) lesions, the definitive etiology of this debilitating polymicrobial disease is still unresolved. To study the microbiomes of 27 DD-infected and 10 healthy interdigital skin samples, we used a combination of different molecular methods. Deep sequencing of the 16S rRNA gene variable regions V1–V2 showed that Treponema, Mycoplasma, Fusobacterium and Porphyromonas were the genera best differentiating the DD samples from the controls. Additional deep sequencing analysis of the most abundant genus, Treponema, targeting another variable region of the 16S rRNA gene, V3–V4, identified 15 different phylotypes, among which Treponema phagedenis-like and Treponema refringens-like species were the most abundant. Although the presence of Treponema spp., Fusobacterium necrophorum and Porphyromonas levii was confirmed by fluorescence in situ hybridization (FISH), the results for Mycoplasma spp. were inconclusive. Extensive treponemal epidermal infiltration, constituting more than 90% of the total bacterial population, was observed in 24 of the 27 DD samples. F. necrophorum and P. levii were superficially located in the epidermal lesions and were present in only a subset of samples. RT-qPCR analysis showed that treponemes were also actively expressing a panel of virulence factors at the site of infection. Our results further support the hypothesis that species belonging to the genus Treponema are major pathogens of DD and also provide sufficient clues to motivate additional research into the role of M. fermentans, F. necrophorum and P. levii in the etiology of DD.
Predicting spatial distribution of pathogens transmitted by ticks in northern Europe

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Section for Bacteriology, Pathology and Parasitology, Wageningen University & Research, National Veterinary Institute Sweden, ANSES - French Agency for Food, Environmental and Occupational Health & Safety, Central Veterinary Institute, Animal and Plant Health Agency
Authors: Cuellar, A. C. (Intern), Schou, K. K. (Intern), Moutailler, S. (Ekstern), Fach, P. (Ekstern), Delannoy, S. (Ekstern), van der Wal, F. (Ekstern), de Koeier, A. (Ekstern), Chirico, J. (Ekstern), Aspán, A. (Ekstern), Juremalm, M. (Ekstern), Mansfield, K. (Ekstern), Phipps, P. (Ekstern), Fooks, T. (Ekstern), Bødker, R. (Intern)
Number of pages: 15
Publication date: 2016

Host publication Information
Title of host publication: 3rd Conference on Neglected Vectors and Vector-Borne Diseases (EurNegVec): with MC and WG Meeting of the COST Action TD1303: Abstract book
Place of publication: ZARAGOZA
Publisher: European Science Foundation
Main Research Area: Technical/natural sciences
Conference: 3rd Conference on Neglected Vectors and Vector-Borne Diseases (EurNegVec): with MC and WG Meeting of the COST Action TD1303, Zaragoza, Spain, 24/05/2016 - 24/05/2016
Electronic versions: abstractszaragoza.pdf
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2016

Predicting spatial distribution of pathogens transmitted by ticks in Northern Europe

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Section for Bacteriology, Pathology and Parasitology, Wageningen University & Research, National Veterinary Institute Sweden, ANSES - French Agency for Food, Environmental and Occupational Health & Safety, Central Veterinary Institute, National Veterinary Institute Sweden, Animal and Plant Health Agency
Authors: Cuellar, A. C. (Intern), Schou, K. K. (Intern), Moutailler, S. (Ekstern), Fach, P. (Ekstern), Delannoy, S. (Ekstern), van der Wal, F. J. (Ekstern), de Koeier, A. (Ekstern), Chirico, J. (Ekstern), Aspán, A. (Ekstern), Juremalm, M. (Ekstern), Mansfield, K. (Ekstern), Phipps, P. (Ekstern), Fooks, T. (Ekstern), Bødker, R. (Intern)
Number of pages: 15
Publication date: 2016

Publication information
Media of output: Powerpoint
**Predicting spatial prevalence of tick pathogens in Northern Europe using satellite imagery**

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Section for Bacteriology, Pathology and Parasitology, ANSES - French Agency for Food, Environmental and Occupational Health & Safety, Wageningen University & Research, Animal and Plant Health Agency, National Veterinary Institute Sweden
Authors: Cuellar, A. C. (Intern), Schou, K. K. (Intern), Moutailler, S. (Ekstern), Fach, P. (Ekstern), Delannoy, S. (Ekstern), van der Wal, F. J. (Ekstern), de Koeiier, A. (Ekstern), Chirico, J. (Ekstern), Aspán, A. (Ekstern), Juremalm, M. (Ekstern), Mansfield, K. (Ekstern), Phipps, P. (Ekstern), Fooks, T. (Ekstern), Bødker, R. (Intern)
Number of pages: 1
Publication date: 2016
Event: Poster session presented at SVEPM, Elsinore, Denmark.
Main Research Area: Technical/natural sciences

**Preparation and self-assembly of amphiphilic polylysine dendrons**

Polylysine dendrons with lipid tails prepared by divergent solid-phase synthesis showed self-assembling properties in aqueous solutions. Herein, we present the synthesis of new amphiphilic polylysine dendrons with variable alkyl chain lengths (C1–C18) at the C-terminal. The dendrons were synthesized in moderate to quantitative yields by divergent solid-phase synthesis (SPS) employing an aldehyde linker. The self-assembling properties of the dendrons in aqueous solutions were studied by small angle neutron scattering (SANS) and dynamic light scattering (DLS). The self-assembling properties were influenced by the length of the alkyl chain and the generation number (Gn). Increasing the temperature and concentration did not have significant impact on the hydrodynamic diameter, but the self-assembling properties were influenced by the pH value. This demonstrated the need for positively charged amines in the head groups for the successful formation of controlled self-assemblies. Dendrons having alkyl chains below C8 did not self-assemble. Well-defined micellar structures observed with SANS were formed with alkyl chain lengths above C12. Large structures detected with DLS for dendrons with alkyl chain lengths above C12 are ascribed to intermicellar aggregates stabilized by hydrophobic and electrostatic forces in accordance with the observed pH effect. Finally, the cytotoxicity of the dendrons was evaluated in mouse fibroblast (NIH/3T3) and human embryonic kidney (HEK 293T) cells at 5, 10 and 20 μM concentrations. The dendrons showed low cytotoxicity, displaying cell viability well above 80%.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Institute for Energy Technology, University of Oslo
Authors: Mirsharghi, S. (Intern), Knudsen, K. D. (Ekstern), Bagherifam, S. (Ekstern), Nyström, B. (Ekstern), Boas, U. (Intern)
Number of pages: 15
Pages: 3597-3611
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: New Journal of Chemistry
Volume: 40
Issue number: 4
ISSN (Print): 1144-0546
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
Prevalence of paratuberculosis in the dairy goat and dairy sheep industries in Ontario, Canada

A cross-sectional study was undertaken (October 2010 to August 2011) to estimate the prevalence of paratuberculosis in the small ruminant dairy industries in Ontario, Canada. Blood and feces were sampled from 580 goats and 397 sheep (lactating and 2 y of age or older) that were randomly selected from 29 randomly selected dairy goat herds and 21 convenience -selected dairy sheep flocks. Fecal samples were analyzed using bacterial culture (BD BACTEC MGIT 960) and polymerase chain reaction (Tetracore); serum samples were tested with the Prionics Parachek enzyme-linked immunosorbent assay (ELISA). Using 3-test latent class Bayesian models, true farm-level prevalence was estimated to be 83.0% [95% probability interval (PI): 62.6% to 98.1%] for dairy goats and 66.8% (95% PI: 41.6% to 91.4%) for dairy sheep. The within-farm true prevalence for dairy goats was 35.2% (95% PI: 23.0% to 49.8%) and for dairy sheep was 48.3% (95% PI: 27.6% to 74.3%). These data indicate that a paratuberculosis control program for small ruminants is needed in
Prevention of foot-and-mouth disease in cattle using a prime-boost-vaccination strategy

Foot-and-mouth disease (FMD) is one of the most economically important infectious diseases of production animals globally. Vaccination can help to control this disease, however, current vaccines are imperfect. They are made using chemically inactivated FMD virus (FMDV) that is produced in mammalian cell culture under high containment. Here, we have expressed the FMDV capsid protein precursor (P1-2A) of strain O1 Manisa alone or with the FMDV 3C protease (3Cpro) using a “single cycle” packaged alphavirus self-replicating RNA based on Semliki Forest virus (SFV). When the FMDV P1-2A was expressed with 3Cpro then processing of the FMDV capsid precursor protein is observed within cells and the proteins assemble into empty capsid particles. In cattle vaccinated once with these rSFV-FMDV vectors alone, anti-FMDV antibodies were elicited but the immune response was insufficient to give protection against FMDV challenge. However, the prior vaccination with these vectors resulted in a much stronger immune response against FMDV post-challenge and the viremia observed was decreased in level and duration. In subsequent experiments, cattle were sequentially vaccinated with a rSFV-FMDV followed by recombinant FMDV empty capsid particles, or vice versa, prior to challenge. Animals given a primary vaccination with the rSFV-FMDV vector and then boosted with FMDV empty capsids showed a strong anti-FMDV antibody response prior to challenge. Following challenge with FMDV, the cattle were protected against disease and no FMDV RNA was detected in their sera. Initial inoculation with empty capsids followed by the rSFV-FMDV was much less effective at combating the FMDV challenge and a large post-challenge boost to the level of anti-FMDV antibodies was observed and clinical disease occurred. This prime-boost system, using reagents that can be generated outside of high-containment facilities, offers significant advantages to achieve control of FMD by vaccination.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, The Pirbright Institute, Karolinska Institutet
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Number of pages: 2
Publication date: 2016
Event: Abstract from 19th European Study group on the molecular Biology of Picornaviruses (Europic 2016), Switzerland.
Main Research Area: Technical/natural sciences
Electronic versions: Europic_Abstract2016Vaccine.pdf
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2016

Profiling and characterization of embryo and seminal fluid extracellular vesicle-associated microRNAs in Sus scrofa: a possible role in differentiation and developmental communication processes

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, University of Gothenburg, Aarhus University
Pages: 169-169
Publication date: 2016
Conference: The Fifth International Meeting of ISEV, Rotterdam, Netherlands, 04/05/2016 - 04/05/2016
Main Research Area: Technical/natural sciences
Publication information
Journal: Journal of Extracellular Vesicles
Volume: 5
Article number: PF7.16
Progression of experimental chronic Aleutian mink disease virus infection

Aleutian mink disease virus (AMDV) is found worldwide and has a major impact on mink health and welfare by decreasing reproduction and fur quality. In the majority of mink, the infection is subclinical and the diagnosis must be confirmed by serology or polymerase chain reaction (PCR). Increased knowledge based on a systematically description of clinical signs, pathology and histopathology might be a tool to reduce the risk of infection from subclinically infected mink to AMDV free herds. The aim of this study was to give a histopathological description of the progression of a chronic experimental infection with a currently circulating Danish strain of AMDV, Saeby/DEN/799.1/05. These results were compared with the pathogenesis of previously published AMDV stains. This experimental AMDV infection resulted in only decreased appetite and soft or discolored feces, primarily within the first 8 weeks after AMDV inoculation. Gross pathology revealed few and inconsistent findings mainly associated with the liver, spleen and kidneys. The majority of the AMDV inoculated wild type mink (n = 41) developed various histopathological changes consistent with AMDV infection in one or more organs: infiltrations of mononuclear cells in liver, kidney and brain, reduced density of lymphocytes and increased numbers of plasma cells in lymph nodes and spleen. Natural infection, as occurred in the sentinel sapphire mink (four of six mink), progressed similar to the experimentally inoculated mink. Experimental AMDV inoculation mainly resulted in subclinical infection with unspecific clinical signs and gross pathology, and more consistent histopathology appearing at any time after AMDV inoculation during the 24 weeks of observation. Thus, the observed histopathology substantiates AMDV infection and no correlation to time of inoculation was found. This confirms that diagnosing AMDV infection requires serology and/or PCR and the Saeby/DEN/799.1/05 AMDV strain results in histopathology consistent with other AMDV strains.
Provision of Amniotic Fluid During Parenteral Nutrition Increases Weight Gain With Limited Effects on Gut Structure, Function, Immunity, and Microbiology in Newborn Preterm Pigs

Background: Small enteral boluses with human milk may reduce the risk of subsequent feeding intolerance and necrotizing enterocolitis in preterm infants receiving parenteral nutrition (PN). We hypothesized that feeding amniotic fluid, the natural enteral diet of the mammalian fetus, will have similar effects and improve growth and gastrointestinal (GI) maturation in preterm neonates receiving PN, prior to the transition to milk feeding. Materials and Methods: Twenty-seven...
pigs, delivered by cesarean section at ~90% of gestation, were provided with PN and also fed boluses with amniotic fluid (AF; n = 13, 24-72 mL/kg/d) or no oral supplements (nil per os [NPO]; n = 14) until day 5 when blood, tissue, and fecal samples were collected for analyses. Results: Body weight gain was 2.7-fold higher in AF vs NPO pigs. AF pigs showed slower gastric emptying, reduced meal-induced release of gastric inhibitory peptide and glucagon-like peptide 2, changed gut microbiota, and reduced intestinal permeability. There were no effects on GI weight, percentage mucosa, villus height, plasma citrulline, hexose absorptive capacity, and digestive enzymes. Intestinal interleukin (IL)-1β levels and expression of IL1B and IL8 were increased in AF pigs, while blood biochemistry and amino acid levels were minimally affected. Conclusion: Enteral boluses of AF were well tolerated in the first 5 days of life in preterm pigs receiving PN. Enteral provision of AF before the initiation of milk feeding may stimulate body growth and improve hydration in preterm infants receiving PN. Furthermore, it may improve GI motility and integrity, although most markers of GI maturation remain unchanged.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Rigshospitalet, University of Copenhagen
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Pages: 552-566
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Parenteral and Enteral Nutrition
Volume: 40
Issue number: 4
ISSN (Print): 0148-6071
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.499 SJR 1.58 CiteScore 3.22
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 1.409 SNIP 1.327 CiteScore 2.88
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.154 SNIP 1.343 CiteScore 2.66
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.366 SNIP 1.515 CiteScore 2.86
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.204 SNIP 1.539 CiteScore 2.67
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.978 SNIP 1.537 CiteScore 2.35
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.883 SNIP 1.559 CiteScore 2.53
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.897 SNIP 1.316
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.811 SNIP 1.126
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.599 SNIP 0.938
Scopus rating (2007): SJR 0.607 SNIP 0.93
Scopus rating (2006): SJR 0.689 SNIP 1.229
QA prime-boost vaccination strategy in prevent serotype O FMDV infection using a "single-cycle" alphavirus vector and empty capsid particles

Introduction
Foot-and-mouth disease (FMD) remains one of the most economically important infectious diseases of production animals globally. Vaccination can help to control this disease, however, current vaccines based on chemically inactivated FMDV, are imperfect and there is a need for new, safe and effective vaccines to control FMD. There is no cross protection between the 7 serotypes but serotype O is the most abundant globally.

Material and methods
The FMDV capsid protein precursor (P1-2A) of strain O1 Manisa has been expressed with the FMDV 3C protease (3Cpro) using a “single cycle” packaged alphavirus self-replicating RNA based on Semliki Forest virus (SFV). Purified O1 Manisa empty capsid particles (ECs) have been prepared using a recombinant vaccinia virus expression system. Cattle have been vaccinated with the SFV-FMDV vectors and boosted subsequently with the ECs and then challenged with serotype O FMDV. The immune response against FMDV achieved by vaccination and infection status following challenge has been determined.

Results
In cattle vaccinated once with these rSFV-FMDV vectors alone, anti-FMDV antibodies were elicited but the immune response was insufficient to give protection against FMDV challenge. However, the vaccination with these vectors resulted in a much stronger immune response against FMDV post-challenge than in naïve animals. In subsequent experiments, cattle were sequentially vaccinated with the rSFV-FMDV vector and then boosted with FMDV empty capsids prior to challenge. Animals given a primary vaccination with the rSFV-FMDV vector and then boosted with FMDV empty capsids showed a strong anti-FMDV antibody response prior to challenge. Following challenge with serotype O FMDV, the cattle were protected against disease and no FMDV RNA was detected in their sera.

Discussion
This prime-boost system, using reagents that can be generated outside of high-containment facilities, offers significant advantages to achieve control of FMD by vaccination.

Raising Backyard Poultry in Rural Bangladesh: Financial and Nutritional Benefits, but Persistent Risky Practices
Poultry is commonly raised by households in rural Bangladesh. In 2007, the Government of Bangladesh began a mass media campaign to disseminate 10 recommended precautions to prevent transmission of H5N1 from poultry to humans. This longitudinal study explored the contribution of backyard poultry on household economy and nutrition and compared poultry-raising practices to government recommendations. From 2009 to 2012, we enrolled a nationally representative sample of 2489 primary backyard poultry raisers from 115 rural villages selected by probability proportional to population
Researchers interviewed the raisers to collect data on poultry-raising practices. They followed the raisers for 2–12 months to collect data on household income and nutrition from poultry. Income from backyard poultry flocks accounted for 2.8% of monthly household income. Return on annual investment (ROI) per flock was 480%. Yearly, median family consumption of eggs was one-fifth of the total produced eggs and three poultry from their own flock. Respondents’ reported practices conflicted with government recommendations. Sixty per cent of raisers had never heard of avian influenza or ‘bird flu’. Among the respondents, 85% handled sick poultry or poultry that died due to illness, and 49% slaughtered or defeathered sick poultry. In 37% of households, children touched poultry. Fifty-eight per cent never washed their hands with soap after handling poultry, while <1% covered their nose and mouth with a cloth when handling poultry. Only 9% reported poultry illness and deaths to local authorities. These reported practices did not improve during the study period. Raising backyard poultry in rural Bangladesh provides important income and nutrition with an excellent ROI. Government recommendations to reduce the risk of avian influenza transmission did not impact the behaviour of poultry producers. Further research should prioritize developing interventions that simultaneously reduce the risk of avian influenza transmission and increase productivity of backyard poultry.
Rapid detection and subtyping of European swine influenza viruses in porcine clinical samples by haemagglutinin- and neuraminidase-specific tetra- and triplex real-time RT-PCRs

Background
A diversifying pool of mammalian-adapted influenza A viruses (IAV) with largely unknown zoonotic potential is maintained in domestic swine populations worldwide. The most recent human influenza pandemic in 2009 was caused by a virus with genes originating from IAV isolated from swine. Swine influenza viruses (SIV) are widespread in European domestic pig populations and evolve dynamically. Knowledge regarding occurrence, spread and evolution of potentially zoonotic SIV in Europe is poorly understood.

Objectives
Efficient SIV surveillance programmes depend on sensitive and specific diagnostic methods which allow for cost-effective large-scale analysis.

Methods
New SIV haemagglutinin (HA) and neuraminidase (NA) subtype- and lineage-specific multiplex real-time RT-PCRs (RT-qPCR) have been developed and validated with reference virus isolates and clinical samples.

Results
A diagnostic algorithm is proposed for the combined detection in clinical samples and subtyping of SIV strains currently circulating in Europe that is based on a generic, M-gene-specific influenza A virus RT-qPCR. In a second step, positive samples are examined by tetraplex HA- and triplex NA-specific RT-qPCRs to differentiate the porcine subtypes H1, H3, N1 and N2. Within the HA subtype H1, lineages “av” (European avian-derived), “hu” (European human-derived) and “pdm” (human pandemic A/H1N1, 2009) are distinguished by RT-qPCRs, and within the NA subtype N1, lineage “pdm” is differentiated. An RT-PCR amplicon Sanger sequencing method of small fragments of the HA and NA genes is also proposed to safeguard against failure of multiplex RT-qPCR subtyping.

Conclusions
These new multiplex RT-qPCR assays provide adequate tools for sustained SIV monitoring programmes in Europe.
Recent breakthroughs have unveiled the many knowledge gaps in Clostridium perfringens-associated necrotic enteritis in chickens: the first International Conference on Necrotic Enteritis in Poultry

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, National Food Institute, Ghent University, University of Guelph
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Number of pages: 2
Pages: 269-270
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Avian Pathology
Volume: 45
Issue number: 3
ISSN (Print): 0307-9457
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.047 SJR 0.871 CiteScore 1.88
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.637 SNIP 0.768 CiteScore 1.46
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.882 SNIP 0.934 CiteScore 1.55
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.037 SNIP 1.237 CiteScore 1.79
Recommended reporting standards for test accuracy studies of infectious diseases of finfish, amphibians, molluscs and crustaceans: the STRADAS-aquatic checklist

Complete and transparent reporting of key elements of diagnostic accuracy studies for infectious diseases in cultured and wild aquatic animals benefits end-users of these tests, enabling the rational design of surveillance programs, the assessment of test results from clinical cases and comparisons of diagnostic test performance. Based on deficiencies in the Standards for Reporting of Diagnostic Accuracy (STARD) guidelines identified in a prior finfish study (Gardner et al. 2014), we adapted the Standards for Reporting of Animal Diagnostic Accuracy Studies-paratuberculosis (STRADAS-paraTB) checklist of 25 reporting items to increase their relevance to finfish, amphibians, molluscs, and crustaceans and provided examples and explanations for each item. The checklist, known as STRADAS-aquatic, was developed and refined by an expert group of 14 transdisciplinary scientists with experience in test evaluation studies using field and experimental samples, in operation of reference laboratories for aquatic animal pathogens, and in development of international aquatic animal health policy. The main changes to the STRADAS-paraTB checklist were to nomenclature related to the species, the addition of guidelines for experimental challenge studies, and the designation of some items as relevant only to experimental studies and ante-mortem tests. We believe that adoption of these guidelines will improve reporting of primary studies of test accuracy for aquatic animal diseases and facilitate assessment of their fitness-for-purpose. Given the importance of diagnostic tests to underpin the Sanitary and Phytosanitary agreement of the World Trade Organization, the principles outlined in this paper should be applied to other World Organisation for Animal Health (OIE)-relevant species.
Removal of Cryptosporidium parvum oocysts in low quality water using Moringa oleifera seed extract as coagulant

The use of different types of low quality water for irrigation in agriculture is common practice in many countries due to limited freshwater resources. Pathogens may contaminate fruit and vegetables when feces contaminated water is used for irrigation or postharvest processing. A laboratory study was carried out to investigate the effect of a coagulant produced from seeds of the Moringa oleifera tree (MO) in reducing Cryptosporidium parvum oocysts and turbidity in wastewater and stream water. Glass jars (n = 60) containing 500 mL wastewater obtained from the inlet to the primary settling tanks from a Danish sewage treatment plant were spiked with 6.1 × 10^5 ± 6.2 × 10^4 oocysts L^-1, while glass jars (n = 18) containing 500 mL stream water were spiked with approx. 100, 1000 or 10,000 oocysts. To half of the wastewater and stream water 4 mL L^-1 of a 5% w/v MO seed extract was added, while the remaining water was left untreated. The water was stirred slowly for 20 min and subsequently left to sediment for 15, 30, 45, 60 or 90 min (wastewater) or 60 min (stream water), with three (stream water) or six (wastewater) replicate glass jars representing each time point. In wastewater, MO seed extracts reduced the C. parvum oocyst load significantly (p = 0.03) by 38% in the interval 15 to 90 min compared to a 0.02% reduction in the untreated wastewater. Furthermore, the number of oocysts L^-1 was significantly (p > 0.0001-p = 0.041) reduced in the treated wastewater at all five sampling times compared to untreated wastewater. Likewise, the oocyst loads in the supernatant of MO treated stream water were noticeably lower compared with untreated stream water at all three spikes. The turbidity was reduced to 10.9 ± 0.3 Nephelometric turbidity units (NTU) (i.e. 94.7% reduction) and 13.7 ± 2.1 NTU (i.e. 91.7% reduction) in the treated wastewater and stream water, respectively. In contrast, the turbidity was 55.3 ± 4.4 NTU and 46.2 ± 1.6 NTU in untreated wastewater and stream water, respectively. M. oleifera seeds are readily available in many tropical countries where the tree is common, and our results clearly demonstrate that MO seed extract may be used by farmers for treatment of different types of surface water prior to irrigation use. Yet, adding MO seed extract to the low quality water did not successfully remove all oocyst. However, treatment of wastewater with MO seed extract significantly improved the water quality with regard to number of oocysts present and turbidity of the water. Further experiments with addition of higher concentrations of MO are needed to establish whether MO seed extract can be used to obtain safe irrigation water free of C. parvum oocysts and other protozoan parasites.

General information
State: Published
Organisations: National Veterinary Institute, University of Copenhagen
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Number of pages: 8
Pages: 1-8
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Food and Waterborne Parasitology
Removal of Escherichia coli in treated wastewater used for food production in Morogoro, Tanzania

The aim of this study was to assess the removal efficiency of Escherichia coli at Mafisa and Mzumbe domestic wastewater treatment ponds in Morogoro, Tanzania. The study was done from October, 2013 to April, 2014. A total of 125 water samples from inlets and subsequent anaerobic, facultative and maturation ponds as well as treated wastewater were collected and analysed for E. coli. The estimated retention times of the wastewater treatment units were 19 and 22 days in Mafisa and Mzumbe ponds, respectively. The concentration of E. coli ranged from 4.70 to 5.60 log cfu/mL in untreated wastewater and was reduced to <1.00 to 2.00 log cfu/mL in the treated wastewater. During rainy and cold seasons, the effluent discharged out at Mafisa during August 2013; and March and April, 2014 was about 2 log cfu/mL while at Mzumbe E. coli concentration in effluent discharged out was up to 1.23 log cfu/mL. The concentration of E. coli in untreated and treated wastewater from the two wastewater treatment ponds study sites were comparable (P<0.05). Reduction of E. coli concentration in wastewater treatment ponds study sites was significant with less reduction seen at Mafisa, during rainy and cold seasons in March, April and August. To conclude, the simple wastewater treatment ponds in the study sites were effective and demonstrated potential for reduction of public health risks associated with use of treated wastewater in agricultural irrigation and aquaculture.

General information
State: Published
Organisations: National Veterinary Institute, Bacteriology & Parasitology
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Number of pages: 7
Pages: 1344-1350
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: African Journal of Microbiology Research
Volume: 10
Issue number: 33
ISSN (Print): 1996-0808
Ratings:
Scopus rating (2015): SJR 0.124 SNIP 1.597
Scopus rating (2014): SJR 0.192 SNIP 1.344
Scopus rating (2013): SJR 0.182 SNIP 1.197
Scopus rating (2012): SJR 0.123 SNIP 0.5
Scopus rating (2011): SJR 0.121 SNIP 12.971
Scopus rating (2010): SJR 0.162 SNIP 0.553
Original language: English
Electronic versions:
DOIs:
10.5897/AJMR2016.8156
Source: FindIt
Source-ID: 2343501655
Publication: Research - peer-review › Journal article – Annual report year: 2017
Reporting the national antimicrobial consumption in Danish pigs: influence of assigned daily dosage values and population measurement

Transparent calculation methods are crucial when investigating trends in antimicrobial consumption over time and between populations. Until 2011, one single standardized method was applied when quantifying the Danish pig antimicrobial consumption with the unit "Animal Daily Dose" (ADD). However, two new methods for assigning values for ADDs have recently emerged, one implemented by DANMAP, responsible for publishing annual reports on antimicrobial consumption, and one by the Danish Veterinary and Food Administration (DVFA), responsible for the Yellow Card initiative. In addition to new ADD assignment methods, Denmark has also experienced a shift in the production pattern, towards a larger export of live pigs. The aims of this paper were to (1) describe previous and current ADD assignment methods used by the major Danish institutions and (2) to illustrate how ADD assignment method and choice of population and population measurement affect the calculated national antimicrobial consumption in pigs (2007-2013). The old VetStat ADD-values were based on SPCs in contrast to the new ADD-values, which were based on active compound, concentration and administration route. The new ADD-values stated by both DANMAP and DVFA were only identical for 48 % of antimicrobial products approved for use in pigs. From 2007 to 2013, the total number of ADDs per year increased by 9 % when using the new DVFA ADD-values, but decreased by 2 and 7 % when using the new DANMAP ADD-values or the old VetStat ADD-values, respectively. Through 2007 to 2013, the production of pigs increased from 26.1 million pigs per year with 18 % exported live to 28.7 million with 34 % exported live. In the same time span, the annual pig antimicrobial consumption increased by 22.2 %, when calculated using the new DVFA ADD-values and pigs slaughtered per year as population measurement (13.0 ADDs/pig/year to 15.9 ADDs/pig/year). However, when based on the old VetStat ADD values and pigs produced per year (including live export), a 10.9 % decrease was seen (10.6 ADDs/pig/year to 9.4 ADDs/pig/year). The findings of this paper clearly highlight that calculated national antimicrobial consumption is highly affected by chosen population measurement and the applied ADD-values.

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, University of Copenhagen, SEGES Pig Research Center
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Number of pages: 9
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Acta Veterinaria Scandinavica (Online)
Volume: 58
Issue number: 1
Article number: 27
ISSN (Print): 0044-605X
Ratings:
- BFI (2018): BFI-level 1
- Web of Science (2018): Indexed yes
- BFI (2017): BFI-level 1
- Scopus rating (2017): SNIP 1.077 SJR 0.655 CiteScore 1.45
- Web of Science (2017): Indexed Yes
- BFI (2016): BFI-level 1
- Scopus rating (2016): CiteScore 1.01 SJR 0.641 SNIP 0.826
- Web of Science (2016): Indexed yes
- BFI (2015): BFI-level 1
- Scopus rating (2015): SJR 0.644 SNIP 1.641 CiteScore 0.98
- BFI (2014): BFI-level 1
- Scopus rating (2014): SJR 0.753 SNIP 1.21 CiteScore 1.54
- BFI (2013): BFI-level 1
- Scopus rating (2013): SJR 0.539 SNIP 1.11 CiteScore 1.41
- ISI indexed (2013): ISI indexed no
- Web of Science (2013): Indexed yes
- BFI (2012): BFI-level 1
- Scopus rating (2012): SJR 0.591 SNIP 0.789 CiteScore 1.26
- ISI indexed (2012): ISI indexed no
- Web of Science (2012): Indexed yes
Retinoic acid signalling is required for the pathogenicity of effector CD4+ T cells during the development of intestinal inflammation

The vitamin A metabolite retinoic acid (RA) seems to be a double-edge sword in CD4+ T cell biology, sustaining the development of foxp3+ Treg cells, but also being essential for the stability of the Th1 lineage. Here we explored the role of RA signalling in CD4+ T cells during the development of intestinal inflammation in the T cell transfer colitis model. RA signalling-deficient CD4+ T cells are less potent at inducing intestinal inflammation compared to their RA signalling-proficient counterparts and exhibit a differentiation skewing towards more IL-17+ and foxp3+ cells, while their capacity to differentiate into Th1 cells is compromised. In vitro studies confirm the inefficacy of RA signalling-deficient T cells to generate bona fide Th1 cells and demonstrate their aberrant increased RORγt expression, while their Th17 differentiation remains unaffected. Surprisingly, RA signalling-deficient and –proficient Tregs are equally competent to inhibit colitis development. Together our results indicate that RA, through its receptor RARα, negatively regulates the early expansion of CD4+ T cells during colitis and is necessary for the generation of colitogenic Th1/Th17 cells, while it is dispensable for the protective function of Treg cells. We are currently deciphering the mechanisms of these effects of RA on CD4+ T cells.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Lund University
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Revisiting the IFN-γ release assay: Whole blood or PBMC cultures? - And other factors of influence

The interferon-γ release assay (IGRA) is a widely used test for the presence of a cell-mediated immune (CMI) response in vitro. This measure is used to test for infection with intracellular pathogens or for validating vaccine efficacy, and it is a widely used test for both human as well as cattle. However, there is no consensus whether to use whole blood cultures or purified PBMCs for the assay, and both cell populations are being used and results compared. Therefore the aim of this study was to compare different culture settings using immune cells from previously vaccinated calves, and to shed light on external factors that could influence the read out in terms of IFN-γ levels. It was found that optimal culture conditions varied between individual animals; when polyclonal activated, cells from whole blood cultures were most responsive, but when activated specifically, the optimal cell concentration/population varied with whole blood, $10 \times 10^6$ cells/ml PBMC and $5 \times 10^6$ cells/ml PBMC being the highest performing conditions. A further investigation of the distribution of cell populations in PBMCs compared to whole blood was conducted, and a significant ($p < 0.001$) decrease in the percentage of CD3+ T lymphocytes within the PBMCs was found. More specifically, this reduction was due to a significant ($p < 0.01$) decrease in the percentage of γδ+ T lymphocytes. Thus measuring immune responses on purified PBMCs might not give a physiologically relevant output. Additionally, it was tested if the choice of incubation plate would interfere with the level of secreted IFN-γ in whole blood cultures from five calves. Six plates (a–f) were tested and no significant difference in absolute levels of IFN-γ was detected in the six plates when cells were polyclonal and specifically activated. However, we observed a significant ($p < 0.05$) higher background level in a flat-bottom plate from Corning® (cat# 3595) (plate d) compared to two different flat-bottom plates from Corning® (cat# 3596) (plate b) and Nunc™ (cat# 167008) (plate a). Furthermore 4 out of 5 calves had maximum specific IFN-γ expression on plate b, and the relative-to-maximum level on this plate was significant ($p < 0.05$) compared to plate a. Altogether these findings highlight the potential weaknesses of the IFN-γ release assay in terms of the many variables that can influence the results, including the cell culture population, the concentration of cells being cultured, and the plastic ware used for the in vitro culture. These findings stress the importance of documenting the precise assay conditions when publishing results of in vitro IFN-γ release assays.

General information
State: Published
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Pages: 24-31
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Immunological Methods
Volume: 434
ISSN (Print): 0022-1759
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.715 SJR 1.289 CiteScore 2.25
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.92 SJR 1.089 SNIP 0.65
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.064 SNIP 0.739 CiteScore 2.07
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.018 SNIP 0.824 CiteScore 1.99
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.087 SNIP 0.834 CiteScore 2.31
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Risk factors for antimicrobial use in Danish rosé veal calves. A register-based study

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, SEGES Cattle
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Number of pages: 1
Publication date: 2016
Event: Poster session presented at SVEPM, Elsinore, Denmark.
Main Research Area: Technical/natural sciences
Electronic versions:
Fertner_Mette.pdf
Source: PublicationPreSubmission
Source-ID: 123559849
Publication: Research - peer-review › Poster – Annual report year: 2016

Risk factors for use of antimicrobials in mink (Neovison vison)

General information
State: Published
Organisations: National Veterinary Institute, Department of Applied Mathematics and Computer Science, Section for Epidemiology, Copenhagen Fur, Copenhagen Fur
Authors: Chriél, M. (Intern), Sommer, H. M. (Intern), Struve, T. (Ekstern), Clausen, J. (Ekstern), Jensen, V. F. (Intern)
Sequence adaptations during growth of rescued classical swine fever viruses in cell culture and within infected pigs

Classical swine fever virus (CSFV) causes an economically important disease of swine. Four different viruses were rescued from full-length cloned cDNAs derived from the Paderborn strain of CSFV. Three of these viruses had been modified by mutagenesis (with 7 or 8 nt changes) within stem 2 of the subdomain III′ of the internal ribosome entry site (IRES) that directs the initiation of protein synthesis. Rescued viruses were inoculated into pigs. The rescued vPader10 virus, without modifications in the IRES, induced clinical disease in pigs that was very similar to that observed previously with the parental field strain and transmission to in-contact pigs occurred. Two sequence reversions, in the NS2 and NS5B coding regions, became dominant within the virus populations in these infected pigs. Rescued viruses, with mutant IRES elements, did not induce disease and only very limited circulation of viral RNA could be detected. However, the animals inoculated with these mutant viruses seroconverted against CSFV. Thus, these mutant viruses were highly attenuated in vivo. All 4 rescued viruses were also passaged up to 20 times in cell culture. Using full genome sequencing, the same two adaptations within each of four independent virus populations were observed that restored the coding sequence to that of the parental field strain. These adaptations occurred with different kinetics. The combination of reverse genetics and in depth, full genome sequencing provides a powerful approach to analyse virus adaptation and to identify key determinants of viral replication efficiency in cells and within host animals.
Sequence-based genotyping of expressed SLA class I alleles by Next Generation Sequencing reveal novel SLA class I haplotypes and alleles in Belgian, Danish and Kenyan fattening pigs and Göttingen minipigs.

The need for typing of the swine leukocyte antigen (SLA) is increasing with the expanded use of pigs as models for human diseases and organ-transplantation experiments, their use in infection studies, and for design of veterinary vaccines. Knowledge of SLA sequences is furthermore a prerequisite for the prediction of CTL epitopes based on predicted MHC binding in pigs. The low number of known SLA class I alleles and the limited knowledge of their prevalence in different pig
breeds, emphasizes the need for efficient SLA typing methods. Here we obtain SLA class I–typing and –expression based on Illumina MiSeq Next Generation Sequencing of barcoded PCR amplicons. Universal primers were designed to generate amplicons spanning exon 2 and exon 3 of the SLA class I genes and predicted to resolve 68% to 88% of all known SLA class I alleles dependent on amplicon size. Based on whole blood mRNA we analyzed the cDNA SLA profiles of 72 pigs from four different pig populations: Göttingen minipigs and Belgian, Kenyan, and Danish fattening pigs. We identified 67 different allele sequences, including 12 novel alleles, and observed 24 haplotypes of which 15 have not been described before. The highest variation in SLA class I profiles was observed in the Danish pigs and the lowest among the Göttingen minipig population, which also had the highest percentage of homozygous individuals. The identification of 12 novel SLA class I alleles from only 72 pigs highlight the fact that there are still numerous unknown SLA class I alleles to be discovered.

In conclusion, we present an NGS-based method to obtain sequence-based high-resolution SLA class I typing based on expressed alleles and provide new information about known and novel alleles and haplotypes and their prevalence in the tested pig populations.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Section for Bacteriology, Pathology and Parasitology, International Livestock Research Institute, Technical University of Denmark
Authors: Sørensen, M. R. (Intern), Ilsøe, M. (Ekstern), Strube, M. L. (Intern), Bishop, R. (Ekstern), Jungersen, G. (Intern)
Number of pages: 1
Publication date: 2016
Event: Abstract from 11th International Veterinary Immunology Symposium, Gold Coast, Australia.
Main Research Area: Technical/natural sciences
Electronic versions: Soerensen_et_al_IVIS_Abstract.pdf
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2016

Sequencing of avian pathogenic Escherichia coli from a colibacillosis outbreak

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Finnish Food Safety Authority
Authors: Pohjanvirta, T. (Ekstern), Ronco, T. (Intern), Pelkonen, S. (Ekstern), Pedersen, K. (Intern)
Number of pages: 1
Publication date: 2016
Event: Poster session presented at 2nd Conference Rapid Microbial NGS and Bioinformatics, Hamburg, Germany.
Main Research Area: Technical/natural sciences
Electronic versions: Evira_RaMi2016_TP0.pdf
Source: PublicationPreSubmission
Source-ID: 124048830
Publication: Research - peer-review › Poster – Annual report year: 2016

Series of Norovirus Outbreaks Caused by Consumption of Green Coral Lettuce, Denmark, April 2016

In early April 2016, an unusual high number of point-source outbreaks of gastrointestinal disease were reported to occur in Denmark. Outbreaks were individually investigated. Two analytical studies were performed. Patient stool samples collected and analysed; positive stool samples were sequenced over the polymerase and/or capsid gene areas. Implicated lettuce heads were collected and analysed for the presence of norovirus. Foods were traced-back and traced-forward and international alert systems applied. A total of 23 linked point-source outbreaks occurred over the course of one week. Fresh green coral lettuce (Lollo Bionda lettuce) had been consumed in all settings. In a cohort study including 234 participants a dish containing green lettuce was associated with illness. Norovirus of Genogroup I (GI) was detected in samples from 28 patients comprising eight of the outbreaks. Sequencing showed GI.P2-G1.2. GI norovirus was detected in one of 20 examined lettuce heads. All lettuce consumed was supplied by the same packer who in turn had bought the lettuce from a wholesaler in France. The two lots of lettuce came from two different growers in different parts of France. Green coral lettuce produced in France was found to have caused a large series of linked norovirus outbreaks in Denmark as established by a number of lines of evidence. A similar incidence occurred in 2010. Fresh lettuce increasingly appear to be a risk food for norovirus infections.

General information
State: Published
Organisations: National Veterinary Institute, National Food Institute, Research Group for Microbial Food Safety
Short time variation in daily shedding of Strep. agalactiae and Staph. aureus determined by bacterial culture and PCR test

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Copenhagen, Aarhus University
Authors: Svennesen, L. (Ekstern), Bennedsgaard, T. W. (Ekstern), Pedersen, K. (Intern), Klaas, I. C. (Ekstern)
Number of pages: 1
Publication date: 2016
Event: Poster session presented at IDF mastitis conference 2016, Nantes, France.
Main Research Area: Technical/natural sciences
Electronic versions:
Poster_Nantes_september_2016_Short_time_variation_in_daily_shedding_of_Strep.pdf
Source: PublicationPreSubmission
Source-ID: 126479174
Publication: Research - peer-review › Poster – Annual report year: 2016

Significantly increased numbers of foetuses positive for porcine parvovirus (PPV) in Denmark in 2015 coincided with a shift in genotype

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, SEGES Pig Research Center
Authors: Krog, J. S. (Intern), Hjulsager, C. K. (Intern), Haugegaard, S. (Ekstern), Larsen, L. E. (Intern)
Pages: 452-452
Publication date: 2016
Event: 24th International Pig Veterinary Society (IPVS) Congress, Dublin, Ireland, 07/06/2016 - 07/06/2016
Main Research Area: Technical/natural sciences
Conference: 24th International Pig Veterinary Society Congress - abstracts book
Title of host publication: 24th International Pig Veterinary Society Congress - abstracts book
Place of publication: Dublin, Ireland
Publisher: Royal Dublin Society
Article number: PO-PF3-156
Electronic versions:
Book of abstracts
Simulating the epidemiological and economic effects of an African swine fever epidemic in industrialized swine populations

African swine fever (ASF) is a notifiable infectious disease with a considerable impact on animal health and is currently one of the most important emerging diseases of domestic pigs. ASF was introduced into Georgia in 2007 and subsequently spread to the Russian Federation and several Eastern European countries. Consequently, there is a non-negligible risk of ASF spread towards Western Europe. Therefore it is important to develop tools to improve our understanding of the spread and control of ASF for contingency planning. A stochastic and dynamic spatial spread model (DTU-DADS) was adjusted to simulate the spread of ASF virus between domestic swine herds exemplified by the Danish swine population. ASF was simulated to spread via animal movement, low- or medium-risk contacts and local spread. Each epidemic was initiated in a randomly selected herd – either in a nucleus herd, a sow herd, a randomly selected herd or in multiple herds simultaneously. A sensitivity analysis was conducted on input parameters. Given the inputs and assumptions of the model, epidemics of ASF in Denmark are predicted to be small, affecting about 14 herds in the worst-case scenario. The duration of an epidemic is predicted to vary from 1 to 76 days. Substantial economic damages are predicted, with median direct costs and export losses of €12 and €349 million, respectively, when epidemics were initiated in multiple herds. Each infectious herd resulted in 0 to 2 new infected herds varying from 0 to 5 new infected herds, depending on the index herd type.

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Ministry of Environment and Food
Authors: Hisham Beshara Halasa, T. (Intern), Bøtner, A. (Intern), Mortensen, S. (Intern), Christensen, H. (Ekstern), Toft, N. (Intern), Boklund, A. (Intern)
Pages: 7-16
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Veterinary Microbiology
Volume: 193
ISSN (Print): 0378-1135
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.7 SJR 1.175 SNIP 1.241
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.363 SNIP 1.206
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.413 SNIP 1.21 CiteScore 2.56
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.291 SNIP 1.256 CiteScore 2.54
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.459 SNIP 1.471 CiteScore 3
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.441 SNIP 1.569 CiteScore 3.18
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.56 SNIP 1.729 CiteScore 3.27
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Simulating the Epidemiological and Economic Impact of Paratuberculosis Control Actions in Dairy Cattle

We describe a new mechanistic bioeconomic model for simulating the spread of Mycobacterium avium subsp. paratuberculosis (MAP) within a dairy cattle herd. The model includes age-dependent susceptibility for infection; age-dependent sensitivity for detection; environmental MAP build up in five separate areas of the farm; in utero infection; infection via colostrum and waste milk, and it allows for realistic culling (i.e., due to other diseases) by including a ranking system. We calibrated the model using a unique dataset from Denmark, including 102 random farms with no control actions against spread of MAP. Likewise, four control actions recommended in the Danish MAP control program were implemented in the model based on reported management strategies in Danish dairy herds in a MAP control scheme. We tested the model parameterization in a sensitivity analysis. We show that a test-and-cull strategy is on average the most cost-effective solution to decrease the prevalence and increase the total net revenue on a farm with low hygiene, but not more profitable than no control strategy on a farm with average hygiene. Although it is possible to eradicate MAP from the farm by implementing all four control actions from the Danish MAP control program, it was not economically attractive since the expenses for the control actions outweigh the benefits. Furthermore, the three most popular control actions against the spread of MAP on the farm were found to be costly and inefficient in lowering the prevalence when used independently.

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Department of Applied Mathematics and Computer Science, Dynamical Systems, University of Copenhagen, SEGES Cattle
Authors: Kirkeby, C. T. (Intern), Græsbøll, K. (Intern), Nielsen, S. S. (Ekstern), Christiansen, L. E. (Intern), Toft, N. (Intern), Rattenborg, E. (Ekstern), Hisham Beshara Halasa, T. (Intern)
Number of pages: 13
Publication date: 2016
Main Research Area: Technical/natural sciences
Simulation of Spread of African Swine Fever, Including the Effects of Residues from Dead Animals

To study the spread of African swine fever (ASF) within a pig unit and the impact of unit size on ASF spread, a simulation model was created. In the model, an animal can be in one of the following stages: susceptible, latent, subclinical, clinical, or recovered. Animals can be infectious during the subclinical stage and are fully infectious during the clinical stage. ASF virus (ASFV) infection through residues of dead animals in the slurries was also modeled in an exponentially fading-out pattern. Low and high transmission rates for ASFV were tested in the model. Robustness analysis was carried out in order to study the impact of uncertain parameters on model predictions. The results showed that the disease may fade out within the pig unit without a major outbreak. Furthermore, they showed that spread of ASFV is dependent on the infectiousness of subclinical animals and the residues of dead animals, the transmission rate of the virus, and importantly the unit size. Moreover, increasing the duration of the latent or the subclinical stages resulted in longer time to disease fade out. The proposed model is a simple and robust tool simulating the spread of ASFV within a pig house taking into account dynamics of ASFV spread and the unit size. The tool can be implemented in simulation models of ASFV spread between herds.
Simultaneous vaccination with PRRS MLV against both PRRSV type 1 and type 2: PRRSV in lungs following challenge

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, SEGES Pig Research Center, Technical University of Denmark, Warsawa University
Authors: Kristensen, C. S. (Ekstern), Kvisgaard, L. K. (Intern), Haugegaard, S. (Ekstern), Pawlowski, M. (Ekstern), Carlsen, S. H. (Ekstern), Stadejek, T. (Ekstern), Larsen, L. E. (Intern)
Pages: 577-577
Publication date: 2016

Host publication information
Title of host publication: 24th International Pig Veterinary Society Congress - abstracts book
Place of publication: Dublin, Ireland
Publisher: Royal Dublin Society
Article number: PO-PW1-089
Main Research Area: Technical/natural sciences
Conference: 24th International Pig Veterinary Society (IPVS) Congress, Dublin, Ireland, 07/06/2016 - 07/06/2016
Electronic versions:
Book of abstracts

Spatial Distribution and Abundance of Culicoides Imicola and Obsolutes Group in Europe

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, Department of Applied Mathematics and Computer Science, Statistics and Data Analysis, Aarhus University, Roskilde University, National Veterinary Institute Sweden, Bernhard Nocht Institute for Tropical Medicine, Norwegian Veterinary Institute, Institute for Veterinary Public Health, Centre de cooperation Internationale en Recherche Agronomique pour le Développement, Universite de Strasbourg, EID Méditerranée, University of the Balearic Islands, Universidad de Zaragoza, Avia-GIS, University of Zurich
Number of pages: 1
Publication date: 2016
Event: Abstract from 3rd Conference on Neglected Vectors and Vector-Borne Diseases, Zaragoza, Spain.
Main Research Area: Technical/natural sciences
Electronic versions:
Cuellar_Abstract_Zaragoza2.pdf

Relations
Activities:
SPATIAL DISTRIBUTION AND ABUNDANCE OF CULICOIDES IMICOLA AND OBSOLETUS GROUP IN EUROPE
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2017

Spatial distribution and abundance of culicoides imicola and obsolutes group in Europe

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Department of Applied Mathematics and Computer Science, Statistics and Data Analysis, Roskilde University, National Veterinary Institute Sweden, Bernhard Nocht Institute for Tropical Medicine, Norwegian Veterinary Institute, Institute for Veterinary Public Health, Centre de cooperation Internationale en Recherche Agronomique pour le Développement, Universite de Strasbourg, EID Méditerranée, Aarhus University, National Veterinary Research Institute
Spatial patterns of Antimicrobial Resistance Genes in Danish Pig Farms

Samples from 687 Danish pig farms were collected at five finisher slaughterhouses in February and March 2015. Faecal samples from five pigs per farm were collected randomly at the slaughter line and pooled into one sample per farm. DNA was extracted from the pooled samples and the level of seven antimicrobial resistance genes, ermB, ermF, sulI, sulII, tet(M), tet(O) and tet(W), was quantified by a high-throughput qPCR. It was evaluated whether the sample method resulted in a study population representative of Danish pig farms with finishers where it was found that the study population was biased towards farms having more finisher and a higher productivity. Spatial cluster analyses were performed in SaTScan®. The results showed significant spatial clusters for ermF, ermB, sulII and tet(W) whereas no significant clusters were found for sulI, tet(M) and tet(O).

General information
State: Published
Organisations: National Veterinary Institute, Epidemiology, Bacteriology & Parasitology, National Food Institute, Research Group for Genomic Epidemiology, University of Copenhagen
Number of pages: 10
Pages: 182-191
Publication date: 2016

Host publication information
Title of host publication: Proceedings of the SVEPM: Annual Meeting 2016
Main Research Area: Technical/natural sciences
Conference: SVEPM, Elsinore, Denmark, 16/03/2016 - 16/03/2016

Relations
Activities:
SPATIAL PATTERNS OF ANTIMICROBIAL RESISTANCE GENES IN DANISH PIG FARMS
Publication: Research - peer-review › Article in proceedings – Annual report year: 2017

Spatial risk of tick borne infections – creating a ScandTick Innovation website for both the public and the health sector based on surveillance data

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Section for Bacteriology, Pathology and Parasitology
Authors: Clausen, C. G. (Intern), Schou, K. K. (Intern), Kirkeby, C. (Intern), Bedker, R. (Intern)
Number of pages: 1
Publication date: 2016
Main Research Area: Technical/natural sciences
Electronic versions:
Abstract_NordTick_Creating_a_ScandTick_Innovation_website_20april2016.pdf
Source: PublicationPreSubmission
Source-ID: 123456779
Spatio-temporal Analysis of the Genetic Diversity of Arctic Rabies Viruses and Their Reservoir Hosts in Greenland

There has been limited knowledge on spatio-temporal epidemiology of zoonotic arctic fox rabies among countries bordering the Arctic, in particular Greenland. Previous molecular epidemiological studies have suggested the occurrence of one particular arctic rabies virus (RABV) lineage (arctic-3), but have been limited by a low number of available samples preventing in-depth high resolution phylogenetic analysis of RABVs at that time. However, an improved knowledge of the evolution, at a molecular level, of the circulating RABVs and a better understanding of the historical perspective of the disease in Greenland is necessary for better direct control measures on the island. These issues have been addressed by investigating the spatio-temporal genetic diversity of arctic RABVs and their reservoir host, the arctic fox, in Greenland using both full and partial genome sequences. Using a unique set of 79 arctic RABV full genome sequences from Greenland, Canada, USA (Alaska) and Russia obtained between 1977 and 2014, a description of the historic context in relation to the genetic diversity of currently circulating RABV in Greenland and neighboring Canadian Northern territories has been provided. The phylogenetic analysis confirmed delineation into four major arctic RABV lineages (arctic 1–4) with viruses from Greenland exclusively grouping into the circumpolar arctic-3 lineage. High resolution analysis enabled distinction of seven geographically distinct subclades (3.I – 3.VII) with two subclades containing viruses from both Greenland and Canada. By combining analysis of full length RABV genome sequences and host derived sequences encoding mitochondrial proteins obtained simultaneously from brain tissues of 49 arctic foxes, the interaction of viruses and their hosts was explored in detail. Such an approach can serve as a blueprint for analysis of infectious disease dynamics and virus-host interdependencies. The results showed a fine-scale spatial population structure in Greenland arctic foxes based on mitochondrial sequences, but provided no evidence for independent isolated evolutionary development of RABV in different arctic fox lineages. These data are invaluable to support future initiatives for arctic fox rabies control and elimination in Greenland.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Friedrich-Loeffler-Institute, University of Alaska Fairbanks, Canadian Food Inspection Agency (CFIA), Animal and Plant Health Agency
Number of pages: 22
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: PLoS Neglected Tropical Diseases (Online)
Volume: 10
Issue number: 7
Article number: e0004779
ISSN (Print): 1935-2735
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.36
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.97
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 4.09
Scopus rating (2014): CiteScore 4.61
Scopus rating (2013): CiteScore 4.72
ISI indexed (2013): ISI indexed yes
Scopus rating (2012): CiteScore 4.75
ISI indexed (2012): ISI indexed yes
Scopus rating (2011): CiteScore 4.64
ISI indexed (2011): ISI indexed no
Web of Science (2011): Indexed yes
Original language: English
Electronic versions:
Spatiotemporal Analysis of the Genetic Diversity of Seal Influenza A(H10N7) Virus, Northwestern Europe

Influenza A viruses are major pathogens for humans, domestic animals, and wildlife, and these viruses occasionally cross the species barrier. In spring 2014, increased mortality of harbor seals (Phoca vitulina), associated with infection with an influenza A(H10N7) virus, was reported in Sweden and Denmark. Within a few months, this virus spread to seals of the coastal waters of Germany and the Netherlands, causing the death of thousands of animals. Genetic analysis of the hemagglutinin (HA) and neuraminidase (NA) genes of this seal influenza A(H10N7) virus revealed that it was most closely related to various avian influenza A(H10N7) viruses. The collection of samples from infected seals during the course of the outbreak provided a unique opportunity to follow the adaptation of the avian virus to its new seal host. Sequence data for samples collected from 41 different seals from four different countries between April 2014 and January 2015 were obtained by Sanger sequencing and next-generation sequencing to describe the molecular epidemiology of the seal influenza A(H10N7) virus. The majority of sequence variation occurred in the HA gene, and some mutations corresponded to amino acid changes not found in H10 viruses isolated from Eurasian birds. Also, sequence variation in the HA gene was greater at the beginning than at the end of the epidemic, when a number of the mutations observed earlier had been fixed. These results imply that when an avian influenza virus jumps the species barrier from birds to seals, amino acid changes in HA may occur rapidly and are important for virus adaptation to its new mammalian host. Influenza A viruses are major pathogens for humans, domestic animals, and wildlife. In addition to the continuous circulation of influenza A viruses among various host species, cross-species transmission of influenza A viruses occurs occasionally. Wild waterfowl and shorebirds are the main reservoir for most influenza A virus subtypes, and spillover of influenza A viruses from birds to humans or other mammalian species may result in major outbreaks. In the present study, various sequencing methods were used to elucidate the genetic changes that occurred after the introduction and subsequent spread of an avian influenza A(H10N7) virus among harbor seals of northwestern Europe by use of various samples collected during the outbreak. Such detailed knowledge of genetic changes necessary for introduction and adaptation of avian influenza A viruses to mammalian hosts is important for a rapid risk assessment of such viruses soon after they cross the species barrier.

General information
State: Published
Organisations: National Veterinary Institute
Authors: Bodewes, R. (Ekstern), Zohari, S. (Ekstern), Krog, J. S. (Intern), Hall, M. D. (Ekstern), Harder, T. C. (Ekstern), Bestebroer, T. M. (Ekstern), van de Bildt, M. W. G. (Ekstern), Spronken, M. I. (Ekstern), Larsen, L. E. (Ekstern), Siebert, U. (Ekstern), Wohlesele, P. (Ekstern), Puff, C. (Ekstern), Seehusen, F. (Ekstern), Baumgärtner, W. (Ekstern), Härkönen, T. (Ekstern), Smits, S. L. (Ekstern), Herfst, S. (Ekstern), Osterhaus, A. D. M. E. (Ekstern), Fouchier, R. A. M. (Ekstern), Koopmans, M. P. (Ekstern), Kuiken, T. (Ekstern), Schultz-Cherry, S. (ed.) (Ekstern)
Number of pages: 9
Pages: 4269-4277
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Virology
Volume: 90
Issue number: 9
ISSN (Print): 0022-538X
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 1.096 SJR 2.853 CiteScore 4.24
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 4.42 SJR 3.114 SNIP 1.124
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 3.282 SNIP 1.132 CiteScore 4.42
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 3.187 SNIP 1.208 CiteScore 4.4
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 3.496 SNIP 1.251 CiteScore 4.92
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 3.19 SNIP 1.222 CiteScore 5.2
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 3.429 SNIP 1.282 CiteScore 5.37
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 3.596 SNIP 1.277
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 3.631 SNIP 1.306
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 3.846 SNIP 1.26
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 3.598 SNIP 1.307
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 3.809 SNIP 1.252
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 3.443 SNIP 1.244
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 3.452 SNIP 1.33
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 3.464 SNIP 1.328
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 3.219 SNIP 1.253
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 3.569 SNIP 1.354
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 4.027 SNIP 1.384
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 4.092 SNIP 1.398
Original language: English
Electronic versions:
J._Virol._2016_Bodewes_4269_77.pdf
DOIs:
10.1128/JVI.03046-15
Links:
http://jvi.asm.org/content/90/9/4269.long

Relations
Projects:
Spatiotemporal Analysis of the Genetic Diversity of Seal Influenza A(H10N7) Virus, Northwestern Europe
Source: FindIt
Source-ID: 2291680733
Publication: Research - peer-review › Journal article – Annual report year: 2016
Spatiotemporal flooding fluctuation analysis: wetland management Bañado La Estrella, Chaco región, Argentina

The wetlands are widely distributed over the Chaco region. Despite their wide territorial extension and major functional role, Bañado la Estrella wetlands have not been appropriately mapped, and this is not a protected area nowadays. Wetlands are ecosystems that depend on periodical flooding, which determine the presence of soils with hydromorphic features and species adapted to permanent or temporary flooding conditions. The bed of the Pilcomayo River began regressing to the west about 30 years ago, creating a wetlands known as the "Bañado la Estrella". We propose an integrated approach, based on satellite imagery analysis (Landsat TM), The NDWI index (Normalized Difference Water) and decision trees, to analyze and characterize seasonal variations (1992-2012) and to map seasonal flooding. We use information about land use and herd distribution (anthropogenic use) and validate it with field data.

Four classes of flooding frequency were defined: permanent flooded areas (80-100 % of the time pixels showed water presence), usually flooded areas (60-100% of the time) and regularly flooded areas (40-60% of the time) during the 1992-2012 period. We are able to delimitate and quantify the total area of Bañado La Estrella wetlands which occupies 1682 km2 including the permanently, usually and regularly flooded areas. This spatio temporal analysis shows that during the dry period the permanently flooded areas were reduced 462 km2 of the total wetland area while the usually flooded area occupied 2 % of the total area and the regularly flooded area occupied 5%. Our results suggest that this method can be used to delimitate different zones, gathering together hydrodynamic and anthropogenic activities, in order to be used as tool for the creation of a future protect area in Argentina.

Spray Dried, Pasteurised Bovine Colostrum Protects Against Gut Dysfunction and Inflammation in Preterm Pigs

OBJECTIVE: Feeding bovine colostrum (BC) improves gut maturation and function, and protects against necrotizing enterocolitis (NEC), relative to formula in newborn preterm pigs. Before BC can be used for preterm infants, it is important to test if the milk processing, required to reduce bacterial load and increase shelf life, may affect bioactivity and efficacy of a BC product. METHODS: We investigated if spray dried, and pasteurised, spray dried BC had protective effects on gut function in preterm pigs, relative to formula. After a 2-day total parenteral nutrition period, preterm pigs were fed formula for a few hours (to induce a pro-inflammatory state) followed by 2 days of formula (FORM, n = 14), BC (COLOS, n = 14), spray dried BC (POW, n = 8), or pasteurised, spray dried BC (POWPAS, n = 9). RESULTS: Spray drying and pasteurisation of BC decreased the concentration of TGF-β1, TGF-β2 and increased protein aggregation. All three BC groups had reduced NEC severity, small intestinal levels of IL-1β, IL-8 and colonic lactic acid levels, and increased intestinal villus height, hexose absorption, and digestive enzyme activities, relative to the FORM group (all P < 0.05). All three BC diets stimulated epithelial cell migration in a wound-healing model with IEC-6 cells. CONCLUSION: Spray drying and pasteurisation affect BC proteins, but do not reduce the trophic and anti-inflammatory effects on the immature intestine. It remains to be studied if BC products will benefit preterm infants just after birth when human milk is often not available.
Strandede havpattedyr som mulig kilde til sygdom hos mennesker

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology
Authors: Alstrup, A. K. O. (Ekstern), Hansen, M. S. (Intern), Schønheyder, H. C. (Ekstern), Fast Jensen, L. (Ekstern)
Pages: 14-17
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Dyrlægemagasinet for Praktiserende Dyrlæger
Volume: 9
Issue number: 3
ISSN (Print): 1603-8002
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Original language: Danish
Electronic versions:
Doc1.pdf
Links:
https://issuu.com/dyrlaegen/docs/dyr20160531
Source: FindIt
Source-ID: 2304135081
Publication: Research - peer-review › Journal article – Annual report year: 2016

Stranding of two sperm whales (Physeter macrocephalus) in the "North Sea trap" at Henne Strand, Denmark
In February 2014 two male sperm whales (Physeter macrocephalus) stranded at Henne Strand, Denmark. One whale (MCE 1644) was found dead, while the other (MCE 1645) was still alive, but drowned during the high tide. To increase our knowledge of sperm whales, conduct forage investigations, post-mortem and diagnostic examinations were carried out. The decay of the carcasses progressed quickly. The whales had large (MCE 1644) or moderate (MCE 1645) numbers of squid beaks (Gonatus fabricii) in the stomachventricles, but no evidence of recent fresh feeding. Both whales had acute dermatitis probably due to trauma during the stranding and skin lesions which could be related to inter – or intraspecific interactions. MCE 1644 had large quantities of bloody fluid in the thorax and bacteriology revealed many Clostridium septicum withherein. Clostridium septicum, a normal commensal in the intestinal tract, can cause severe localized or systemic infections. The finding of large volumes of bloody pleural fluid with large quantities of C. septicum suggests that MCE 1644 died of infection. However, reservations must be taken due to the pronounced decay of the carcass. Sperm whales have strong social bonds where they follow each other, which could explain why MCE 1645 stranded alive without signs of disease.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Aarhus University Hospital, Danzoovet, Fisheries and Maritime Museum, Danish Museum of Natural History, Aalborg University Authors: Hansen, M. S. (Intern), Alstrup, A. K. O. (Ekstern), Hansen, J. H. (Ekstern), Al-Sabi, M. N. S. (Intern), Nonnemann, B. (Intern), Jensen, L. F. (Ekstern), Hedayat, A. (Ekstern), Jensen, T. H. (Ekstern)
Number of pages: 7
Pages: 35-41
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Aquatic Mammals
Volume: 42
Issue number: 1
ISSN (Print): 0167-5427
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.618 SJR 0.474 CiteScore 0.83
Streptococcus agalactiae Serotype IV in Humans and Cattle, Northern Europe

Streptococcus agalactiae is an emerging pathogen of nonpregnant human adults worldwide and a reemerging pathogen of dairy cattle in parts of Europe. To learn more about interspecies transmission of this bacterium, we compared contemporaneously collected isolates from humans and cattle in Finland and Sweden. Multilocus sequence typing identified 5 sequence types (STs) (ST1, 8, 12, 23, and 196) shared across the 2 host species, suggesting possible interspecies transmission. More than 54% of the isolates belonged to those STs. Molecular serotyping and pilus island typing of those isolates did not differentiate between populations isolated from different host species. Isolates from humans and cattle differed in lactose fermentation, which is encoded on the accessory genome and represents an adaptation to the bovine mammary gland. Serotype IV-ST196 isolates were obtained from multiple dairy herds in both countries. Cattle may constitute a previously unknown reservoir of this strain.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology
Authors: Lyhs, U. (Intern), Kulkas, L. (Ekstern), Katholm, J. (Ekstern), Waller, K. P. (Ekstern), Saha, K. (Ekstern), Tomusk, R. J. (Ekstern), Zadoks, R. N. (Ekstern)
Number of pages: 7
Pages: 2097-2103
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Emerging Infectious Diseases
Volume: 22
Issue number: 12
ISSN (Print): 1080-6040
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 4.78 SJR 3.278 SNIP 1.916
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 4.92 SJR 3.428 SNIP 2.198
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 3.101 SNIP 2.012 CiteScore 4.23
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 3.509 SNIP 2.406 CiteScore 4.59
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 3.254 SNIP 2.266 CiteScore 4.68
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 2.858 SNIP 2.131 CiteScore 4.25
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 2.785 SNIP 2.19 CiteScore 4.46
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 3.021 SNIP 2.319
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 3.168 SNIP 2.701
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 3.231 SNIP 2.277
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 2.709 SNIP 2.341
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 2.879 SNIP 2.345
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 2.816 SNIP 2.297
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 2.683 SNIP 2.562
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 2.267 SNIP 2.373
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 3.094 SNIP 2.545
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 2.346 SNIP 2.904
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.522 SNIP 2.856
Scopus rating (1999): SJR 1.71 SNIP 2.61

Original language: English
IMMUNOLOGY, INFECTIOUS, GROUP-B STREPTOCOCCUS, NONPREGNANT ADULTS, ANTIMICROBIAL RESISTANCE, MASTITIS PATHOGENS, MULTIPLEX PCR, UNITED-STATES, DAIRY HERDS, BOVINE, COLONIZATION, DISEASE, Europe, Streptococcus agalactiae, bacteria, bovine mastitis, cattle, host specificity, human, molecular epidemiology, zoonoses
Sublethal concentrations of ichthyotoxic alga Prymnesium parvum affect rainbow trout susceptibility to viral haemorrhagic septicaemia virus

Ichthyotoxic algal blooms are normally considered a threat to maricultured fish only when blooms reach lethal cell concentrations. The degree to which sublethal algal concentrations challenge the health of the fish during blooms is practically unknown. In this study, we analysed whether sublethal concentrations of the ichthyotoxic alga Prymnesium parvum affect the susceptibility of rainbow trout Oncorhynchus mykiss to viral haemorrhagic septicaemia virus (VHSV). During exposure to sublethal algal concentrations, the fish increased production of mucus on their gills. When fish were exposed to the algae for 12 h prior to the addition of virus, a marginal decrease in the susceptibility to VHSV was observed compared to fish exposed to VHSV without algae. If virus and algae were added simultaneously, inclusion of the algae increased mortality by 50% compared to fish exposed to virus only, depending on the experimental setup. We concluded that depending on the local exposure conditions, sublethal concentrations of P. parvum could affect susceptibility of fish to infectious agents such as VHSV.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, University of Copenhagen, Aarhus University
Authors: Andersen, N. G. (Ekstern), Lorenzen, E. (Ekstern), Boutrup, T. S. (Intern), Hansen, P. J. (Ekstern), Lorenzen, N. (Ekstern)
Number of pages: 9
Pages: 187-195
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Diseases of Aquatic Organisms
Volume: 117
Issue number: 3
ISSN (Print): 0177-5103
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.95 SJR 0.675 CiteScore 1.7
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.95 SJR 0.893 SNIP 0.92
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.973 SNIP 0.943 CiteScore 1.96
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.895 SNIP 0.889 CiteScore 1.86
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.831 SNIP 0.928 CiteScore 1.77
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.919 SNIP 1.092 CiteScore 2.04
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.12 SNIP 1.164 CiteScore 2.29
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.918 SNIP 0.948
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.897 SNIP 0.985
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.865 SNIP 0.995
Scopus rating (2007): SJR 0.951 SNIP 1.05
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.875 SNIP 0.966
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.909 SNIP 1.033
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.992 SNIP 1.097
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.942 SNIP 1.188
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 1.199 SNIP 1.217
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 1.35 SNIP 1.193
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.16 SNIP 1.215
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 1.193 SNIP 1.139
Original language: English
Viral haemorrhagic septicemia virus, Susceptibility, Harmful algal blooms, Fish Disease, Oncorhynchus mykiss, VHSV, Aquatic Science, Ecology, Evolution, Behavior and Systematics, Fish disease
DOIs: 10.3354/dao02946
Source: FindIt
Source-ID: 2288696639
Publication: Research - peer-review › Journal article – Annual report year: 2016

Subtypning af influenza på danske minkfarme i 2014

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Hjulsager, C. K. (Intern), Krog, J. S. (Intern), Chriél, M. (Intern), Larsen, G. (Intern), Larsen, L. E. (Intern)
Pages: 109-113
Publication date: 2016

Host publication information
Title of host publication: Faglig årsberetning 2015 : Kopenhagen Fur
Place of publication: Aarhus N
Publisher: Kopenhagen Fur
Main Research Area: Technical/natural sciences
Electronic versions:
Faglig_årsberetning_2015.pdf
Publication: Research › Report chapter – Annual report year: 2016

TCR gamma delta(+)CD8 alpha beta(+) T cell in health and disease: a novel and functionally active subpopulation of T cells enriched within the gut
TCRγδ+CD8αβ+ T cell in health and disease: a novel and functionally active subpopulation of T-cells enriched within the gut

γδ T-cells have been implicated in the pathogenesis of immune-mediated diseases such as inflammatory bowel disease (IBD). However, a potential role of different immune cell subsets in IBD and also in the process of mucosal healing upon treatment is unknown. γδ T-cells have been divided into CD8αα+ and CD8β- T-cells. By using flow cytometry and RT-PCR, we described for the first time an novel subset of human γδ T-cells expressing CD8αβ heterodimers on their surface. We found that these TCRγδ+CD8αβ+ T-cell subset exist in both human peripheral blood as well as in the gut, however they were differentially enriched within the gut. TCRγδ+CD8αβ+ T-cells displayed high cytotoxic activity by expressing Fas Ligand on their surface and also producing Granzyme B and Perforin. We showed that these cells can produce INFγ and TNFα but they did not show the ability to produce IL-17 in healthy individuals. In patients with IBD, we found a decrease in the percentage of intestinal CD8αβ+ γδ T-cells compared to healthy controls. Moreover, the percentage of TCRγδ+CD8αβ+ T-cells of γδ T-cells showed a negative correlation with Crohn's disease activity. Three months of anti-TNFα (adalimumab) therapy increased the percentage of TCRγδ+CD8αβ+ T-cells close to the level of healthy controls. These results suggest that TCRγδ+CD8αβ+ T-cells might possibly play a role in gut inflammation and also intestinal wound healing after anti-TNFα treatment. These results are likely to have implications for the development of novel therapies to treat mucosal inflammatory diseases.

General information
State: Published
Organisations: National Veterinary Institute, T-cells & Molecular Mechanisms, Lund University
Authors: Kadivar, M. (Ekstern), Petersson, J. (Ekstern), Bekiaris, V. (Intern), Marsal, J. (Ekstern), Svensson, L. (Ekstern)
Pages: 154-154
Publication date: 2016
Conference: ICI 2016 International Congress of Immunology, Melbourne, Australia, 21/08/2016 - 21/08/2016
Main Research Area: Technical/natural sciences

Publication information
Journal: European Journal of Immunology
Volume: 46
Issue number: Suppl. 1
ISSN (Print): 0014-2980
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.59 SJR 2.206 SNIP 0.92
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.61 SJR 2.525 SNIP 0.927
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.588 SNIP 0.965 CiteScore 3.85
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.672 SNIP 0.972 CiteScore 3.83
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 2.876 SNIP 1.05 CiteScore 4.3
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
Testing experimental subunit furunculosis vaccines for rainbow trout
Aeromonas salmonicida subsp. salmonicida (AS) is the etiological agent of typical furunculosis in salmonid fish. The disease causes bacterial septicemia and is a major fish health problem in salmonid aquaculture worldwide, inducing high morbidity and mortality. In this study we vaccinated rainbow trout with subunit vaccines containing protein antigens that were selected based on an in silico antigen discovery approach. Thus, the proteome of AS strain A449 was analyzed by an antigen discovery platform and its proteins consequently ranked by their predicted ability to evoke protective immune response against AS. Fourteen proteins were prepared in 3 different experimental subunit vaccine combinations and used to vaccinate rainbow trout by intraperitoneal (i.p.) injection. We tested the proteins for their ability to elicit antibody production and protection. Thus, fish were exposed to virulent AS 7 weeks post-vaccination by applying a novel, multi-puncture challenge method. The immune response in fish was evaluated following vaccination and challenge by measuring antibody levels and recording survival. The control group showed 56 % mortality whereas the groups of fish vaccinated with experimental subunit vaccines exhibited significantly lower mortalities (17-30 %). These results imply that in silico-predicted protective protein antigens of AS have significant protective properties and should be considered for further validation as potential candidates for a subunit vaccine against furunculosis.
Classical swine fever (CSF) is one of the most important viral diseases of domestic pigs (Sus scrofa domesticus) and wild boar (Sus scrofa). For at least 4 decades, several European Union member states were confronted with outbreaks among wild boar and, as it had been shown that infected wild boar populations can be a major cause of primary outbreaks in domestic pigs, strict control measures for both species were implemented. To guarantee early detection and to demonstrate freedom from disease, intensive surveillance is carried out based on a hunting bag sample. In this context, virologic investigations play a major role in the early detection of new introductions and in regions immunized with a conventional vaccine. The required financial resources and personnel for reliable testing are often large, and sufficient sample sizes to detect low virus prevalences are difficult to obtain. We conducted a simulation to model the possible impact of changes in sample size and sampling intervals on the probability of CSF virus detection based on a study area of 65 German hunting grounds. A 5-yr period with 4,652 virologic investigations was considered. Results suggest that low prevalences could not be detected with a justifiable effort. The simulation of increased sample sizes per sampling interval showed only a slightly better performance but would be unrealistic in practice, especially outside the main hunting season. Further studies on other approaches such as targeted or risk-based sampling for virus detection in connection with (marker) antibody surveillance are needed.
The costs of preventive activities for exotic contagious diseases - A Danish case study of foot and mouth disease and swine fever: a Danish case study of foot and mouth disease and swine fever

The present paper provides an overview of the costs of preventive activities, currently undertaken in Denmark, related to foot and mouth disease (FMD) and classical and African swine fever (SF). Only costs held between outbreaks were included. Costs were divided into public costs and costs paid by the pig and cattle industries, respectively. Data were retrieved from multiple sources such as databases, legal documents, official statistics, yearly reports and expert opinions. As no previous studies have assessed such costs, data collection and estimation procedures were discussed and decided upon in a group of experts from universities, industry, and public authorities. The costs of each preventive activity were related to the type of activity, the number of times the activity was carried out and the share of costs that could be associated with FMD or SF. Uncertainty about parameters was incorporated in the analysis by assuming that the FMD/SF shares of costs as well as total costs for each activity could take on a most likely as well as a minimum and maximum value. A high degree of transparency was prioritized in the cost analysis, which enables reproducibility and easy access to conducting sensitivity analyses. A total of 27 FMD/SF preventive activities were identified. The estimated median (minimum-maximum) of total costs amounted to €32 (18-50) million in 2013. The single most costly FMD/SF related activity, amounting to €8 (5-13) million or 26% of total costs, was a national legal requirement to clean lorries immediately after transportation of live animals. The distribution of costs between stakeholders was estimated to be as follows: pig industry 63%, cattle industry 27%, and the public authorities 10%. Most of the activities focused on reducing the probability of spreading FMD/SF, while only a few activities were directed mainly towards reducing the probability of introduction. Legally required FMD/SF activities (mainly based on EU legislation) accounted for 60% of the activities, while FMD/SF related measures agreed on at sector level and measures implemented due to individual initiatives, such as farmer's investment in specially built delivery facilities, each accounted for 20%. (C) 2016 Elsevier B.V. All rights reserved.

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, University of Copenhagen, Danish Agriculture and Food Council, Danish Veterinary and Food Administration, SEGES Cattle
Authors: Denver, S. (Ekstern), Alban, L. (Ekstern), Boklund, A. (Intern), Houe, H. (Ekstern), Mortensen, S. (Ekstern), Rattenborg, E. (Ekstern), Tamstorf, T. V. (Ekstern), Zobbe, H. (Ekstern), Christensen, T. (Ekstern)
Number of pages: 10
Pages: 111-120
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
The effects of vitamin A supplementation with measles vaccine on leucocyte counts and in vitro cytokine production

As WHO recommends vitamin A supplementation (VAS) at vaccination contacts after age 6 months, many children receive VAS together with measles vaccine (MV). We aimed to investigate the immunological effect of VAS given with MV. Within a randomised placebo-controlled trial investigating the effect on overall mortality of providing VAS with vaccines in Guinea-Bissau, we conducted an immunological sub-study of VAS v. placebo with MV, analysing leucocyte counts, whole blood in vitro cytokine production, vitamin A status and concentration of C-reactive protein (CRP). VAS compared with placebo was associated with an increased frequency of CRP≥5 mg/l (28 v. 12 %; P=0·005). Six weeks after supplementation, VAS had significant sex-differential effects on leucocyte, lymphocyte, monocyte and basophil cell counts, decreasing them in males but increasing them in females. Mainly in females, the effect of VAS on cytokine responses differed by previous VAS: in previous VAS recipients, VAS increased the pro-inflammatory and T helper cell type 1 (Th1) cytokine responses, whereas VAS decreased these responses in previously unsupplemented children. In previous VAS recipients, VAS was associated with increased IFN-γ responses to phytohaemagglutinin in females (geometric mean ratio (GMR): 3·97; 95 % CI 1·44, 10·90) but not in males (GMR 0·44; 95 % CI 0·14, 1·42); the opposite was observed in previously unsupplemented children. Our results corroborate that VAS provided with MV has immunological effects, which may depend on sex and previous VAS. VAS may increase the number of leucocytes, but also repress both the innate and lymphocyte-derived cytokine responses in females, whereas this repression may be opposite if the females have previously received VAS.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Statens Serum Institut, Leiden University Medical Center, Aarhus University
Authors: Jensen, K. J. (Intern), Fisker, A. B. (Ekstern), Andersen, A. (Ekstern), Sartono, E. (Ekstern), Yazdanbakhsh, M. (Ekstern), Aaby, P. (Ekstern), Erikstrup, C. (Ekstern), Benn, C. S. (Ekstern)
Number of pages: 10
Pages: 619-628
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: British Journal of Nutrition
Volume: 115
Issue number: 4
ISSN (Print): 0007-1145
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.555 SJR 1.756 CiteScore 3.65
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.46 SJR 2.055 SNIP 1.535
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.583 SNIP 1.442 CiteScore 3.52
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.532 SNIP 1.273 CiteScore 3.18
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 2.746 SNIP 2.479 CiteScore 3.61
The evolution of antimicrobial peptide resistance in Pseudomonas aeruginosa is shaped by strong epistatic interactions

Colistin is an antimicrobial peptide that has become the only remaining alternative for the treatment of multidrug-resistant Gram-negative bacterial infections, but little is known of how clinical levels of colistin resistance evolve. We use in vitro experimental evolution and whole-genome sequencing of colistin-resistant Pseudomonas aeruginosa isolates from cystic fibrosis patients to reconstruct the molecular evolutionary pathways open for high-level colistin resistance. We show that the evolution of resistance is a complex, multistep process that requires mutation in at least five independent loci that synergistically create the phenotype. Strong intergenic epistasis limits the number of possible evolutionary pathways to resistance. Mutations in transcriptional regulators are essential for resistance evolution and function as nodes that potentiate further evolution towards higher resistance by functionalizing and increasing the effect of the other mutations. These results add to our understanding of clinical antimicrobial peptide resistance and the prediction of resistance evolution.
The future of antiviral immunotoxins

There is a constant need for new therapeutic interventions in a wide range of infectious diseases. Over the past few years, the immunotoxins have entered the stage as promising antiviral treatments. Immunotoxins have been extensively explored in cancer treatment and have achieved FDA approval in several cases. Indeed, the design of new anticancer immunotoxins is a rapidly developing field. However, at present, several immunotoxins have been developed targeting a variety of different viruses with high specificity and efficacy. Rather than blocking a viral or cellular pathway needed for virus replication and dissemination, immunotoxins exert their effect by killing and eradicating the pool of infected cells. By targeting a virus-encoded target molecule, it is possible to obtain superior selectivity and drastically limit the side effects,
which is an immunotoxin-related challenge that has hindered the success of immunotoxins in cancer treatment. Therefore, it seems beneficial to use immunotoxins for the treatment of virus infections. One recent example showed that targeting of virus-encoded 7 transmembrane (7TM) receptors by immunotoxins could be a future strategy for designing ultraspecific antiviral treatment, ensuring efficient internalization and hence efficient eradication of the pool of infected cells, both in vitro and in vivo. In this review, we provide an overview of the mechanisms of action of immunotoxins and highlight the advantages of immunotoxins as future anti-viral therapies.

**General information**

State: Published
Organisations: National Veterinary Institute, Section for Virology, University of Copenhagen
Authors: Spiess, K. (Ekstern), Høy Jakobsen, M. (Ekstern), Kledal, T. N. (Intern), Rosenkilde, M. M. (Ekstern)
Number of pages: 15
Pages: 911-925
Publication date: 2016
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Journal of Leukocyte Biology
Volume: 99
Issue number: 6
ISSN (Print): 0741-5400
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.98 SJR 2.04 CiteScore 3.56
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4 SJR 2.473 SNIP 1.09
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.459 SNIP 1.141 CiteScore 3.95
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.589 SNIP 1.173 CiteScore 3.94
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 2.651 SNIP 1.188 CiteScore 4.22
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 2.624 SNIP 1.269 CiteScore 4.6
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 2.538 SNIP 1.303 CiteScore 4.5
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.555 SNIP 1.22
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 2.498 SNIP 1.185
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 2.647 SNIP 1.08
Scopus rating (2007): SJR 2.443 SNIP 1.093
Scopus rating (2006): SJR 2.562 SNIP 1.142
Scopus rating (2005): SJR 2.399 SNIP 1.144
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 2.199 SNIP 1.062
Scopus rating (2003): SJR 2.186 SNIP 1.066
Scopus rating (2002): SJR 2.227 SNIP 1.03
Swine influenza presents a substantial disease burden for pig populations worldwide and poses a potential pandemic threat to humans. There is considerable diversity in both H1 and H3 influenza viruses circulating in swine due to the frequent introductions of viruses from humans and birds coupled with geographic segregation of global swine populations. Much of this diversity is characterized genetically but the antigenic diversity of these viruses is poorly understood. Critically, the antigenic diversity shapes the risk profile of swine influenza viruses in terms of their epizootic and pandemic potential. Here, using the most comprehensive set of swine influenza virus antigenic data compiled to date, we quantify the antigenic diversity of swine influenza viruses on a multi-continental scale. The substantial antigenic diversity of recently circulating viruses in different parts of the world adds complexity to the risk profiles for the movement of swine and the potential for swine-derived infections in humans.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Number of pages: 17
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: eLife
Volume: 5
Article number: e12217
ISSN (Print): 2050-084X
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.572 SJR 7.121 CiteScore 6.88
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 5.41 SJR 7.296 SNIP 1.506
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 7.741 SNIP 1.654 CiteScore 4.91
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 7.888 SNIP 1.664 CiteScore 4.85
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 6.086 SNIP 1.562 CiteScore 4.24
Original language: English
epidemiology, global health, human, infectious disease, influenza, microbiology, pandemic, swine, virus
Electronic versions:
elife_12217.pdf
The H3K4me3/2 histone demethylase RBR-2 controls axon guidance by repressing the actin-remodeling gene wsp-1

The dynamic regulation of histone modifications is important for modulating transcriptional programs during development. Aberrant H3K4 methylation is associated with neurological disorders, but how the levels and the recognition of this modification affect specific neuronal processes is unclear. Here, we show that RBR-2, the sole homolog of the KDM5 family of H3K4me3/2 demethylases in Caenorhabditis elegans, ensures correct axon guidance by controlling the expression of the actin regulator wsp-1. Loss of rbr-2 results in increased levels of H3K4me3 at the transcriptional start site of wsp-1, with concomitant higher wsp-1 expression responsible for defective axon guidance. In agreement, overexpression of WSP-1 mimics rbr-2 loss, and its depletion restores normal axon guidance in rbr-2 mutants. NURF-1, an H3K4me3-binding protein and member of the chromatin-remodeling complex NURF, is required for promoting aberrant wsp-1 transcription in rbr-2 mutants and its ablation restores wild-type expression of wsp-1 and axon guidance. Thus, our results establish a precise role for epigenetic regulation in neuronal development by demonstrating a functional link between RBR-2 activity, H3K4me3 levels, the NURF complex and the expression of WSP-1.
The impact of dietary swine plasma immunoglobulins on intestinal microbiota and general health in weaner piglets

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Section for Bacteriology, Pathology and Parasitology
Authors: Hedegaard, C. J. (Intern), Strube, M. L. (Intern), Jensen, T. K. (Intern), Heegaard, P. M. H. (Intern)
Number of pages: 1
Publication date: 2016
Event: Poster session presented at 2nd international symposium on alternatives to antibiotics (ATA), Paris, France.
Main Research Area: Technical/natural sciences
Electronic versions:
POSTER_ATA_2016.pdf
Publication: Research - peer-review › Poster – Annual report year: 2016

The impact of microclimatic temperature on vector-borne disease transmission in Denmark

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology
Authors: Haider, N. (Intern), Kristensen, B. (Intern), Kirkeby, C. (Intern), Toft, N. (Intern), Bødker, R. (Intern)
Number of pages: 1
Publication date: 2016
Event: Poster session presented at SVEPM, Elsinore, Denmark.
Main Research Area: Technical/natural sciences
Electronic versions:
Haider_Najmul.pdf
Source: PublicationPreSubmission
Source-ID: 123369531
Publication: Research - peer-review › Poster – Annual report year: 2016

The level of embryonation influences detection of Ostertagia ostertagi eggs by semi-quantitative PCR
The Internal Transcribed Spacer 2 (ITS2) is a candidate diagnostic marker of the pathogenic cattle nematode Ostertagia ostertagi. The aims of this study were: (i) to document and quantify how the developement of O. ostertagi eggs affects ITS2 copies under different storage conditions, and (ii) to suggest optimal storage conditions for faecal samples in a diagnostic pipeline that involves detection and semi-quantification by real-time semi-quantitative polymerase chain reaction (qPCR). Eggs of Ostertagia ostertagi were obtained from fresh faeces and stored at 4 °C or 25 °C under aerobic or anaerobic conditions.
(vacuum packing) conditions. Development was monitored by microscopy for up to 336 h, and the ITS2 copies were determined by qPCR from a fixed number of parasites. Under aerobic conditions at 25 °C, embryonation and a significant increase of ITS2 copies (P
The Non-structural Protein 5 and Matrix Protein Are Antigenic Targets of T Cell Immunity to Genotype 1 Porcine Reproductive and Respiratory Syndrome Viruses

The porcine reproductive and respiratory syndrome virus (PRRSV) is the cause of one of the most economically important diseases affecting swine worldwide. Efforts to develop a next-generation vaccine have largely focused on envelope glycoproteins to target virus-neutralizing antibody responses. However, these approaches have failed to demonstrate the necessary efficacy to progress toward market. T cells are crucial to the control of many viruses through cytolysis and cytokine secretion. Since control of PRRSV infection is not dependent on the development of neutralizing antibodies, it has been proposed that T cell-mediated immunity plays a key role. Therefore, we hypothesized that conserved T cell antigens represent prime candidates for the development a novel PRRS vaccine. Antigens were identified by screening a proteome-wide synthetic peptide library with T cells from cohorts of pigs rendered immune by experimental infections with a closely related (subtype 1) or divergent (subtype 3) PRRSV-1 strain. Dominant T cell IFN-gamma responses were directed against the non-structural protein 5 (NSP5), and to a lesser extent, the matrix (M) protein. The majority of NSP5-specific CD8 T cells and M-specific CD4 T cells expressed a putative effector memory phenotype and were polyfunctional as assessed by coexpression of TNF-alpha and mobilization of the cytotoxic degranulation marker CD107a. Both antigens were generally well conserved among strains of both PRRSV genotypes. Thus, M and NSP5 represent attractive vaccine candidate T cell antigens, which should be evaluated further in the context of PRRSV vaccine development.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Animal and Plant Health Agency, University of Veterinary Medicine, University of Surrey, University College London
Authors: Mokhtar, H. (Ekstern), Pedrera, M. (Ekstern), Frossard, J. (Ekstern), Biffar, L. (Ekstern), Hammer, S. E. (Ekstern), Kvisgaard, L. K. (Intern), Larsen, L. E. (Intern), Stewart, G. R. (Ekstern), Somavarapu, S. (Ekstern), Steinbach, F. (Ekstern), Graham, S. P. (Ekstern)
Number of pages: 14
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Frontiers in Immunology
Volume: 7
Article number: 40
ISSN (Print): 1664-3224
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SJR 2.803 SNIP 1.484 CiteScore 5.62
Web of Science (2017): Indexed yes
Scopus rating (2016): CiteScore 5.37 SJR 3.034 SNIP 1.476
Web of Science (2016): Indexed yes
Scopus rating (2015): SJR 2.827 SNIP 1.277 CiteScore 5.09
Web of Science (2015): Indexed yes
Scopus rating (2014): SJR 2.389 SNIP 1.057 CiteScore 4.24
Web of Science (2014): Indexed yes
Scopus rating (2013): SJR 1.908 SNIP 0.855 CiteScore 3.55
ISI indexed (2013): ISI indexed no
Scopus rating (2012): SJR 0.809 SNIP 0.193 CiteScore 1.38
ISI indexed (2012): ISI indexed no
Scopus rating (2011): SJR 0.121
Web of Science (2011): Indexed yes
Original language: English
IMMUNOLOGY, EXPERIMENTAL CHALLENGE, LYMPHOCYTE SUBSETS, CLINICAL-DISEASE, SYNDROME PRRS, IFN-GAMMA, PIGS, VACCINE, RESPONSES, SWINE, IDENTIFICATION, porcine reproductive and respiratory syndrome virus, T cell, IFN-gamma, antigen identification, phenotype and function, vaccine, IFN-γ
Electronic versions:
fimmu_07_00040.pdf
DOIs:
10.3389/fimmu.2016.00040
The pig as a large preclinical model for therapeutic human anti-cancer vaccine development

Development of therapeutic cancer vaccines has largely been based on rodent models and the majority failed to establish therapeutic responses in clinical trials. We therefore used pigs as a large animal model for human cancer vaccine development due to the large similarity between the porcine and human immunome. We administered peptides derived from porcine IDO, a cancer antigen important in human disease, formulated in Th1-inducing adjuvants to outbred pigs. By in silico prediction 136 candidate IDO-derived peptides were identified and peptide-SLA class I complex stability measurements revealed 89 stable (t½ ≥ 0.5 hour) complexes with expressed SLA alleles. By IFN-γ ELISpot we showed that it was possible to break the peripheral tolerance and induce a cell-mediated response to an endogenous antigen. Mounting a proper Th1 response is highly dependent on peptide dose; we therefore designed a dose titration study with 15 Göttlingen minipigs receiving intraperitoneal injections of either 1 µg, 10 µg or 100 µg of 30-31mer peptides covering the majority of IDO-derived potential cytotoxic T lymphocyte (CTL) epitopes. Peptides were formulated in CAF09, an adjuvant comprised of cationic DDA liposomes decorated with poly (I:C) and MMG as immune modulators. Interestingly, the 1 µg group was the only one showing responses to all immunization peptides following seven injections as determined by IFN-γ ELISpot. These data show that a reduction in dose can result in a highly specific Th1-biased response. To test the CTL functionality we designed an in vivo cytotoxicity assay, where purified autologous PBMCs fluorescently labelled and pulsed with IDO-derived target peptides were administered intravenously into each donor and killing capacity was measured by flow cytometry. All animals receiving 10 µg peptide immunizations showed specific killing of peptide-pulsed target cells one week post i.v. transfer with certain animals reaching close to 60% specific killing capacity in vivo.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Section for Virology, University of Copenhagen, Technical University of Denmark, Copenhagen University Hospital
Authors: Overgaard, N. H. (Intern), Frøsig, T. M. (Intern), Welner, S. (Intern), Rasmussen, M. (Ekstern), Ilsøe, M. (Ekstern), Sørensen, M. R. (Intern), Andersen, M. H. (Ekstern), Buus, S. (Ekstern), Jungersen, G. (Intern)
Number of pages: 1
Pages: 1102-1102
Publication date: 2016
Conference: ICI 2016 International Congress of Immunology, Melbourne, Australia, 21/08/2016 - 21/08/2016
Main Research Area: Technical/natural sciences

Publication information
Journal: European Journal of Immunology
Volume: 46
Issue number: S1
ISSN (Print): 0014-2980
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.59 SJR 2.206 SNIP 0.92
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.61 SJR 2.525 SNIP 0.927
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.588 SNIP 0.965 CiteScore 3.85
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.672 SNIP 0.972 CiteScore 3.83
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 2.876 SNIP 1.05 CiteScore 4.3
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
The pig as a large preclinical model for therapeutic human anti-cancer vaccine development

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Section for Virology, State Serum Institute, University of Copenhagen, Technical University of Denmark, Statens Serum Institut
Number of pages: 1
Publication date: 2016
Event: Abstract from 11th International Veterinary Immunology Symposium, Gold Coast, Australia.
Main Research Area: Technical/natural sciences
Electronic versions:
IVIS_2016_abstract_Overgaard_et_al.pdf
Source: PublicationPreSubmission
Source-ID: 127762619
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2016

The policy implications of urban open space commercial vegetable farmers’ willingness and ability to pay for reclaimed water for irrigation in Kumasi, Ghana

The acute waste management problems, coupled with the proliferation of small scale industries in many developing countries, make low quality water treatment before use inevitable in the long run. These industries have the potential to discharge effluent containing chemicals and heavy metals into the environment. The indiscriminative use of pharmaceutical products by households in many of these countries is another source of health concern. Low quality water treatment in these countries has however been hampered by the high cost of infrastructure provision and maintenance. Cost-sharing among stakeholders appears to be a promising strategy to finance and maintain the wastewater treatment infrastructure. In this study therefore, the willingness and ability of urban open space commercial vegetable farmers to pay
for reclaimed water for irrigation purposes has been assessed. One hundred open space commercial vegetable farmers and four vegetable farmers' associations were selected and interviewed in Kumasi in Ghana using semi-structured interview schedules and interview guides respectively. The results of the study show that approximately three out of every five vegetable farmers were willing to pay for reclaimed water for irrigation. The results further show that the probability of being willing to pay by farmers who agreed that the current water they used for irrigation was harmful is approximately 5.3 times greater than that of those who did not. The analysis of the farmers' ability to pay revealed that all the farmers would be capable of paying for reclaimed water at a price of US$0.11/m³. This has implications for land tenure security and vegetable consumers' willingness to pay higher prices for the produce.

General information
State: Published
Organisations: National Veterinary Institute, National Food Institute, Research Group for Genomic Epidemiology, DHI Hørsholm, Kwame Nkrumah University of Science and Technology
Authors: Amponsah, O. (Ekstern), Vigre, H. (Intern), Braimah, I. (Ekstern), Schou, T. W. (Ekstern), Abaidoo, R. C. (Ekstern)
Number of pages: 38
Pages: e00078
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Heliyon
Volume: 2
Issue number: 3
ISSN (Print): 2405-8440
Ratings:
Scopus rating (2017): CiteScore 1.23 SJR 0.355 SNIP 0.572
Scopus rating (2016): CiteScore 0.62 SJR 0.187 SNIP 0.72
Original language: English
Agricultural economics, Agriculture, Development
Electronic versions:
1_s2.0_S2405844015303492_main.pdf
1_s2.0_S2405844015303492_main.pdf
DOIs:
10.1016/j.heliyon.2016.e00078

Bibliographical note
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Source: Findit
Source-ID: 2302993723
Publication: Research - peer-review › Journal article – Annual report year: 2016

The potential for vector borne infections in the Nordic area now and in the future

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Technical University of Denmark
Authors: Bødker, R. (Intern), Cuellar, A. C. (Intern), Haider, N. (Ekstern)
Number of pages: 35
Publication date: 2016

Publication information
Media of output: Powerpoint
Original language: English
Publisher: Technical University of Denmark (DTU)
Main Research Area: Technical/natural sciences
Electronic versions:
Rene_Boedker_Trondheim_June_2016_final_PDF.pdf
Publication: Research › Sound/Visual production (digital) – Annual report year: 2016

The preterm pig as a model of premature infant gait ataxia
Aims/background Compromised gait, balance and motor coordination (ataxia) as observed in cases of cerebral palsy is a serious complication to premature birth. The cerebellum is a central region with regards to these brain functions and its development shows high sensitivity to premature birth. Our group has over many years refined a pig model of premature birth focusing on gut and immune system development. Phenotypically, we have observed distinct motoric problems e.g.
falls, tiptoe walking and swaying in preterm pigs relative to term born counterparts, indicating compromised brain function. The aim of this study was to compare gait patterns and cerebellar neurodevelopmental gene expression of preterm and term piglets. Methods We compared gait patterns and T-maze performance of caesarean born preterm (3 litters, 90% gestation) and term born pigs (1 litter, 100% gestation) recorded at five distinct postnatal days. MatLab was used to determine a list of spatiotemporal gait characteristics e.g. stride length/ frequency, "duty factor" and asymmetry indices. These data were paralleled by qPCR of >60 selected neurodevelopmental genes of isolated cerebellar tissue. Results While most genes did not differ significantly, we found higher (fold change [1.5-2]) mRNA levels of Midkine, Doublecortin, Neurotrophin3, p75 and Ephrin-B1 in preterms. Preliminary results from gait and T-maze showed significant functional differences between terms and preterms. Conclusions The preterm pig shows functional delays relative to terms, yet the limited cerebellar gene expression differences (mainly related to angiogenesis) suggest other brain regions e.g. motor cortex and basal ganglia to also be involved in compromised gait.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, University of Copenhagen, University of Antwerp
Authors: Bergström, A. (Ekstern), Ryom, K. (Ekstern), Vanden Hole, C. (Ekstern), Andersen, A. D. (Ekstern), Skovgaard, K. (Intern), Van Ginneken, C. (Ekstern), Thymann, T. (Ekstern), Sangild, P. T. (Ekstern)
Number of pages: 1
Publication date: 2016
Event: Abstract from 10th FENS Forum of Neuroscience 2016, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Electronic versions:
FENS2016_abstract_Bergstrom_FINAL.pdf
Source: PublicationPreSubmission
Source-ID: 122152945
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2016

The role of cattle movement in determining the incidence risk of Mycoplasma bovis in Danish dairy herds between 2013-2014

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Technical University of Denmark, University of Copenhagen
Authors: Arede, M. (Intern), Nielsen, L. R. (Ekstern), Halasa, T. (Ekstern), Toft, N. (Intern), Nielsen, P. K. (Ekstern)
Number of pages: 1
Publication date: 2016
Event: Poster session presented at SVEPM, Elsinore, Denmark.
Main Research Area: Technical/natural sciences
Electronic versions:
NYT.pdf
Source: FindIt
Source-ID: 2306027668
Publication: Research - peer-review › Poster – Annual report year: 2016

Towards control of LA-MRSA - Simulation modeling of LA-MRSA spread between pig farms

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Statens Serum Institut
Authors: Schulz, J. (Intern), Toft, N. (Intern), Boklund, A. (Intern), Larsen, J. (Ekstern), Hisham Beshara Halasa, T. (Intern)
Number of pages: 1
Publication date: 2016
Event: Poster session presented at SVEPM, Elsinore, Denmark.
Main Research Area: Technical/natural sciences
Electronic versions:
SVEPM_Poster_Jana_Sonnenburg.pdf
Source: PublicationPreSubmission
Source-ID: 127047463
Publication: Research - peer-review › Poster – Annual report year: 2016
Tracking the elusive cytotoxic T cell response in pigs

Quantitative and qualitative assessment of antigen-specific cytotoxic T cell (CTL) responses in pigs is not a straightforward process. Through the years we have developed a series of reagents, tools and protocols to characterize peptide-specific CTL responses in pigs.

The most common recombinant SLA heavy chains were produced and peptide binding motifs were determined by assays measuring the affinity and stability of the peptide-SLA complex (pSLA) interaction. These results have been used to train neural networks to predict the binding of any pSLA (http://www.cbs.dtu.dk/services/). Recombinant SLA molecules complexed with verified binding peptides can be assembled to SLA multimers for staining of peptide-specific CTLs, and measured by flow cytometry, as we have shown with FMDV and influenza. This, however, requires SLA-matched pigs for which we have developed two methods: a sequence-based, high-resolution SLA genotyping method by standard PCR for specific detection of eight in-house SLA molecules; and a next-generation sequencing method for parallel detection of up to 50 samples of barcoded cDNA PCR products spanning exon 2 and 3. The latter for a wider characterization of expressed alleles in candidate pigs.

The in vivo generation of CTL responses to antigens following peptide immunizations is thought to require cross-presentation in appropriate dendritic cells (DC). In mice this was linked to targeting of CD103+DCs recruited after intraperitoneal immunizations. We have therefore developed a protocol for intraperitoneal delivery of peptides formulated in poly(I:C)/MMG-decorated liposomes (CAF09) to investigate the influence of peptide dose on the generation of CTL vs. antibody responses. Finally, the induced CTL killing was assessed by an in vivo cytotoxicity assay, where purified autologous PBMCs, fluorescently labeled and pulsed with target peptides, were reinjected into the donor. The in vivo killing of peptide-pulsed cells was measured by flow cytometry relative to non-pulsed PBMCs at different time points after cell transfer.
Unravelling the nature of non-specific effects of vaccines—A challenge for innate immunologists

Epidemiological observations have shown that vaccines can influence morbidity and mortality more than can be ascribed to target-disease immunity. A growing number of immunological studies have helped identify possible biological mechanisms to explain these so-called nonspecific effects (NSE) of vaccines, including heterologous T-cell reactivity and innate immune memory or ‘trained innate immunity’, which involves epigenetic reprogramming of innate immune cells. Here, we review the epidemiological evidence for NSE as well as human, animal and in vitro immunological data that could explain these NSE, and discuss priorities for future epidemiologic and immunologic studies to further unravel the biology and optimize the benefits of current and new vaccines.
Unrecognized circulation of SAT 1 foot-and-mouth disease virus in cattle herds around Queen Elizabeth National Park in Uganda

Foot-and-mouth disease (FMD) is endemic in Uganda in spite of the control measures used. Various aspects of the maintenance and circulation of FMD viruses (FMDV) in Uganda are not well understood; these include the role of the African buffalo (Syncerus caffer) as a reservoir for FMDV. To better understand the epidemiology of FMD at the livestock-wildlife-interface, samples were collected from young, unvaccinated cattle from 24 pastoral herds that closely interact with wildlife around Queen Elizabeth National Park in Uganda, and analysed for evidence of FMDV infection. In total, 37 (15 %) of 247 serum samples had detectable antibodies against FMDV non-structural proteins (NSPs) using a pan-serotypic assay. Within these 37 sera, antibody titres ≥ 80 against the structural proteins of serotypes O, SAT 1, SAT 2 and SAT 3 were detected by ELISA in 5, 7, 4 and 3 samples, respectively, while neutralizing antibodies were only detected against serotype O in 3 samples. Two FMDV isolates, with identical VP1 coding sequences, were obtained from probang samples from clinically healthy calves from the same herd and are serotype SAT 1 (topotype IV (EA-I)). Based on the VP1 coding sequences, these viruses are distinct from previous cattle and buffalo SAT 1 FMDV isolates obtained from the same area (19-30 % nucleotide difference) and from the vaccine strain (TAN/155/71) used within Uganda (26 % nucleotide difference). Eight herds had only one or a few animals with antibodies against FMDV NSPs while six herds had more substantial evidence of prior infection with FMDV. There was no evidence for exposure to FMDV in the other ten herds. The two identical SAT 1 FMDV VP1 sequences are distinct from former buffalo and cattle isolates from the same area, thus, transmission between buffalo and cattle was not demonstrated. These new SAT 1 FMDV isolates differed significantly from the vaccine strain used to control Ugandan FMD outbreaks, indicating a need for vaccine matching studies. Only six herds had clear serological evidence for exposure to O and SAT 1 FMDV. Scattered presence of antibodies against FMDV in other herds may be due to the occasional introduction of animals to the area or maternal antibodies from past infection and/or vaccination. The evidence for asymptomatic FMDV infection has implications for disease control strategies in the area since this obstructs early disease detection that is based on clinical signs in FMDV infected animals.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Dhikusooka, M. T. (Ekstern), Ayebazibwe, C. (Ekstern), Namatovu, A. (Ekstern), Belsham, G. (Intern), Siegismund, H. R. (Ekstern), Wekesa, S. N. (Ekstern), Balinda, S. N. (Ekstern), Muwanika, V. B. (Ekstern), Tjørnehøj, K. (Intern)
Number of pages: 13
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: B M C Veterinary Research
Volume: 12
Issue number: 1
ISSN (Print): 1746-6148
Ratings:
BFI (2018): BFI-level 1
Using Merkel cell polyomavirus specific TCR gene therapy for treatment of Merkel cell carcinoma

T cell receptor gene-therapy has entered the clinic and shown potential for successful cancer treatment. However, the clinical evaluation has also highlighted the need for selection of truly cancerspecific targets. Merkel cell carcinoma (MCC) is a highly aggressive skin cancer associated with Merkel cell polyomavirus (MCPyV). Due to the clear viral correlation CD8+ T cells specific for viral epitopes could potentially form cancer-specific targets in MCC patients. We have identified MCPyV specific T cells using a high-throughput platform for T-cell enrichment and combinatorial encoding of fluorescence-labeled major histocompatibility complex (MHC) class I multimers. We identified 35 T cell epitopes among 398 MCPyV derived peptides analyzed. Strikingly, T-cell responses against the two oncogenic MCPyV proteins Large T antigen and small T antigen were exclusively present in blood of MCC patients when compared to healthy donors. We demonstrate both the processing and presentation of oncoprotein-derived epitopes, as well as lytic activity of specific T cells towards MHC matched MCC cells. Demonstrating the presence of oncoprotein-specific T cells among tumorinfiltrating lymphocytes ex vivo further substantiated the relevance of the identified epitopes. The viral epitopes represents specific targets and should be ideal for TCR-gene therapy approaches. We have isolated and sequenced MCPyV oncogenic protein specific T cell receptors and are currently testing in vitro transduction systems with the purpose of introducing the TCRs into human PBMC, injecting them into immune deficient NOG mice carrying HLA matched MCPyV positive tumor to investigate the tumor rejection capacity of these gene-modified T cells.
Vector-borne disease surveillance in livestock populations: a critical review of literature recommendations and implemented surveillance (BTV-8) in five European countries

Preparedness against vector-borne threats depends on the existence of a long-term, sustainable surveillance of vector-borne disease and their relevant vectors. This work reviewed the availability of such surveillance systems in five European countries (Denmark, France, The Netherlands, Sweden and United Kingdom, part of the CoVetLab network). A qualitative assessment was then performed focusing on surveillance directed particularly to BTV-8. Information regarding surveillance activities were reviewed for the years 2008 and 2012. The results were then complemented with a critical scoping review of the literature aimed at identifying disease surveillance strategies and methods that are currently suggested as best suited to target vector-borne diseases in order to guide future development of surveillance in the countries in question.

Passive surveillance was found to be efficient for early detection of diseases during the early phase of introduction into a free country. However, its value diminished once the disease has been established in a territory. Detection of emerging diseases was found to be very context and area specific, and thus active surveillance designs need to take the available epidemiological, ecological and entomological information into account. This was demonstrated by the effectiveness of the bulk milk surveillance in detecting the first case in Sweden, highlighting the need for output based standards to allow the most effective, context dependent, surveillance strategies to be used. Preparedness was of fundamental importance in determining the timeliness of detection and control in each country and that this in turn was heavily influenced by knowledge of emerging diseases in neighboring countries. Therefore it is crucial to share information on outbreaks between researchers and decision-makers and across borders continually in order to react timely in case of an outbreak. Furthermore, timely reaction to an outbreak was heavily influenced by availability of control measures (vaccines), which is also strengthened if knowledge is shared quickly between countries. The assessment of the bluetongue surveillance in the affected countries showed that the degree of voluntary engagement varied, and that it is important to engage the public by general awareness and dissemination of results. The degree of engagement will also aid in establishing a passive surveillance system.
Virulence determinants within the E2 glycoprotein of Classical Swine Fever Virus

Classical Swine Fever is a highly contagious disease of pigs caused by Classical Swine Fever Virus (CSFV), a member of the pestivirus genus within the family Flaviviridae. The E2 glycoprotein of CSFV has been shown to be an important factor for the virulence of the virus. In a recent study, we have identified a specific motif within the E2 glycoprotein that contributes to the virulence of the highly virulent CSFV strain Koslov (Fahnøe et al. 2014). This motif comprises residues S74 and L75 in the N-terminal domain of E2 (S763 and L764 in the polyprotein). Evidence points towards involvement of this motif in virulence. CSFV strains encoding L763 and P764 represent the predominant alleles across all published full-length CSFV genomes, whereas the S763/L764 combination is only seen in highly virulent strains. In this study, mutations were introduced into the consensus cDNA clone of the highly virulent CSFV strain Koslov to evaluate the virulence of a set of E2 mutants with modifications in the encoded residues 763 and 764; these mutants are termed; vKos_SP, vKos_LP and vKos_LL, respectively. Animal infection experiments were performed to compare virulence of these E2 mutants in comparison to vKos (with the SL motif). The results indicate that the E2 residues 763-64 play an important role in CSFV virulence.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Johnston, C. M. (Intern), Fahnøe, U. (Intern), Lohse, L. (Intern), Belsham, G. (Intern), Rasmussen, T. B. (Intern)
Number of pages: 1
Publication date: 2016
Event: Abstract from Keystone Symposia on Molecular and Cellular Biology, Austin, United States.
Main Research Area: Technical/natural sciences
Electronic versions:
Johnston_et_al_plusRNAvirus_meeting_keystone.pdf
Source: PublicationPreSubmission
Source-ID: 127611632
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2016

Virulence of viral haemorrhagic septicaemia virus (VHSV) genotype III in rainbow trout

In general, viral haemorrhagic septicemia virus (VHSV) isolates from marine fish species in European waters (genotypes GIIb, GII and GIII) are non- to low virulent in rainbow trout. However, a VHSV isolation was made in 2007 from a disease outbreak in sea farmed rainbow trout in Norway. The isolate, named NO-2007-50-385, was demonstrated to belong to GIII. This isolate has attracted attention to assess which of the viral genome/proteins might be associated with the virulence in rainbow trout. In this study, we describe the difference of virulence in rainbow trout between the NO-2007-50-385 and 4p168 isolates as representatives of virulent and non-virulent GIII isolates, respectively. Rainbow trout were bath challenged with VHSV NO-2007-50-385 for 1 and 6 h, resulting in cumulative mortalities of 5 and 35%, respectively. No mortality was observed in the rainbow trout groups immersed with the genotype III VHSV isolate 4p168 for 1 and 6 h. The viral titre in organs from fish challenged with NO-2007-50-385 for 6 h increased more rapidly than those exposed for 1 h. By in vitro studies it was demonstrated that the final titres of VHSV DK-3592B (GI), NO-2007-50-385 and 4p168 inoculated
on EPC cells were very similar, whereas when inoculated on the rainbow trout cell line RTG-2 the titre of the non-virulent 4p168 isolate was 3-4 logs below the two other VHSV isolates. Based on a comparative analysis of the entire genome of the genotype III isolates, we suggest that substitutions of amino acids in positions 118-123 of the nucleo-protein are candidates for being related to virulence of VHSV GIII in rainbow trout.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Fisheries Research Agency
Authors: Ito, T. (Ekstern), Kurita, J. (Ekstern), Mori, K. (Ekstern), Olesen, N. J. (Intern)
Number of pages: 13
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Veterinary Research
Volume: 47
Issue number: 1
Article number: 4
ISSN (Print): 0928-4249
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 1.139 SJR 1.266
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): SJR 1.44 SNIP 1.303
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.537 SNIP 1.153 CiteScore 2.66
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.453 SNIP 1.423 CiteScore 2.46
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.681 SNIP 1.701 CiteScore 3.13
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.461 SNIP 1.45 CiteScore 2.97
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.712 SNIP 1.655 CiteScore 3.85
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.531 SNIP 1.606
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.489 SNIP 1.689
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.578 SNIP 2.002
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.749 SNIP 2.189
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.353 SNIP 1.936
Vis jeres værd, universiteter

**General information**
State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Kledal, T. N. (Intern)
Pages: 2-2
Publication date: 2016
Main Research Area: Technical/natural sciences

**Publication information**
Journal: Boersen
ISSN (Print): 0105-0729

West Nile fever: En virussygdom, der spredes sig i Europa
Status over West Nile virus i Europa og det danske overvågningsprogram.

**General information**
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Section for Virology, Fødevarestyrelsen, University of Copenhagen
Authors: Lohse, L. (Intern), Madsen, J. J. (Ekstern), Huda, A. (Ekstern), Bødker, R. (Intern), Thorup, K. (Ekstern), Polacek, C. (Intern), Bøtner, A. (Intern)
Pages: 10-13
Publication date: 2016
Main Research Area: Technical/natural sciences

**Publication information**
Journal: Dansk Veterinaertidsskrift
Volume: 2016
Issue number: 8
ISSN (Print): 0106-6854

BFI (2018): BFI-level 1
What to look for when monitoring animal diseases?

**General information**

**State:** Published  
**Organisations:** National Veterinary Institute, Section for Epidemiology, University of Copenhagen  
**Authors:** Lopes Antunes, A. C. (Intern), Jensen, D. (Ekstern), Hisham Beshara Halasa, T. (Intern), Toft, N. (Intern)  
**Number of pages:** 1  
**Publication date:** 2016  
**Event:** Poster session presented at SVEPM, Elsinore, Denmark.

**Main Research Area:** Technical/natural sciences

**Electronic versions:**

West_Nile_fever_DVT_08_2016.pdf  
Links:

Source: PublicationPreSubmission  
Source-ID: 124120862  
Publication: Research › Journal article – Annual report year: 2016

Why do neonatal piglets get diarrhoea?

**General information**

**State:** Published  
**Organisations:** National Veterinary Institute, Pig Research Centre, SEGES Pig Research Center  
**Authors:** Kongsted, H. (Ekstern), Bækbo, P. (Ekstern), Hjulsager, C. K. (Intern), Jorsal, S. E. L. (Intern)  
**Pages:** 169-169  
**Publication date:** 2016

**Host publication information**

**Title of host publication:** 24th International Pig Veterinary Society Congress - abstracts book  
**Place of publication:** Dublin, Ireland  
**Publisher:** Royal Dublin Society  
**Article number:** O-MIS-001  
**Main Research Area:** Technical/natural sciences  
**Conference:** 24th International Pig Veterinary Society (IPVS) Congress, Dublin, Ireland, 07/06/2016 - 07/06/2016  
**Electronic versions:**

AnaCarolina_Antunes.pdf  
Source: PublicationPreSubmission  
Source-ID: 122708284  
Publication: Research ‒ peer-review › Poster – Annual report year: 2016
Widespread presence of mrsa CC398 in the danish production of farmed mink (neovison vison)

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Statens Serum Institut, State Serum Institute, Technical University of Denmark
Authors: Hansen, J. E. (Intern), Rhod Larsen, A. (Ekstern), Skov, R. L. (Ekstern), Chriél, M. (Intern), Larsen, G. (Intern), Angen, Ø. (Ekstern), Larsen, J. (Ekstern), Corvera Kløve Lassen, D. (Ekstern), Pedersen, K. (Intern)
Pages: 70-71
Publication date: 2016

Host publication information
Title of host publication: The Danish Microbiological Society Annual Congress 2016 : Programme & Abstracts
Place of publication: Copenhagen
Publisher: American Society for Microbiology
Article number: P54
Main Research Area: Technical/natural sciences
Conference: Danish Microbiological Society Annual Congress 2016, Copenhagen, Denmark, 14/11/2016 - 14/11/2016
Electronic versions:
Programme & Abstracts book
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2016

Danske køer foretrækker drenge, mens amerikanske køer foretrækker piger
Nyt studie fra DTU viser, at en dansk malkeko giver mere mælk, hvis hendes kalv er en tyrekalv. I USA derimod giver køen mest mælk, hvis kalven er en kvie. Forskellen overrasker forskerne, som troede, at køerne var mere ens.

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology
Authors: Græsbøll, K. (Intern)
Publication date: 15 Aug 2015

Publication information
Type: Netartikel
Source/Publisher: Videnskab.dk
Last modified date: 15/08/2015
Main Research Area: Technical/natural sciences
Electronic versions:
videnskab_2015.pdf
Links:

Bibliographical note
Artikel for 'Forskerzonen' på videnskab.dk
Source: PublicationPreSubmission
Source-ID: 118750203
Publication: Research › Internet publication – Annual report year: 2015

Role and prevalence of antibiosis and the related resistance genes in the environment
It becomes increasingly clear that the basis of antibiotic resistance problem among bacterial pathogens is not confined to the borders of clinical microbiology but has broader ecological and evolutionary associations. This Research Topic "Role and prevalence of antibiosis and the related resistance genes in the environment" in Frontiers in Microbiology, section Antimicrobials, Resistance and Chemotherapy, presents the examples of occurrence and diversity of antibiotic resistance genes in the wide range of environments, from the grasslands of the Colombian Andes, to the dairy farms and small animal veterinary hospitals in the United Stated, and to the various enviroments of Continental Europe and Indochina. Besides, various genetic mechanisms and selection/co-selection factors contributing to the dissemination and maintenance of antibiotic resistance genes are presented. The topic is finalized by the mathematical modeling approach to access the probability of rare horizontal gene transfer events in bacterial populations.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Lyon
112 Presence of bacteria in the endometrium and oviduct of cows with pyometra as detected by fluorescence in situ hybridization

The objective of the study was to identify the location of the present bacteria in the uterus and oviducts of cows with pyometra. Pyometra is one of the postpartum infectious diseases in cattle that can result in infertility and thereby affect reproduction performance. Reproductive tracts (n = 21) were collected at a slaughterhouse in Denmark and sent to The University of Copenhagen for examination and sampling. The uteri were included in the study when the following criteria were met: the cow was more than 21 days postpartum, the uterus was distended with pus, the cervix was closed, and a corpus luteum was present in one or both ovaries. A full thickness uterine tissue sample from the previous pregnant horn and both oviducts were sampled and then fixed in formalin. The tissues were trimmed, processed by routine methods, embedded in paraffin, sectioned at 3 microns, and prepared for fluorescence in situ hybridization using a probe targeting the 16S ribosomal RNA of the domain bacteria (i.e. targeting all bacteria regardless of species). Using fluorescence microscopy, the presence of bacteria within or on the surface of the endometrium and in the oviducts were noted. The endometrial biopsies from all cows (n = 21) contained bacteria, while 75% (16/21) of the cows had bacteria in one or both oviducts. The bacteria were located on the luminal surface and in the lamina propria in 38.1% (8/21) of the uterine biopsies. In the remaining 62% of the uterine biopsies, the bacteria were only located above the basal membrane. Regarding the oviduct biopsies, the bacteria were located on the luminal surface and in lamina propria in 9.5% (2/21) of the biopsies, whereas the bacteria were located only above the basal membrane in 90.5% of the biopsies. In conclusion, 1) bacteria are present in the uteri and oviducts of cows with pyometra and 2) the bacteria are primarily located on the luminal epithelia surface above the basal membrane. Further analyses will investigate which specific species of bacteria that are located in the lamina propria of the uterine and oviduct biopsies.
A Bayesian herd-level diagnostic test evaluation - Mycoplasma bovis

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, University of Copenhagen
Authors: Nielsen, P. K. (Intern), Petersen, M. B. (Ekstern), Nielsen, L. R. (Ekstern), Hisham Beshara Halasa, T. (Intern), Toft, N. (Intern)
Number of pages: 1
Publication date: 2015
Event: Poster session presented at Annual Meeting of the Society of Veterinary Epidemiology and Preventive medicine, Ghent, Belgium.
Main Research Area: Technical/natural sciences
Electronic versions:
SVEPM_2015_poster_pkani_DTE.pdf
Source: FindIt
Source-ID: 2265056936
Publication: Research - peer-review › Poster – Annual report year: 2015

Accelerated apoptosis of neutrophils in familial Mediterranean fever
The causative mutations for familial Mediterranean fever (FMF) are located in the MEFV gene, which encodes pyrin. Pyrin modulates the susceptibility to apoptosis via its PYD domain, but how the mutated versions of pyrin affect apoptotic processes are poorly understood. Spontaneous and induced rates of systemic neutrophil apoptosis as well as the levels of proteins involved in apoptosis were investigated ex vivo in patients with FMF using flow cytometry and RT-qPCR. The freshly collected neutrophils from the patients in FMF remission displayed a significantly larger number of cells spontaneously entering apoptosis compared to control (6.27 ± 2.14 vs. 1.69 ± 0.18%). This elevated ratio was retained after 24 h incubation of neutrophils in the growth medium (32.4 ± 7.41 vs. 7.65 ± 1.32%). Correspondingly, the mRNA level for caspase-3 was also significantly increased under these conditions. In response to the inducing agents, the
neutrophils from FMF patients also displayed significantly elevated apoptotic rates compared to control. The elevated rates, however, can be largely explained by the higher basal ratio of apoptotic cells in the former group. Monitoring of several proteins involved in apoptosis has not revealed any conventional mechanisms contributing to the enhanced apoptotic rate of neutrophils in FMF. Although the exact molecular mechanisms of accelerated neutrophil apoptosis in FMF remain unknown, it may provide a protection against excessive inflammation and tissue damage due to a massive infiltration of neutrophils in the acute period of the disease.

**General information**
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, National Academy of Sciences of the Republic of Armenia, Yerevan State Medical University, Scientific Centre of Drug and Medical Technology Expertise JSC
Authors: Manukyan, G. (Ekstern), Aminov, R. (Intern), Hakobyan, G. (Ekstern), Davtyan, T. (Ekstern)
Number of pages: 7
Publication date: 2015
Main Research Area: Technical/natural sciences

**Publication information**
Journal: Frontiers in Immunology
Issue number: 6
Article number: 239
ISSN (Print): 1664-3224
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SJR 2.803 SNIP 1.484 CiteScore 5.62
Web of Science (2017): Indexed yes
Scopus rating (2016): CiteScore 5.37 SJR 3.034 SNIP 1.476
Web of Science (2016): Indexed yes
Scopus rating (2015): SJR 2.827 SNIP 1.277 CiteScore 5.09
Web of Science (2015): Indexed yes
Scopus rating (2014): SJR 2.389 SNIP 1.057 CiteScore 4.24
Web of Science (2014): Indexed yes
Scopus rating (2013): SJR 1.908 SNIP 0.855 CiteScore 3.55
ISI indexed (2013): ISI indexed no
Scopus rating (2012): SJR 0.809 SNIP 0.193 CiteScore 1.38
ISI indexed (2012): ISI indexed no
Scopus rating (2011): SJR 0.121
Web of Science (2011): Indexed yes
Original language: English
Electronic versions:
Accel_apoptosis.pdf
DOI:
10.3389/fimmu.2015.00239
Links:
Source: PublicationPreSubmission
Source-ID: 110602553
Publication: Research - peer-review › Journal article – Annual report year: 2015

A cell culture-adapted Classical swine fever virus phenotype does not require the 476Arg Ems mutation

**General information**
State: Published
Organisations: National Veterinary Institute, Section for Virology, Friedrich Loeffler Institute
Authors: Drager, C. (Ekstern), Blome, S. (Ekstern), Beer, M. (Ekstern), Reimann, I. (Ekstern), Rasmussen, T. B. (Intern)
Number of pages: 1
Pages: 137-137
Publication date: 2015
A comparison of 2 screening questionnaires for clinical assessment of canine cognitive dysfunction

Canine cognitive dysfunction (CCD) is a neurobehavioral syndrome occurring in some senior dogs. The diagnosis is currently primarily dependent on owner-based questionnaires addressing changes in behavior and daily routines and the exclusion of other conditions which may display clinical signs mimicking CCD. A number of CCD screening questionnaires have been published, but whether the choice of questionnaire might influence the diagnosis of CCD or not, is unclear. The objective of the present study was to correlate the total scores from 2 CCD screening questionnaires which were developed on the basis of very different strategies. The study population consisted of 50 dogs more than 8 years of age. The dogs were evaluated clinically, and the 2 questionnaires were given in a face-to-face interview with the owners. The study found a significant correlation (r= 0.83, P <0.0001) between the 2 questionnaires. The ability to identify dogs with multiple and severe signs of CCD were equally good. This is of importance for research studying CCD case definitions and for comparisons between studies using different questionnaires. If evaluation for longitudinal changes is needed, the canine cognitive rating scale may prove more useful for assessing disease progression.

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, University of Copenhagen
Authors: Schütt, T. (Ekstern), Toft, N. (Intern), Berendt, M. (Ekstern)
Pages: 452-458
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Veterinary Behavior
Volume: 10
Issue number: 6
ISSN (Print): 1558-7878
Ratings:
Web of Science (2018): Indexed yes
Scopus rating (2017): SNIP 0.898 SJR 0.782 CiteScore 1.59
Web of Science (2017): Indexed Yes
Scopus rating (2016): SJR 0.685 SNIP 0.926 CiteScore 1.48
Scopus rating (2015): SJR 0.556 SNIP 0.861 CiteScore 1.22
Web of Science (2015): Indexed yes
Scopus rating (2014): SJR 0.541 SNIP 0.678 CiteScore 0.94
Scopus rating (2013): SJR 0.409 SNIP 0.793 CiteScore 1.21
Scopus rating (2012): SJR 0.465 SNIP 0.983 CiteScore 1.15
Scopus rating (2011): SJR 0.271 SNIP 0.626 CiteScore 0.69
Scopus rating (2010): SJR 0.407 SNIP 0.596
Scopus rating (2009): SJR 0.294 SNIP 0.395
Scopus rating (2008): SJR 0.228 SNIP 0.244
Scopus rating (2007): SJR 0.13 SNIP 0.023
Original language: English
Veterinary (all), Ageing, Canine dementia, Cognitive dysfunction, Dog, Questionnaire
DOI: 10.1016/j.jveb.2015.07.036
Source: FindIt
Source-ID: 2280113775
Publication: Research - peer-review › Journal article – Annual report year: 2015
Aeromonas salmonicida infection in vaccinated rainbow trout: influence of challenge methods and environmental factors on challenge success

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Copenhagen, Vaxxinova
Authors: Chettri, J. K. (Ekstern), Skov, J. (Ekstern), Jaafar, R. M. (Ekstern), Krossøy, B. (Ekstern), Kania, P. W. (Ekstern), Dalsgaard, I. (Intern), Buchmann, K. (Ekstern)
Pages: 58-58
Publication date: 2015

Host publication information
Title of host publication: 17th International Conference on Diseases of Fish And Shellfish : Abstract book
Place of publication: Las Palmas
Publisher: European Association of Fish Pathologists
Article number: O-050
Main Research Area: Technical/natural sciences
Conference: 17th International Conference on Diseases of Fish and Shellfish, Las Palmas, Spain, 07/09/2015 - 07/09/2015
Electronic versions:
Book_of_abstracts_17th_International_conference_on_Diseases_of_Fish_and_Shellfish.pdf
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2015

Age- and Sex-Associated Effects on Acute-Phase Proteins in Göttingen Minipigs
Göttingen minipigs are a useful model for diseases having an inflammatory component, and the associated use of acute-phase proteins (APP) as biomarkers of inflammation warrants establishment of their reference ranges. The objective of this study was to establish reference values for selected APP in Göttingen minipigs and to investigate the effects of age, sex, and various stimuli on these ranges. Serum concentrations of C-reactive protein (CRP), serum amyloid A (SAA), haptoglobin, pig major acute-phase protein (PMAP), albumin, and porcine α-1 acid glycoprotein (PAGP) were evaluated in 4 age groups (6, 16, 24 and 40-48 wk) of male and female Göttingen minipigs. In addition, minipigs were tested under 2 housing conditions, after acute LPS challenge, and after diet-induced obesity with and without mild diabetes. Changing the pigs to a new environment induced significant increases in CRP, PMAP, haptoglobin and PAGP and a decrease in albumin. An acute LPS stimulus increased CRP, PMAP, haptoglobin, and SAA; PAGP was unchanged and albumin decreased. Obese pigs with and without diabetes showed increases in CRP and PAGP, albumin decreased, and haptoglobin and SAA were unchanged. PMAP was increased only in obese pigs without diabetes. In conclusion, reference values for CRP, PMAP, haptoglobin, SAA; PAGP was unchanged and albumin decreased. Obese pigs with and without diabetes showed increases in CRP and PAGP, albumin decreased, and haptoglobin and SAA were unchanged. PMAP was increased only in obese pigs without diabetes. In conclusion, reference values for CRP, PMAP, haptoglobin, SAA; PAGP and albumin were established for male and female Göttingen minipigs of different ages. These APP were influenced by age and sex, underlining the importance of considering these factors when designing and interpreting studies including aspects of inflammation. In addition, an APP response was verified after both acute and chronic stimuli.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, University of Copenhagen
Authors: Christoffersen, B. Ø. (Ekstern), Jensen, S. J. (Ekstern), Ludvigsen, T. P. (Ekstern), Nilsson, S. K. (Ekstern), Grossi, A. B. (Ekstern), Heegaard, P. M. H. (Intern)
Number of pages: 9
Pages: 333-341
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Comparative Medicine
Volume: 65
Issue number: 4
ISSN (Print): 1532-0820
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.283 SJR 0.342 CiteScore 0.78
Web of Science (2017): Indexed Yes
Aleutian Mink Disease Virus in Free-Ranging Mink from Sweden

Aleutian mink disease (AMD) is a chronic viral disease in farmed mink and the virus (AMDV) has been found in many free-ranging mink (Neovison vison) populations in Europe and North America. In this study, AMDV DNA and AMDV antibodies were analysed in 144 free-ranging mink hunted in Sweden. Associations between being AMDV infected (defined as positive for both viral DNA and antibodies) and the weight of the spleen, liver, kidneys, adrenal glands and body condition were calculated and the sequences of ten AMDV isolates were analysed in order to characterize the genetic relationships.

In total, 46.1% of the mink were positive for AMDV antibodies and 57.6% were positive for AMDV DNA. Twenty-two percent of the mink tested on both tests (n = 133) had dissimilar results. The risk of having AMDV antibodies or being positive for AMDV DNA clearly increased with age and the majority of the mink that were two years or older were infected. Few macroscopic changes were found upon necropsy. However, the relative weight of the spleen was sexually dimorphic and was found to be slightly, but significantly (rho = 0.006), heavier in AMDV infected male mink than uninfected. No association between AMDV infection and body condition, weight of the kidneys, liver or adrenal glands were found.

Several different strains of AMDV were found across the country. Two of the AMDV sequences from the very north of Sweden did not group with any of the previously described groups of strains. In summary, AMDV seems to be prevalent in wild mink in Sweden and may subtly influence the weight of the spleen.

General information
State: Published
A major population of mucosal memory CD4+ T cells, coexpressing IL-18Rα and DR3, display innate lymphocyte functionality

Mucosal tissues contain large numbers of memory CD4+ T cells that, through T-cell receptor-dependent interactions with antigen-presenting cells, are believed to have a key role in barrier defense and maintenance of tissue integrity. Here we identify a major subset of memory CD4+ T cells at barrier surfaces that coexpress interleukin-18 receptor alpha (IL-18Rα) and death receptor-3 (DR3), and display innate lymphocyte functionality. The cytokines IL-15 or the DR3 ligand tumor necrosis factor (TNF)-like cytokine 1A (TL1a) induced memory IL-18Rα+DR3+CD4+ T cells to produce interferon-gamma, TNF-α, IL-6, IL-5, IL-13, granulocyte-macrophage colony-stimulating factor (GM-CSF), and IL-22 in the presence of IL-12/IL-18. TL1a synergized with IL-15 to enhance this response, while suppressing IL-15-induced IL-10 production. TL1a- and IL-15-mediated cytokine induction required the presence of IL-18, whereas induction of IL-5, IL-13, GM-CSF, and IL-22 was IL-12 independent. IL-18Rα+DR3+CD4+ T cells with similar functionality were present in human skin, nasal polyps, and, in particular, the intestine, where in chronic inflammation they localized with IL-18-producing cells in lymphoid aggregates. Collectively, these results suggest that human memory IL-18Rα+DR3+CD4+ T cells may contribute to antigen-independent innate responses at barrier surfaces.
Amniotic fluid and colostrum as potential diets in the critical care of preterm infants

Amniotic fluid is the enteral “diet” of the developing fetus, while the first mammary gland secretion, colostrum, is the natural diet of the newborn mammal. Both diets contain nutrients but also growth factors, immune-modulating components, and antibacterial agents that support perinatal organ development, particularly of the gastrointestinal (GI) tract. Birth requires a sudden transition to nutrient uptake via the GI tract and exposure to microorganisms. Ingestion of amniotic fluid before birth and of colostrum just after birth helps to adapt GI functions and provides protection against detrimental immune responses. Experimental studies indicate that these fluids may also have beneficial effects in certain GI disease conditions, particularly those related to immature digestive and immune function. We provide a brief review of the functions and composition of mammalian amniotic fluid and colostrum, and we describe how these fluids may have a therapeutic potential for GI conditions in some pediatric patients, particularly preterm infants. The composition of the two fluids varies widely among different species and the effects are likely highly species specific. Some effects may however be species independent, maybe allowing colostrum from one species (i.e., lactating cows) to be used as the first enteral diet for infants for whom mother’s milk is lacking. The use of amniotic fluid and bovine colostrum in the critical care of neonates is still at an experimental stage, but animal studies have shown promising results.

General information
State: Published
Organisations: National Veterinary Institute, University of Copenhagen
Authors: Støy, A. C. F. (Intern), Viberg Østergaard, M. (Ekstern), Torp Sangild, P. (Ekstern)
Number of pages: 13
Pages: 1109-1121
Publication date: 2015

A multi-dimensional dynamic linear model for monitoring slaughter pig production

Scientists and farmers still lack an efficient way to unify the large number of different types of data series, which are increasingly being generated in relation to automatic herd monitoring. Such a unifying model should be able to account for the correlations between the various types of data, resulting in a model which could potentially yield more information than can be gained from the individual components separately. Here we present such a model for monitoring slaughter pig production, in the form of a multivariate dynamic linear model. This model unifies three types of data (live weight, feed-and water consumption), measured at different levels of detail (individual pig and double-pen level) and with different observational frequencies (weekly and daily), using series collected for the Danish PigIT project. The presented three-dimensional model serves as a proof of concept, and it should be straightforward to expand it with additional data types.

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, University of Copenhagen
Authors: Jensen, D. B. (Ekstern), Cornou, C. (Ekstern), Toft, N. (Intern), Kristensen, A. (Ekstern)
Number of pages: 8
Publication date: 2015
Event: Paper presented at 7th European Conference on Precision Livestock Farming (EC-PLF), Milan, Italy.
Main Research Area: Technical/natural sciences
Analysis of Recent Serotype O Foot-and-Mouth Disease Viruses from Livestock in Kenya: Evidence of Four Independently Evolving Lineages

Foot-and-mouth disease (FMD) is endemic in Kenya where four serotypes (O, A, SAT 1 and SAT 2) of the virus are currently in circulation. Within 2010 and 2011, the National Laboratory recorded an increase in the number of FMD outbreaks caused by serotype O virus. The characteristics of these viruses were determined to ascertain whether these were independent outbreaks or one single strain spreading throughout the country. The sequences of the complete VP1-coding region were analysed from viruses sampled within different areas of Kenya during 2010 and 2011. The results indicated that the 2010 to 2011 outbreaks in Kenya were caused by four independent strains. By comparison with earlier type O isolates from Eastern Africa, it was apparent that the outbreaks were caused by viruses from three different lineages of topotype EA-2 and a fourth virus strain belonging to topotype EA-4. The topotypes EA-1 and EA-3 were not detected from these outbreaks. Implications of these results for FMD control in Eastern Africa are discussed.

General information

State: Published
Organisations: National Veterinary Institute, Section for Virology, The Pirbright Institute, Makerere University, University of Copenhagen, Ministry of Livestock Development
Authors: Wekesa, S. N. (Ekstern), Muwanika, V. B. (Ekstern), Siegismund, H. R. (Ekstern), Sangula, A. K. (Ekstern), Namatovu, A. (Ekstern), Dhikusooka, M. T. (Ekstern), Tjørnehøj, K. (Intern), Balinda, S. N. (Ekstern), Wadsworth, J. (Ekstern), Knowles, N. J. (Ekstern), Belsham, G. (Intern)
Number of pages: 10
Pages: 305-314
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information

Journal: Transboundary and Emerging Diseases
Volume: 62
Issue number: 3
ISSN (Print): 1865-1674
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.87 SJR 1.147 SNIP 1.488
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.16 SJR 1.046 SNIP 0.998
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.305 SNIP 1.249 CiteScore 2.29
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.048 SNIP 1.207 CiteScore 2.23
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.975 SNIP 1.123 CiteScore 2.33
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.847 SNIP 1.178 CiteScore 2.04
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
A novel challenge method with aeromonas salmonicida in rainbow trout for evaluation of furunculosis vaccines

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Copenhagen, Vaxxinova
Authors: Marana, M. H. (Ekstern), Skov, J. (Ekstern), Chettri, J. K. (Ekstern), Krossøy, B. (Ekstern), Dalsgaard, I. (Intern), Kania, P. (Ekstern), Buchmann, K. (Ekstern)
Pages: 172-172
Publication date: 2015

Host publication information
Title of host publication: 17th International Conference on Diseases of Fish And Shellfish : Abstract book
Place of publication: Las Palmas
Publisher: European Association of Fish Pathologists
Article number: O-164
Main Research Area: Technical/natural sciences
Conference: 17th International Conference on Diseases of Fish and Shellfish, Las Palmas, Spain, 07/09/2015 - 07/09/2015
Electronic versions:
Book_of_abstracts_17th_International_conference_on_Diseases_of_Fish_and_Shellfish.pdf
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2015

Anthelmintic activity of sesquiterpene lactones from forage chicory against Ascaris suum

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Section for Immunology and Vaccinology, University of Copenhagen
Anthelmintic effects of sa infoin against different catt le nematodes may be linked to concentration of condensed tannins in different gut compartments

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Copenhagen, University of Reading
Authors: Desrues, O. (Ekstern), Pena-Espinoza, M. A. (Intern), Hansen, T. V. (Ekstern), Mueller-Harvey, I. (Ekstern), Enemark, H. (Intern), Thamsborg, S. M. (Ekstern)
Number of pages: 1
Pages: 58-58
Publication date: 2015

Host publication information
Title of host publication: 25th International Conference of the World Association for the Advancement of Veterinary Parasitology : Abstract Book
Place of publication: Liverpool, United Kingdom
Main Research Area: Technical/natural sciences
Conference: 25th International Conference of the World Association for the Advancement of Veterinary Parasitology, Liverpool, United Kingdom, 16/08/2015 - 16/08/2015
Electronic versions:
Desrues_et_al_WAAVP2015.pdf
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2015

Antibiotika til mink fra 2007-2012

General information
State: Published
Organisations: Department of Applied Mathematics and Computer Science , Statistics and Data Analysis, Division of Epidemiology and Microbial Genomics, National Veterinary Institute, Copenhagen Fur
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Pages: 34-37
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Dansk Pelsdyravl
Issue number: 2
ISSN (Print): 0011-6424
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Original language: Danish
Electronic versions:
Medicin_til_mink_Dansk_pelsdyravl_2015.pdf
Links:
http://ipaper.ipapercms.dk/KopenhagenFur/DanskPelsdyravlFebruar2015/?Page=34
Source: PublicationPreSubmission
Source-ID: 106132030
Publication: Research - peer-review › Journal article – Annual report year: 2015
Application of qPCR assays for diagnosing causes of viral mink diarrhea. Preliminary results

Gastrointestinal (GI) disorders is the main cause for submitting mink (Neovison vison) carcasses for post-mortem examination at the National Veterinary Institute in Denmark and has been described as the predominant cause of disease and mortality in the Danish mink production (Rattenborg et al. 1999). Diarrhea in mink can be caused by infectious agents (virus, bacteria and parasites) and food-related/multifactorial conditions. Known enteric viral infections are mink enteritis virus (MEV) and mink astrovirus. Coronaviruses and caliciviruses have also been implicated as potential causes or contributors to diarrhea in mink. Rotavirus is poorly described in mink, but has previously been demonstrated in feces from mink pups with and without clinical signs (Jorgensen et al. 1996). The pathogenicity of these viruses could be related to viral load, virulence and the age of the mink. Therefore, there is a need for a quantitative diagnostic approach. We have developed new or adapted previously published real-time PCR/RT-PCR assays for MEV, astrovirus, rota- and coronavirus diagnostics.

The technical test validation was initially carried out on archived diarrhea samples from diagnosed positive animals and on normal and diarrhea samples from a case-control study. In order to further validate the applicability of the assays, a testing scheme for normal and affected farms was set up and initiated in June 2015. This protocol will allow optimization of test characteristics (sensitivity, specificity and predictive value) and assessment of the validity of using pooled samples in order to reduce test costs.
A Recombinant Multi-Stage Vaccine against Paratuberculosis Significantly Reduces Bacterial Level in Tissues without Interference in Diagnostics

A new (FET11) recombinant vaccine against paratuberculosis was developed based on recombinant antigens from acute and latent stages of Mycobacterium avium subsp. paratuberculosis (Map) infection. In two experiments 28 calves and 15 goats were orally inoculated with live Map in their third week of life and post-exposure vaccinated at different times after inoculation or with different vaccine constructs. In contrast to common whole-cells vaccination, the FET11 vaccine did not interfere with tests for paratuberculosis or bovine tuberculosis as no measurable antibody responses by ID Screen® ELISA, PPDj-specific IFN-γ responses or positive PPDa or PPDb skin tests developed in vaccinees. Antibodies and cell-mediated immune responses were developed against FET11 antigens, however. At necropsy 8 or 12 months of age, relative Map burden was determined in a number of gut tissues by quantitative IS900 PCR and revealed significantly reduced levels of Map and reduced histopathology. Diagnostic tests for antibody responses and cell-mediated immune responses, used as surrogates of infection, corroborated the observed vaccine efficacy: Five of seven non-vaccinated calves seroconverted in ID Screen® ELISA at 32 to 40 weeks p.i. indicating the progression of infection, while only four of 14 FET11 vaccinated calves seroconverted at 40-52 weeks p.i. Similarly, PPDj-induced IFN-γ responses increased over time in non-vaccinated calves, while FET11 vaccinated calves had significantly reduced PPDj IFN-γ assay responses from 40 to 52 weeks compared to non-vaccinated calves. These results indicate the FET11 vaccine can be used to accelerate eradication of paratuberculosis while surveillance or test-and-manage control programs for tuberculosis and Johne’s disease remain in place. Funded by EMIDA ERA-NET (219235), PoC East Denmark and Danish Research Council (FTP 274-08-0166)

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, State Serum Institute
Authors: Jungersen, G. (Intern), Thakur, A. (Intern), Aagaard, C. (Ekstern), Mikkelsen, H. (Ekstern), Andersen, P. (Ekstern)
Number of pages: 1
Publication date: 2015
Event: Abstract from Immunity to Veterinary Pathogens 2015, Keystone, United States.
Main Research Area: Technical/natural sciences
Electronic versions:
Jungersen_multistage_MAP_vaccine_Abstract_Keystone_2015.pdf
Source: PublicationPreSubmission
Source-ID: 118952771
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2015

A review of the human vs. porcine female genital tract and associated immune system in the perspective of using minipigs as a model of human genital Chlamydia infection

Sexually transmitted diseases constitute major health issues and their prevention and treatment continue to challenge the health care systems worldwide. Animal models are essential for a deeper understanding of the diseases and the development of safe and protective vaccines. Currently a good predictive non-rodent model is needed for the study of genital chlamydia in women. The pig has become an increasingly popular model for human diseases due to its close similarities to humans. The aim of this review is to compare the porcine and human female genital tract and associated immune system in the perspective of genital Chlamydia infection. The comparison of women and sows has shown that despite some gross anatomical differences, the structures and proportion of layers undergoing cyclic alterations are very similar. Reproductive hormonal cycles are closely related, only showing a slight difference in cycle length and source of luteolysing hormone. The epithelium and functional layers of the endometrium show similar cyclic changes. The immune system in pigs is very similar to that of humans, even though pigs have a higher percentage of CD4(+)/CD8(+) double positive T cells. The genital immune system is also very similar in terms of the cyclic fluctuations in the mucosal antibody levels, but differs slightly regarding immune cell infiltration in the genital mucosa - predominantly due to the influx of
neutrophils in the porcine endometrium during estrus. The vaginal flora in Göttingen Minipigs is not dominated by lactobacilli as in humans. The vaginal pH is around 7 in Göttingen Minipigs, compared to the more acidic vaginal pH around 3.5-5 in women. This review reveals important similarities between the human and porcine female reproductive tracts and proposes the pig as an advantageous supplementary model of human genital Chlamydia infection.

**General information**

State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, University of Copenhagen, State Serum Institute
Authors: Lorenzen, E. (Ekstern), Follmann, F. (Ekstern), Jungersen, G. (Intern), Agerholm, J. S. (Ekstern)
Number of pages: 13
Publication date: 2015
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Veterinary Research
Volume: 46
Issue number: 1
Article number: 116
ISSN (Print): 0928-4249
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 1.139 SJR 1.266
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): SJR 1.44 SNIP 1.303
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.537 SNIP 1.153 CiteScore 2.66
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.453 SNIP 1.423 CiteScore 2.46
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.681 SNIP 1.701 CiteScore 3.13
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.461 SNIP 1.45 CiteScore 2.97
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.712 SNIP 1.655 CiteScore 3.85
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.531 SNIP 1.606
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.489 SNIP 1.689
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.578 SNIP 2.002
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.749 SNIP 2.189
Web of Science (2007): Indexed yes
A space-time analysis of Mycoplasma bovis in Denmark

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, University of Copenhagen
Number of pages: 1
Publication date: 2015
Event: Poster session presented at Annual Meeting of the Society of Veterinary Epidemiology and Preventive medicine, Ghent, Belgium.
Main Research Area: Technical/natural sciences
Electronic versions:
PosterSEVPM_Margarida_new_.pdf
Source: FindIt
Source-ID: 2265057602
Publication: Research - peer-review › Poster – Annual report year: 2015

Assessment of Methods to Quantify Livestock Associated MRSA in Pig Herds

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Section for Epidemiology, National Food Institute, University of Copenhagen, Statens Serum Institut
Authors: Hansen, J. E. (Intern), Sørensen, A. I. V. (Intern), Espinosa-Gongora, C. (Ekstern), Larsen, A. R. (Ekstern), Larsen, J. (Ekstern), Skov, R. (Ekstern), Pedersen, K. (Intern)
Pages: 28-28
Publication date: 2015

Host publication information
Title of host publication: 4th ASM-ESCMID Conference on Methicillin-resistant Staphylococci in Animals: Final program and abstracts
Place of publication: Chicago, Illinois
Publisher: American Society for Microbiology
Main Research Area: Technical/natural sciences
Source: PublicationPreSubmission
Assessment of the probability of introducing Mycobacterium tuberculosis into Danish cattle herds

Tuberculosis is a zoonosis caused by Mycobacterium spp. International trade in cattle is regulated with respect to Mycobacterium bovis (M. bovis) but not Mycobacterium tuberculosis (M. tuberculosis), despite that cattle can become infected with both species. In this study we estimated the annual probability (PIntro) of introducing M. tuberculosis into the Danish cattle population, by the import of cattle and/or by immigrants working in Danish cattle herds. Data from 2013 with date, number, and origin of imported live cattle were obtained from the Danish cattle database. Information on immigrants working in Danish cattle herds was obtained through a questionnaire sent to Danish cattle farmers. The gained inputs were fed into three stochastic scenario trees to assess the PLintro for the current and alternative test-and-manage strategies, such as testing of imported animals and/or testing immigrant workers with the tuberculin skin test. We considered the population of Danish farmers and practitioners free of tuberculosis, because in Denmark, the incidence of the disease in humans is low and primarily related to immigrants and socially disadvantaged people.

The median annual probability of introducing M. tuberculosis into the Danish cattle population due to imported live cattle was 0.008% (90% P.I.: 0.0007%; 0.03%), while the probability due to immigrant workers was 4.1% (90% P.I.: 0.8%; 12.1%). The median combined probability (PIntro) due to imported cattle plus workers was 4.1% (90% P.I.: 0.8%; 12.6%). Hence, on average at least one introduction each 24 (90% P.I.: 8; 125) years could be expected. Imported live cattle appeared to play a marginal role on the overall annual PIntro, because they represented only approximately 0.2% of the median annual probability. By testing immigrant workers the overall annual PIntro could be reduced to 0.2% (90% P.I.: 0.04%; 0.7%).

Thus, testing of immigrant workers could be considered as a risk mitigation strategy to markedly reduce the likelihood of...
introducing M. tuberculosis into the Danish cattle population, if the risk is considered unacceptable by the veterinary public health authorities.

General information
State: Published
Organisations: National Veterinary Institute, University of Copenhagen, Knowledge Centre for Agriculture, Danish Agriculture and Food Council
Authors: Foddai, A. (Intern), Nielsen, L. R. (Ekstern), Krogh, K. (Ekstern), Alban, L. (Ekstern)
Pages: 92-98
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Preventive Veterinary Medicine
Volume: 122
Issue number: 1-2
ISSN (Print): 0167-5877
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 1.31 SJR 1.144 CiteScore 2.26
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.2 SJR 1.249 SNIP 1.361
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.282 SNIP 1.177 CiteScore 2.1
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.27 SNIP 1.407 CiteScore 2.37
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.264 SNIP 1.529 CiteScore 2.49
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.265 SNIP 1.436 CiteScore 2.45
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.194 SNIP 1.295 CiteScore 2.24
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.156 SNIP 1.284
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.032 SNIP 1.338
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.056 SNIP 1.258
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.009 SNIP 1.353
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.06 SNIP 1.277
Web of Science (2006): Indexed yes
Assessment of the probability of introduction of bovine tuberculosis to Danish cattle farms via imports of live cattle from abroad and immigrant workers

Denmark has been recognized as officially free (OTF) from bovine tuberculosis (bTB) since 1980. In this study, we estimated the annual probability (PIntro) of introducing Mycobacterium bovis into the Danish cattle population, through (a) imports of cattle and (b) foreign personnel working in Danish cattle herds. Data from 2000 to 2013 with date, number and origin of imported live cattle were obtained from the Danish Cattle Federation. Information on immigrants working in Danish cattle herds was obtained through a questionnaire sent by email to a sample of Danish cattle farmers (N = 460). Inputs obtained from data analysis, expert opinion, the questionnaire and literature were fed into three stochastic scenario tree models used to simulate the effect of import trade patterns, and contact between immigrant workers and cattle. We also investigated the opportunity of testing animals imported from OTF countries by tuberculin skin test and animals from non-OTF countries by interferon-γ test (IFN-γ), exemplified by using year 2009 where the number of imported animals was higher than usual.

Results showed that PIntro is driven mainly by importation of live cattle. The combined median annual probability of introducing M. bovis into the Danish cattle population by either imported live cattle or infectious immigrant workers, ranged from 0.3% (90% prediction interval (P.I.): 0.04%:1.4%) in 2001 to 4.9% (90% P.I.: 0.6%; 19.2%) in 2009. The median of the median PIntro estimates from the 14 years was 0.7% (median of 90% P.I.: 0.08%; 3.5%). Hence, on average, at least one introduction each 143 years could be expected, if the annual number of imported animals does not change remarkably in the future.

If the number of imported animals increases, compared to the years we analyzed, additional testing of imported cattle might be considered. For example, in 2009, PIntro would have been reduced from 4.9% to 0.8% (90% P.I.: 0.1%; 4.7%) if animals from OTF countries had been tested with the tuberculin skin test and animals from non-OTF countries had been tested with the IFN-γ test.

The presented model could be used easily in other countries with similar bTB status to Denmark, where wildlife represents a negligible probability of infection for domestic cattle and where the imported live cattle represent the main pathway of bTB introduction into the local cattle population.

General information
State: Published
Organisations: National Veterinary Institute, University of Copenhagen, Knowledge Centre for Agriculture, Danish Agriculture and Food Council
Authors: Foddai, A. (Intern), Nielsen, L. R. (Ekstern), Krogh, K. (Ekstern), Alban, L. (Ekstern)
Pages: 306-317
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Preventive Veterinary Medicine
Volume: 122
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 1.31 SJR 1.144 CiteScore 2.26
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.2 SJR 1.249 SNIP 1.361
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.282 SNIP 1.177 CiteScore 2.1
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.27 SNIP 1.407 CiteScore 2.37
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.264 SNIP 1.529 CiteScore 2.49
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.265 SNIP 1.436 CiteScore 2.45
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.194 SNIP 1.295 CiteScore 2.24
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.156 SNIP 1.284
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.032 SNIP 1.338
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.056 SNIP 1.258
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.009 SNIP 1.353
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.06 SNIP 1.277
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.931 SNIP 1.414
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.812 SNIP 1.146
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.846 SNIP 1.323
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.857 SNIP 1.427
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 1.045 SNIP 1.48
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 0.623 SNIP 1.261
Associations between biosecurity and outbreaks of canine distemper on Danish mink farms in 2012-2013

During 8 months from July 2012 to February 2013, a major outbreak of canine distemper involving 64 mink farms occurred on the Danish peninsula of Jutland. The canine distemper outbreak was associated with exposure of farmed mink to infected wild carnivores and could represent a deficit in biosecurity on the mink farms. The aim of this study was to investigate the extent and association of specific biosecurity measures with the outbreak. The study was carried out in an epidemiological case-control design. The case group consisted of the 61 farms, which had a confirmed outbreak of canine distemper from July 2012 to February 2013. The control group included 54 farms without an outbreak of canine distemper in 2012 or 2013, selected as the closest geographical neighbour to a case farm. The results showed that significantly more control than case farms had vaccinated their mink against canine distemper virus. Mortality was only assessed on the case farms, and there was a non-significantly lower mortality on vaccinated farms than on the non-vaccinated farms. Furthermore, the proportion of farms with observations of wild red foxes (Vulpes vulpes) inside the farm enclosures were larger for case farms, indicating that the control farms had a better biosecurity or were not equally exposed to canine distemper virus. Generally, all farms had very few specific precautions at the gate entrance in respect to human visitors as well as animals. The use of biosecurity measures was very variable in both case and control farms. Not using plastic boot covers, presence of dogs and cats, presence of demarcated area for changing clothes when entering and leaving the farm area and presence of hand washing facilities significantly lowered the odds of the farm having a canine distemper virus outbreak. The results of the study indicate that consistent use of correct vaccination strategies, implementation of biosecurity measures and limiting human and animal access to the mink farm can be important factors in reducing the risk for canine distemper outbreaks.
Avian bornavirus in free-ranging waterfowl in North America and Europe

The first avian bornavirus (ABV) was identified in 2008 by researchers investigating the cause of proventricular dilation disease in psittacine birds 3,4. A distinctly separate genotype (ABV-CG) was discovered in 2009 in association with neurological disease in free-ranging Canada geese (Branta canadensis) and trumpeter swans (Cygnus buccinator) in Ontario, Canada 1. Since then this genotype, now identified as ABBV-1, has been identified from a variety of wild avian species 5, predominantly waterfowl, in North America at prevalences ranging from 10 to 50%, and in 2014 an additional genotype was identified in mallard ducks (Anas platyrhynchos) 2. In order to determine whether avian bornavirus was present in European waterfowl, the brains of 333 hunter killed geese in Denmark were examined by real time RT-PCR for the presence of avian bornavirus; seven birds (2.1%) were positive. Sequences were 98.18-99.83 % identical to each other, and 97.38-98.06 % identical to a reference sequence of ABBV-1 from North America. This is the first finding of ABV in wild waterfowl in Europe, and extends the range of waterfowl species in which the virus has been identified to include the pink-footed goose (Anser brachyrhynchus), greylag goose (Anser anser), and barnacle goose (Branta leucopsis).
Given the migration paths of these species, avian bornavirus is likely to have a much wider geographic range than has previously been suspected.

**General information**
**State:** Published
**Organisations:** National Veterinary Institute, University of Copenhagen, Toronto Zoo, University of Guelph, Copenhagen Zoo
**Authors:** Brinkmann, J. (Ekstern), Thomsen, A. F. (Ekstern), Bertelsen, M. F. (Ekstern), Hjulsager, C. K. (Intern), Chriél, M. (Intern), Delnatte, P. (Ekstern), Okjic, D. (Ekstern), Smith, D. A. (Ekstern)
**Publication date:** 2015
**Event:** Abstract from 64th Annual International Conference of the Wildlife Disease Association, Queensland, Australia.
**Main Research Area:** Technical/natural sciences
**Electronic versions:** Avian_bornavirus_Europe_abstract_WDA_2015.pdf

**Bibliographical note**
Source: PublicationPreSubmission
Source-ID: 112051423
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2015

**Bacteriophage Resistance Mechanisms in the Fish Pathogen Flavobacterium psychrophilum: Linking Genomic Mutations to Changes in Bacterial Virulence Factors**
Flavobacterium psychrophilum is an important fish pathogen in salmonid aquaculture worldwide. Due to increased antibiotic resistance, pathogen control using bacteriophages has been explored as a possible alternative treatment. However, the effective use of bacteriophages in pathogen control requires overcoming the selection for phage resistance in the bacterial populations. Here, we analyzed resistance mechanisms in F. psychrophilum after phage exposure using whole-genome sequencing of the ancestral phage-sensitive strain 950106-1/1 and six phage-resistant isolates. The phage-resistant strains had all obtained unique insertions and/or deletions and point mutations distributed among intergenic and genic regions. Mutations in genes related to cell surface properties, gliding motility, and biosynthesis of lipopolysaccharides and cell wall were found. The observed links between phage resistance and the genetic modifications were supported by direct measurements of bacteriophage adsorption rates, biofilm formation, and secretion of extracellular enzymes, which were all impaired in the resistant strains, probably due to superficial structural changes. The clustered regularly interspaced short palindromic repeat (CRISPR) region was unaffected in the resistant isolates and thus did not play a role as a resistance mechanism for F. psychrophilum under the current conditions. All together, the results suggest that resistance in F. psychrophilum was driven by spontaneous mutations, which were associated with a number of derived effects on the physiological properties of the pathogen, including reduced virulence under in vitro conditions. Consequently, phage-driven physiological changes associated with resistance may have implications for the impact of the pathogen in aquaculture, and these effects of phage resistance on host properties are therefore important for the ongoing exploration of phage-based control of F. psychrophilum.

**General information**
**State:** Published
**Organisations:** National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Copenhagen
**Authors:** Castillo, D. (Ekstern), Christiansen, R. H. (Intern), Dalsgaard, I. (Intern), Madsen, L. (Intern), Middelboe, M. (Ekstern)
**Number of pages:** 11
**Pages:** 1157-1167
**Publication date:** 2015
**Main Research Area:** Technical/natural sciences

**Publication information**
**Journal:** Applied and Environmental Microbiology
**Volume:** 81
**Issue number:** 3
**ISSN (Print):** 0099-2240
**Ratings:**
- BFI (2018): BFI-level 2
- Web of Science (2018): Indexed yes
- BFI (2017): BFI-level 2
- Scopus rating (2017): CiteScore 3.99
- Web of Science (2017): Indexed yes
Bat Coronaviruses circulating in Danish bats

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, University of Copenhagen, Central Veterinary Institute
Authors: Rasmussen, T. B. (Intern), Chriél, M. (Intern), Baagøe, H. J. (Ekstern), Fjederholt, E. (Ekstern), Kooi, E. A. (Ekstern), Belsham, G. (Intern), Betnér, A. (Intern)
Number of pages: 1
Pages: 252-252
Publication date: 2015

Host publication information
Title of host publication: Xth International Congress for Veterinary Virology
Place of publication: Montpellier, France
Main Research Area: Technical/natural sciences
Conference: 10th International Congress for Veterinary Virology, Montpellier, France, 31/08/2015 - 31/08/2015
Electronic versions:
EPIZONE_Abstract_Coronavirus_in_bats_TBRUR.pdf
Source: PublicationPreSubmission
Source-ID: 116892687
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2015

Bat Coronaviruses circulating in Danish bats

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, University of Copenhagen, Central Veterinary Institute
Authors: Rasmussen, T. B. (Intern), Chriél, M. (Intern), Baagøe, H. J. (Ekstern), Fjederholt, E. (Ekstern), Kooi, E. A. (Ekstern), Belsham, G. (Intern), Betnér, A. (Intern)
Number of pages: 1
Publication date: 2015
Event: Poster session presented at 10th International Congress for Veterinary Virology, Montpellier, France.
Main Research Area: Technical/natural sciences
Electronic versions:
EPIZONE_Poster_Coronavirus_in_bats_TBRUR_150825_final.pdf
Publication: Research - peer-review › Poster – Annual report year: 2015

Battling Bluetongue and Schmallenberg virus: Local scale behavior of transmitting vectors

General information
State: Published
Organisations: Department of Applied Mathematics and Computer Science, Statistics and Data Analysis, National Veterinary Institute, Section for Epidemiology
Authors: Stockmarr, A. (Intern), Kirkeby, C. (Intern), Bødker, R. (Intern)
Number of pages: 23
Publication date: 2015

Publication information
Media of output: PowerPoint
Original language: English
Main Research Area: Technical/natural sciences
Electronic versions:
Infectious_Diseases_1008_2015_Anders_Stockmarr.pdf

Relations
Activities:
Battling Bluetongue and Schmallenberg virus: Local scale behavior of transmitting vectors
Publication: Research › Sound/Visual production (digital) – Annual report year: 2015

Baylisascaris procyonis in wild raccoons (Procyon lotor) in Denmark
The nematode Baylisascaris procyonis, which may cause severe clinical disease in humans and animals, is emerging in Europe after its introduction with raccoons (Procyon lotor) from North America. B. procyonis has a broad spectrum of
paratenic hosts, including rodents, birds, wild carnivores and primates, which are severely affected by the migrating larval stages of the parasite. We report here the recovery of B. procyonis from two out of 18 examined wild raccoons in Denmark. The parasites were identified based on morphology and their identity was confirmed by partial sequencing of the 18S rRNA gene. Follow-up telephone interviews of staffs in nine zoos housing captive raccoons and veterinarians supervising these zoos showed that knowledge of B. procyonis and its zoonotic potential were sparse. Eggs of B. procyonis were detected in two raccoons kept in one of three zoos that submitted fecal samples following the telephone interviews. Continuous monitoring and increased awareness are needed to reduce further spread of the parasite and to limit the public health risks associated with baylisascariasis.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, National Food Institute
Authors: Al-Sabi, M. N. S. (Intern), Chriél, M. (Intern), Hansen, M. S. (Intern), Enemark, H. (Intern)
Number of pages: 4
Pages: 55-58
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Parasitology
Volume: 1-2
ISSN (Print): 0031-1820
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 0.946 SJR 1.194 CiteScore 2.45
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): SJR 1.085 SNIP 0.927 CiteScore 2.37
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.34 SNIP 1.059 CiteScore 2.62
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.05 SNIP 1.009 CiteScore 2.3
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.157 SNIP 0.908 CiteScore 2.45
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.026 SNIP 1.004 CiteScore 2.55
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.183 SNIP 1.02 CiteScore 2.63
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.13 SNIP 0.935
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 0.976 SNIP 0.943
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.086 SNIP 0.975
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 0.977 SNIP 0.988
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.908 SNIP 0.994
Beskytter de eksisterende vacciner godt nok mod PCV2-mutant (PCV2d)?

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Larsen, L. E. (Intern), Krog, J. S. (Intern), Hjulsager, C. K. (Intern)
Pages: 48-48
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Dansk Veterinaertidsskrift
Issue number: 13
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
ISI indexed (2012): ISI indexed no
BFI (2011): BFI-level 1
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
BFI (2009): BFI-level 1
BFI (2008): BFI-level 1
Original language: Danish
Electronic versions:
Larsen, 2015, PCV2_DVT.pdf
Source: PublicationPreSubmission
Source-ID: 118962830
Publication: Research - peer-review › Journal article – Annual report year: 2015
Big Data fra jord til bord
Danske landmænd og virksomhederne i fødevaresektoren har gode forudsætninger for at drage nytte af den rivende udvikling inden for indsamling og bearbejdning af data:

• Danmark har en stærk fødevaresektor. Det skyldes bl.a., at alle dele af værdikæden arbejder tæt sammen. Fra primærproducenterne, over forarbejdningsindustrien, agroindustrien til videns- og forskningsmiljøerne. Effektiv ressourceudnyttelse og fokus på optimering i hele værdikæden gør sektoren i stand til at konkurere på verdensmarkedet.

• Danske fødevarevirksomheder har altid været gode til at opdyrke nye forretningsmodeller og finde nye innovative veje til øget værdiskabelse. For eksempel gennem smartere måder at producere på, levere produkterne på eller at indarbejde større værdi i produkterne, så de kan sælges med større fortjeneste.

• Dansk landbrug og hele værdikæden i fødevaresektoren producerer store mængder af data. Det skyldes bl.a. et højt automatizationsniveau og myndighedernes krav til dokumentation af fødevarekvaliteten, når de danske producenter leverer fødevarer til forbrugerne verden over. Der er imidlertid et stort spring fra at råde over store mængder af data til at bruge dem aktivt i forretningsudviklingen. Denne rapport viser, hvordan Big Data kan være ét af omdrejningspunkter krav til dokumentation af fødevarekvaliteten, når de danske producenter leverer fødevarer til forbrugerne verden over. Der er imidlertid et stort spring fra at råde over store mængder af data til at bruge dem aktivt i forretningsudviklingen. Denne rapport viser, hvordan Big Data kan være ét af omdrejningspunkter
Booster immersion vaccination using diluted *Yersinia ruckeri* bacterin confers protection against ERM in rainbow trout

A single immersion vaccination of rainbow trout fry using a *Yersinia ruckeri* bacterin confers immunity to reinfection but only for a shorter period. A longer protective period is needed in practical trout farming and we have shown that booster vaccination prolongs immunity. Due to economic considerations and management practices it is not possible to immersion vaccinate large trout (20–30 g) with the recommended high bacterin concentration. We here demonstrate that booster vaccination using dilutions of the bacterin (1:100, 1:1000 and 1:2000) with increased exposure time (1 h, 2 h) confers a higher and longer lasting immunity although a short term (30 s) booster in 1:10 bacterin proved superior. This has practical implications for fish farmers because this diluted booster vaccination over longer time can be applied when farmers handle and transport fish between ponds and farms. Therefore such a practice will not challenge farm management and economy. Increased antibody levels were recorded after challenge of vaccinated fish but not after immersion vaccination alone which suggests that immersion induces priming of memory cells.

**General information**

**State:** Published  
**Organisations:** National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Copenhagen  
**Authors:** Chettri, J. K. (Ekstern), Mohammad, R. J. (Ekstern), Skov, J. (Ekstern), Kania, P. W. (Ekstern), Dalsgaard, I. (Intern), Buchmann, K. (Ekstern)  
**Number of pages:** 5  
**Pages:** 1-5  
**Publication date:** 2015  
**Main Research Area:** Technical/natural sciences  
**Publication information**  
**Journal:** Aquaculture  
**Volume:** 440  
**ISSN (Print):** 0044-8486  
**Ratings:**  
BFI (2018): BFI-level 2  
Web of Science (2018): Indexed yes  
BFI (2017): BFI-level 2  
Scopus rating (2017): CiteScore 3.05 SJR 1.152 SNIP 1.58  
Web of Science (2017): Indexed yes  
BFI (2016): BFI-level 2  
Scopus rating (2016): CiteScore 2.75 SJR 1.122 SNIP 1.51  
Web of Science (2016): Indexed yes  
BFI (2015): BFI-level 2  
Scopus rating (2015): SJR 1.107 SNIP 1.256 CiteScore 2.12  
Web of Science (2015): Indexed yes
Booster-vaccinering med fortyndet dypvaccine mod rødmundsge forlænger beskyttelsesperioden

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Copenhagen
Broadening the repertoire of melanoma-associated T-cell epitopes

Immune therapy has provided a significant breakthrough in the treatment of metastatic melanoma. Despite the remarkable clinical efficacy and established involvement of effector CD8 T cells, the knowledge of the exact peptide-MHC complexes recognized by T cells on the tumor cell surface is limited. Many melanoma-associated T-cell epitopes have been described, but this knowledge remains largely restricted to HLA-A2, and we lack understanding of the T-cell recognition in the context of other HLA molecules. We selected six melanoma-associated antigens (MAGE-A3, NY-ESO-1, gp100, Mart1, tyrosinase and TRP-2) that are frequently recognized in patients with the aim of identifying novel T-cell epitopes restricted to HLA-A1, -A3, -A11 and -B7. Using in silico prediction and in vitro confirmation, we identified 127 MHC ligands and analyzed the T-cell responses against these ligands via the MHC multimer-based enrichment of peripheral blood from 39 melanoma patients and 10 healthy donors. To dissect the T-cell reactivity against this large peptide library, we used combinatorial-encoded MHC multimers and observed the T-cell responses against 17 different peptide-MHC complexes in the patient group and four in the healthy donor group. We confirmed the processing and presentation of HLA-A3-restricted T-cell epitopes from tyrosinase (TQYESGSMDK) and gp100 (LIYRRRLMK) and an HLA-A11-restricted T-cell epitope from gp100 (AVGATKVPR) via the cytolytic T-cell recognition of melanoma cell lines and/or K562 cells expressing the appropriate antigen and HLA molecule. We further found T-cell reactivity against two of the identified sequences among tumor-infiltrating lymphocytes from melanoma patients, suggesting a potential clinical relevance of these sequences.

General information

State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, University Hospital Herlev
Authors: Frøsig, T. M. (Intern), Lyngaa, R. B. (Intern), Met, Ö. (Ekstern), Larsen, S. K. (Ekstern), Donia, M. (Ekstern), Svane, I. M. (Ekstern), Straten, P. T. (Ekstern), Hadrup, S. R. (Intern)
Pages: 609-620
Publication date: 2015
Main Research Area: Technical/natural sciences
Chemokine receptor 9 (CCR9) is required for the homeostatic recruitment of T cells to the mucosa of the small intestine. Accordingly, CCR9 has been suggested as a potential target to inhibit the recruitment of proinflammatory effector T cells (Teff) in inflammatory bowel disease (IBD). Since the contribution of CCR9 to the recruitment of Teff in inflammation is not entirely clear, we aimed to address this question using IFABP-tOva mice. These mice express Ovalbumin (Ova) specifically in small intestinal epithelial cells, which allows triggering of acute inflammation following transfer of Ova-specific CD8+ T cells (OT-I cells) and adjuvant treatment. Strikingly, intestinal inflammation in IFABP-tOva mice could also be triggered following transfer of CCR9-deficient OT-I cells, demonstrating that CCR9 is not required for homing of Teff cells. Interestingly, OT-I cells transferred to IFABP-tOva mice did not only differentiate into Teff, but also into FoxP3+ CD8+ Tregs, which in contrast to Teff cells expressed high levels of CCR9. Indeed, recruitment and expansion of this regulatory subset in the small intestine was strongly dependent on CCR9. Hence, our data show that Teff and regulatory T cell subsets use distinct mechanisms for migration to the small intestine and suggest that inhibition of CCR9 in IBD could be more harmful than useful.

General information
CCRL1/ACKR4 is expressed in key thymic microenvironments but is dispensable for T lymphopoiesis at steady state in adult mice

Thymus colonisation and thymocyte positioning are regulated by interactions between CCR7 and CCR9, and their respective ligands, CCL19/CCL21 and CCL25. The ligands of CCR7 and CCR9 also interact with the atypical receptor CCRL1 (also known as ACKR4), which is expressed in the thymus and has recently been reported to play an important role in normal alpha beta T-cell development. Here, we show that CCRL1 is expressed within the thymic cortex, predominantly by MHC-IIlowCD40- cortical thymic epithelial cells and at the subcapsular zone by a population of podoplanin+ thymic epithelial cells in mice. Interestingly, CCRL1 is also expressed by stromal cells which surround the pericytes of vessels at the corticomedullary junction, the site for progenitor cell entry and mature thymocyte egress from the thymus. We show that CCRL1 suppresses thymocyte progenitor entry into the thymus, however, the thymus size and cellularity are the same in adult WT and CCRL1−/− mice. Moreover, CCRL1−/− mice have no major perturbations in T-cell populations at different stages of thymic differentiation and development, and have a similar rate of thymocyte migration into the blood. Collectively, our findings argue against a major role for CCRL1 in normal thymus development and function.
CD4+ T-cell lines used to evaluate a Mycobacterium avium subsp. paratuberculosis (MAP) peptide vaccine

The aim of the study was to establish a protocol for generation of MAP-specific T-cell lines and to use these lines for evaluation of a peptide vaccine. A protocol for culturing T-cell lines from peripheral blood of goats naturally infected with MAP was established. CD4+ T cells were positively selected using an anti CD4 mAb and Dynabeads. Sorted CD4+ cells were cultivated with purified protein derivative from MAP (PPDj) or E. coli sonicate, IL-2, and IL-15. After two cultivation cycles, T cells were tested for recall responses in a proliferative T-cell assay. T-cell line responses were in average 92 % for PPDj, and -3 % for E. coli sonicate. CD4+ T-cell lines stimulated with PPDj showed a 6 fold increase in IFN-γ production compared to controls. These results indicated that the T-cell lines were MAP-specific.

The protocol was subsequently used to evaluate MAP-specific peptides as vaccine antigens. T-cell lines were now generated by cultivating CD4+ cells with peptides instead of PPDj. Initially, both healthy and MAP-infected goats were vaccinated with 119 peptides defined by in silico analysis. Cellular responses to the peptides were not detected using standard IFN-γ plasma ELISA. However, testing of T-cell lines from the MAP-infected goats identified peptides that induced strong proliferative responses. The 23 peptides inducing the strongest responses were used in a second vaccination trial with healthy goat kids. Vaccinated kids developed strong IFN-γ and antibody responses, and these MAP-specific peptides show great potential for use in a subunit vaccine.

Generation of T-cell lines was a valuable tool for selecting MAP vaccine antigens, and the protocol can also be applied for identifying vaccine candidates for other diseases.

General information

State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Norwegian Veterinary Institute, Technical University of Denmark, Statens Serum Institut
Challenges for bovine viral diarrhoea virus antibody detection in bulk milk by antibody enzyme-linked immunosorbent assays due to changes in milk production levels

Background: Bovine viral diarrhoea (BVD) is considered eradicated from Denmark. Currently, very few (if any) Danish cattle herds could be infected with BVD virus (BVDV). The Danish antibody blocking enzyme-linked immunosorbent assay (ELISA) has been successfully used during the Danish BVD eradication program, initiated in 1994. During the last decade, the cattle herd size has increased while the prevalence of BVDV has decreased. In this study, we investigated how these changes could affect the performance of the Danish blocking ELISA and of the SVANOVIR® BVDV-Ab indirect ELISA. The latter has successfully been used to eradicate BVD in Sweden. Data (2003–2010) on changes in median herd size and milk production levels, occurrence of viremic animals and bulk milk surveillance were analysed. Additionally, the Danish blocking ELISA and the SVANOVIR ELISA were compared analyzing milk and serum samples. The prevalence of antibody positive milking cows that could be detected by each test was estimated, by diluting positive individual milk samples and making artificial milk pools. Results: During the study period, the median herd size increased from 74 (2003) to 127 cows (2010), while the prevalence of BVDV infected herds decreased from 0.51 to 0.02 %. The daily milk yield contribution of a single seropositive cow to the entire daily bulk milk was reduced from 1.61 % in 2003 to 0.95 % in 2010 due to the increased herd size. It was observed that antibody levels in bulk milk decreased at national level. Moreover, we found that when testing bulk milk, the SVANOVIR® BVDV-Ab can detect a lower prevalence of seropositive lactating cows, compared to the Danish blocking ELISA (0.78 % vs. 50 %). Values in the SVANOVIR® BVDV-Ab better relate to low concentrations of antibody positive milk (R2 = 94-98 %), than values in the blocking ELISA (R2 = 23–75 %). For sera, the two ELISAs performed equally well. Conclusions: The SVANOVIR ELISA is recommended for analysis of bulk milk samples in the current Danish situation, since infected dairy herds e.g. due to import of infected cattle can be detected shortly after BVDV introduction, when only few lactating cows have seroconverted. In sera, the two ELISAs can be used interchangeably.
Challenges for Serology-Based Characterization of Foot-and-Mouth Disease Outbreaks in Endemic Areas; Identification of Two Separate Lineages of Serotype O FMDV in Uganda in 2011

Control of foot-and-mouth disease (FMD) in Uganda by ring vaccination largely depends on costly trivalent vaccines, and use of monovalent vaccines could improve the cost effectiveness. This, however, requires application of highly specific diagnostic tests. This study investigated outbreaks of FMD in seven Ugandan districts, during 2011, using the PrioCHECK((R)) FMDV NS ELISA, solid-phase blocking ELISAs (SPBEs) and virus neutralization tests (VNTs), together with virological analyses for characterization of the responsible viruses. Two hundred and eighteen (218) cattle and 23
goat sera as well as 82 oropharyngeal fluid/epithelial tissue samples were collected. Some 50% of the cattle and 17% of the goat sera were positive by the PrioCHECK® FMDV NS ELISA, while SPBEs identified titres 80 for antibodies against serotype O FMD virus (FMDV) in 51% of the anti-NSP positive cattle sera. However, 35% of the anti-NSP positive cattle sera had SPBE titres 80 against multiple serotypes, primarily against serotypes O, SAT 1 and SAT 3. Comparison of SPBEs and VNTs for the detection of antibodies against serotypes O, SAT 1 and SAT 3 in 72 NSP positive cattle sera showed comparable results against serotype O (P=0.181), while VNTs detected significantly fewer samples positive for antibodies against SAT 1 and SAT 3 than the SPBEs (P

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Ministry of Agriculture, Animal Industry and Fisheries, Makerere University, University of Copenhagen
Authors: Namatovu, A. (Ekstern), Belsham, G. (Intern), Ayebazibwe, C. (Ekstern), Dhikusooka, M. T. (Ekstern), Wekesa, S. N. (Ekstern), Siegismund, H. R. (Ekstern), Muwanika, V. B. (Ekstern), Tjørnehøj, K. (Intern)
Number of pages: 13
Pages: 522-534
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Transboundary and Emerging Diseases
Volume: 62
Issue number: 5
ISSN (Print): 1865-1674
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.87 SJR 1.147 SNIP 1.488
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.16 SJR 1.046 SNIP 0.998
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.305 SNIP 1.249 CiteScore 2.29
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.048 SNIP 1.207 CiteScore 2.23
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.975 SNIP 1.123 CiteScore 2.33
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.847 SNIP 1.178 CiteScore 2.04
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.939 SNIP 1.124 CiteScore 2.05
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.761 SNIP 0.983
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.601 SNIP 0.907
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.363 SNIP 0.707
Web of Science (2008): Indexed yes
Changing medication method influences total amount of administered antimicrobials

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology
Authors: Fertner, M. E. (Intern), Boklund, A. (Intern), Toft, N. (Intern)
Publication date: 2015
Main Research Area: Technical/natural sciences
Electronic versions:
Poster_SVEPM_2015.pdf
Source: PublicationPreSubmission
Source-ID: 110974355
Publication: Research - peer-review › Poster – Annual report year: 2015

Characterisation of recent foot-and-mouth disease viruses from African buffalo (Syncerus caffer) and cattle in Kenya is consistent with independent virus populations

Background
Understanding the epidemiology of foot-and-mouth disease (FMD), including roles played by different hosts, is essential for improving disease control. The African buffalo (Syncerus caffer) is a reservoir for the SAT serotypes of FMD virus (FMDV). Large buffalo populations commonly intermingle with livestock in Kenya, yet earlier studies have focused on FMD in the domestic livestock, hence the contribution of buffalo to disease in livestock is largely unknown. This study analysed 47 epithelia collected from FMD outbreaks in Kenyan cattle between 2008 and 2012, and 102 probang and serum samples collected from buffalo in three different Kenyan ecosystems; Maasai-Mara (MME) (n=40), Tsavo (TSE) (n=33), and Meru (ME) (n=29).

Results
Antibodies against FMDV non-structural proteins were found in 65 of 102 (64%) sera from buffalo with 44/102 and 53/102 also having neutralising antibodies directed against FMDV SAT 1 and SAT 2, respectively. FMDV RNA was detected in 42% of the buffalo probang samples by RT-qPCR (Cycle Threshold (Ct) ≤32). Two buffalo probang samples were positive by VI and were identified as FMDV SAT 1 and SAT 2 by Ag-ELISA, while the latter assay detected serotypes O (1), A (20), SAT 1 (7) and SAT 2 (19) in the 47 cattle epithelia. VP1 coding sequences were generated for two buffalo and 21 cattle samples. Phylogenetic analyses revealed SAT 1 and SAT 2 virus lineages within buffalo that were distinct from those detected in cattle.

Conclusions
We found that FMDV serotypes O, A, SAT 1 and SAT 2 were circulating among cattle in Kenya and cause disease, but only SAT 1 and SAT 2 viruses were successfully isolated from clinically normal buffalo. The buffalo isolates were genetically distinct from isolates obtained from cattle. Control efforts should focus primarily on reducing FMDV circulation among livestock and limiting interaction with buffalo. Comprehensive studies incorporating additional buffalo viruses are recommended.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Foot-and-Mouth Disease Laboratory, Makerere University, Kenya Wildlife Service, University of Copenhagen
Characterization of eelpout rhabdovirus (ERV) on cell culture

**General information**
State: Published
Organisations: National Veterinary Institute, Section for Virology, National Veterinary Institute Sweden, Swedish Agency for Marine and Water Management
Authors: Blomkvist, E. (Ekstern), Alfjorden, A. (Ekstern), Hakhverdyan, M. (Ekstern), Boutrup, T. S. (Intern), Ahola, H. (Ekstern), Ljunghager, F. (Ekstern), Hagström, Å. (Ekstern), Olesen, N. J. (Intern), Juremalm, M. (Ekstern), Leijon, M. (Ekstern), Valarcher, J. (Ekstern), Axen, C. (Ekstern)
Pages: 228-228
Publication date: 2015

**Host publication information**
Title of host publication: 17th International Conference on Diseases of Fish And Shellfish : Abstract book
Place of publication: Las Palmas
Publisher: European Association of Fish Pathologists
Article number: P-004
Main Research Area: Technical/natural sciences
Conference: 17th International Conference on Diseases of Fish and Shellfish, Las Palmas, Spain, 07/09/2015 - 07/09/2015
Electronic versions:
Book_of_abstracts_17th_International_conference_on_Diseases_of_Fish_and_Shellfish.pdf
Publication: Research - peer-review » Conference abstract in proceedings – Annual report year: 2015


To investigate the foot-and-mouth disease virus (FMDV) serotypes circulating in Uganda’s cattle population, both serological and virological analyses of samples from outbreaks that occurred during 2012-2013 were performed. Altogether, 79 sera and 60 oropharyngeal fluid (OP)/tissue/oral swab samples were collected from herds with reported FMD outbreaks in seven different Ugandan districts. Overall, 61/79 (77%) of the cattle sera were positive for antibodies against FMDV by PrioCHECK® FMDV NS ELISA and solid phase blocking ELISA detected titres ≥ 80 for serotypes O, SAT 1, SAT 2 and SAT 3 in 41, 45, 30 and 45 of these 61 seropositive samples, respectively. Virus neutralisation tests detected the highest levels of neutralising antibodies (titres ≥ 45) against serotype O in the herds from Kween and Rakai districts, against SAT 1 in the herd from Nwoya district and against SAT 2 in the herds from Kiruhura, Isingiro and Ntungamo districts. Consistent with the detection of high levels of neutralising antibodies against SAT 2, was the isolation of a SAT 2 FMDV from Isingiro; sequencing (for the VP1 coding region) indicated that this virus belonged to lineage I within this serotype, like the currently used vaccine strain. From the Wakiso district 11 tissue/swab samples were collected; serotype A FMDV, genotype Africa (G-I), was isolated from the epithelial samples. This study shows that within a period of less than one year, FMD outbreaks in Uganda were caused by four different serotypes namely O, A, SAT 1 and SAT 2. Therefore, to enhance the control of FMD in Uganda, there is need for efficient and timely determination of outbreak virus strains/serotypes and vaccine matching. The value of incorporating serotype A antigen into the imported vaccines along with the current serotype O, SAT 1 and SAT 2 strains should be considered.

**General information**
State: Published
Organisations: National Veterinary Institute, Section for Virology, Ministry of Agriculture, Animal Industry and Fisheries, Makerere University, University of Copenhagen
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Number of pages: 17
Publication date: 2015
Main Research Area: Technical/natural sciences

**Publication information**
Journal: P L o S One
Volume: 10
Issue number: 2
Article number: e011481
ISSN (Print): 1932-6203
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Characterization of gene expression profiles to chronic infection with Mycobacterium avium subspecies paratuberculosis

Mycobacterium avium subsp. paratuberculosis (Map) causes paratuberculosis, a chronic enteritis of ruminants. The aim of the study was to use high-throughput reverse transcriptase (RT) qPCR to describe intestinal gene expression patterns in response to different levels of Map infection with a large panel of immunologically relevant genes.

For the study we selected samples of 6 calves that were all experimentally infected with Map at two weeks of age and based on serology, histology and Map tissue load were classified as protected (n=2) or unprotected (n=2) after vaccination, or un-vaccinated infected controls (n=2). From each calf, 7 intestinal tissue samples and 3 lymph node samples, collected at 10 months of age, were used for cDNA synthesis. Expression of a total of 37 selected genes including inflammatory, Th1 and Th17 related genes were explored.

The results showed that Map infection, as expected, leads to increased expression of local IFN-γ. Expression of IL-10 also increased as a result of Map infection, and this increase was more correlated to the amount of Map than IFN-γ, indicating a shift towards a regulatory environment as infection progress. Th17-mediated immune responses were suppressed at this stage. Gene expression of all other genes could not be interpreted in relation to infection status.

High throughput RT qPCR can be used for exploring gene expression patterns in response to Map infection but larger study groups are needed to fully understand which are key mechanisms and pathways responsible for protection or
Characterization of the bacterial gut microbiota of piglets suffering from new neonatal porcine diarrhoea

Background: In recent years, new neonatal porcine diarrhoea (NNPD) of unknown aetiology has emerged in Denmark. NNPD affects piglets during the first week of life and results in impaired welfare, decreased weight gain, and in the worst-case scenario death. Commonly used preventative interventions such as vaccination or treatment with antibiotics, have a limited effect on NNPD. Previous studies have investigated the clinical manifestations, histopathology, and to some extent, microbiological findings; however, these studies were either inconclusive or suggested that Enterococci, possibly in interaction with Escherichia coli, contribute to the aetiology of NNPD. This study examined ileal and colonic luminal contents of 50 control piglets and 52 NNPD piglets by means of the qPCR-based Gut Microbiotassay and 16 samples by 454 sequencing to study the composition of the bacterial gut microbiota in relation to NNPD. Results: NNPD was associated with a diminished quantity of bacteria from the phyla Actinobacteria and Firmicutes while genus Enterococcus was more than 24 times more abundant in diarrhoeic piglets. The number of bacteria from the phylum Fusobacteria was also doubled in piglets suffering from diarrhoea. With increasing age, the gut microbiota of NNPD affected piglet and control piglets became more diverse. Independent of diarrhoeic status, piglets from first parity sows (gilts) possessed significantly more bacteria from family Enterobacteriaceae and species E. coli, and fewer bacteria from phylum Firmicutes. Piglets born to gilts had 25 times higher odds of having NNPD compared with piglets born to multiparous sows. Finally, the co-occurrence of genus Enterococcus and species E. coli contributed to the risk of having NNPD. Conclusion: The results of this study support previous findings that points towards genus Enterococcus and species E. coli to be involved in the pathogenesis of NNPD. Moreover, the results indicate that NNPD is associated with a disturbed bacterial composition and larger variation between the diarrhoeic piglets.
Characterization of the PRRSV strain circulating in a PRRSV type 1 positive herd before, during and after vaccination with a PRRSV type 1 vaccine

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Danish Pig Production
Authors: Kvisgaard, L. K. (Intern), Kristensen, C. S. (Ekstern), Hjulsager, C. K. (Intern), Larsen, L. E. (Intern)
Number of pages: 1
Publication date: 2015
Event: Abstract from 7th International Symposium on Emerging and Re-emerging Pig Diseases, Kyoto, Japan.
Main Research Area: Technical/natural sciences
Electronic versions: iserpd2015abstract_FINAL.pdf
DOI: 10.1186/s12917-015-0419-4

Bibliographical note
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Original language: English

NNPD, Neonatal, Piglet, Diarrhoea, qPCR, Microbiota, Gut Microbiotassay, 454 sequencing

Electronic versions:

DOIs:
10.1186/s12917-015-0419-4
Characterizing novel endogenous retroviruses from genetic variation inferred from short sequence reads

From Illumina sequencing of DNA from brain and liver tissue from the lion, Panthera leo, and tumor samples from the pike-perch, Sander lucioperca, we obtained two assembled sequence contigs with similarity to known retroviruses. Phylogenetic analyses suggest that the pike-perch retrovirus belongs to the epsilonretroviruses, and the lion retrovirus to the gammaretroviruses. To determine if these novel retroviral sequences originate from an endogenous retrovirus or from a recently integrated exogenous retrovirus, we assessed the genetic diversity of the parental sequences from which the short Illumina reads are derived. First, we showed by simulations that we can robustly infer the level of genetic diversity from short sequence reads. Second, we find that the measures of nucleotide diversity inferred from our retroviral sequences significantly exceed the level observed from Human Immunodeficiency Virus infections, prompting us to conclude that the novel retroviruses are both of endogenous origin. Through further simulations, we rule out the possibility that the observed elevated levels of nucleotide diversity are the result of co-infection with two closely related exogenous retroviruses.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, University of Copenhagen, Statens Seruminstitute Authors: Mourier, T. (Ekstern), Mollerup, S. (Ekstern), Vinner, L. (Ekstern), Kjartansdóttir, K. R. (Ekstern), Guldberg Freslev, T. (Ekstern), Boutrup, T. S. (Intern), Nielsen, L. P. (Ekstern), Willerslev, E. (Ekstern), Hansen, A. J. (Ekstern)
Number of pages: 11
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Scientific Reports
Volume: 5
Article number: 15644
ISSN (Print): 2045-2322
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.36 SJR 1.533 SNIP 1.245
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.63 SJR 1.692 SNIP 1.354
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.034 SNIP 1.597 CiteScore 5.3
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.163 SNIP 1.554 CiteScore 4.75
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.998 SNIP 1.57 CiteScore 4.06
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.531 SNIP 0.962 CiteScore 2.44
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
ISI indexed (2011): ISI indexed no
Original language: English
Electronic versions:
srep15644.pdf
DOIs:
10.1038/srep15644
Links:
http://www.nature.com/articles/srep15644
**Checkpoint inhibitors in cancer immunotherapy: Cross reactivity of a CTLA-4 antibody and IDO-inhibitor L-1MT in pigs**

Blockade of checkpoint inhibitors has recently shown very convincing results in the treatment of cancer. One key target is CTLA-4, which has been demonstrated to be a potent negative regulator of lymphocyte activation. The treatment with the FDA-approved fully human CTLA-4 monoclonal antibody Ipilimumab increases anticancer T-cell reactivity and overall survival of metastatic cancer patients. Indole-amine 2,3-dioxygenase (IDO) is another checkpoint inhibitor which suppresses T-cell immunity by the depletion of tryptophan in the T-cell microenvironment, and also inhibition of IDO by L-1-Methyltryptophan (L-1MT) has shown promising results in clinical phase I/II studies of human cancer such as epithelial ovarian cancer.

Pre-clinical immune therapeutic studies are usually performed with mice, but Ipilimumab is not reactive with mouse cells. Recent studies indicate that the pig may be a more suitable animal model for studies of immune reactivity due to higher similarity of the immunome between pig and man. This study is part of the CANVACPIG project “Accelerating development of vaccines against cancer with pigs as a large animal model” and investigates the reactivity of a fully human monoclonal anti CTLA-4 antibody and L-1MT on porcine immune cells.

At the genome level, the homology between human and pig CTLA-4 and IDO is 86% and 73%, respectively, while the homology to the mouse is 75% and 63%. Our preliminary in vitro studies indicate that the monoclonal anti CTLA-4 antibody induces a non-specific activation of porcine T cells. This will be further investigated to provide the basis for in vivo studies investigating checkpoint inhibitor blockade in combination with other cancer immunotherapies. Eventually our goal is to establish pigs as an alternative large animal model for development and formulation of new human cancer vaccines.

**Circulating Extracellular microRNA in Systemic Autoimmunity**

MicroRNAs (miRNAs) are differentially regulated in healthy, activated, inflamed, neoplastic, or otherwise pathological cells and tissues. While their main functions are executed intracellularly, many miRNAs can reproducibly be detected extracellularly in plasma and serum. This circulating, extracellular miRNA is protected against degradation by complexation with carrier proteins and/or by being enclosed in subcellular membrane vesicles. This, together with their tissue- and disease-specific expression, has fuelled the interest in using circulating miRNA profiles as harbingers of disease, i.e., as diagnostic analytes and as clues to dysregulated pathways in disease. Many studies show that inflammation and immune dysregulation, e.g., in autoimmune diseases, are associated with distinct miRNA expression changes in targeted tissues and in innate and adaptive immunity cells such as lymphocytes, natural killer cells, neutrophil granulocytes, and monocyte-macrophages. Exploratory studies (only validated in a few cases) also show that specific profiles of circulating miRNAs are associated with different systemic autoimmune diseases including systemic lupus erythematosus (SLE), systemic sclerosis, and rheumatoid arthritis. Even though the link between cellular alterations and extracellular profiles is still unpredictable, the data suggest that circulating miRNAs in autoimmunity may become diagnostically useful. Here, we review important circulating miRNAs in animal models of inflammation and in systemic autoimmunity and summarize some proposed functions of miRNAs in immune regulation and dysregulation. We conclude that the studies suggest new hypotheses and additional experiments, and that further diagnostic development is highly dependent on analytical method development and on obtaining sufficient numbers of uniformly processed samples from clinically well-characterized patients and controls.
Clinical utility and performance of sock sampling in weaner pig diarrhoea

Low pathogen diarrhoea is a group-level diagnosis, characterised by non-haemorrhagic diarrhoea. In the current study, the apparent prevalence of low pathogen diarrhoea outbreaks in Danish herds was investigated along with the clinical utility of a laboratory examination for intestinal disease, agreement between three consecutive herd examinations from the same herd and agreement between quantitative PCR results from pooled faecal samples and sock samples. Twenty-four veterinarians submitted faecal and sock samples for quantitative PCR testing from outbreaks of diarrhoea in nursery pigs (n=38 herds) where the farmer or veterinarian had decided that antimicrobial treatment was necessary. The veterinarians were asked to fill in a questionnaire and participate in telephone interviews. The apparent prevalence of low pathogen diarrhoea was 0.18 (95% CI: 0.08–0.34). Agreement between the veterinarians’ clinical aetiological diagnosis and the pooled faecal sample was 0.18 (95% CI: 0.08–0.34), and Cohen’s Kappa was 0.03 (95% CI: −0.08 to 0.14). Antibiotic treatment or prevention strategies were changed in 0.63 (95% CI: 0.46–0.78) of the herds, and the veterinarians indicated that, for 0.32 (95% CI: 0.18–0.50) of the herds, changes were related to the diagnostic results from the laboratory examination performed in the study. In 0.16 (95% CI: 0.05–0.36) of the herds, the same infections were demonstrated at all three consecutive examinations. No herds had three consecutive diarrhoea outbreaks classified as low pathogen diarrhoea. For the quantitative results (log10 of the summed amounts of Lawsonia intracellularis, Brachyspira pilosicoli, Escherichia coli F4 and F18) agreement between pooled faecal samples and sock samples was evaluated. Lin’s concordance correlation coefficient was 0.69 (95% CI: 0.48–0.82), and the mean difference between the two types of samples was −0.38 log10 bacteria/g faeces (SD=1.59 log10 bacteria/g faeces; 95% CI: −0.90 to 0.14 log10 bacteria/g faeces). Agreement for the dichotomised results was 0.89 (95% CI: 0.75–0.97) when test results were classified as low pathogen diarrhoea or not, and Cohen’s Kappa was 0.61 (95% CI: 0.26–0.95). In relation to detection of the individual infections, agreement was 0.63 (95% CI: 0.46–0.78), and Cohen’s Kappa was 0.53 (95% CI: 0.34–0.71). In conclusion, low pathogen diarrhoea is a common finding amongst diarrhoea outbreaks that are subjected to antibiotic batch treatment in Danish nursery pigs. Sock samples seem to offer a reliable diagnostic method with impact on clinical decisions for treatment and prevention. However, both the diarrhoea type and the aetiology change with time in the majority of herds, indicating a potential need for frequent diagnostic examinations.
Cognitive Function, Progression of Age-related Behavioral Changes, Biomarkers, and Survival in Dogs More Than 8 Years Old

Background
Canine cognitive dysfunction (CCD) is an age-dependent neurodegenerative condition dominated by changes in behavioral patterns. Cohort studies investigating cognitive status in dogs are lacking.

Objectives
To investigate cognitive function, progression of age-related behavioral changes, survival, and possible biomarkers of CCD in aged dogs.
Animals
Fifty-one dogs >8 years old; 21 with no cognitive deficits, 17 with mild cognitive impairments (MCI) and 13 with CCD. Methods
Longitudinal study. Recruitment period of 12 months and an observational period of 24 months including a baseline and 3 planned subsequent assessments. Cognitive status was determined using validated questionnaires. Plasma A- peptides were quantified using commercial ELISA assays and cytokines by a validated immunoassay.

Results
Signs characterizing dogs with CCD were aimless wandering, staring into space, avoid getting patted, difficulty finding dropped food and anxiety. Thirty-three percent of dogs with a normal cognitive status progressed to MCI and 22% classified as MCI progressed to CCD during the study period. For 6 dogs diagnosed with CCD, signs of cognitive dysfunction increased with time. A diagnosis of CCD did not affect survival. The level of plasma A(42) was significantly increased (P < .05) in the CCD group (92.8 ± 24.0 pg/mL) compared to the MCI (77.0 ± 12.3 pg/mL) and normal group (74.9 ± 10.0 pg/mL), but no significant differences in concentrations of systemic inflammatory markers were detected.

Conclusions
Canine cognitive dysfunction is a progressive disorder with an individual variability in the rate of cognitive decline and clinical signs. Plasma A(42) seems to be an interesting plasma biomarker of CCD.

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, University of Copenhagen
Authors: Schütt, T. (Ekstern), Berendt, M. (Ekstern), Toft, N. (Intern)
Pages: 1569-1577
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Veterinary Internal Medicine
Volume: 29
Issue number: 6
ISSN (Print): 0891-6640
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 1.787 SJR 1.481 CiteScore 2.38
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): SJR 1.35 SNIP 1.286 CiteScore 2.06
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.217 SNIP 1.233 CiteScore 2.09
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.273 SNIP 1.495 CiteScore 2.08
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.541 SNIP 1.674 CiteScore 2.24
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.301 SNIP 1.522 CiteScore 2.08
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.604 SNIP 1.499 CiteScore 1.98
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.626 SNIP 1.691
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.502 SNIP 1.578
BFI (2008): BFI-level 2
Comment on "5-Azacytidine Promotes an Inhibitory T-Cell Phenotype and Impairs Immune Mediated Antileukemic Activity"

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology
Authors: Frøsig, T. M. (Intern), Hadrup, S. R. (Intern)
Number of pages: 3
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Mediators of Inflammation
Article number: 871641
ISSN (Print): 0962-9351
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.049 SJR 1.37 CiteScore 3.46
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 1.51 SNIP 1.123 CiteScore 3.52
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.485 SNIP 1.142 CiteScore 3.35
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.287 SNIP 0.994 CiteScore 2.9
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.364 SNIP 1.142 CiteScore 3.19
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.18 SNIP 1.117 CiteScore 3.3
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.238 SNIP 0.95 CiteScore 3.22
ISI indexed (2011): ISI indexed yes
Comparative evaluation of infection methods and environmental factors on challenge success: Aeromonas salmonicida infection in vaccinated rainbow trout

When testing vaccine-induced protection an effective and reliable challenge method is a basic requirement and we here present a comparative study on different challenge methods used for infection of rainbow trout Oncorhynchus mykiss with Aeromonas salmonicida, a bacterial pathogen eliciting furunculosis. Fish were vaccinated with three different adjuvanted trivalent vaccines containing formalin killed A. salmonicida, Vibrio anguillarum O1 and O2a. These were 1) the commercial vaccine Alpha Ject 3000, 2) an experimental vaccine with water in paraffin oil adjuvant, 3) an experimental vaccine with water in paraffin oil in water adjuvant. Fish were then exposed to A. salmonicida challenge using i.p. injection, cohabitation in freshwater, cohabitation in saltwater (15 ppt) or combined fresh/saltwater cohabitation. Cohabitation reflects a more natural infection mode and was shown to give better differentiation of vaccine types compared to i.p. injection of live bacteria. The latter infection mode is less successful probably due to the intra-abdominal inflammatory reactions (characterized in this study according to the Speilberg scale) induced by i.p. vaccination whereby injected live bacteria more effectively become inactivated at the site of injection. Compared to cohabitation in freshwater, cohabitation in saltwater was less efficient probably due to reduced survivability of A. salmonicida in saltwater, which was also experimentally verified in vitro.

General information

State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Copenhagen, Vaxxinova Norway AS
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Number of pages: 11
Pages: 485-495
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information

Journal: Fish and Shellfish Immunology
Volume: 44
Issue number: 2
ISSN (Print): 1050-4648
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Comparative genome analysis of Clostridium perfringens isolates from healthy and necrotic enteritis infected poultry and diseased pigs

Introduction: Clostridium perfringens causes gastrointestinal diseases in both humans and domestic animals. Type A strains are the main cause of necrotic enteritis (NE) in chickens, which is a significant economic issue in the international poultry industry. TheNetB and Cpb2 toxins seem to be important for the development of NE in chickens and piglets, respectively, while the role of these toxins is less well elucidated in diseased turkeys.

Methods: We carried out comparative genomic analysis of 40 C. perfringens genomes from healthy and NE-suffering chickens and turkeys, and diseased pigs using whole-genome data.

Results: Analyses of virulence gene content including VirR boxes showed that netB was primarily found among NE isolates from chickens, while cpl2 dominated the isolates from diseased pigs. The pathogenicity loci NELoc-1, -2 and -3 were primarily observed in NE isolates from poultry and most commonly in chickens, whereas only NELoc-2 was common among isolates from diseased turkeys. Furthermore, conjugative plasmid transfer genes were identified in the majority of all isolates, and VirR boxes were found upstream of genes that are essential in the NE pathogenesis.

Conclusions:
• netB, NELoc-1 and -3 seem to play an important role in the NE pathogenesis in chickens, whereas cpl2 is important in diseased pigs.
• The VirSR two-component system is involved in regulating NE-associated virulence genes.
• Conjugative plasmid genes are widely spread among C. perfringens.
• WGS is a powerful tool to investigate virulence properties and population genetic structure of C. perfringens.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Statens Serum Institut
Authors: Ronco, T. (Intern), Lyhs, U. (Intern), Stegger, M. (Ekstern), Andersen, P. S. (Ekstern), Pedersen, K. (Intern)
Pages: 89-89
Publication date: 2015

Comparative genomic analysis of Clostridium perfringens isolates from healthy and diseased livestock production animals

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Statens Serum Institut
Authors: Ronco, T. (Intern), Lyhs, U. (Intern), Stegger, M. (Ekstern), Andersen, P. S. (Ekstern), Pedersen, K. (Intern)
Publication date: 2015

Comparison of individual and pooled samples for quantification of antimicrobial resistance genes in swine feces by high-throughput qPCR

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Section for Epidemiology, University of Copenhagen
Authors: Clasen, J. (Intern), Mellerup, A. (Intern), Olsen, J. E. (Ekstern), Angen, Ø. (Intern), Folkesson, S. A. (Intern), Hisham Beshara Halasa, T. (Intern), Toft, N. (Intern), Birkegård, A. C. (Intern)
Number of pages: 1
Publication date: 2015
Event: Poster session presented at Annual General Meeting of the European College of Veterinary Public Health 2015, Belgrade, Serbia.
Comparison of individual and pooled samples for quantification of antimicrobial resistance genes in swine feces by high-throughput qPCR

There is a considerable societal interest in the careful monitoring of antimicrobial resistance (AMR) levels in human and animal populations. Sampling and data analysis can be both costly and time consuming. Optimization of sample pooling procedures is therefore important to reduce costs and analysis times. The objective of this study was to estimate how many individual fecal samples are needed to pool to get a representative sample for quantification of AMR-genes in a Danish pig herd. 20 individual fecal samples were collected from one section in a Danish pig herd. One to five rectal fecal samples were taken from each pen with respect to the number of pigs in the pen. A total of 48 pools were made of increasing number of individual samples. The levels of 9 different AMR-genes were quantified using dynamic qPCR arrays on the BioMark HD system (Fluidigm©). DNA was extracted using the Maxwell® 16 Blood DNA Purification Kit (Promega). DNA concentrations were diluted to 40 ng/μl. The efficiency of the primers was determined using standard curves. Obtained results were normalized with 16S ribosomal DNA. There were large variations in the levels of AMR-genes between individual samples. As the number of samples in a pool increased a decrease in sample variation was observed. A steady state in the sample variation was seen when pooling five or more samples. No significant difference was found between pools of five samples and pools of more. There were a significant difference between pools of five or more samples and pools of less (p < 0.0001). In order to quantify the level of AMR-genes pools of five individual samples will give a result representative of the pig herd. The findings of this study could be used in planning of observational studies.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Section for Epidemiology, University of Copenhagen
Authors: Clausen, J. (Intern), Mellerup, A. (Intern), Olsen, J. E. (Ekstern), Angen, Ø. (Intern), Folkesson, S. A. (Intern), Toft, N. (Intern), Birkergård, A. C. (Intern)
Pages: 27-27
Publication date: 2015

Comparison of output-based approaches used to substantiate bovine tuberculosis free status in Danish cattle herds

We compared two published studies based on different output-based surveillance models, which were used for evaluating the performance of two meat inspection systems in cattle and to substantiate freedom from bovine tuberculosis (bTB) in Denmark. The systems were the current meat inspection methods (CMI) vs. the visual-only inspection (VOI). In one study, the surveillance system sensitivity (SSe) was estimated to substantiate the bTB free status. The other study used SSe in the estimation of the probability of freedom (PFree), based on the epidemiological concept of negative predictive value to substantiate the bTB free status. Both studies found that changing from CMI to VOI would markedly decrease the SSe. However, the two studies reported diverging conclusions regarding the effect on the substantiation of Denmark as a bTB free country, if VOI were to be introduced. The objectives of this work were: (a) to investigate the reasons why conclusions based on the two models differed, and (b) to create a hybrid model based on elements from both studies to evaluate the impact of a change from CMI to VOI. The hybrid model was based on the PFree approach to substantiate freedom from bTB and was parameterized with inputs according to the newest available information. The PFree was updated on an annual basis for each of 42 years of test-negative surveillance data (1995–2037), while assuming a low (<1%) annual probability of introduction of bTB into Danish cattle herds. The most important reasons for the difference between the study conclusions were: the approach chosen to substantiate the bTB free status (SSe vs. PFree) and the number of years of surveillance data considered. With the hybrid model, the PFree reached a level >95% after the first year of surveillance and remained ≥96% with both the CMI and VOI systems until the end of the analyzed period. It is appropriate to use the PFree of the surveillance system to substantiate confidence in bTB free status, when test-negative surveillance
results can be documented over an extended period of time, while maintaining a low probability of introduction of bTB into the cattle population. For Denmark, the probability of introduction of bTB should be kept <1% on an annual basis to sustain the high confidence in freedom over time. The results could be considered when deciding if the CMI can be replaced by VOI in cattle abattoirs of countries for which bTB freedom can be demonstrated.

General information
State: Published
Organisations: National Veterinary Institute, University of Copenhagen, Danish Agriculture and Food Council
Authors: Foddai, A. (Intern), Rosenbaum Nielsen, L. (Ekstern), Willeberg, P. (Intern), Alban, L. (Ekstern)
Number of pages: 9
Pages: 21-29
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Preventive Veterinary Medicine
Volume: 121
Issue number: 1-2
ISSN (Print): 0167-5877
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 1.31 SJR 1.144 CiteScore 2.26
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.2 SJR 1.249 SNIP 1.361
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.282 SNIP 1.177 CiteScore 2.1
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.27 SNIP 1.407 CiteScore 2.37
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.264 SNIP 1.529 CiteScore 2.49
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.265 SNIP 1.436 CiteScore 2.45
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.194 SNIP 1.295 CiteScore 2.24
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.156 SNIP 1.284
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.032 SNIP 1.338
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.056 SNIP 1.258
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.009 SNIP 1.353
Web of Science (2007): Indexed yes
Complete genome sequence of eelpout rhabdovirus (ERV) identified by deep sequencing of viral RNA

**General information**
State: Published
Organisations: National Veterinary Institute, Section for Virology, National Veterinary Institute Sweden, Swedish Agency for Marine and Water Management
Authors: Hakhverdyan, M. (Ekstern), Areskog, M. (Ekstern), Blomkvist, E. (Ekstern), Alfjorden, A. (Ekstern), Boutrup, T. S. (Intern), Ahola, H. (Ekstern), Ljunghager, F. (Ekstern), Hagström, Å. (Ekstern), Olesen, N. J. (Intern), Juremalm, M. (Ekstern), Valarcher, J. (Ekstern), Axen, C. (Ekstern), Leijon, M. (Ekstern)
Pages: 341-341
Publication date: 2015

Host publication information
Title of host publication: 17th International Conference on Diseases of Fish and Shellfish : Abstract book
Place of publication: Las Palmas
Publisher: European Association of Fish Pathologists
Article number: P-117
Main Research Area: Technical/natural sciences
Conference: 17th International Conference on Diseases of Fish and Shellfish, Las Palmas, Spain, 07/09/2015 - 07/09/2015
Electronic versions:
Book_of_abstracts_17th_International_conference_on_Diseases_of_Fish_and_Shellfish.pdf
Publication: Research - peer-review » Conference abstract in proceedings – Annual report year: 2015

Complete Genome Sequence of the Human Gut Symbiont Roseburia hominis
We report here the complete genome sequence of the human gut symbiont Roseburia hominis A2-183(T) (= DSM 16839(T) = NCIMB 14029(T)), isolated from human feces. The genome is represented by a 3,592,125-bp chromosome with 3,405 coding sequences. A number of potential functions contributing to host-microbe interaction are identified.

**General information**
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Aberdeen
Authors: Travis, A. J. (Ekstern), Kelly, D. (Ekstern), Flint, H. J. (Ekstern), Aminov, R. (Intern)
Number of pages: 2
Publication date: 2015
Main Research Area: Technical/natural sciences

**Publication information**
Concurrent host-pathogen gene expression in the lungs of pigs challenged with Actinobacillus pleuropneumoniae

Background: Actinobacillus pleuropneumoniae causes pleuropneumonia in pigs, a disease which is associated with high morbidity and mortality, as well as impaired animal welfare. To obtain in-depth understanding of this infection, the interplay between virulence factors of the pathogen and defense mechanisms of the porcine host needs to be elucidated. However, research has traditionally focused on either bacteriology or immunology; an unbiased picture of the transcriptional responses can be obtained by investigating both organisms in the same biological sample. Results: Host and pathogen responses in pigs experimentally infected with A. pleuropneumoniae were analyzed by high-throughput RT-qPCR. This approach allowed concurrent analysis of selected genes encoding proteins known or hypothesized to be important in the acute phase of this infection. The expression of 17 bacterial and 31 porcine genes was quantified in lung samples obtained within the first 48 hours of infection. This provided novel insight into the early time course of bacterial genes involved in synthesis of pathogen-associated molecular patterns (lipopolysaccharide, peptidoglycan, lipoprotein) and genes involved in pattern recognition (TLR4, CD14, MD2, LBP, MYD88) in response to A. pleuropneumoniae. Significant up-regulation of proinflammatory cytokines such as IL1β, IL6, and IL8 was observed, correlating with protein levels, infection status and histopathological findings. Host genes encoding proteins involved in iron metabolism, as well as bacterial genes encoding exotoxins, proteins involved in adhesion, and iron acquisition were found to be differentially expressed according to disease progression. By applying laser capture microdissection, porcine expression of selected genes could be confirmed in the immediate surroundings of the invading pathogen. Conclusions: Microbial pathogenesis is the product of interactions between host and pathogen. Our results demonstrate the applicability of high-throughput RT-qPCR for the elucidation of dual-organism gene expression analysis during infection. We showed differential expression of 12 bacterial and 24 porcine genes during infection and significant correlation of porcine and bacterial gene expression. This is the first study investigating the concurrent transcriptional response of both bacteria and host at the site of infection during porcine respiratory infection.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Section for Bacteriology, Pathology and Parasitology
Authors: Brogaard, L. (Intern), Schou, K. K. (Intern), Heegaard, P. M. H. (Intern), Hansen, M. S. (Intern), Jensen, T. K. (Intern), Skovgaard, K. (Intern)
Number of pages: 15
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: B M C Genomics
Volume: 16
Issue number: 417
ISSN (Print): 1471-2164
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SJR 2.11 SNIP 1.151 CiteScore 4.08
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.05 SJR 2.163 SNIP 1.096
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.348 SNIP 1.159 CiteScore 4.3
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.327 SNIP 1.199 CiteScore 4.18
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 2.195 SNIP 1.188 CiteScore 4.39
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 2.236 SNIP 1.243 CiteScore 4.61
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 2.307 SNIP 1.191 CiteScore 4.38
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.142 SNIP 1.037
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 2.21 SNIP 1.012
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 2.287 SNIP 1.007
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 2.12 SNIP 1.039
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.878 SNIP 0.927
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 2.287 SNIP 0.915
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 2.218 SNIP 0.728
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 1.94 SNIP 0.571
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 7.349 SNIP 0.529
Scopus rating (2001): SJR 0.132 SNIP 0.016

Original language: English
and amino acids, 10066, Biochemistry studies - Lipids, 10068, Biochemistry studies - Carbohydrates, 10069, Biochemistry studies - Minerals, 12502, Pathology - General, 16004, Respiratory system - Physiology and biochemistry, 16006, Respiratory system - Pathology, 17002, Endocrine - General, 31000, Physiology and biochemistry of bacteria, 31500, Genetics of bacteria and viruses, 36002, Medical and clinical microbiology - Bacteriology, 38002, Veterinary science - General and methods, 38004, Veterinary science - Pathology, Infection, Molecular Genetics, Veterinary Medicine, pathogen-associated molecular patterns, pleuropneumonia Pleuropneumonia (MeSH) respiratory system disease pathology, mortality, Biochemistry and Molecular Biophysics, Medical Sciences, lungs respiratory system, high-throughput RT-qPCR laboratory techniques, genetic techniques, histopathological examination laboratory techniques, histology and cytology techniques, laser capture microdissection laboratory techniques, histology and cytology techniques, BIOTECHNOLOGY, GENETICS, GRAM-NEGATIVE BACTERIA, ACUTE-PHASE RESPONSE, EXPERIMENTAL- INFECTION, PULMONARY-LESIONS, VIRULENCE FACTORS, PROTEINS, IDENTIFICATION, INDUCTION, IRON, RECEPTOR, High-throughput RT-qPCR, Transcriptional analysis, Host-pathogen interactions, Innate immunity, Actinobacillus pleuropneumoniae, Respiratory infection, Laser capture microdissection

Electronic versions:
Concurrent_host_pathogen_gene_expression_in_the_lungs_of_pigs_challenged_with_Actinobacillus_pleuropneumoniae.pdf
DOIs:
10.1186/s12864-015-1557-6

Bibliographical note
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Source: FindIt
Source-ID: 275180778
Publication: Research - peer-review › Journal article – Annual report year: 2015

Context dependent development of lymphoid organ mesenchymal subsets fromBP3-Gp38+ PDGFRβ+/α+CD34+ vascular adventitial precursors
Lymphoid associated mesenchymal stromal cells are believed to play essential roles in immune and organ homeostasis however our knowledge regarding the functional heterogeneity and ontogeny of these cells remains limited.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, University of Birmingham, Lund University
Number of pages: 1
Publication date: 2015
Event: Abstract from 1st International Venice Thymus Meeting, San Servolo Island, Italy.
Main Research Area: Technical/natural sciences
Electronic versions:
poster_venice_K_Sitnik.pdf
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2015

Convergent synthesis of degradable dendrons based on L-malic acid
New degradable polyester dendrons based on the cellular tricarboxylic acid cycle component L-malic acid were synthesized up to the third generation by convergent synthesis. The dendron wedges could be introduced in a stepwise, highly regioselective fashion. HMBC-NMR revealed that the C1-carbonyl on malic acid was exclusively esterified, before the reaction of the second dendron wedge at C4 took place. Degradation studies on a first generation dendron analyzed by HPLC showed that hydrolytic degradation of the dendron most profoundly takes place at pH 4 and pH 9 with the highest degradation rate at alkaline pH. NMR shows that the dendron degrades to malic acid and fumaric acid derivatives. Preliminary studies performed in the cell culture show low toxicity of the dendrons in concentrations of up to 50 μg mL⁻¹.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, University of Copenhagen
Authors: Meyhoff, U. (Ekstern), Riber, U. (Intern), Boas, U. (Intern)
Pages: 1161-1171
Creation of Functional Viruses from Non-Functional cDNA Clones Obtained from an RNA Virus Population by the Use of Ancestral Reconstruction

RNA viruses have the highest known mutation rates. Consequently it is likely that a high proportion of individual RNA virus genomes, isolated from an infected host, will contain lethal mutations and be non-functional. This is problematic if the aim is to clone and investigate high-fitnes, functional cDNAs and may also pose problems for sequence-based analysis of viral evolution. To address these challenges we have performed a study of the evolution of classical swine fever virus (CSFV) using deep sequencing and analysis of 84 full-length cDNA clones, each representing individual genomes from a moderately virulent isolate. In addition to here being used as a model for RNA viruses generally, CSFV has high socioeconomic importance and remains a threat to animal welfare and pig production. We find that the majority of the investigated genomes are non-functional and only 12% produced infectious RNA transcripts. Full length sequencing of cDNA clones and deep sequencing of the parental population identified substitutions important for the observed phenotypes. The investigated cDNA clones were furthermore used as the basis for inferring the sequence of functional viruses. Since each unique clone must necessarily be the descendant of a functional ancestor, we hypothesized that it should be possible to produce functional clones by reconstructing ancestral sequences. To test this we used phylogenetic methods to infer two ancestral sequences, which were then reconstructed as cDNA clones. Viruses rescued from the reconstructed cDNAs were tested in cell culture and pigs. Both reconstructed ancestral genomes proved functional, and displayed distinct phenotypes in vitro and in vivo. We suggest that reconstruction of ancestral viruses is a useful tool for experimental and computational investigations of virulence and viral evolution. Importantly, ancestral reconstruction can be done even on the basis of a set of sequences that all correspond to non-functional variants.
Cryptosporidium and Giardia in Danish organic pig farms: seasonal and age-related variation in prevalence, infection intensity and species/genotypes

Although pigs are commonly infected with Cryptosporidium spp. and Giardia duodenalis, including potentially zoonotic species or genotypes, little is known about age-related infection levels, seasonal differences and genetic variation in naturally infected pigs raised in organic management systems. Therefore, the current study was conducted to assess seasonal and age-related variations in prevalence and infection intensity of Cryptosporidium and Giardia, evaluate zoonotic potential and uncover correlations between species/genotypes, infection intensity and faecal consistency. Shedding of oocysts and cysts ((oo-) cysts) was monitored at quarterly intervals (September 2011 to June 2012) in piglets (n=152), starter pigs (n=234), fatteners (n=230) and sows (n=240) from three organic farms in Denmark. (Oo-) cysts were quantified by immunofluorescence microscopy; and 56/75 subsamples from Cryptosporidium infected pigs were successfully analysed by PCR amplification and partial sequencing of the small subunit (SSU) 18S rRNA and
hsp70 genes, while 13/67 Giardia subsamples were successfully analysed by amplification and partial sequencing of the 18S rRNA and the gdh genes. Altogether, Cryptosporidium or Giardia infections were observed in 40.9% (350/856) and 14.0% (120/856) of the pigs, respectively, including 8.2% (70/856) infected with both parasites. Prevalence, intensity of infections and presence of Cryptosporidium species varied significantly between age-groups; 53.3% piglets, 72.2% starter pigs, 40.4% fatteners and 2.9% sows were infected with Cryptosporidium, whereas 2.0% piglets, 27.4% starter pigs, 17.8% fatteners and 5.0% sows were infected with Giardia. The overall prevalence was stable throughout the year, except for dual-infections that were more prevalent in September and December (p<0.05). The infection intensity was age-related for both parasites, and dual-infected pigs tended to excrete lower levels of oocysts compared to pigs harbouring only Cryptosporidium. Likewise, pigs infected with C. scrofarum excreted fewer oocysts (mean CPG: 54,848±94,508CI: 9085–118,781) compared to pigs infected with C. suis (mean OPG: 351,035±351,035CI: 67,953–634,117). No correlation between faecal consistency and (oo-) cyst excretion levels was observed. Of the successfully genotyped isolates, 38/56 (67.9%) were C. scrofarum and 18/56 (32.1%) were C. suis, while the livestock specific G. duodenalis Assemblage E was detected in 11/13 (84.6%) isolates and the potentially zoonotic Assemblage A was identified in 2/13 (15.4%) isolates. Piglets exclusively hosted C. suis, with one exception, while starter pigs and fatteners predominantly hosted C. scrofarum. As organic pigs are partly reared outdoors, environmental contamination with Cryptosporidium and Giardia is inevitable. Nevertheless, the present data indicate that the potential public health risk associated with both of these parasites in Danish organic pig production seems to be negligible.
Danish holsteins favor bull offspring: Biased Milk Production as a Function of Fetal Sex, and Calving Difficulty

In a previous study from 2014 it was found that US Holstein cows that gave birth to heifer calves produced more milk than cows having bull calves. We wanted to assess whether this is also true for Danish cattle. Data from 578 Danish Holstein herds were analysed with a mixed effect model and contrary to the findings in the US, we found that cows produced higher volumes of milk if they had a bull calf compared to a heifer calf. We found a significantly higher milk production of 0.28% in the first lactation period for cows giving birth to a bull calf, compared to a heifer calf. This difference was even higher when cows gave birth to another bull calf, so having two bull calves resulted in a difference of 0.52% in milk production compared to any other combination of sex of the offspring. Furthermore, we found that farmer assisted calvings were associated with a higher milk yield. Cows with no farmer assistance or with veterinary assistance during the most recent calving produced less milk. There were also indications that dams would favor a bull fetus by decreasing milk production during the second pregnancy if the calf born in the first parity was a heifer. We hypothesize that size of calves is a confounding factor for milk production. However, calving weight was not available in the present data set to test this hypothesis.

General information
State: Published
Organisations: Department of Applied Mathematics and Computer Science, National Veterinary Institute, Section for Epidemiology, Dynamical Systems, University of Copenhagen
Authors: Græsbøll, K. (Intern), Kirkeby, C. (Intern), Nielsen, S. S. (Ekstern), Christiansen, L. E. (Intern)
Number of pages: 12
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: PLoS One
Volume: 10
Issue number: 4
Article number: e0124051
Danish sea reared rainbow trout suffer from furunculosis despite vaccination - How can applied research help to solve the problem?

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Aarhus University, Danish Aquaculture Organisation, University of Copenhagen, Vaxxinova
Authors: Skall, H. F. (Ekstern), Lorenzen, E. (Ekstern), Kjær, T. E. (Ekstern), Henriksen, N. (Ekstern), Dalsgaard, I. (Intern), Madsen, S. B. (Ekstern), Buchmann, K. (Ekstern), Krossøy, B. (Ekstern), Lorenzen, N. (Ekstern)
Danske PPV-stammer har ændret sig genetisk

I 2015 er der set en markant stigning i antallet af positive fund af porcin parvovirus (PPV) i indsendelser til undersøgelse af svineaborter (Tabel 1).

PPV forekommer udbredt i svinebesætninger og kan forårsage reproduktionsproblemer. Disse kan imidlertid kontrolleres med vacciner, der dog ikke forhinder infektion og virusudskillelse fra soerne, men beskytter mod reproduktionsproblemerne.

PPV-viruspartiklerne er meget modstandsdygtige overfor nedbrydelse i omgivelserne, så da virus formodentlig findes i de fleste besatninger, er det vigtigt med effektiv vaccination af alle avlsdyr for at beskytte mod PPV-relaterede reproduktionsproblemer.

Tidligere studier har vist, at europæiske PPV-virus, inklusive de danske, kan inddeles i to grupper (genotyper) baseret på forskelle i deres gensekvenser. For at undersøge de danske PPV-virus fra 2015 nærmere, har vi bestemt DNAsekvensen af hele virusgenomet fra fire af de positive indsendelser fra 2015.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Hjulsager, C. K. (Intern), Krog, J. S. (Intern), Larsen, L. E. (Intern)
Pages: 47-47
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Dansk Veterinaertidsskrift
Issue number: 15
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
ISI indexed (2012): ISI indexed no
BFI (2011): BFI-level 1
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
BFI (2009): BFI-level 1
BFI (2008): BFI-level 1
Original language: Danish
Electronic versions:
16021_2_.pdf
Source: PublicationPreSubmission
Source-ID: 118964661
Publication: Research - peer-review › Journal article – Annual report year: 2015
Design and Validation of Conditional Ligands for HLA-B*08:01, HLA-B*15:01, HLA-B*35:01, and HLA-B*44:05

We designed conditional ligands restricted to HLA-B*08:01, 2B*35:01, and 2B*44:05 and proved the use of a conditional ligand previously designed for HLA-B*15:02 together with HLA-B*15:01. Furthermore, we compared the detection capabilities of specific HLA-B*15:01-restricted T cells using the HLA-B*15:01 and HLA-B*15:02 major histocompatibility complex (MHC) multimers and found remarkable differences in the staining patterns detected by flow cytometry. These new conditional ligands greatly add to the application of MHC-based technologies in the analyses of T-cell recognition as they represent frequently expressed HLA-B molecules. This expansion of conditional ligands is important to allow T-cell detection over a wide range of HLA restrictions, and provide comprehensive understanding of the T-cell recognition in a given context.
Det danske beredskab for havpattedyr

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Fisheries and Maritime Museum
Authors: Alstrup, A. K. O. (Ekstern), Hansen, M. S. (Intern), Jensen, L. F. (Ekstern)
Pages: 12-14
Publication date: 2015
Main Research Area: Technical/natural sciences

Detection of aeromonas salmonicida in fish tissue by real-time PCR

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology
Authors: Bartkova, S. (Intern), Kokotovic, B. (Intern), Dalsgaard, I. (Intern)
Pages: 359-359
Publication date: 2015
Main Research Area: Technical/natural sciences

Host publication information
Title of host publication: 17th International Conference on Diseases of Fish And Shellfish : Abstract book
Place of publication: Las Palmas
Publisher: European Association of Fish Pathologists
Article number: P-135
Main Research Area: Technical/natural sciences
Conference: 17th International Conference on Diseases of Fish and Shellfish, Las Palmas, Spain, 07/09/2015 - 07/09/2015
Electronic versions:
Detection of Aeromonas salmonicida in fish tissue by real-time PCR

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology
Authors: Bartkova, S. (Intern), Kokotovic, B. (Intern), Dalsgaard, I. (Intern)
Number of pages: 1
Event: Poster session presented at 17th International Conference on Diseases of Fish and Shellfish, Las Palmas, Spain.
Main Research Area: Technical/natural sciences
Electronic versions:
Poster.pdf
Source: PublicationPreSubmission
Source-ID: 116616319
Publication: Research › Poster – Annual report year: 2015

Detection of African Swine Fever Virus DNA in Blood Samples Stored on FTA Cards from Asymptomatic Pigs in Mbeya Region, Tanzania

The aim of the study was to assess whether blood samples collected onto FTA® cards could be used in combination with real-time PCR for the detection of African swine fever virus (ASFV) DNA in samples from resource-poor settings under the assumption that asymptomatically (sub-clinically) infected pigs may be present. Blood samples were collected from clinically healthy pigs from Mbeya Region, Tanzania. The blood samples were stored on FTA® cards and analysed by real-time PCR assays in duplicate; three pigs had high levels of viral DNA (Ct values of 27-29), and three pigs had a low level of viral DNA (Ct 36-45). Four pigs were positive in one of the duplicate samples only, but clear products of the expected size were obtained when the reactions were analysed by gel electrophoresis. For comparison, blood samples from pigs experimentally infected with either a pathogenic (OURT T88/1) or a non-pathogenic (OURT T88/3) isolate of ASFV were collected, stored on FTA® cards and analysed in the same way. The blood from pigs infected with the OURT T88/1 isolate showed high levels of viral DNA (Ct 22-33), whereas infection with non-pathogenic OURT T88/3 isolate resulted in only low levels of viral DNA (Ct 39) in samples collected at 10-14 days after inoculation.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Sokoine University of Agriculture, University of Copenhagen
Authors: Braae, U. C. (Ekstern), Johansen, M. V. (Ekstern), Ngowi, H. A. (Ekstern), Rasmussen, T. B. (Intern), Nielsen, J. (Intern), Uttenthal, Å. (Intern)
Number of pages: 4
Pages: 87-90
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Transboundary and Emerging Diseases
Volume: 62
Issue number: 1
ISSN (Print): 1865-1674
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.87 SJR 1.147 SNIP 1.488
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.16 SJR 1.046 SNIP 0.998
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.305 SNIP 1.249 CiteScore 2.29
Web of Science (2015): Indexed yes
Detection of American lineage low pathogenic avian influenza viruses in Uria lomvia in Greenland

In early March 2014, unusual high numbers of wild bird Thick-billed Murre (Uria lomvia), order Charadriiformes, were found dead at the coast of South Greenland. To investigate the cause of death, 45 birds were submitted for diagnosis at the National Veterinary Institute, Technical University of Denmark. Five birds were randomly selected for diagnostic investigation and samples were taken from the cadavers (pooled oropharyngeal swabs, cloacal swabs, lung/trachea/heart tissues and liver/spleen/kidney tissues, and separate preparation of stomach from a single bird). Avian influenza virus (AIV) with subtype H11N2 was detected in all pools by RT-PCR. Virus was isolated from embryonated chicken-eggs by allantoic inoculation from all pools except the liver/spleen/kidney pool. Full-genome sequencing of AIV isolate revealed American lineage origin of genes. The remaining 40 birds were subsequently screened for AIV in oropharyngeal and cloacal swab specimens from each bird by RT-PCR. American lineage H11N2 AIV was detected in both oropharyngeal and cloacal swabs from one bird, and American lineage low pathogenic AIV with subtype H5N1 was detected in the cloacal swab from another bird. The sparse and mixed subtype occurrence of AIV together with an emaciated appearance of the birds, suggests that the Murre die-off may not have been caused by infection with AIV, but that the birds could have died from starvation. However, here we present the first characterization of AIVs from Greenland and our results supports the idea that wild birds in Greenland could be involved in the movement of AIV between North America and Europe.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Detection of antibodies specific to koi herpesvirus (KHV) by serum neutralization test

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, ANSES - French Agency for Food, Environmental and Occupational Health & Safety, Friedrich Loeffler Institute, Instituto Zooprofilattico Sperimentale delle Venezie, National Veterinary Research Institute, Wageningen University & Research
Authors: Cabon, J. (Ekstern), Louboutin, L. (Ekstern), Castric, J. (Ekstern), Bergmann, S. M. (Ekstern), Bovo, G. (Ekstern), Matras, M. (Ekstern), Haenen, O. (Ekstern), Olesen, N. J. (Intern), Morin, T. (Ekstern)
Pages: 115-115
Publication date: 2015

Host publication information
Title of host publication: 17th International Conference on Diseases of Fish And Shellfish : Abstract book
Place of publication: Las Palmas
Publisher: European Association of Fish Pathologists
Article number: O-107
Main Research Area: Technical/natural sciences
Conference: 17th International Conference on Diseases of Fish and Shellfish, Las Palmas, Spain, 07/09/2015 - 07/09/2015
Electronic versions:
Book_of_abstracts_17th_International_conference_on_Diseases_of_Fish_and_Shellfish.pdf
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2015

Detection of PRRSV in air sampled inside and outside PRRSV-positive herds in Denmark

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Technical University of Denmark, Svinevet Pig Practise, Boehringer Ingelheim Danmark A/S
Authors: Priebe, A. (Ekstern), Kvisgaard, L. K. (Intern), Rathkjen, P. H. (Ekstern), Hjulsager, C. K. (Intern), Havn, K. (Ekstern), Larsen, L. E. (Intern)
Number of pages: 1
Publication date: 2015
Event: Abstract from International Porcine Reproductive And Respiratory Syndrome Congress, Ghent, Belgium.
Main Research Area: Technical/natural sciences
Electronic versions:
abstract1_pribe_final.pdf
Source: PublicationPreSubmission
Source-ID: 119056081
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2015

Development and Characterization of Probe-Based Real Time Quantitative RT-PCR Assays for Detection and Serotyping of Foot-And-Mouth Disease Viruses Circulating in West Eurasia.
Rapid and accurate diagnosis of foot-and-mouth disease (FMD) and virus serotyping are of paramount importance for control of this disease in endemic areas where vaccination is practiced. Ideally this virus characterization should be achieved without the need for virus amplification in cell culture. Due to the heterogeneity of FMD viruses (FMDVs) in different parts of the world, region specific diagnostic tests are required. In this study, hydrolysableprobe-based real time reverse transcription quantitative polymerase chain reaction (RTqPCR) assays were developed for specific detection and serotyping of the FMDVs currently circulating in West Eurasia. These assays were evaluated, in parallel with pan-FMDV
diagnostic assays and earlier serotype-specific assays, using field samples originating from Pakistan and Afghanistan containing FMD viruses belonging to different sublineages of OPanAsia A-Iran05 and Asia-1 (Group-II and Group-VII (Sindh-08)). In addition, field samples from Iran and Bulgaria, containing FMDVs belonging to the O-PanAsia sublineages were also tested. Each of the three primer/probe sets was designed to be specific for just one of the serotypes O, A and Asia-1 of FMDV and detected the RNA from the target viruses with cycle threshold (Ct) values comparable with those obtained with the serotype independent pan-FMDV diagnostic assays. No cross-reactivity was observed in the assays between the heterotypic viruses circulating in the region. The assays reported here have higher diagnostic sensitivity (100% each for serotypes O and Asia-1, and 92% [95% CI = 81.4–100%] for serotype A positive samples) and specificity (100% each for serotypes O, A and Asia-1 positive samples) for the viruses currently circulating in West Eurasia compared to the serotyping assays reported earlier. Comparisons of the sequences of the primers and probes used in these assays and the corresponding regions of the circulating viruses provided explanations for the poor recognition of some of the viruses by the earlier assays. These new assays should help in the early detection and typing of serotype O, A and Asia-1 FMDVs circulating in West Eurasia to enable improved disease control.

**General information**

State: Published
Organisations: National Veterinary Institute, Section for Virology, University of Malakand
Authors: Jamal, S. M. (Ekstern), Belsham, G. (Intern)
Publication date: 2015
Main Research Area: Technical/natural sciences

**Publication information**

Journal: PLoS One
Volume: 10
Issue number: 8
Article number: e0135559
ISSN (Print): 1932-6203
Ratings:

- BFI (2018): BFI-level 1
- Web of Science (2018): Indexed yes
- BFI (2017): BFI-level 1
- Scopus rating (2017): CiteScore 3.01 SJR 1.164 SNIP 1.111
- Web of Science (2017): Indexed yes
- BFI (2016): BFI-level 1
- Scopus rating (2016): CiteScore 3.11 SJR 1.236 SNIP 1.101
- Web of Science (2016): Indexed yes
- BFI (2015): BFI-level 1
- Scopus rating (2015): SJR 1.427 SNIP 1.136 CiteScore 3.32
- Web of Science (2015): Indexed yes
- BFI (2014): BFI-level 1
- Scopus rating (2014): SJR 1.559 SNIP 1.148 CiteScore 3.54
- Web of Science (2014): Indexed yes
- BFI (2013): BFI-level 1
- Scopus rating (2013): SJR 1.772 SNIP 1.153 CiteScore 3.94
- ISI indexed (2013): ISI indexed yes
- Web of Science (2013): Indexed yes
- BFI (2012): BFI-level 1
- Scopus rating (2012): SJR 1.982 SNIP 1.156 CiteScore 4.15
- ISI indexed (2012): ISI indexed yes
- Web of Science (2012): Indexed yes
- BFI (2011): BFI-level 1
- Scopus rating (2011): SJR 2.425 SNIP 1.233 CiteScore 4.58
- ISI indexed (2011): ISI indexed no
- Web of Science (2011): Indexed yes
- BFI (2010): BFI-level 1
- Scopus rating (2010): SJR 2.705 SNIP 1.178
- Web of Science (2010): Indexed yes
- BFI (2009): BFI-level 1
- Scopus rating (2009): SJR 2.614 SNIP 1.046
Development and comparison of a generic multiple-locus variable-number tandem repeat analysis with PFGE for typing of Salmonella enterica subsp. enterica

Aims
Salmonella enterica subsp. enterica causes salmonellosis in humans and animals. Serovar specific multiple-locus variable-number tandem repeat analysis (MLVA) is widely used for Salmonella surveillance; however, isolates have to be serotyped prior to MLVA typing and only the most common serovars can be typed. We developed a MLVA scheme for high discriminatory typing of Salmonella.

Methods and Results
Sixty-six unique VNTRs were investigated and the polymorphisms of seven promising VNTRs were evaluated with a panel of 163 diverse isolates of 14 serotypes of significance for human health. Five VNTRs were selected for MLVA analysis. The discriminatory power was evaluated within serovars by 163 isolates and MLVA yielded 79 genotypes (DI of 0.9790) and PFGE revealed 87 genotypes (DI of 0.9989). MLVA divided each serotype into 2-8 different profiles and identified six pairs of outbreak-related strains.

Conclusions
The technique showed a high discriminatory power within most serotypes comparable with or better than that of PFGE. This MLVA assay makes it possible to use a single typing method for Salmonella surveillance and outbreak investigations. This allows inexpensive and fast surveillance for laboratories without resources for both serotyping and molecular typing, e.g. PFGE or sequence-based methods, and thereby improve the effectiveness of epidemiological investigations of Salmonella infections globally.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, State Serum Institute
Authors: Kjeldsen, M. K. (Intern), Torpdahl, M. (Ekstern), Pedersen, K. (Intern), Nielsen, E. M. (Ekstern)
Pages: 1707-1717
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Applied Microbiology
Volume: 119
Issue number: 6
ISSN (Print): 1364-5072
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.41
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.41
Development of a real-time RT-PCR assay that detects a broad range of Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) Type 1 subtypes

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Parco Technologico Padano
Authors: Kvisgaard, L. K. (Intern), Hjulsager, C. K. (Intern), Botti, S. (Ekstern), Larsen, L. E. (Intern)
Number of pages: 1
Publication date: 2015
Event: Abstract from International Porcine Reproductive And Respiratory Syndrome Congress, Ghent, Belgium.
Main Research Area: Technical/natural sciences
Electronic versions:
Development_of_a_real_time_RT_PCR_assay_final.pdf
Source: PublicationPreSubmission
Source-ID: 119055993
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2015
Different clinical, virological, serological and tissue tropism outcomes of two new and one old Belgian type 1 subtype 1 porcine reproductive and respiratory virus (PRRSV) isolates

In this study, the pathogenic behavior of PRRSV 13V091 and 13V117, isolated in 2013 from two different Belgian farms with enzootic respiratory problems shortly after weaning in the nursery, were compared with the Belgian strain 07V063 isolated in 2007. Full-length genome sequencing was performed to identify their origin. Twelve weeks-old pigs were inoculated intranasally (IN) with 13V091, 13V117 or 07V063 (9 pigs/group). At 10 days post inoculation (dpi), 4 animals from each group were euthanized and tissues were collected for pathology, virological and serological analysis. 13V091 infection resulted in the highest respiratory disease scores and longest period of fever. Gross lung lesions were more pronounced for 13V091 (13%), than for 13V117 (7%) and 07V063 (11%). The nasal shedding and viremia was also most extensive with 13V091. The 13V091 group showed the highest virus replication in conchae, tonsils and retropharyngeal lymph nodes. 13V117 infection resulted in the lowest virus replication in lymphoid tissues. 13V091 showed higher numbers of sialoadhesin-infected cells/mm(2) in conchae, tonsils and spleen than 13V117 and 07V063. Neutralizing antibody response with 07V063 was stronger than with 13V091 and 13V117. It can be concluded that (i) 13V091 is a highly pathogenic type 1 subtype 1 PRRSV strain that replicates better than 07V063 and 13V117 and has a strong tropism for sialoadhesin-cells and (ii) despite the close genetic relationship between 13V117 and 07V063, 13V117 has an increased nasal replication and shedding, but a decreased replication in lymphoid tissues compared to 07V063.
Differential induction of total IgE by two Salmonella enterica serotypes

The main goal of this study was to establish how the inflammation caused by infection with two different Salmonella enterica serotypes, S. Typhimurium and S. Enteritidis, may lead to the predisposition to allergy as measured by total IgE level in the blood. Infection by S. Typhimurium did not affect the systemic IgE concentration while in S. Enteritidis-infected patients there was a significant 3.5-fold increase. This effect was especially profound in patients >4 years old, with up to the 8-fold increase above the norm. The degree of dysbiosis in these two infections measured with the comparative counts of cultivated bacteria showed an inverse relationship with the IgE concentration. Earlier we reported the elevated level of IL-17 in patients infected by S. Enteritidis. In the current study a significant correlation was found between the concentrations of IL-17 and IgE suggesting a possible role played by this cytokine in triggering the production of IgE in response to S. Enteritidis infection.
Disease associated population effects of commercial fish and shellfish species (ToR g)

Pathogens are increasingly reported from populations of aquatic animals. Variations in the frequency and abundance of pathogens depend on spatial or temporal factors as well as those related to host effects such as age or condition. Similarly, the development of a disease is a function of the combined effects of the pathogen, host and environmental factors. Diseases may be one of several biological and non-biological factors regulating the abundance and composition of stocks or populations of aquatic organisms. Here we review evidence for population effects associated with diseases in wild marine gastropods, bivalves, crustaceans, and fishes. The report provides information on the types of diseases, together with data on diagnostic criteria, causative agents, geographical ranges and effects at the individual and population level. A dis-cussion of the significance of the findings and references to key publications are provided. The overview shows that the effects of diseases may occur at various life stages of affected hosts. The extent to which these effects lead to measurable population changes (e.g., in growth, reproduction, mortality, recruitment, population demography, geographical distribution) is best evidenced in those populations already subject to long-term population level monitoring, such as in commercial species. However, quantitative evidence of population effects is so far scarce. From the information available, it may be concluded that some diseases play a much larger role in population performance and dynamics in marine fish and shellfish than previously recognised. Therefore, methods for incorporating disease data into population/stock assessment models should be further explored. In the first instance, this will be relevant for commercial species, for which most information is available. However, the development of realistic mathematical models, taking into account population effects of diseases, are becoming also more relevant for non-commercial species, e.g., as part of coastal zone management or assessments of general marine ecology in the context of a more holistic ecosystem approach to marine management.
Disease management mitigates risk of pathogen transmission from farmed salmon

Open marine net pens facilitate virus and sea lice transfer, occasionally leading to infections and outbreaks of disease in farmed salmon. A review of 3 salmon pathogens (infectious salmon anaemia virus [ISAV], salmon alphavirus [SAV] and the salmon louse Lepeophtheirus salmonis) shows that increased risk of exposure to neighbouring farms is inversely related to distance from and directly related to biomass at the source of infection. Epidemiological techniques integrating data from oceanography, diagnostics and pathogen shedding rates and viability contribute to improved understanding of pathogen transmission pathways among farms and permit the designation of areas of risk associated with sources of infection. Occupation of an area of risk may increase the likelihood of exposure, infection and disease among susceptible fish. Disease mitigation in mariculture occurs at 2 scales: area-based (coordinated stocking, harvesting and falling) and farm-based (vaccination, early pathogen detection, veterinary prescribed treatments and depopulation or early harvest in the event of viral disease). Collectively, implementation of mitigation measures results in virus disease outbreaks of shorter duration with lower mortality and therefore reduces the likelihood of pathogen transmission. In contrast, the mitigation of sea lice transmission is less likely to be effective in some areas due to the loss of parasite sensitivity to therapeutants and to dissemination of larval lice when parasites occur below management thresholds. For wild populations, risk of pathogen spillback is estimated from farm-based epidemiological data; however, validation, particularly for ISAV and SAV, is required using direct surveillance.
Dødelig sygdom på fremmarch: Afrikansk svinepest

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology
Authors: Chriél, M. (Intern), Boklund, A. (Intern)
Pages: 130-131
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Jaeger
Issue number: 12
ISSN (Print): 0906-415X
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
Dynamic expression of leukocyte innate immune genes in whole blood from horses with lipopolysaccharide-induced acute systemic inflammation

Background: In horses, insights into the innate immune processes in acute systemic inflammation are limited even though these processes may be highly important for future diagnostic and therapeutic advances in high-mortality disease conditions as the systemic inflammatory response syndrome (SIRS) and sepsis. Therefore, the aim of this study was to investigate the expression of 31 selected blood leukocyte immune genes in an equine model of acute systemic inflammation to identify significantly regulated genes and to describe their expression dynamics during a 24-h experimental period. Systemic inflammation was induced in 6 adult horses by the intravenous injection of 1 μg lipopolysaccharide (LPS) per kg bw. Sixteen blood samples were collected for each horse at predetermined intervals and analyzed by reverse transcription quantitative real-time PCR. Post-induction expression levels for each gene were compared with baseline levels. Results: Systemic inflammation was confirmed by the presence of clinical and hematological changes which were consistent with SIRS. The clinical response to LPS was transient and brief as all horses except one showed unaltered general demeanor after 24 h. Twenty-two leukocyte genes were significantly regulated at at least one time point during the experimental period. By close inspection of the temporal responses the dynamic changes in mRNA abundance revealed a very rapid onset of both pro- and anti-inflammatory mediators and a substantial variation in both expression magnitudes and duration of changes between genes. A majority of the 22 significantly regulated genes peaked within the first 8 h after induction, and an on-going, albeit tightly controlled, regulation was seen after 24 h despite approximate clinical recovery. Conclusions: This first broad study of gene expressions in blood leukocytes during equine acute LPS-induced systemic inflammation thoroughly characterized a highly regulated and dynamic innate immune response. These results provide new insights into the molecular mechanisms of equine systemic inflammation.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, University of Copenhagen, Swedish University of Agricultural Sciences
Authors: Vinther, A. M. L. (Ekstern), Skovgaard, K. (Intern), Heegaard, P. M. H. (Intern), Andersen, P. H. (Ekstern)
Number of pages: 11
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: BMC Veterinary Research
Volume: 11
ISSN (Print): 1746-6148
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.108 SJR 0.934 CiteScore 2.16
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.83 SJR 0.87 SNIP 1.011
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.981 SNIP 1.009 CiteScore 1.86
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.943 SNIP 1.018 CiteScore 1.81
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Early gradual feeding with bovine colostrum improves gut function and NEC resistance relative to infant formula in preterm pigs

It is unclear when and how to start enteral feeding for preterm infants when mother’s milk is not available. We hypothesized that early and slow advancement with either formula or bovine colostrum stimulates gut maturation and prevents necrotizing enterocolitis (NEC) in preterm pigs, used as models for preterm infants. Pigs were given either total parenteral nutrition (TPN, n = 14) or slowly advancing volumes (16–64 ml·kg⁻¹·day⁻¹) of preterm infant formula (IF, n = 15) or bovine colostrum (BC, n = 13), both given as adjunct to parenteral nutrition. On day 5, both enteral diets increased intestinal mass (27 ± 1 vs. 22 ± 1 g/kg) and glucagon-like peptide 2 release, relative to TPN (P < 0.05). The incidence of mild NEC lesions was higher in IF than BC and TPN pigs (60 vs. 0 and 15%, respectively, P <0.05). Only the IF pigs showed reduced gastric emptying and gastric inhibitory polypeptide release, and increased tissue proinflammatory cytokine levels (IL-1_ and IL-8, P <0.05) and expression of immunerelated genes (AOAH, LBP, CXCL10, TLR2), relative to TPN. The IF pigs also showed reduced intestinal villus-to-crypt ratio, lactose digestion, and some plasma amino acids (Arg, Cit, Gin, Tyr, Val), and higher intestinal permeability, compared with BC pigs (all P <0.05). Colonic microbiota analyses showed limited differences among groups. Early feeding with formula induces intestinal dysfunction whereas bovine colostrum supports gut maturation when mother’s milk is absent during the first week after preterm birth. A dietdependent feeding guideline may be required for newborn preterm infants.
Echinococcus multilocularis genotyping by the microsatellite EMSB, state of the art

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of France-Comté, ANSES - French Agency for Food, Environmental and Occupational Health & Safety, National Veterinary Institute Sweden
Authors: Knapp, J. (Ekstern), Umhang, G. (Ekstern), Wahlström, H. (Ekstern), Enemark, H. (Intern), Saarma, U. (Ekstern) , Gottstein, B. (Ekstern), Millon, L. (Ekstern)
Number of pages: 1
Publication date: 2015
Event: Abstract from 6th Conference of the Scandinavian-Baltic Society for Parasitology (CSBSP6), Uppsala, Sweden.
Main Research Area: Technical/natural sciences
Electronic versions:
15.04_SBSP_Em_genotyping_state_of_the_art.pdf
Source: PublicationPreSubmission
Source-ID: 108239754
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2015

Effect of hydrogen peroxide and/or Flavobacterium psychrophilum on the gills of rainbow trout, Oncorhynchus mykiss (Walbaum)
The immune response and morphological changes in the gills of rainbow trout fry after immersion in hydrogen peroxide (H2O2), Flavobacterium psychrophilum or combined exposure were examined. The gills were sampled 4, 48, 125 and 192 h after exposure, and the regulation of expression of the following genes was investigated using qPCR: IgT, IgM, CD8, CD4, MHC I, MHC II, IL-4/13A, TcR-δ, IL-10, IL-1β, IL-17, SAA and FoxP3. Bacteria were not observed in haematoxylin-and-eosin-stained gill tissue, but the presence of F. psychrophilum 16S rRNA was detected using qPCR. The 16S rRNA levels were correlated with gene expression. Although pretreatment with H2O2 before immersion in F. psychrophilum did not significantly alter the amount of bacteria found in the gill, the immune response was influenced: exposure to F. psychrophilum resulted in a negative correlation with expression of IL-17c1, MHC I and MHC II, while pretreatment with H2O2 resulted in a positive correlation with IL-4/13A and IgM. Exposure to either H2O2 or F. psychrophilum influenced the regulation of gene expression and damaged tissue. Exposure to both combined altered the immune response to infection and postponed healing of gill tissue.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Copenhagen
Authors: Henriksen, M. M. M. (Intern), Kania, P. W. (Ekstern), Buchmann, K. (Ekstern), Dalsgaard, I. (Intern)
Number of pages: 12
Pages: 259-270
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Fish Diseases
Volume: 38
Issue number: 3
ISSN (Print): 0140-7775
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.82
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Effect of variation in oxytetracycline treatment of Lawsonia intracellularis diarrhea in nursery pigs on treatment-efficacy and resistance development

A Danish research project, MINIRESIST, investigated the consequences of varying doses and treatment strategies for oxytetracycline treatment of Lawsonia intracellularis diarrhea in nursery pigs. Batches of nursery pigs in five herds were randomly allocated to one of five treatment protocols (batch treatment orally with high, normal and low doses; penwise treatment with normal dose and injection treatment with normal dose). Outcomes, in terms of reduction of L. intracellularis determined by qPCR, growth rate and fecal dry matter content (determined on 30 pigs per batch in 61 batches), and levels of tetracyclineresistant coliforms, and quantification of resistance genes in intestinal content (determined on 15 pigs per batch in 80 batches), were determined and analyzed statistically. These studies were supplemented with in silico simulation of phenotypic resistance development in the intestine based on in vitro determined growth characteristics of porcine commensal E. coli in the presence of tetracycline. Low-dose batch-treatment did not differ significantly from normal and high dose treatment in terms of reduction of L. intracellularis, and phenotypic resistance levels under field conditions also did not differ statistically depending on dosing levels. qPCR results were shown to add to phenotypic resistance-determination with information on selected genes. Injection treatment resulted in the lowest number of resistant bacteria, but also in the lowest overall cure rate, probably because treatment was based on fecal scores, which have low sensitivity for diarrhea. Simulation studies suggested that resistance development was mostly dependent on the duration
of the treatment and the total amount of oxytetracycline used per pig. Ongoing field testing has been initiated to confirm
this conclusion, since no field experimentation has yet been performed with variation of duration of treatment. In
conclusion, batch treatment with the lowest dose was recommended from both a disease and a resistance point of view.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Department of Applied
Mathematics and Computer Science, University of Copenhagen, National Veterinary Institute, Technical University of
Denmark
Authors: Larsen, I. (Ekstern), Mellerup, A. (Intern), Zachariasen, C. (Ekstern), Niels, S. S. (Ekstern), Folkesson, S. A.
(Intern), Angen, Ø. (Ekstern), Christiansen, L. (Ekstern), Grøsbøll, K. (Intern), Damborg, P. (Ekstern), Nielsen, J. P.
(Ekstern), Olsen, J. E. (Ekstern)
Pages: 135-135
Publication date: 2015

Host publication information
Title of host publication: Safepork 2015 Proceedings Book: Epidemiology and control of hazards in pork production chain : SAFEPORK, One health approach under a concept of farm to fork
Main Research Area: Technical/natural sciences
Electronic versions:
Effect_of_variation_in_oxytetracycline_treatment_of_Lawsonia_intr.pdf
Links:
http://lib.dr.iastate.edu/safepork/2015/allpapers/18/
Source: PublicationPreSubmission
Source-ID: 124155738
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2016

Effects of adjuvant Montanide™ ISA 763 A VG in rainbow trout injection vaccinated against Yersinia ruckeri
Enteric redmouth disease (ERM) caused by the fish pathogen Yersinia ruckeri is a major threat to freshwater production of
rainbow trout (Oncorhynchus mykiss) throughout all life stages. Injection vaccination of rainbow trout against Y. ruckeri
infection has been shown to confer better protection compared to the traditionally applied immersion vaccination. It may be
hypothesized, based on experience from other vaccines, that adjuvants may increase the protective level of ERM injection
vaccines even more. Controlled comparative vaccination studies have been performed to investigate effects of the oil
adjuvant Montanide™ ISA 763 A VG (Seppic) when added to an experimental Y. ruckeri bacterin (containing both biotype
1 and 2 of serotype O1). A total of 1000 fish with mean weight 19 g was divided into five different groups (in duplicated
tanks 2 x 100 fish per group): 1) non-vaccinated control fish (NonVac), 2) fish injected with a commercial vaccine
(AquaVac® Relera™) (ComVac), 3) fish injected with an experimental vaccine (ExpVac), 4) fish injected with an
experimental vaccine + adjuvant (ExpVacAdj) and 5) fish injected with adjuvant alone (Adj). Injection of the experimental
vaccine (both adjuvanted and non-adjuvanted) induced a significantly higher antibody (IgM) level, increased occurrence of
IgM(+) cells in spleen tissue and significant up-regulation of several immune genes. Additional experiments using a higher
challenge dosage suggested an immune enhancing effect of the adjuvant as the challenge produced 100% mortality in the
NonVac group, 60% mortality in both of ComVac and Adj groups and only 13 and 2.5% mortalities in the ExpVac and the
ExpVacAdj groups, respectively.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of
Copenhagen
Authors: Jaafar, R. M. (Ekstern), Chettri, J. K. (Intern), Dalsgaard, I. (Intern), Al-Jubury, A. (Ekstern), Kania, P. W.
(Ekstern), Skov, J. (Ekstern), Buchmann, K. (Ekstern)
Number of pages: 10
Pages: 797-806
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Fish and Shellfish Immunology
Volume: 47
Issue number: 2
ISSN (Print): 1050-4648
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
Effects of Roux-en-Y gastric bypass on fasting and postprandial inflammation-related parameters in obese subjects with normal glucose tolerance and in obese subjects with type 2 diabetes

Background: Obesity is characterized by low grade inflammation and an altered secretion of inflammatory cytokines from the adipose tissue. Weight loss has shown to reduce inflammation; however, changes in cytokine profiles during massive weight loss are not well described. The present study explored the hypothesis that Roux-en-Y gastric bypass (RYGB) reduces circulating levels of pro-inflammatory cytokines, while increasing anti-inflammatory cytokines in obese subjects with type 2 diabetes (T2D) and in obese normal glucose tolerant (NGT) subjects. Methods: Thirteen obese subjects with T2D (weight; 129 +/- 14 kg, glycated hemoglobin (HbA1c); 7.0 +/- 0.9%, body mass index (BMI); 43.2 +/- 5.3 kg/m(2), mean +/- SD) and twelve matched obese NGT subjects (weight; 127 +/- 15 kg, HbA1c; 5.5 +/- 0.4%, BMI; 41.5 +/- 4.8 kg/m(2), mean +/- SD) were examined before, one week, three months, and one year after surgery. Interleukin (IL)-6, leptin, adiponectin, IL-8, transforming growth factor beta (TGF-beta), and the incretin hormone glucagon-like peptide-1 (GLP-1) were measured in the fasting state and during a liquid meal. Insulin resistance was evaluated by HOMA-IR.

Results: Weight loss did not differ between the two groups. Before surgery, HbA1c was higher and HOMA-IR lower in T2D patients, however, converged to the values of NGT subjects one year after surgery. Circulating cytokine concentrations did not differ between the two groups at any time point. One week after surgery, circulating IL-6 and IL-8 were increased, while adiponectin and leptin were reduced compared with pre-surgical concentrations. Three months after surgery, IL-8 was increased, leptin was reduced, and no change was observed for IL-6, TGF-beta, and adiponectin. One year after surgery, concentrations of IL-6, TGF-beta, and leptin were significantly reduced compared to before surgery, while adiponectin was significantly increased. Conclusions: One year after RYGB, fasting concentrations of IL-6 and leptin were reduced, while no changes were observed in IL-8, TGF-beta and adiponectin in both T2D and NGT obese subjects. This study is the first to examine IL-8 and TGF-beta in obese subject after RYGB. Resolution of inflammation could offer a potential explanation for the health improvement associated with major weight loss after bariatric surgery.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Zealand Pharma A/S, Hvidovre Hospital
Authors: Bovbjerg, K. K. L. (Intern), Jorgensen, N. B. (Ekstern), Just, R. (Ekstern), Heegaard, P. M. H. (Intern), Madsbad, S. (Ekstern)
Number of pages: 12
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Diabetology & Metabolic Syndrome
Volume: 7
Issue number: 12
ISSN (Print): 1758-5996
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.033 SJR 0.943 CiteScore 2.5
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 1.006 SNIP 0.993 CiteScore 2.36
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.924 SNIP 1.048 CiteScore 2.53
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.858 SNIP 1.196 CiteScore 2.69
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.807 SNIP 1.255 CiteScore 2.68
ISI indexed (2013): ISI indexed yes
Scopus rating (2012): SJR 0.722 SNIP 0.919 CiteScore 2.2
ISI indexed (2012): ISI indexed no
Scopus rating (2011): SJR 0.517 SNIP 1.014 CiteScore 1.62
ISI indexed (2011): ISI indexed no
Elucidating the T-cell reactivity against porcine IDO and RhoC to establish the pig as an animal model for vaccine development against human cancer

Immune therapy of cancer has recently experienced a great breakthrough with prolonged overall survival in patients with metastatic disease following the use of checkpoint inhibitors and T cell therapy with ex vivo expanded CD8+ cytotoxic T cells (CTLs). In the further development of immune therapies against cancer, vaccine formulations tailored to mount in vivo CTL responses towards co-delivered cancer antigens will be an important hallmark. Recognition of antigen-derived peptides presented in the context of major histocompatibility complex (MHC) class I molecules on cancer cells is a requirement for activation of CTLs. Previously, the development of therapeutic anti-cancer vaccines have largely been based on rodent models, in particular mice; however the majority of these fail to establish a therapeutic response once put into clinical trials. Pigs have the potential of serving as a model superior to rodents as they are more closely related to humans in terms of immunology and physiology. Here, we introduce pigs as a supplementary large animal model for human cancer vaccine development via the use of our unique technology for swine leukocyte antigen (SLA) production. IDO and RhoC, two tumor antigens previously identified as important players in human cancer development and progression, were used as vaccine targets. Using peptide-MHC-I binding predictors we identified IDO-derived and RhoC-derived candidate peptides potentially binding to five different broadly distributed SLA molecules. We measured the peptide-SLA complex stability of these and found a total of 89 stable (t½ ≥ 0.5 hours) peptide-MHC complexes with SLA-1*04:01, -1*07:02, -2*04:01, -2*05:02 and/or -3*04:01. For a pilot study, 12 pigs were immunized with overlapping 20-mer peptides spanning the entire IDO and RhoC sequences formulated in a panel of CTL-inducing adjuvants. Vaccine and adjuvant efficacy will be evaluated through immunological assays among others including ex vivo stimulation of whole blood with identified stable SLA-binding peptides and quantification of peptide-specific CTLs. Hence, these data elucidate the potential in using pigs as a large animal model for human anti-cancer vaccine development.

Embryonation of Ostertagia ostertagi eggs affects the outcome of real-time quantitative PCR

The aims of this study were to assess how the development of Ostertagia ostertagi eggs into first-stage larva (L1) affects the copy numbers of the Internal Transcribed Spacer region 2 (ITS2) of the ribosomal DNA; and based on these results, to suggest optimal storage conditions for faecal samples prior to detection and quantification by real-time quantitative polymerase chain reaction (qPCR). Fresh O. ostertagi eggs were isolated from cattle faeces and stored at 4°C or 25°C under aerobic or anaerobic conditions. Embryonation was monitored by microscopy and the ITS2 copies were determined by qPCR at predetermined intervals for up to 336 h. Under aerobic conditions, L1 was observed after 24 h at 25°C, while development to L1 took 336 h at 4°C. A corresponding significant increase of the ITS2 copies was also observed (p < 0.0001). However, anaerobic conditions inhibited embryonation at both temperatures and no significant effect of storage on ITS2 copies was noticed (p = 0.8984). ITS2 copies were significantly higher in L1 compared with copies in unembryonated eggs (p < 0.0001) and with lower coefficients of variation for L1 (33%) compared with unembryonated eggs (266%). In conclusion, storage conditions affect the outcome of qPCR analysis for the quantitative determination of O. ostertagi eggs in cattle faeces. Cold storage at 4°C for up to 3 days or anaerobic vacuum packing at 25°C for up to 336 h will entail no undesirable effects on ITS2 copies.
ERM immersion vaccination and adjuvants

Two candidate adjuvants were tested with a commercial ERM dip vaccine (AquaVac™ Relera, MSD Animal Health) for rainbow trout in an experimental design compatible with common vaccination practices at farm level, i.e. immersion of fish in vaccine (±adjuvant) for 30 s. The adjuvants were the commercial product Montanide™ IMS 1312 VG PR (SEPPIC), and a soluble and ≥98% pure β-glucan from yeast (Saccharomyces cerevisiae) (Sigma-Aldrich). Hence, five experimental groups in duplicate were established and exposed to vaccine and adjuvants in the following combinations: AquaVac™ Relera (alone); AquaVac™ Relera + Montanide™; AquaVac™ Relera + β-glucan; Montanide™ (alone); and β-glucan (alone). Approximately 450 degree days post-vaccination, the fish were bath-challenged with live Yersinia ruckeri to produce survival curves. Blood, skin and gills were sampled at selected time points during the course of the experiment to test for plasma Ab levels and lysozyme activity, and the regulation of immune relevant genes and cells in external, mucosal tissues. Preliminary results show 96% to 100% survival of vaccinated fish with and without any of the two adjuvants, whereas unvaccinated controls and fish exposed to β-glucan alone experienced 58% and 60% survival, respectively (calculated at day 24 post-challenge). Montanide™ alone gave rise to an intermediate level of 72% survival. Lysozyme activity levels in plasma were markedly elevated at day 3 and day 24 post-challenge in fish exposed to Montanide™ alone or β-glucan alone compared to fish from any of the three vaccinated groups.

Establishing the pig as a large animal model for vaccine development against human cancer

Immunotherapy has increased overall survival of metastatic cancer patients, and cancer antigens are promising vaccine targets. To fulfill the promise, appropriate tailoring of the vaccine formulations to mount in vivo cytotoxic T cell (CTL) responses toward co-delivered cancer antigens is essential. Previous development of therapeutic cancer vaccines has largely been based on studies in mice, and the majority of these candidate vaccines failed to induce therapeutic responses in the subsequent human clinical trials. Given that antigen dose and vaccine volume in pigs are translatable to humans and the porcine immunome is closer related to the human counterpart, we here introduce pigs as a supplementary large animal model for human cancer vaccine development. IDO and RhoC, both important in human cancer development and progression, were used as vaccine targets and 12 pigs were immunized with overlapping 20mer peptides spanning the entire porcine IDO and RhoC sequences formulated in CTL-inducing adjuvants: CAF09, CASAC, Montanide ISA 51 VG, or PBS. Taking advantage of recombinant swine MHC class I molecules (SLAs), the peptide-SLA complex stability was measured for 198 IDO- or RhoC-derived 9-11mer peptides predicted to bind to SLA-1*04:01, −1*07:02, −2*04:01, −2*05:02, and/or −3*04:01. This identified 89 stable (t½ ≥ 0.5 h) peptide-SLA complexes. By IFN-γ release in PBMC cultures we monitored the vaccine-induced peptide-specific CTL responses, and found responses to both IDO- and RhoC-derived peptides across all groups with no adjuvant being superior. These findings support the further use of pigs as a large animal model for vaccine development against human cancer.
Evaluation of the effect of percolation and NaCl solutions on viral haemorrhagic septicaemia virus (VHSV) under experimental conditions

In the present Danish "Ministerial order no. 965 of 18/07/2013 regarding authorisation and operation of aquaculture farms and sale of aquatic organisms and products thereof" fish cutting plants have according to 20 the possibility to get rid of their wastewater by percolation. To examine the effect of percolation on viral haemorrhagic septicaemia virus (VHSV) a sand column experiment has been performed. VHSV was infused onto a column packed with gravel as top and bottom layer (in total 22 cm) and dug sand (76 cm). Over a period of 18 h 3.9 x 10^{10} TCID50 VHSV was pumped onto the column where after tap water was added over the rest of the experimental period. The experiment ran over 7 days. During that period samples were collected from the outlet for virological examination. The sampling was most intense in the period where there was the highest risk of VHSV escaping the column. VHSV was not isolated from any of the outlet samples. As the sensitivity of the virological examination was 13.9 TCID50/ml a reduction of >4 log was shown at the outlet. Percolation thus seems to be a usable method for sanitation of water contaminated with VHSV. Changes in temperature, pH, earth types etc. may potentially change the reduction. Some of the fish cutting plants also produce smoked trout fillets using brine in the process. It was tested whether a high NaCl solution will inactivate VHSV. After 20 h with a salinity of 20.9% no inactivation was observed.

Statement of relevance
Fish processing plants slaughtering VHS diseased fish may discharge wastewater containing the disease causing virus. In order to protect both farmed and wild fish it is important that this virus does not get in contact with other fish. This manuscript concerns the fate of VHSV when percolated through the ground. In Denmark this is an approved method to get rid of the wastewater. To our knowledge, for fish pathogenic viruses, this kind of investigation has never been published before and the presented knowledge is therefore new and valuable. (C) 2015 Elsevier B.V. All rights reserved.
Evaluation of the immune response in rainbow trout fry, *Oncorhynchus mykiss* (Walbaum), after waterborne exposure to *Flavobacterium psychrophilum* and/or hydrogen peroxide

The immune response in rainbow trout fry against *Flavobacterium psychrophilum* was elucidated using an immersion-based challenge with or without prior exposure to hydrogen peroxide (H$_2$O$_2$). Samples were taken from the head kidney 4, 48, 125 and 192 h after immersion, and the regulation of several genes was examined. Bacterial load was assessed based on the presence of 16S rRNA and correlated with gene expression, and the levels of specific antibodies in the blood were measured 50 days post-infection. Separately, both H$_2$O$_2$ and *F. psychrophilum* influenced gene expression, and pre-treatment with H$_2$O$_2$ influenced the response to infection with *F. psychrophilum*. Pre-treatment with H$_2$O$_2$ also affected correlation between gene regulation and pathogen load for several genes. A delay in antibody production in H$_2$O$_2$-treated fish in the early phase of infection was indicated, but H$_2$O$_2$ exposure did not affect antibody levels 50 days post-infection. An increasing amount of *F. psychrophilum* 16S rRNA was found in the head kidneys of infected fish pre-treated with H$_2$O$_2$ relative to the *F. psychrophilum* group. The results show that a single pre-treatment with H$_2$O$_2$ impairs the response against *F. psychrophilum* and may intensify infection.

**General information**

**State:** Published

**Organisations:** National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, National Veterinary Institute, University of Copenhagen

**Authors:** Henriksen, M. M. M. (Intern), Kania, P. W. (Ekstern), Buchmann, K. (Intern), Dalsgaard, I. (Intern)

**Number of pages:** 12

**Pages:** 55-66

**Publication date:** 2015

**Main Research Area:** Technical/natural sciences

**Publication information**

**Journal:** Journal of Fish Diseases

**Volume:** 38

**ISSN (Print):** 0140-7775

**Ratings:**

- BFI (2018): BFI-level 1
- Web of Science (2018): Indexed yes
- BFI (2017): BFI-level 1
- Scopus rating (2017): CiteScore 1.82
- Web of Science (2017): Indexed yes
- BFI (2016): BFI-level 1
- Scopus rating (2016): CiteScore 2.12
- Web of Science (2016): Indexed yes
- BFI (2015): BFI-level 1
- Scopus rating (2015): CiteScore 1.71
- Web of Science (2015): Indexed yes
- BFI (2014): BFI-level 1
Experimental infection of cattle with ovine Dichelobacter nodosus isolates

Dichelobacter nodosus is the main causative agent of ovine footrot, and there are strong indications that the bacterium can be transferred to cattle grazing on the same pasture as sheep. The aim of this study was to investigate if benign and virulent D. nodosus strains isolated from sheep can be transferred to the interdigital skin of cattle under experimental conditions. Further, we wanted to observe the impact of such infection on bovine foot health, and test the effect of topical chlortetracycline (Cyclo spray®: Eurovet) on the infection. Six heifers were included in the study. After an initial 18-day maceration period, three heifers were inoculated on one single foot with a benign strain and three with a virulent strain by adding bacterial suspension in a bandage. The bandages were left on for 17 days, and when removed, D. nodosus was isolated from all six heifers. All six heifers developed interdigital dermatitis. In five of the heifers D. nodosus organisms were demonstrated within the epidermis. Twenty-four days after treatment with chlortetracycline all heifers were negative by cultivation, but tested positive for D. nodosus by polymerase chain reaction (PCR). Two of the six heifers still tested positive for D. nodosus by PCR 49 days after treatment. After 70 days, all heifers tested negative for D. nodosus. This study shows that both virulent and benign D. nodosus strains originating from sheep can be transferred to naïve heifers under experimental conditions. Further, the study supports the hypothesis that infections with virulent D. nodosus in cattle are associated with interdigital dermatitis. No conclusion regarding the treatment of D. nodosus infection with chlortetracycline was possible.

General information

State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Norwegian Veterinary Institute, Norwegian University of Life Sciences, Norwegian Sheep Health Service
Authors: Knape-Poindécker, M. (Ekstern), Jørgensen, H. J. (Ekstern), Jensen, T. K. (Intern), Tesfamichael, B. (Ekstern), Ulvund, M. J. (Ekstern), Hektoen, L. (Ekstern), Fjeldaas, T. (Ekstern)
Feeding chicory (Cichorium intybus) selectively reduces Ostertagia ostertagi infection levels in cattle

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Copenhagen
Authors: Pena-Espinoza, M. A. (Intern), Desruès, O. (Ekstern), Hansen, T. (Ekstern), Thamsborg, S. M. (Ekstern), Enemark, H. (Intern)
Number of pages: 1
Pages: 299-299
Publication date: 2015

Host publication information
Title of host publication: 25th International Conference of the World Association for the Advancement of Veterinary Parasitology: Abstract Book
Place of publication: Liverpool, United Kingdom
Main Research Area: Technical/natural sciences
Conference: 25th International Conference of the World Association for the Advancement of Veterinary Parasitology, Liverpool, United Kingdom, 16/08/2015 - 16/08/2015
Electronic versions:
Pe_a_Espinoza_et_al_in_vivo_WAAVP2015.pdf
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2015

First detection of bonamia ostreae in native flat oysters from the limfjord in denmark

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Section for Virology
Authors: Madsen, L. (Intern), Thomassen, H. E. H. (Intern)
Pages: 92-92
Publication date: 2015

Host publication information
Title of host publication: 17th International Conference on Diseases of Fish And Shellfish: Abstract book
Place of publication: Las Palmas
Publisher: European Association of Fish Pathologists
Article number: O-084
Main Research Area: Technical/natural sciences
Conference: 17th International Conference on Diseases of Fish and Shellfish, Las Palmas, Spain, 07/09/2015 - 07/09/2015
Electronic versions:
Book_of_abstracts_17th_International_conference_on_Diseases_of_Fish_and_Shellfish.pdf
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2015

Fishpathogens.eu/noda: a free and handy online platform for Betanodavirus targeted research and data sharing
Viral nervous necrosis (VNN) is a severe neuropathological disease affecting a broad variety of finfish species worldwide. The causative agents of VNN are small viruses with a bi-segmented RNA genome known as betanodaviruses. At least four species with distinct but yet insufficiently characterized epidemiological features are recognized. The spread of VNN to an increasing number of host species, its wide geographic extent and its economical and ecological impacts justify the
importance of collating as much molecular data as possible for tracing the origin of viral isolates and highlight the need for a freely accessible tool for epidemiological and molecular data sharing and consultation. For this purpose, we established a web-based specific database using the www.fishpathogens.eu platform, with the aim of collecting molecular and epidemiological information on VNN viruses, with relevance to their control, management and research studies.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Instituto Zooprofilattico Sperimentale delle Venezie, ANSES - French Agency for Food, Environmental and Occupational Health & Safety, Symantix Ltd., Imperial College London
Authors: Mikkelsen, S. S. (Intern), Panzarin, V. (Ekstern), Jonstrup, S. P. (Intern), Bigarré, L. (Ekstern), Baud, M. (Ekstern), Gray, T. (Ekstern), Agapow, P. (Ekstern), Olesen, N. J. (Intern)
Number of pages: 6
Pages: 755-760
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Fish Diseases
Volume: 38
Issue number: 8
ISSN (Print): 0140-7775
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.82
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.12
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 1.71
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 1.99
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 1.74
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 1.7
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.09
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Web of Science (2008): Indexed yes
Web of Science (2007): Indexed yes
Web of Science (2006): Indexed yes
Web of Science (2005): Indexed yes
Fluorescence In Situ Hybridization for the Tissue Detection of Bacterial Pathogens Associated with Porcine Infections.

Fluorescence in situ hybridization (FISH) is an efficient technique for the identification of specific bacteria in tissue of both experimental and spontaneous infections. The method detects specific sequences of nucleic acids by hybridization of fluorescently labeled probes to complementary target sequences within intact cells. FISH allows direct histological localization of the bacteria in the tissue and thereby a correlation between the infection and the histopathological changes present. This chapter presents protocols for FISH identification of bacterial pathogens in fixed deparaffinized tissue samples mounted on glass slides. Two different methods are presented: one is illustrated with the use of peptide nucleic acid (PNA) that is carried out directly on glass slides (Method I), whereas the other is exemplified by using a DNA probe in a Shandon rack (Method II). In the two methods, both PNA and DNA probes can be used.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology
Authors: Elvang Jensen, H. (Ekstern), Jensen, L. K. (Ekstern), Barington, K. (Ekstern), Pors, S. E. (Ekstern), Bjarnsholt, T. (Ekstern), Boye, M. (Intern)
Number of pages: 16
Pages: 219-234
Publication date: 2015

Host publication information
Title of host publication: Veterinary Infection Biology: Molecular Diagnostics and High-Throughput Strategies
Volume: 1247
Place of publication: New York
Publisher: Springer Science+Business Media
Editors: Cunha, M. V., Inácio, J.
Edition: 1
Chapter: 17

Series: Methods in Molecular Biology
ISSN: 1064-3745
Main Research Area: Technical/natural sciences
Bacteria, DNA, PNA, FISH, Fluorescence, Hybridization, In situ, Porcine, rRNA, Tissue
DOI:
10.1007/978-1-4939-2004-4_17
Source: PublicationPreSubmission
Source-ID: 102384351
Publication: Research - peer-review › Book chapter – Annual report year: 2015

Foot-and-Mouth Disease
Foot-and-mouth disease (FMD) is an economically important, highly contagious disease of cloven-hoofed animals characterised by the appearance of vesicles (blisters) on the feet and in, and around, the mouth. The causative agent, foot-and-mouth disease virus (FMDV), was the first mammalian virus to be discovered. It has a ribonucleic acid (RNA) genome enclosed within a protein coat (capsid). The virus replicates very rapidly within the cytoplasm of cells. The RNA genome has to function both as a messenger RNA (mRNA) and as a template for RNA replication. The RNA encodes a single large polyprotein that is processed, by virus-encoded proteases, to about 12 mature products (plus functionally important precursors) that are required for virus replication and assembly. Some of these viral proteins modify host cell activities to block antivirus defence systems. Thus, this small virus displays a remarkably complex array of biological activities.
Foot-and-Mouth Disease Virus Serotype SAT 3 in Long-Horned Ankole Calf, Uganda

After a 16-year interval, foot-and-mouth disease virus serotype SAT 3 was isolated in 2013 from an apparently healthy long-horned Ankole calf that grazed close to buffalo in Uganda. The emergent virus strain is ≈20% different in nucleotide sequence (encoding VP1 [viral protein 1]) from its closest relatives isolated previously from buffalo in Uganda.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, The Pirbright Institute
Authors: Belsham, G. (Intern), Charleston, B. (Ekstern), Jackson, T. (Ekstern), Paton, D. J. (Ekstern)
Number of pages: 9
Publication date: 2015

Host publication information
Title of host publication: Encyclopedia of Life Sciences
Publisher: Wiley
Main Research Area: Technical/natural sciences
Animals, Virus, Vesicles, Picornavirus, RNA, Integrins
DOIs: 10.1002/9780470015902.a0001024.pub
Source: PublicationPreSubmission
Source-ID: 105956609
Publication: Research - peer-review » Encyclopedia chapter – Annual report year: 2015
Fugleinfluenzavirus H10N7 spredte sig blandt danske sæler i 2014

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Section for Virology
Authors: Hjulsager, C. K. (Intern), Krog, J. S. (Intern), Hansen, M. S. (Intern), Chriél, M. (Intern), Larsen, L. E. (Intern)
Pages: 42-42
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Dansk Veterinaertidsskrift
Issue number: 9
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Fund af Bonamia ostreae i danske østers fra Limfjorden

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology
Authors: Madsen, L. (Intern)
Pages: 41
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Dansk Veterinærtidsskrift
Volume: 98
Issue number: 8
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
ISI indexed (2012): ISI indexed no
BFI (2011): BFI-level 1
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
BFI (2009): BFI-level 1
BFI (2008): BFI-level 1
Original language: English
Electronic versions:
Madsen_2015_DVT_nr8_s41.pdf
Source: PublicationPreSubmission
Source-ID: 110840762
Publication: Communication › Journal article – Annual report year: 2015

Gastrointestinal parasites in Danish cats
**Gastrointestinal parasites of cats in Denmark assessed by necropsy and concentration McMaster technique**

The large population of feral cats in Denmark may potentially transmit pathogens to household cats and zoonotic parasites to humans. A total of 99 euthanized cats; feral cats (n = 92) and household cats with outdoor access (n = 7), were collected from March to May 2014 from the Zealand region, Denmark. The sedimentation and counting technique (SCT) was used to isolate helminths and coproscopy was done by concentration McMaster technique (c-McMaster). Overall, 90.1% of the cats were infected and a total of 10 species were recorded by SCT: 5 nematode species: Toxocara cati (84.8%), Ollulanus tricuspis (13.1%), Aonchotheca putorii (7.1%), Paersonema spp. (3.0%), Strongyloides spp. (1.0%); 3 cestodes: Hydatigera taeniaeformis (36.4%), Mesocestoides sp. (3.0%), Dipylidium caninum (1.0%); and 2 trematodes: Cryptocotyle spp. (5.1%) and Pseudamphistomum truncatum (1.0%). O. tricuspis was the second most common gastrointestinal nematode of cats but had the highest intensity of infection. For T. cati, prevalence and worm burden were significantly higher in feral than household cats. No juvenile cats were infected with H. taeniaeformis, and age thus had a significant effect on prevalence and worm burdens of this species. Rural cats had a higher prevalence and worm burden of A. putorii than urban cats. By c-McMaster, ascarid, capillarid, strongyloid or taeniid type eggs were found in 77.9% of the cats while Cystoisospora felis was found in 2.1%. The sensitivity of the c-McMaster was 82.5% for T. cati but 26.5% for taeniid eggs, using the SCT as gold standard. A positive correlation between faecal egg counts and worm burdens was seen for T. cati, but not for taeniid eggs (assumed to be H. taeniaeformis). Coprological examination also detected the eggs of extraintestinal Capillariidae species including Eucoleus aerophilus and Eucoleus boehmi, but further necropsy studies are needed to confirm these findings.

**General information**

State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Copenhagen
Authors: Takeuchi-Storm, N. (Intern), Mejer, H. (Ekstern), Al-Sabi, M. N. S. (Intern), Olsen, C. S. (Ekstern), Thamsborg, S. M. (Ekstern), Enemark, H. (Intern)
Pages: 327-332
Publication date: 2015
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Veterinary Parasitology
Volume: 214
Issue number: 3-4
ISSN (Print): 0304-4017
Ratings:
- BFI (2018): BFI-level 2
- Web of Science (2018): Indexed yes
- BFI (2017): BFI-level 1
- Scopus rating (2017): SNIP 1.215 SJR 1.275 CiteScore 2.55
- Web of Science (2017): Indexed Yes
- BFI (2016): BFI-level 1
- Scopus rating (2016): CiteScore 2.49 SJR 1.228 SNIP 1.218
- Web of Science (2016): Indexed yes
- BFI (2015): BFI-level 1
- Scopus rating (2015): SJR 1.21 SNIP 1.309 CiteScore 2.46
- Web of Science (2015): Indexed yes
- BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.324 SNIP 1.42 CiteScore 2.53
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.262 SNIP 1.437 CiteScore 2.63
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.163 SNIP 1.439 CiteScore 2.6
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.233 SNIP 1.429 CiteScore 2.61
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.254 SNIP 1.347
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.138 SNIP 1.414
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.117 SNIP 1.21
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.007 SNIP 1.421
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.932 SNIP 1.442
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.846 SNIP 1.437
Scopus rating (2004): SJR 0.883 SNIP 1.168
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.81 SNIP 1.233
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.919 SNIP 1.146
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.61 SNIP 1.123
Scopus rating (2000): SJR 0.841 SNIP 1.183
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 0.812 SNIP 1.042
Original language: English
Parasitology, Veterinary (all), Cat, Concentration McMaster technique, Denmark, Helminths, Sedimentation and counting technique
DOIs: 10.1016/j.vetpar.2015.06.033
Source: FindIt
Source-ID: 2279650767
Publication: Research - peer-review › Journal article – Annual report year: 2015

**Genetics of VHSV in Europe**

**General information**
State: Published
Organisations: National Veterinary Institute, Section for Virology, Friedrich Loeffler Institute, University of Bern, Wageningen University & Research, Aarhus University, ANSES - French Agency for Food, Environmental and Occupational Health & Safety, Instituto Zooprofilattico Sperimentale delle Venezie
Authors: Cieslak, M. (Ekstern), Baud, M. (Ekstern), Diserens, N. (Ekstern), Engelsma, M. (Ekstern), Haenen, O. (Ekstern), Mousakhani, S. (Ekstern), Olesen, N. J. (Intern), Panzarin, V. (Ekstern), Skall, H. F. (Ekstern), Wahl, T. (Ekstern), Schütze, H. (Ekstern)
Pages: 55-55
Genomic approach to high resolution typing of Mycoplasma bovis

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology
Authors: Shukla, A. (Intern), Kokotovic, B. (Intern)
Number of pages: 1
Publication date: 2015
Event: Poster session presented at Progress in human and animal mycoplasmology, Pendik/Istanbul, Turkey.
Main Research Area: Technical/natural sciences
Electronic versions:
Poster_Istanbul.pdf
Source: PublicationPreSubmission
Source-ID: 115272742
Publication: Research - peer-review › Poster – Annual report year: 2015

Göttingen minipig model of diet-induced atherosclerosis: influence of mild streptozotocin-induced diabetes on lesion severity and markers of inflammation evaluated in obese, obese and diabetic, and lean control animals

From a pharmacological perspective, readily-available, well-characterized animal models of cardiovascular disease, including relevant in vivo markers of atherosclerosis are important for evaluation of novel drug candidates. Furthermore, considering the impact of diabetes mellitus on atherosclerosis in human patients, inclusion of this disease aspect in the characterization of a such model, is highly relevant. The objective of this study was to evaluate the effect of mild streptozotocin-induced diabetes on ex- and in vivo end-points in a diet-induced atherosclerotic minipig model. Castrated male Göttingen minipigs were fed standard chow (CD), atherogenic diet alone (HFD) or with superimposed mild streptozotocin-induced diabetes (HFD-D). Circulating markers of inflammation (C-reactive protein (CRP), oxidized low-density lipoprotein (oxLDL), plasminogen activator inhibitor-1, lipid and glucose metabolism were evaluated together with coronary and aortic atherosclerosis after 22 or 43 diet-weeks. Group differences were evaluated by analysis of variance for parametric data and Kruskal-Wallis test for non-parametric data. For qualitative assessments, Fisher's exact test was applied. For all analyses, p

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, University of Copenhagen, Novo Nordisk A/S
Authors: Ludvigsen, T. P. (Ekstern), Kirk, R. K. (Ekstern), Christoffersen, B. Ø. (Ekstern), Pedersen, H. (Ekstern), Martinussen, T. (Ekstern), Kildegaard, J. (Ekstern), Heegaard, P. M. H. (Intern), Lykkesfeldt, J. (Ekstern), Olsen, L. H. (Ekstern)
Number of pages: 12
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Translational Medicine
Volume: 13
Issue number: 1
Article number: 312
ISSN (Print): 1479-5876
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
Habitatrelateret føde hos RÆV (Vulpes vulpes) i landbrugsområder

General information
State: Published
Organisations: National Veterinary Institute, Aarhus University, Danmarks Jægerforbund
Authors: Pagh, S. (Ekstern), Tjørnløv, R. S. (Forskerdatabase), Kjær Illeman, J. (Ekstern), Tolsgaard, S. (Ekstern), Chriél, M. (Intern)
Number of pages: 12
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Flora og Fauna
Volume: 121
Issue number: 1-2
High prevalence of Alaria alata in farmed wild boars (Sus scrofa) in Denmark – preliminary results of ongoing surveillance of zoonotic parasites

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, National Food Institute
Authors: Enemark, H. L. (Intern), Al-Sabi, M. N. S. (Intern), Takeuchi-Storm, N. (Intern), Larsen, G. (Intern), Chriél, M. (Intern)
Publication date: 2015
Event: Abstract from 25th International Conference of the World Association for the Advancement of Veterinary Parasitology, Liverpool, United Kingdom.
Main Research Area: Technical/natural sciences
Source: FindIt
Source-ID: 2282296519
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2015

High-throughput Gene Expression Analysis In Pigs As Model For Respiratory Infections

Influenza A virus infections have great impact on human health and welfare and significant resources are linked to influenza epidemics due to excess hospitalizations and lost productivity. Up to 15% of the human population is affected when Influenza spreads around the world in seasonal epidemics (WHO).

Animal models are essential in understanding the mechanisms involved in human infectious disease and for the development of effective prevention and treatment strategies. It is increasingly realized that large animal models like the pig are exceptionally human like and serve as an excellent model for disease and inflammation. Pigs are fully susceptible to human influenza, and have been demonstrated to be involved in influenza evolution and ecology. Pigs share many similarities with humans regarding lung physiology and innate immune cell infiltration of the respiratory system and thus seem to be an obvious large animal model for respiratory infections. This study aimed at providing a better understanding of the involvement of circulating non-coding RNA and innate immune factors in porcine blood leukocytes during influenza virus infection. By employing the pig as a model we were able to perform highly controlled experimental infections and to study changes of symptoms, viral titer, and expression of microRNAs/mRNAs as the influenza infection progresses in
time, generating information that would be difficult to obtain from human patients.

The Gram-negative bacterium Actinobacillus pleuropneumoniae causes pneumonia in pigs, a disease which is associated with high morbidity and mortality, as well as impaired animal welfare. The rapidly evolving pneumonia is characterized by large areas of lung necrosis resulting from the combined effect of tissue damage caused by the bacteria, and a strong proinflammatory immune response. To obtain in-depth understanding of this infection, concurrent gene expression of host and pathogen in lung samples collected from pigs experimentally infected with A. pleuropneumoniae was studied. We applied high-throughput RT-qPCR for the simultaneous analysis of host and pathogen gene expression. This parallel analysis was done in lung tissue samples as well as in the immediate surroundings of infection loci after laser capture microdissection. Regulation of gene expression of several immune factors was observed in agreement with protein levels of these factors in lung tissue, infection status and histopathological findings.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Section for Bacteriology, Pathology and Parasitology, Section for Virology, IDT-Biologika GmbH, Technical University of Denmark
Authors: Skovgaard, K. (Intern), Brogaard, L. (Intern), Schou, K. K. (Intern), Larsen, L. E. (Intern), Mortensen, S. (Ekstern), Dürwald, R. (Ekstern), Schengel, M. (Ekstern), Heegaard, P. M. H. (Intern)
Number of pages: 1
Publication date: 2015
Event: Abstract from 7th international qPCR & NGS Event Symposium & Industrial Exhibition & Application Workshops, Germany.
Main Research Area: Technical/natural sciences

Host-pathogen Interaction at the Intestinal Mucosa Correlates With Zoonotic Potential of Streptococcus suis
Background. Streptococcus suis has emerged as an important cause of bacterial meningitis in adults. The ingestion of undercooked pork is a risk factor for human S. suis serotype 2 (SS2) infection. Here we provide experimental evidence indicating that the gastrointestinal tract is an entry site of SS2 infection. Methods. We developed a noninvasive in vivo model to study oral SS2 infection in piglets. We compared in vitro interaction of S. suis with human and porcine intestinal epithelial cells (IEC). Results. Two out of 15 piglets showed clinical symptoms compatible with S. suis infection 24–48 hours after ingestion of SS2. SS2 was detected in mesenteric lymph nodes of 40% of challenged piglets. SS2 strains isolated from patients showed significantly higher adhesion to human IEC compared to invasive strains isolated from pigs. In contrast, invasive SS9 strains showed significantly higher adhesion to porcine IEC. Translocation across human IEC, which occurred predominately via a paracellular route, was significantly associated with clonal complex 1, the predominant zoonotic genotype. Adhesion and translocation were dependent on capsular polysaccharide production. Conclusions. SS2 should be considered a food-borne pathogen. S. suis interaction with human and pig IEC correlates with S. suis serotype and genotype, which can explain the zoonotic potential of SS2.

General information
State: Published
Organisations: National Veterinary Institute, University of Amsterdam, Wageningen IMARES, Academic Medical Center, Animal Health Service
Authors: Ferrando, M. L. (Ekstern), de Greeff, A. (Ekstern), van Rooijen, W. J. M. (Ekstern), Stockhofe-Zurwieden, N. (Ekstern), Nielsen, J. (Intern), Wichgers Schreur, P. J. (Ekstern), Pannekoek, Y. (Ekstern), Heuvelink, A. (Ekstern), van der Ende, A. (Ekstern), Smith, H. (Ekstern), Schultz, C. (Ekstern)
Number of pages: 11
Pages: 95-105
Publication date: 2015
Main Research Area: Technical/natural sciences
Publication information
Journal: Journal of Infectious Diseases
Volume: 212
Issue number: 1
ISSN (Print): 0022-1899
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Hvordan ser afrikansk svinepest ud i danske grise II?: Rapport over smitteforsøg i drægtige søer 2014

Denne artikel beskriver forløbet af et eksperimentelt forsøg i danske, drægtige søer og fostre podet med afrikansk svinepestvirus(African swine fever virus = ASFV). Formålet med forsøget var at tilvejebringe viden om det kliniske og patologiske billede ved infektion med den ASFV-stamme(ASFV Georgia 2007), der cirkulerer i Rusland og omegn (nu også EU). Forsøget efterfølger et tidligere smitteforsøg gennemført i danske fravænningsgrise med samme isolat (se faktaboks 1). Forsøget skulle samtidig fastlægge, hvilket diagnostisk materiale det er optimalt at udtage fra drægtige søer/nyfødte grise i en mistankesituation. Endelig, indgik forsøget i den løbende opdatering og undervisning af...
beredskabsdyrlæger i Fødevarestyrelsen om eksotiske virussygdomme i husdyr. Denne aktivitet foregår i et samarbejde mellem DTU Veterinærinstituttet og Fødevarestyrelsen. Via besøg på Lindholm med ekskursion til stald- og laboratoriefaciliteter holdes beredskabsdyrlægerne ajour med det kliniske og patologiske billede af de udefrakommende virustrusler, der cirkulerer i husdyr i landene omkring Danmark.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Lohse, L. (Intern), Strandbygaard, B. (Intern), Nielsen, J. (Intern), Uttenthal, Å. (Intern), Rasmussen, T. B. (Intern), Belsham, G. (Intern), Bøtner, A. (Intern)
Pages: 21-23
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Dansk Veterinaertidsskrift
Volume: 9
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
ISI indexed (2012): ISI indexed no
BFI (2011): BFI-level 1
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
BFI (2009): BFI-level 1
BFI (2008): BFI-level 1
Original language: English
Electronic versions: Hvordan_ser_afrikansk_svinepest_ud_i_danske_grise_Il_Lohse_et_al.pdf
Source: PublicationPreSubmission
Source-ID: 114766961
Publication: Communication › Journal article – Annual report year: 2015

iCull – A bioeconomic model for herd management and disease control
General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Department of Applied Mathematics and Computer Science, Dynamical Systems, University of Copenhagen
Authors: Kirkeby, C. (Intern), Græsbøll, K. (Intern), Nielsen, S. S. (Ekstern), Christiansen, L. E. (Intern), Toft, N. (Intern), Hisham Beshara Halasa, T. (Intern)
Number of pages: 1
Publication date: 2015
Main Research Area: Technical/natural sciences

Relations
Activities:
SVEPM Annual Meeting 2015
Publication: Research › Poster – Annual report year: 2015
Identification and complete genome analysis of novel picornavirus in bovine in Japan
We identified novel viruses in feces from cattle with diarrhea collected in 2009 in Hokkaido Prefecture, Japan, by using a metagenomics approach and determined the (near) complete sequences of the virus. Sequence analyses revealed that they had a standard picornavirus genome organization, i.e. 5' untranslated region (UTR) - L- P1 (VP4- VP3- VP2- VP1) - P2 (2A- 2B- 2C) - P3 (3A- 3B- 3C-3D) - 3'UTR- poly(A). They are closely related to other unclassified Chinese picornaviruses; bat picornaviruses group 1-3, feline picornavirus, and canine picornavirus, sharing 45.4-51.4% (P1), 38.0-44.9% (P2), and 49.6-53.3% (P3) amino acid identities, respectively. The phylogenetic analyses and detailed genome characterization showed that they, together with the unclassified Chinese picornaviruses, grouped as a cluster for the P1, 2C, 3CD and VP1 coding regions. These viruses had conserved features (e.g. predicted protein cleavage sites, presence of a leader protein, 2A, 2C, 3C, and 3D functional domains), suggesting they have a common ancestor. Reverse-transcription-PCR assays, using specific primers designed from the 5'UTR sequence of these viruses, showed that 23.0% (20/87) of fecal samples from cattle with diarrhea were positive, indicating the prevalence of these picornavirus in the Japanese cattle population in Hokkaido Prefecture. However, further studies are needed to investigate the pathogenic potential and etiological role of these viruses in cattle.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Tokyo University of Agriculture and Technology, Nippon Veterinary and Life Science University, National Institute of Infectious Diseases
Pages: 205-212
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Virus Research
Volume: 210
ISSN (Print): 0168-1702
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.901 SJR 1.147 CiteScore 2.58
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 1.208 SNIP 0.917 CiteScore 2.55
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.253 SNIP 0.9 CiteScore 2.56
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.213 SNIP 0.926 CiteScore 2.63
BFI (2013): BFI-level 1
ISI indexed (2013): ISI indexed yes
Scopus rating (2013): SJR 1.3 SNIP 1.105 CiteScore 2.94
Web of Science (2013): Indexed yes
ISI indexed (2012): ISI indexed yes
Scopus rating (2012): SJR 1.21 SNIP 1.05 CiteScore 2.9
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.271 SNIP 1.216 CiteScore 3.04
ISI indexed (2011): ISI indexed yes
ISI indexed (2010): ISI indexed yes
Scopus rating (2010): SJR 1.244 SNIP 1.081
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.313 SNIP 1.042
Web of Science (2009): Indexed yes
Identification of Highly Pathogenic Microorganisms by Matrix-Assisted Laser Desorption Ionization–Time of Flight Mass Spectrometry: Results of an Interlaboratory Ring Trial

In the case of a release of highly pathogenic bacteria (HPB), there is an urgent need for rapid, accurate, and reliable diagnostics. MALDI-TOF mass spectrometry is a rapid, accurate, and relatively inexpensive technique that is becoming increasingly important in microbiological diagnostics to complement classical microbiology, PCR, and genotyping of HPB. In the present study, the results of a joint exercise with 11 partner institutions from nine European countries are presented. In this exercise, 10 distinct microbial samples, among them five HPB, Bacillus anthracis, Brucella canis, Burkholderia mallei, Burkholderia pseudomallei, and Yersinia pestis, were characterized under blinded conditions. Microbial strains were inactivated by high-dose gamma irradiation before shipment. Preparatory investigations ensured that this type of inactivation induced only subtle spectral changes with negligible influence on the quality of the diagnosis. Furthermore, pilot tests on nonpathogenic strains were systematically conducted to ensure the suitability of sample preparation and to optimize and standardize the workflow for microbial identification. The analysis of the microbial mass spectra was carried out by the individual laboratories on the basis of spectral libraries available on site. All mass spectra were also tested against an in-house HPB library at the Robert Koch Institute (RKI). The averaged identification accuracy was 77% in the first case and improved to >93% when the spectral diagnoses were obtained on the basis of the RKI library. The compilation of complete and comprehensive databases with spectra from a broad strain collection is therefore considered of paramount importance for accurate microbial identification.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Robert Koch Institute, Public Health Agency of Sweden, Austrian Agency for Health and Food Safety, National Center for Epidemiology, Friedrich Loeffler Institute, Bundeswehr Institute of Microbiology, Norwegian Institute of Public Health, National Institute for Nuclear, Chemical and Biological Protection, Spiez Laboratory, Mabritec AG, L. Spallanzani National Institute for Infectious Diseases
Authors: Lasch, P. (Ekstern), Wahab, T. (Ekstern), Weil, S. (Ekstern), Pályi, B. (Ekstern), Tomaso, H. (Ekstern), Zange, S. (Ekstern), Kiland Granerud, B. (Ekstern), Drevinek, M. (Ekstern), Kokotovic, B. (Intern), Wittwer, M. (Ekstern), Pflüger, V. (Ekstern), Di Caro, A. (Ekstern), Stäubämmier, M. (Ekstern), Grunow, R. (Ekstern), Jacob, D. (Ekstern)
Number of pages: 9
Pages: 2632-2640
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Clinical Microbiology
Volume: 53
Issue number: 8
ISSN (Print): 0095-1137
Ratings:
BFI (2018): BFI-level 1
Immune and inflammatory responses in pigs infected with *Trichuris suis* and *Oesophagostomum dentatum*

The aim of the present study was to investigate parasite induced immune responses in pigs co-infected with *Trichuris suis* and *Oesophagostomum dentatum* as compared to mono-species infected pigs. *T. suis* is known to elicit a strong immune response leading to rapid expulsion, and a strong antagonistic effect on *O. dentatum* populations has been observed in co-infected pigs. Forty-eight helminth naïve pigs were allocated into 4 groups in a 2-factorial design. Two groups were trickle inoculated with either 10 *T. suis* eggs/kg/day (Group T) or 20 *O. dentatum* L3/kg/day (Group O). Group OT was infected with same levels of both *T. suis* and *O. dentatum* (Group OT) and Group C remained uninfected. In each group, six pigs were necropsied after 35 days and the remaining pigs after 71 days. Parasite E/S-antigen specific serum antibodies were quantified by an in-direct ELISA. qPCR was used to measure the expression of immune function related genes in the mucosa of proximal colon and the draining lymph node. Highly significant interactions were identified for *O. dentatum* specific IgG1 (p < 0.0001) and IgG2 (p < 0.0006) antibodies with a remarkable 2-fold higher antibody response in group OT pigs as compared to group O. These findings indicated that *T. suis* enhanced the antibody response against *O. dentatum* in Group OT. The gene expression data confirmed a strong Type 2 response to *T. suis* (e.g. marked increase in IL-13, ARG1 and CCL11) and clearly weaker in amplitude and/or delayed onset response to *O. dentatum* in the single infected group. Interactions were found between the two nematodes with regard to several cytokines, e.g. the increase in IL-13 observed in Group T was absent in Group OT (p = 0.06, proximal colon mucosa, 35 and 71 p.i.). Some of these immune response-related interactions may support, or even partially explain, the observed interactions between the two worm populations in co-infected pigs.

**General information**

State: Published

Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, University of Copenhagen, National Veterinary Institute Sweden, United States Department of Agriculture

Authors: Andreasen, A. (Ekstern), Petersen, H. H. (Intern), Kringel, H. (Ekstern), Iburg, T. M. (Ekstern), Skovgaard, K. (Intern), Dawson, H. (Ekstern), Urban Jr., J. F. (Ekstern), Thamsborg, S. M. (Ekstern)

Pages: 249-258

Publication date: 2015

Main Research Area: Technical/natural sciences

**Publication information**

Journal: Veterinary Parasitology

Volume: 207

Issue number: 3-4

ISSN (Print): 0304-4017

Ratings:

BFI (2018): BFI-level 2

Web of Science (2018): Indexed yes

BFI (2017): BFI-level 1

Scopus rating (2017): SNIP 1.215 SJR 1.275 CiteScore 2.55

Web of Science (2017): Indexed Yes

BFI (2016): BFI-level 1

Scopus rating (2016): CiteScore 2.49 SJR 1.228 SNIP 1.218

Web of Science (2016): Indexed yes

BFI (2015): BFI-level 1

Scopus rating (2015): SJR 1.21 SNIP 1.309 CiteScore 2.46

Web of Science (2015): Indexed yes

BFI (2014): BFI-level 1

Scopus rating (2014): SJR 1.324 SNIP 1.42 CiteScore 2.53

Web of Science (2014): Indexed yes

BFI (2013): BFI-level 1

Scopus rating (2013): SJR 1.262 SNIP 1.437 CiteScore 2.63

ISI indexed (2013): ISI indexed yes

Web of Science (2013): Indexed yes
Immune gene expression in the spleen of chickens experimentally infected with Ascaridia galli

Ascaridia galli is a gastrointestinal nematode infecting chickens. Chickens kept in alternative rearing systems or at free-range experience increased risk for infection with resulting high prevalences. A. galli infection causes reduced weight gain, decreased egg production and in severe cases increased mortality. More importantly, the parasitised chickens are more susceptible to secondary infections and their ability to develop vaccine-induced protective immunity against other diseases may be compromised. Detailed information about the immune response to the natural infection may be exploited to enable future vaccine development. In the present study, expression of immune genes in the chicken spleen during an experimental infection with A. galli was investigated using the Fluidigm (R) BioMark (TM) microfluidic qPCR platform which combines automatic high-throughput with attractive low sample and reagent consumption. Spleenic transcription of immunological genes was compared between infected chickens and non-infected controls at week 2, 6, and 9 p.i. corresponding to different stages of parasite development/maturation. At week 2 p.i. increased expression of IL-13 was observed in infected chickens. Increased expression of MBL, CRP, IFN-alpha, IL-1 beta, IL-8, IL-12 beta and IL-18 followed at week 6 p.i. and at both week 6 and 9 p.i. expression of DEF beta 1 was highly increased in infected chickens. In summary, apart from also earlier reported increased expression of the Th2 signature cytokine IL-13 we observed only few differentially expressed genes at week 2 p.i. which corresponds to the larvae histotrophic phase. In contrast, we observed increased expression of pro-inflammatory cytokines and acute phase proteins in infected chickens, by week 6 p.i. where the larvae re-enter the intestinal lumen. Increased expression of DEF beta 1 was observed in infected chickens at week 6 p.i. but also at week 9 p.i. which corresponds to a matured stage where adult worms are present in the intestinal lumen. (C) 2015 Elsevier B.V. All rights reserved.
An epidemic of foot-and-mouth disease (FMD) in a FMD-free country with large exports of livestock and livestock products would result in profound economic damage. This could be reduced by rapid and efficient control of the disease spread. The objectives of this study were to estimate the economic impact of a hypothetical FMD outbreak in Denmark based on changes to the economic assumptions of the model, and to investigate whether the control of an FMD epidemic can be improved by combining the enlargement of protection or surveillance zones with pre-emptive depopulation or emergency vaccination. The stochastic spatial simulation model DTU-DADS was used to simulate the spread of FMD in Denmark. The control strategies were the basic EU and Danish strategy, pre-emptive depopulation, suppressive or protective vaccination, enlarging protection or surveillance zones, and a combination of pre-emptive depopulation or emergency vaccination with enlarged protection or surveillance zones. Herds are detected either based on basic detection through the appearance of clinical signs, or as a result of surveillance in the control zones. The economic analyses consisted of direct costs and export losses. Sensitivity analysis was performed on uncertain and potentially influential input parameters. Enlarging the surveillance zones from 10 to 15 km, combined with pre-emptive depopulation over a 1-km radius around detected herds resulted in the lowest total costs. This was still the case even when the different input parameters were changed in the sensitivity analysis. Changing the resources for clinical surveillance did not affect the epidemic consequences. In conclusion, an FMD epidemic in Denmark would have a larger economic impact on the agricultural sector than previously anticipated. Furthermore, the control of a potential FMD outbreak in Denmark may be improved by combining pre-emptive depopulation with an enlarged protection or surveillance zone.
Increased B and T Cell Responses in M. bovis Bacille Calmette-Guérin Vaccinated Pigs Co-Immunized with Plasmid DNA Encoding a Prototype Tuberculosis Antigen

The only tuberculosis vaccine currently available, bacille Calmette-Guérin (BCG) is a poor inducer of CD8+ T cells, which are particularly important for the control of latent tuberculosis and protection against reactivation. As the induction of strong CD8+ T cell responses is a hallmark of DNA vaccines, a combination of BCG with plasmid DNA encoding a prototype TB antigen (Ag85A) was tested. As an alternative animal model, pigs were primed with BCG mixed with empty vector or codon-optimized pAg85A by the intradermal route and boosted with plasmid delivered by intramuscular electroporation. Control pigs received unformulated BCG. The BCG-pAg85A combination stimulated robust and sustained Ag85A-specific antibody, lymphoproliferative, IL-6, IL-10 and IFN-γ responses. IgG1/IgG2 antibody isotype ratio reflected the Th1 helper type biased response. T lymphocyte responses against purified protein derivative of tuberculin (PPD) were induced in all (BCG) vaccinated animals, but responses were much stronger in BCG-pAg85A vaccinated pigs. Finally, Ag85A-specific IFN-γ producing CD8+ T cells were detected by intracellular cytokine staining and a synthetic peptide, spanning Ag85A131-150 and encompassing two regions with strong predicted SLA-1*0401/SLA-1*0801 binding affinity, was promiscuously recognized by 6/6 animals vaccinated with the BCG-pAg85A combination. Our study provides a proof of concept in a large mammalian species, for a new Th1 and CD8+ targeting tuberculosis vaccine, based on BCG-plasmid DNA co-administration.
Increased microbe-receptor contact in early life – approaching immune regulation

The crucial colonization in early life educates immune receptors and cells of the body to form the immune system that we depend on during maintenance, disease, and repair. When regulatory mechanisms fail and the system itself becomes the
cause of disease, we should look to the proposed early window of opportunity, where it may be possible to affect the developing immune system towards tolerance.

We hypothesize that increased contact in early life between immune receptors and microbial-associated molecular patterns (MAMP), like TLR-4 and LPS, favors a regulatory immune environment later in life. Dextran Sulphate Sodium interrupts the barrier function of the gut wall by shaving the mucus layer. In low doses it may have the desired contact-increasing effect without inducing colitis-related disease.

Following low-dose DSS treatment in early life of BALB/c mice, we did a gene expression screening in ileum and colon together with cell counts in the spleen and mesenteric lymph nodes combined with sequencing the gut microbiota. We investigated the effect of DSS alone, and in combination with Ampicillin and LPS to elucidate the importance of bacterial ligands.

Our study shows that DSS changes the gut microbiota, and Ampicillin itself can act protective as well as activating on inflammatory markers in a time-dependent manner. It is apparent that DSS works differently in the ileum and colon for some genes. In some cases LPS as only ligand reduces inflammatory markers, but overall it is confirmed that the abundance in bacterial ligands is the most important factor for immune regulation.

The work was funded by LIFEPHARM and the Danish 3G Centre under the Danish Council for Strategic Research.

Influenza A(H10N7) Virus in Dead Harbor Seals, Denmark
Since April 2014, an outbreak of influenza in harbor seals has been ongoing in northern Europe. In Denmark during June-August, 152 harbor seals on the island of Anholt were found dead from severe pneumonia. We detected influenza A(H10N7) virus in 2 of 4 seals examined.
Influenza A H10N7 virus in dead harbor seals in Denmark 2015.pdf

DOIs:
10.3201/eid2104.141484

Source: FindIt
Source-ID: 274626359

Publication: Research - peer-review › Journal article – Annual report year: 2015
Influenza A virus H10N7 detected in dead harbor seals (Phoca vitulina) at several locations in Denmark 2014.

Influenza A virus (IAV) affects a wide range of species, though waterfowl is regarded the natural host for most IAV subtypes. Avian influenza (AI) viruses replicate in the intestinal tract of birds and are mainly transmitted by the fecal-oral route. Pinnipeds share the same shoreline habitats as many waterfowl species and are therefore potentially exposed to AIV. Outbreaks of AI in seals have been described in North America and Asia but prior to 2014 never in Europe. In 2014 massive deaths of harbor seals (Phoca vitulina) were reported in Northern Europe. In Denmark, harbor seals were initially found dead on the Danish island Anholt in Kattegat, which is the sea surrounded by Denmark, Norway and Sweden. Between June and August, 152 harbor seals were found dead. Four seals were submitted to the National Veterinary Institute in Denmark and diagnosed with severe pneumonia. Influenza A virus of the subtype H10N7 was detected in two out of four seals. Subsequently IAV was detected in dead harbor seals at several locations in Denmark. The IAV outbreak appeared to move with time to the west through the Limfjord to the North Sea and further down south along the west coast of Jutland to the Wadden Sea. Outbreaks were subsequently reported from Germany and The Netherlands. The aim of this study was to characterize the viruses detected at the several locations by molecular and phylogenetic analysis. All viruses were subtyped as H10N7 with genes of avian origin. The HA and NA genes of the viruses were highly similar to H10N7 IAV detected in harbor seals in Sweden in the spring of 2014 and in Germany in the autumn of 2014, suggesting that the same strain of virus had spread from Sweden to Denmark and further on to Germany.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Section for Virology, Anholt Gartneri & Naturpleje, Aalborg University
Publication date: 2015
Event: Abstract from 3rd International Symposium on Neglected Influenza Viruses, Athens, Georgia, United States.
Main Research Area: Technical/natural sciences
Electronic versions:
Abstract_H10N7_s_ler_submittet_3rd_Negl_Inf_Symposium.pdf

Inhibition studies of natural resin acids to Clostridium perfringens and Escherichia coli O149

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology
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Number of pages: 1
Publication date: 2015
Event: Abstract from 1st International Conference on Necrotic Enteritis in Poultry, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Electronic versions:
Abstract_book_NE_Conference_final.pdf

In situ prebiotics: enzymatic release of galacto-rhamnogalacturonan from potato pulp in vivo in the gastrointestinal tract of the weaning piglet

Prebiotics may be efficient for prevention of intestinal infections in humans and animals by increasing the levels of beneficial bacteria and thereby improving gut health. Using purified prebiotics may however not be cost-effective in the livestock production industry. Instead, prebiotic fibres may be released directly in the gastro-intestinal tract by feeding enzymes with a suitable substrate and allowing the prebiotics to be produced in situ. Using low doses, 0.03 % enzyme-to-substrate ratio, of the enzymes pectin lyase and polygalacturonase in combination with potato pulp, a low-value industrial by-product, we show that high molecular weight galacto-rhamnogalacturonan can be solubilized in the stomach of weaning piglets. The release of this fiber is in the order of 22–38 % of the theoretical amount, achieved within 20 min. The catalysis takes place mainly in the stomach of the animal and is then followed by distribution through the small intestines. To our knowledge, this is the first paper describing targeted production of prebiotics in an animal model.
In situ prebiotics for weaning piglets: In vitro production and fermentation of potato galactorhamnogalacturonan

Post weaning diarrhea (PWD) in pigs is a leading cause of economic loss in pork production worldwide. The current practice of using antibiotics and zinc to treat PWD is unsustainable due to the potential of antibiotic resistance and ecological disturbance, and novel methods are required. In this study, an in vitro model was used to test the possibility of producing prebiotic fiber in situ in the gastro-intestinal tract (GI-tract) of the piglet and the prebiotic activity of the resulting fiber in the terminal ileum. Soluble fiber were successfully produced from potato pulp, an industrial waste product, with a minimal enzyme dose in a simulated upper GI-model extracting 26.9 % of initial dry matter. The fiber was rich in galactose and galacturonic acid and was fermented at 2.5, 5 or 10 g/L in a glucose-free media inoculated with the gut contents of piglet terminal ileum. Fermentations of 5 g/L inulin or 5 g/L of a purified potato fiber were used as controls. The fibers showed high fermentability, evident by a dose-dependent drop in pH and increase in organic acids, with lactate in particularly being increased. Deep sequencing showed a significant increase in Lactobacillus and Veillonella and an insignificant increase in Clostridium as well as a decrease in Streptococcus. Multivariate analysis showed clustering of the treatment groups, with the purified potato fiber being clearly separated from the other groups as the microbiota composition was 60 % Lactobacillus and almost free of Clostridium. For animal studies, a dosage corresponding to the 5 g/L treatment is suggested.
Intestinal colonization of broiler chickens by Campylobacter spp. in an experimental infection study

Consumption of poultry meat is considered as one of the main sources of human campylobacteriosis, and there is clearly a need for new surveillance and control measures based on quantitative data on Campylobacter spp. colonization dynamics in broiler chickens. We conducted four experimental infection trials, using four isolators during each infection trial to evaluate colonization of individual broiler chickens by Campylobacter jejuni over time. Individual and pooled faecal samples were obtained at days 4, 7 and 12 post-inoculation (p.i.) and caecal samples at day 12 p.i. There were large differences between broiler chickens in the number of C. jejuni in caecal and faecal material. Faecal samples of C. jejuni ranged from 4·0 to 9·4 log c.f.u./g and from 4·8 to 9·3 log c.f.u./g in the caeca. Faecal c.f.u./g decreased with time p.i. Most variation in c.f.u. for faecal and caecal samples was attributed to broiler chickens and a minor part to isolators, whereas infection trials did not affect the total variance. The results showed that pooled samples within isolators had lower c.f.u./g compared to the arithmetic mean of the individual samples. There was a significant correlation between faecal c.f.u./g at days 4 and 7 p.i., days 7 and 12 p.i. and for caecal and faecal c.f.u./g at day 12 p.i.
Intrabronchial Microdialysis: Effects of Probe Localization on Tissue Trauma and Drug Penetration into the Pulmonary Epithelial Lining Fluid

Recent intrabronchial microdialysis data indicate that the respiratory epithelium is highly permeable to drugs. Of concern is whether intrabronchial microdialysis disrupts the integrity of the respiratory epithelium and thereby alters drug penetration into the pulmonary epithelial lining fluid (PELF). The objective of this study was to investigate the effect of intrabronchial microdialysis on the integrity of the bronchial epithelium. Microdialysis sampling in PELF in proximal (n=4) and distal bronchi (n=4) was performed after intravenous inulin and florfenicol administration in anaesthetized pigs. Inulin was used as a marker molecule of permeability of the epithelium, and florfenicol was used as test drug. Bronchial tissue was examined by histopathology (distal and proximal bronchi) and gene expression analysis (RT-qPCR, proximal bronchi) at the termination of the experiment (6.5hr). The microdialysis probe caused overt tissue trauma in distal bronchi, whereas no histopathological lesions were observed in proximal bronchi. A moderate up-regulation of the pro-inflammatory cytokines IL1B, IL6 and acute-phase reactant serum amyloid A was seen in proximal bronchi surrounding the microdialysis probes suggesting initiation of an inflammatory response. The observed up-regulation is considered to have limited impact on drug penetration during short-term studies. Inulin penetrated the respiratory epithelium in both proximal and distal bronchi without any correlation to histopathological lesions. Likewise, florfenicol penetration into PELF was unaffected by bronchial histopathology. However, this independency of pathology on drug penetration may not be valid for other antibiotics. We conclude that short-term microdialysis drug quantification can be performed in proximal bronchi without disruption of tissue integrity.

General information
State: Published
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Number of pages: 9
Pages: 242-250
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Basic & Clinical Pharmacology & Toxicology
Volume: 117
Issue number: 4
ISSN (Print): 1742-7835
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.51
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.57
BFI (2015): BFI-level 1
Intramuscular Priming and Intranasal Boosting Induce Strong Genital Immunity Through Secretory IgA in Minipigs Infected with Chlamydia trachomatis

International efforts in developing a vaccine against Chlamydia trachomatis have highlighted the need for novel immunization strategies for the induction of genital immunity. In this study, we evaluated an intramuscular (IM) prime/intranasal boost vaccination strategy in a Göttingen Minipig model with a reproductive system very similar to humans. The vaccine was composed of C. trachomatis subunit antigens formulated in the Th1/Th17 promoting CAF01 adjuvant. IM priming immunizations with CAF01 induced a significant cell-mediated interferon gamma and interleukin 17A response and a significant systemic high-titered neutralizing IgG response. Following genital challenge, intranasally boosted groups mounted an accelerated, highly significant genital IgA response that correlated with enhanced bacterial clearance on day 3 post infection. By detecting antigen-specific secretory component (SC), we showed that the genital IgA was locally produced in the genital mucosa. The highly significant inverse correlation between the vaginal IgA SC response and the chlamydial load suggests that IgA in the minipig model is involved in protection against C. trachomatis. This is important both for our understanding of protective immunity and future vaccination strategies against C. trachomatis and genital pathogens in general.

General information
State: Published
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Number of pages: 12
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Frontiers in Immunology
Issue number: 6
Article number: 628
ISSN (Print): 1664-3224
Ratings:
BFI (2018): BFI-level 1
Involvement of IRF4 dependent dendritic cells in T cell dependent colitis

Inflammatory Bowel Disease (IBD) is a chronic non-curable inflammatory disease of the intestine that affects as many as 1.4 million persons in the United States and 2.2 million persons in Europe. IBD results from abnormal immune response to bacterial components of the commensal microflora in genetically susceptible individuals and pathogenic CD4+ T cells, which accumulate in the inflamed mucosa, are believed to be key drivers of the disease. While dendritic cells (DCs) are important in the priming of intestinal adaptive immunity and tolerance their role in the initiation and perpetuation of chronic intestinal inflammation remains unclear. In the current study we used the CD45RBhi T cell transfer model of colitis to determine the role of IRF4 dependent DCs in intestinal inflammation. In this model naïve CD4+ T cells when transferred into RAG-/- mice, proliferate and expand in response to bacterial derived luminal antigen, localize to the intestinal mucosa and induce colitis. Adoptive transfer of naïve T cells into CD11cCre.IRF4fl/fl.RAG-1-/- mice resulted in reduced monocyte recruitment to the intestine and mesenteric lymph nodes (MLN) compared to Cre- controls. Inflammatory cytokines including IFNγ, TNFα and IL-6 also were reduced in the serum and intestinal tissues of these mice. Additionally CD11cCre.IRF4fl/fl.RAG-1-/- mice displayed significantly reduced numbers of CD4+ T cells in intestinal draining mesenteric lymph nodes and spleen but not the colonic lamina propria. Collectively these results suggest an important role for IRf4 dependent DCs in T cell driven colitis.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Lund University
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Number of pages: 1
Publication date: 2015
Event: Abstract from Keystone Symposia on Molecular and Cellular Biology - Dendritic Cells and Macrophages Reunited, Montreal, Canada.
Main Research Area: Technical/natural sciences
Electronic versions:
Involvement_of_IRF4_dependent_dendritic_cells_in_T_cell_dependent_colitis.docx
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2015
which accumulate in the inflamed mucosa, are believed to be key drivers of the disease. While dendritic cells (DCs) are important in the priming of intestinal adaptive immunity and tolerance their role in the initiation and perpetuation of chronic intestinal inflammation remains unclear. In the current study we used the CD45RBhi T cell transfer model of colitis to determine the role of IRF4 dependent DCs in intestinal inflammation. In this model naïve CD4+ T cells when transferred into RAG-1-/- mice, proliferate and expand in response to bacterial derived luminal antigen, localize to the intestinal mucosa and induce colitis. Adoptive transfer of naïve T cells into CD11cCre.IRF4fl/fl.RAG-1-/- mice resulted in reduced monocyte recruitment to the intestine and mesenteric lymph nodes (MLN) compared to Cre- controls. Inflammatory cytokines including IFNγ, TNFα and IL-6 also were reduced in the serum and intestinal tissues of these mice. Additionally CD11cCre.IRF4fl/fl.RAG-1-/- mice displayed significantly reduced numbers of CD4+ T cells in intestinal draining mesenteric lymph nodes and spleen but not the colonic lamina propria. Collectively these results suggest an important role for Irf4 dependent DCs in T cell driven colitis.

Involvement of two microRNAs in the early immune response to DNA vaccination against a fish rhabdovirus

Mechanisms that account for the high protective efficacy in teleost fish of a DNA vaccine expressing the glycoprotein (G) of Viral hemorrhagic septicemia virus (VHSV) are thought to involve early innate immune responses mediated by interferons (IFNs). Microribonucleic acids (miRNAs) are a diverse class of small (18–22 nucleotides) endogenous RNAs that potently mediate post-transcriptional silencing of a wide range of genes and are emerging as critical regulators of cellular processes, including immune responses. We have recently reported that miR-462 and miR-731 were strongly induced in rainbow trout infected with VHSV. In this study, we analyzed the expression of these miRNAs in fish following administration of the DNA vaccine and their potential functions. Quantitative RT-PCR analysis revealed the increased levels of miR-462, and miR-731 in the skeletal muscle tissue at the site of vaccine administration and in the liver of vaccinated fish relative to empty plasmid backbone-injected controls. The increased expression of these miRNAs in the skeletal muscle correlated with the increased levels of the type I interferon (IFN)-inducible gene Mx, type I IFN and IFN-γ genes at the vaccination site. Intramuscular injection of fish with either type I IFN or IFN-γ plasmid construct resulted in the upregulation of miR-462 and miR-731 in the skeletal muscle tissue at the site of vaccine administration and in the liver of vaccinated fish relative to empty plasmid backbone-injected controls. The increased expression of these miRNAs in the skeletal muscle correlated with the increased levels of the type I interferon (IFN)-inducible gene Mx, type I IFN and IFN-γ genes at the vaccination site. Intramuscular injection of fish with either type I IFN or IFN-γ plasmid construct resulted in the upregulation of miR-462 and miR-731 at the site of injection, suggesting that the induction of these miRNAs is elicited by IFNs. To analyze the function of miR-462 and miR-731, specific silencing of these miRNAs using anti-miRNA oligonucleotides was conducted in poly I:C-treated rainbow trout fingerlings. Following VHSV challenge, anti-miRNA-injected fish had faster development of disease and higher mortalities than control fish, indicating that miR-462/731 may be involved in IFN-mediated protection conferred by poly I:C.
IRF8-dependent DCs Play a Key Role in the Regulation of CD8 T Cell Responses to Epithelial-derived Antigen in the Steady State but not Inflammation

The intestinal immune system has the complex task of generating tolerance towards harmless antigens derived from our diet, commensal microflora or tissue, while maintaining the ability to mount protective immune responses to mucosal
Much of our understanding regarding the regulation of mucosal T cell responses stems from studies on CD4+ T cells. However, the intestinal mucosa is a major entry site for intracellular pathogens, whose control requires cross-presentation of cell-associated antigens for the induction of protective CD8+ T cell responses. To assess the regulation of mucosal CD8+ T cell priming and differentiation in the steady state and inflammatory setting, we utilized IFABP-tOva mice, in which Ovalbumin (Ova) is expressed as an epithelial-derived antigen in the small intestine. In this model Ova-specific CD8+ T cells were found to differentiate into two distinct subsets, CD107a/b+ cytotoxic T cells (CTLs) and FoxP3+ CD8+ T cells with regulatory potential. Interestingly, neither IRF8 nor IRF4 expression by intestinal dendritic cells (DCs) was crucial for the expansion of CTLs. In contrast, presence of IRF8 but not IRF4-dependent DCs was critical for the development of FoxP3+ CD8+ T cells in the steady state. However in the inflammatory setting, expansion of the FoxP3+ subset was not affected by the absence of IRF8-dependent DCs, suggesting that other subsets of intestinal antigen presenting cells (APCs) can compensate their function in an inflammatory milieu. Collectively these findings further our understanding of the mechanisms regulating CD8+ T cell responses in the intestinal mucosa and have potential implications for mucosal vaccine design.

Isolation of VHS and IHN from recent outbreaks on croatian rainbow trout farms

The aim of this report is to give detailed information on the diagnostic examination on transmissible spongiform encephalopathies (TSE) performed in Denmark during 2014. The present annual report is the 19th on this topic published by the National Veterinary Institute, Technical University of Denmark (DTU-VET).


The DTU-VET is the national reference laboratory of bovine spongiform encephalopathy (BSE) and TSE/Scrapie, and therefore the results of all neuropathological examinations on BSE and Scrapie in Denmark are given in the present report as in previous years.
Latent class analysis of bulk tank milk PCR and ELISA testing for herd level diagnosis of Mycoplasma bovis

The bacterium Mycoplasma bovis causes disease in cattle of all ages. An apparent increase in the occurrence of M. bovis associated outbreaks among Danish dairy cattle herds since 2011 has prompted a need for knowledge regarding herd-level diagnostic performance. Therefore, the objective of this study was to evaluate the herd-level diagnostic performance of an indirect ELISA test by comparison to a real-time PCR test when diagnosing M. bovis in cattle herds of bulk tank milk. Bulk tank milk samples from Danish dairy herds (N=3437) were analysed with both the antibody detecting BIO K 302 M. bovis ELISA kit and the antigen detecting PathoProof Mastitis Major-3 kit. As none of these are considered a gold standard test for herd-level diagnostics we applied a series of Bayesian latent class analyses for a range of ELISA cut-off values. The negative and positive predictive values were calculated for hypothetical true national prevalences (1, 5, 10, 15 and 20%) of infected herds. We estimated that the ELISA test had a median sensitivity and specificity of 60.4 [37.5-96.2 95% Posterior Credibility Interval] and 97.3 [94.0-99.8 95% PCI] at the currently recommended cut-off (37% Optical density Coefficient). These changed to 43.5 [21.1-92.5 95% PCI] and 99.6 [98.8-100 95% PCI] if the cut-off was increased to 50 ODC%. In addition, herd-level diagnosis by ELISA would result in fewer false positives at a cut-off value of 50 ODC% compared to 37 ODC% without compromising the negative predictive value.
**Leuconostoc rapi sp. nov., isolated from sous-vide cooked rutabaga**

A Gram-positive, ovoid lactic acid bacterium, strain LMG 27676T, was isolated from a spoiled sous-vide cooked rutabaga. 16S rRNA gene sequence analysis indicated that the novel strain belongs to the genus Leuconostoc, with Leuconostoc kimchi and Leuconostoc miyukkimchi as nearest neighbours (99.1 and 98.8% 16S rRNA gene sequence similarity towards the type strain, respectively). Phylogenetic analysis of the 16S rRNA gene, multilocus sequence analysis of the pheS, rpoA and atpA genes, and biochemical and genotypic characteristics allowed to differentiate strain LMG 27676T from all established Leuconostoc species. Strain LMG 27676T (= DSMZ 27776) therefore represents a new species, for which the name Leuconostoc rapi sp. nov. is proposed.
Lipidated alpha-Peptide/beta-Peptoid Hybrids with Potent Antiinflammatory Activity

In this study, we investigated, optimized, and characterized a novel subclass of host defense peptide (HDP) mimics based on a-peptide/beta-peptoid hybrid oligomers with an alternating cationic/hydrophobic design with respect to their ability to modulate the pro-inflammatory response by human primary leukocytes upon exposure to bacterial components. Structureactivity studies revealed that certain lipidated a-peptide/beta-peptoid hybrid oligomers possess anti-inflammatory activities in the submicromolar range with low cytotoxicity, and that the anti-inflammatory activity of the HDP mimics is dependent on the length and position of the lipid element(s). The resulting lead compound, Pam-(Lys-beta NSpe)(6)-NH2, blocks LPS-induced cytokine secretion with a potency comparable to that of polymyxin B. The mode of action of this HDP mimic appears not to involve direct LPS interaction since it, in contrast to polymyxin B, displayed only minor activity in the Limulus amebocyte lysate assay. Flow cytometry data showed specific interaction of a fluorophore-labeled lipidated a-peptide/beta-peptoid hybrid with monocytes and granulocytes indicating a cellular target expressed by these leukocyte subsets.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, University of Copenhagen
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Number of pages: 13
Pages: 801-813
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Medicinal Chemistry
Volume: 58
Issue number: 2
ISSN (Print): 0022-2623
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 6.25
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 6.06
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 2.529 SNIP 1.631 CiteScore 5.66
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 2.259 SNIP 1.693 CiteScore 5.55
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 2.293 SNIP 1.78 CiteScore 5.65
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 2.33 SNIP 1.756 CiteScore 5.52
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 2.259 SNIP 1.706 CiteScore 5.48
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.99 SNIP 1.586
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 2.012 SNIP 1.636
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 2.146 SNIP 1.615
Scopus rating (2007): SJR 2.085 SNIP 1.648
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.864 SNIP 1.713
Scopus rating (2005): SJR 1.9 SNIP 1.72
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 1.915 SNIP 1.841
Scopus rating (2003): SJR 1.721 SNIP 1.918
Scopus rating (2002): SJR 1.702 SNIP 1.806
Scopus rating (2001): SJR 1.655 SNIP 1.81
Scopus rating (2000): SJR 1.765 SNIP 1.804
Scopus rating (1999): SJR 1.791 SNIP 1.83
Original language: English
DOIs:
10.1021/jm501341h
Source: Findit
Source-ID: 274175593
Publication: Research - peer-review › Journal article – Annual report year: 2015

Long Range RNA-RNA interactions with the genome of classical swine fever virus

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Hadsbjerg, J. (Intern), Rasmussen, T. B. (Intern), Belsham, G. (Intern)
Number of pages: 1
Publication date: 2015
Event: Poster session presented at 10th International Congress for Veterinary Virology, Montpellier, France.
Main Research Area: Technical/natural sciences
Electronic versions:
PosterEpiESVV_final300dpi.pdf
Publication: Research - peer-review › Poster – Annual report year: 2015

Long Range RNA-RNA interactions with the genome of classical swine fever virus

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Hadsbjerg, J. (Intern), Rasmussen, T. B. (Intern), Belsham, G. (Intern)
Number of pages: 1
Publication date: 2015
Event: Poster session presented at 9th Annual Meeting of EPIZONE, Montpellier, France.
Main Research Area: Technical/natural sciences
Electronic versions:
PosterEpiESVV_final300dpi.pdf
Low-dose antibiotics: current status and outlook for the future

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Albert Einstein College of Medicine of Yeshiva University, University of Tennessee, Osaka University, Parnell Pharmaceuticals
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Pages: 112-113
Publication date: 2015

Host publication information
Title of host publication: Mechanisms of antibiotic resistance
Publisher: Frontiers Media SA
ISBN (Print): 978-2-88919-453-7
Series: Frontiers Research Topics
ISSN: 1664-8714
Main Research Area: Technical/natural sciences
Electronic versions: Book_Mechanisms_of_Antibiotic_Resistance.PDF
DOIs: 10.3389/fmicb.2014.00478

Lymphocyte Trafficking to Mucosal Tissues
Lymphocytes are the key cells of the adaptive immune system that provide antigen-specific responses tailored to the context of antigen exposure. Through cytokine release and antibody production, lymphocytes orchestrate and amplify the recruitment and function of other immune cells and contribute to host defense against invading pathogens and the pathogenesis of many inflammatory diseases. Lymphocyte function is critically dependent on their ability to traffic into the correct anatomic locations at the appropriate times. This process is highly regulated and requires that lymphocytes interact with various homing molecules and respond to tightly regulated navigational cues.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Harvard Medical School
Authors: Mikhak, Z. (Ekstern), Agace, W. W. (Intern), Luster, A. D. (Ekstern)
Pages: 805-830
Publication date: 2015

Host publication information
Title of host publication: Mucosal Immunology
Publisher: Elsevier
Volume: 1
Editors: Mestecky, J., Strober, W., Russell, M. W., Cheroutre, H., Lambrecht, B. N., Kelsall, B. L.
Edition: 4
ISBN (Print): 978-0-12-415847-4
Main Research Area: Technical/natural sciences
DOIs: 10.1016/B978-0-12-415847-4.00040-9

Mass mortalities in baltic sea eelpout (zoarces viviparous) caused by a new rhabdovirus

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, National Veterinary Institute Sweden, Swedish Agency for Marine and Water Management
Matrix-assisted laser desorption/ionization time of flight, MALDI-TOF, mass spectrometry for identification of fish pathogenic bacteria

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, National Veterinary Institute Sweden, Central Veterinary Institute
Authors: Jansson, E. (Ekstern), Eriksson, E. (Ekstern), Säker, E. (Ekstern), Dalsgaard, I. (Intern), Nonnemann, B. (Intern), Roozenburg, I. (Ekstern), Haenen, O. (Ekstern)
Number of pages: 2
Publication date: 2015
Event: Abstract from 17th International Conference on Diseases of Fish and Shellfish, Las Palmas, Spain.
Main Research Area: Technical/natural sciences
Electronic versions:
Extention_EAFP_MALDI_TOF.pdf
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2015

Matrix-assisted laser desorption/ionization time of flight, MALDI-TOF, mass spectrometry for identification of fish pathogenic bacteria

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, National Veterinary Institute Sweden, Central Veterinary Institute
Authors: Jansson, E. (Ekstern), Eriksson, E. (Ekstern), Säker, E. (Ekstern), Dalsgaard, I. (Intern), Nonnemann, B. (Intern), Roozenburg, I. (Ekstern), Haenen, O. (Ekstern)
Number of pages: 1
Publication date: 2015
Event: Poster session presented at 17th International Conference on Diseases of Fish and Shellfish, Las Palmas, Spain.
Main Research Area: Technical/natural sciences
Electronic versions:
17th_International_Conference_on_Diseases_of_Fish_And.pdf
Publication: Research - peer-review › Poster – Annual report year: 2015

Matrix-assisted laser desorption/ionization time of flight, meldi-tof, mass spectrometry for identification of fish pathogenic bacteria

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, National Veterinary Institute Sweden, Central Veterinary Institute, Wageningen University & Research
Authors: Jansson, E. (Ekstern), Eriksson, E. (Ekstern), Säker, E. (Ekstern), Dalsgaard, I. (Intern), Nonnemann, B. (Intern), Roozenburg, I. (Ekstern), Haenen, O. (Ekstern)
Pages: 384-384
Publication date: 2015
Mean effective sensitivity for Mycobacterium avium subsp. paratuberculosis infection in cattle herds

Background: Mycobacterium avium subsp. paratuberculosis (MAP) infections in cattle are generally challenging to detect and cost-effective test strategies are consequently difficult to identify. MAP-specific antibody ELISAs for milk and serum are relatively inexpensive, but their utility is influenced by a number of factors such as herd size, herd composition and diagnostic sensitivity. The sensitivity of the test increases with the age of the tested animal, and therefore the general, or "mean effective sensitivity" (defined as the mean of the sensitivities for all animals within a population, MES), for detecting MAP within a herd is dependent upon the age distribution of the herd. For this study we used a dataset of cattle from 4,259 dairy herds and 4,078 non-dairy herds. The aim was to investigate the MES for groups of cattle considered to be reasonable entities for MAP surveillance and control, in order to assist the decision-makers in planning and optimizing these programs economically. We compared six different groups of cattle (three dairy and three non-dairy) in Denmark by calculating the MES for each herd in each group.

Results: The distribution of MES showed a large variation within and between groups, and in some groups we found a bimodal distribution of MES. Dairy herds generally showed higher MES than non-dairy herds. Dairy herds in a control programme for paratuberculosis showed a MES similar to all other dairy herds from which animals >2.0 years were tested (both groups had a median MES = 0.60). For the non-dairy groups, the sensitivity became much higher when animals <2.0 years and herds with less than 25 cattle were excluded, resulting in a median MES of 0.65.

Conclusion: The results showed that MES could indicate the effectiveness of testing different cattle groups for MAP, given that the data used are unbiased.

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Department of Applied Mathematics and Computer Science, Dynamical Systems, University of Copenhagen
Authors: Kirkeby, C. (Intern), Græsbøll, K. (Intern), Hisham Beshara Halasa, T. (Intern), Toft, N. (Intern), Nielsen, S. S. (Ekstern)
Number of pages: 6
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: B M C Veterinary Research
Volume: 11
Issue number: 1
Article number: 190
ISSN (Print): 1746-6148
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.108 SJR 0.934 CiteScore 2.16
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.83 SJR 0.87 SNIP 1.011
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.981 SNIP 1.009 CiteScore 1.86
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.943 SNIP 1.018 CiteScore 1.81
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.861 SNIP 0.853 CiteScore 1.85
Mechanisms of antibiotic resistance

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Tennessee, Osaka University, University of Washington, California State University, University of Strathclyde, Chinese Academy of Sciences
Number of pages: 3
Pages: 5-7
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication Information
Journal: Frontiers in Microbiology
Volume: 6
Article number: 34
ISSN (Print): 1664-302X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 4.19 SJR 1.699 SNIP 1.174
Mechanisms of antibiotic resistance

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Tennessee, Osaka University, California State University, Chinese Academy of Sciences
Number of pages: 226
Publication date: 2015

Publication information
Publisher: Frontiers Media SA
ISBN (Print): 978-2-88919-453-7
Original language: English
Series: Frontiers Research Topics
ISSN: 1664-8714
Main Research Area: Technical/natural sciences
DOIs:
10.3389/978-2-88919-453-7
Source: PublicationPreSubmission
Source-ID: 110880934
Publication: Research - peer-review › Book – Annual report year: 2015

MicroRNA regulation of TLRs in a post-influenza animal model
Introduction
Substantial morbidity and mortality is caused by secondary bacterial infections occurring in individuals after influenza A
virus (IAV) infection. Results from studies in mice suggest that this may in part be due to a lack of responsiveness to Toll-like receptor (TLR) ligands in the post-IAV infected individual. Using the pig as an animal model, we have identified microRNAs (miRNAs) that are differentially expressed in lung tissue two weeks after challenge compared to uninfected controls, i.e. well after the infection has cleared. The role for differential expression of miRNA at this late time point remains unclear. We therefore seek to examine the potential involvement of miRNAs in the translational regulation of TLRs and associated proteins, thus contributing to the lowered responsiveness to bacterial TLR ligands at this late time point, making the individual vulnerable to secondary infections.

Methods and outcome
Pigs were experimentally challenged with a Danish reassortant IAV strain (A/sw/Denmark/12687/03(H1N2)). Lung tissue was harvested 14 days after challenge, as well as from uninfected control animals. Using RNAseq and high-throughput RT-qPCR, we quantified the expression of relevant miRNAs (e.g. miR-335 and miR-146a-5p) and mRNA levels of relevant miRNA targets. Transcriptional analysis at the site of infection reveals a set of miRNAs to be regulated one week after the pigs had cleared the IAV infection (i.e. two weeks after challenge). This set included miRNAs experimentally validated or in silico predicted to bind to and regulate transcripts of TLRs and relevant co-factors and transcription factors (online tools). The antiviral immune response elicited by IAV infection thus includes late miRNA regulation, which in turn may be at the expense of host responsiveness to bacterial TLR ligands.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Section for Virology, IDT-Biologika GmbH
Authors: Brogaard, L. (Intern), Heegaard, P. M. H. (Intern), Larsen, L. E. (Intern), Dürrwald, R. (Ekstern), Schlegel, M. (Ekstern), Skovgaard, K. (Intern)
Number of pages: 1
Publication date: 2015
Main Research Area: Technical/natural sciences
Electronic versions:
Abstract_TOLL2015_Louise_Brogaard_1.pdf

Bibliographical note
Poster presentation
Source: PublicationPreSubmission
Source-ID: 118949835
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2015

Microsatellite typing of Echinococcus multilocularis from naturally infected Danish and Swedish red foxes (Vulpes vulpes)

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, ANSES - French Agency for Food, Environmental and Occupational Health & Safety, National Veterinary Institute Sweden, University of France-Comté
Number of pages: 1
Publication date: 2015
Event: Abstract from 6th Conference of the Scandinavian-Baltic Society for Parasitology (CSBSP6), Uppsala, Sweden.
Main Research Area: Technical/natural sciences
Electronic versions:
15.04_SBSP_Microsatellite_typing_of_Em.pdf
Source: PublicationPreSubmission
Source-ID: 108239777
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2015

MLVA analysis of Salmonella

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Statens Serum Institut
Authors: Kristine Kjeldsen, M. (Ekstern), Torpdal, M. (Ekstern), Pedersen, K. (Intern), Nielsen, E. M. (Ekstern)
Number of pages: 1
Molecular characterization of AI viruses from poultry and wild bird surveillance in Denmark

Infection with avian influenza virus (AIV) in poultry may cause devastating disease although the same virus may not cause disease in wild birds. Since AIV viruses can be exchanged between poultry and wild birds, surveillance in wild birds provides important knowledge for control of disease in poultry. AIV’s from the Danish wild bird active surveillance were characterized, focusing on viruses from 2012, and from outbreaks of AI in poultry in Denmark. The matrix (M) gene from more than 50 viruses of different subtypes and the hemagglutinin (HA) gene from more than 30 subtype H5 low pathogenic viruses were sequenced and compared by alignment and phylogenetic analyses. The aim was to evaluate: the origin of viruses from outbreaks of AI in Danish poultry, the design of active surveillance in Denmark, and the suitability of the molecular diagnostic RT-PCR tests employed. All M-genes from Danish viruses grouped phylogenetically with Eurasian lineage viruses. Grouping among Danish sequences was not correlated to place or to the time of sampling within the same year, although there was a tendency to grouping according to the year of sampling. Similar results were observed for H5 sequences. M and H5/H7 gene sequences from poultry showed a high degree of similarity to Danish wild bird sequences, suggesting exchange of viruses between geographically close wild birds and poultry. Significant drift was observed in both M and H5 gene sequences that are important for adequate molecular diagnostics, thus highlighting the importance of continuous surveillance and molecular characterization of AI viruses.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, University of Copenhagen
Authors: Larsen, L. E. (Intern), Kroeg, J. S. (Intern), Madsen, J. J. (Ekstern), Thorup, K. (Ekstern), Hjulsager, C. K. (Intern)
Event: From abstract 9th International Symposium on Avian Influenza, Athens, Georgia, United States.
Main Research Area: Technical/natural sciences
Electronic versions:
Molecular_characterization_of_AI_viruses_from_poultry_and_wild_bird_surveillance_in_Denmark_til_ORBIT.pdf

Bibliographical note
Abstract for oral presentation by Charlotte K Hjulsager at 9th International Symposium on Avian Influenza, Athens, Georgia, US. April 12-15, 2015.
Source: PublicationPreSubmission
Source-ID: 112051314
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2015

Molecular Epidemiology and Evolution of Influenza Viruses Circulating within European Swine between 2009 and 2013

The emergence in humans of the A(H1N1)pdm09 influenza virus, a complex reassortant virus of swine origin, highlighted the importance of worldwide influenza virus surveillance in swine. To date, large-scale surveillance studies have been reported for southern China and North America, but such data have not yet been described for Europe. We report the first large-scale genomic characterization of 290 swine influenza viruses collected from 14 European countries between 2009 and 2013. A total of 23 distinct genotypes were identified, with the 7 most common comprising 82% of the incidence. Contrasting epidemiological dynamics were observed for two of these genotypes, H1HuN2 and H3N2, with the former showing multiple long-lived geographically isolated lineages, while the latter had short-lived geographically diffuse lineages. At least 32 human-swine transmission events have resulted in A(H1N1)pdm09 becoming established at a mean frequency of 8% across European countries. Notably, swine in the United Kingdom have largely had a replacement of the endemic Eurasian avian virus-like (“avian-like”) genotypes with A(H1N1)pdm09-derived genotypes. The high number of reassortant genotypes observed in European swine, combined with the identification of a genotype similar to the A(H3N2)v genotype in North America, underlines the importance of continued swine surveillance in Europe for the purposes of maintaining public health. This report further reveals that the emergences and drivers of virus evolution in swine differ at the global level.

IMPORTANCE The influenza A(H1N1)pdm09 virus contains a reassortant genome with segments derived from separate virus lineages that evolved in different regions of the world. In particular, its neuraminidase and matrix segments were derived from the Eurasian avian virus-like (“avian-like”) lineage that emerged in European swine in the 1970s. However, while large-scale genomic characterization of swine has been reported for southern China and North America, no equivalent study has yet been reported for Europe. Surveillance of swine herds across Europe between 2009 and 2013 revealed that the A(H1N1)pdm09 virus is established in European swine, increasing the number of circulating lineages in
the region and increasing the possibility of the emergence of a genotype with human pandemic potential. It also has implications for veterinary health, making prevention through vaccination more challenging. The identification of a genotype similar to the A(H3N2)v genotype, causing zoonoses at North American agricultural fairs, underlines the importance of continued genomic characterization in European swine.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Wellcome Trust Sanger Institute, Animal and Plant Health Agency, University of Oxford, Ghent University, Ploufragan-Pluzané Laboratory, Istituto Zooprofilattico Sperimentale della Lombardia e dell’Emilia, Kimron Veterinary Institute, National Food Chain Safety Office, Merial S.A.S., Laboratorios HIPRA SA, Panstwowy Instytut Weterynaryjny, IDT-Biologika GmbH, Finnish Food Safety Authority, Central Veterinary Institute
Pages: 9920-9931
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Virology
Volume: 89
Issue number: 19
ISSN (Print): 0022-538X
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 1.096 SJR 2.853 CiteScore 4.24
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 4.42 SJR 3.114 SNIP 1.124
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 3.282 SNIP 1.132 CiteScore 4.42
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 3.187 SNIP 1.208 CiteScore 4.4
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 3.496 SNIP 1.251 CiteScore 4.92
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 3.19 SNIP 1.222 CiteScore 5.2
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 3.429 SNIP 1.282 CiteScore 5.37
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 3.596 SNIP 1.277
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 3.631 SNIP 1.306
Molecular tracing of VHS in Denmark

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Norwegian Veterinary Institute, Friedrich Loeffler Institute, Danish Veterinary and Food Administration
Authors: Mikkelsen, S. S. (Intern), Schuetze, H. (Ekstern), Korsholm, H. (Ekstern), Jensen, B. B. (Ekstern), Bruun, M. S. (Intern), Olesen, N. J. (Intern)
Pages: 194-194
Publication date: 2015

Host publication information
Title of host publication: 17th International Conference on Diseases of Fish And Shellfish : Abstract book
Place of publication: Las Palmas
Publisher: European Association of Fish Pathologists
Article number: O-186
Main Research Area: Technical/natural sciences
Conference: 17th International Conference on Diseases of Fish and Shellfish, Las Palmas, Spain, 07/09/2015 - 07/09/2015
Electronic versions:
Book_of_abstracts_17th_International_conference_on_Diseases_of_Fish_and_Shellfish.pdf
Source: PublicationPreSubmission
Source-ID: 118580288
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2015

Monitoring PRRS based on laboratory submissions: a simulation study to evaluate detection algorithms performance

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology
Authors: Lopes Antunes, A. C. (Intern), Dorea, F. (Ekstern), Hisham Beshara Halasa, T. (Intern), Toft, N. (Intern)
Monitoring PRRS based on laboratory submissions: A simulation study to evaluate detection algorithms performance.

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, National Veterinary Institute Sweden
Authors: Lopes Antunes, A. C. (Intern), Dorea, F. (Ekstern), Hisham Beshara Halasa, T. (Intern), Toft, N. (Intern)
Number of pages: 1
Publication date: 2015
Main Research Area: Technical/natural sciences
Electronic versions:
ACANTUNES.ECVPH15.pdf
Source: PublicationPreSubmission
Source-ID: 116878342
Publication: Research - peer-review › Poster – Annual report year: 2015

Monitoring PRRS sero-prevalence in Danish breeding herds: Evaluation of algorithms performance

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, National Veterinary Institute Sweden
Authors: Lopes Antunes, A. C. (Intern), Dorea, F. (Ekstern), Hisham Beshara Halasa, T. (Intern), Toft, N. (Intern)
Number of pages: 1
Publication date: 2015
Event: Poster session presented at Annual Conference of The Society for Veterinary Epidemiology and Preventive Medicine, Ghent, Belgium.
Main Research Area: Technical/natural sciences
Electronic versions:
AC_SVEPM_FINAL.pdf
Source: PublicationPreSubmission
Source-ID: 107222841
Publication: Research - peer-review › Poster – Annual report year: 2015

Morphological and molecular analyses of larval taeniid species in small mammals from contrasting habitats in Denmark
Taeniid infections in intermediate hosts manifest themselves as extraintestinal larval stages which, in early development, lack species-specific characteristics. The inability to distinguish infections of zoonotic importance such as Echinococcus multilocularis from other taeniid infections that have mainly veterinary significance stimulated the development of species-specific molecular diagnostics. In this study, the prevalence of taeniid infections in potential intermediate hosts was evaluated using both morphological diagnosis and a newly described multiplex Polymerase Chain Reaction (PCR) for species determination. Small mammals (N=719) were trapped in three different types of habitats in north-east Zealand, Denmark. The sensitivity of the multiplex PCR (90.5%) exceeded that of morphological examination (57.9%) for identifying 95 taeniid infections. The use of the multiplex PCR resulted in higher prevalence rates due to improved detection of immature liver infections with Hydatigera taeniaeformis and Versteria mustelae, but did not affect the observed prevalence rates of peritoneal metacestodes of Taenia polycantha. The prevalence of taeniid infections showed a significant difference according to habitat type, potentially identifying a 'sylvatic' transmission and an 'urban' transmission with
marked variation among different taeniid species. Versteria mustelae and T. polyacantha were more prevalent in rural forests, while infections with H. taeniaeformis were dominant in urban parks/forests and in residential and farm gardens. The multiplex PCR facilitated a better utilization of wildlife samples by yielding a higher number of definitive diagnoses of ambiguous taeniid infections in liver lesions, allowing for more accurate epidemiological data and, hence, a more accurate risk assessment.

**General information**

State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Copenhagen
Authors: Al-Sabi, M. N. S. (Intern), Jensen, P. M. (Ekstern), Chrestensen, M. U. (Ekstern), Kapel, C. M. O. (Ekstern)
Number of pages: 6
Pages: 112-117
Publication date: 2015
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Journal of Helminthology
Volume: 89
Issue number: 1
ISSN (Print): 0022-149X
Ratings:

BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.712 SJR 0.553 CiteScore 1.28
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.544 SNIP 0.745 CiteScore 1.13
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.586 SNIP 0.859 CiteScore 1.23
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.466 SNIP 0.745 CiteScore 0.98
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.599 SNIP 0.776 CiteScore 1.23
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.596 SNIP 0.903 CiteScore 1.38
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.639 SNIP 0.783 CiteScore 1.22
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.721 SNIP 0.763
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.404 SNIP 0.635
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.752 SNIP 0.921
Scopus rating (2007): SJR 0.478 SNIP 0.829
Scopus rating (2006): SJR 0.456 SNIP 0.665
Scopus rating (2005): SJR 0.32 SNIP 0.526
Scopus rating (2004): SJR 0.405 SNIP 0.764
Scopus rating (2003): SJR 0.477 SNIP 0.881
Scopus rating (2002): SJR 0.536 SNIP 0.719
Scopus rating (2001): SJR 0.439 SNIP 0.839
MyD88 Signaling Regulates Steady-State Migration of Intestinal CD103⁺ Dendritic Cells Independently of TNF-α and the Gut Microbiota

Intestinal homeostasis and induction of systemic tolerance to fed Ags (i.e., oral tolerance) rely on the steady-state migration of small intestinal lamina propria dendritic cells (DCs) into draining mesenteric lymph nodes (MLN). The majority of these migratory DCs express the α integrin chain CD103, and in this study we demonstrate that the steady-state mobilization of CD103⁺ DCs into the MLN is in part governed by the IL-1R family/TLR signaling adaptor molecule MyD88. Similar to mice with complete MyD88 deficiency, specific deletion of MyD88 in DCs resulted in a 50–60% reduction in short-term accumulation of both CD103⁺CD11b⁺ and CD103⁺CD11b⁻ DCs in the MLN. DC migration was independent of caspase-1, which is responsible for the inflammasomedependent proteolytic activation of IL-1 cytokine family members, and was not affected by treatment with broad-spectrum antibiotics. Consistent with the latter finding, the proportion and phenotypic composition of DCs were similar in mesenteric lymph from germ-free and conventionally housed mice. Although TNF-α was required for CD103⁺ DC migration to the MLN after oral administration of the TLR7 agonist R848, it was not required for the steady-state migration of these cells. Similarly, TLR signaling through the adaptor molecule Toll/IL-1R domain-containing adapter inducing IFN-β and downstream production of type I IFN were not required for steady-state CD103⁺ DC migration. Taken together, our results demonstrate that MyD88 signaling in DCs, independently of the microbiota and TNF-α, is required for optimal steady-state migration of small intestinal lamina propria CD103⁺ DCs into the MLN.
BFI (2017): BFI-level 2
Scopus rating (2017): SJR 2.837 SNIP 1.112 CiteScore 4.55
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 4.79 SJR 3.474 SNIP 1.176
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 3.571 SNIP 1.26 CiteScore 5.05
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 3.744 SNIP 1.271 CiteScore 5.03
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 3.909 SNIP 1.35 CiteScore 5.61
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 4.011 SNIP 1.362 CiteScore 5.82
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 4.06 SNIP 1.347 CiteScore 5.67
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 4.165 SNIP 1.306
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 4.157 SNIP 1.338
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 4.609 SNIP 1.322
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 4.655 SNIP 1.375
Web of Science (2007): Indexed yes
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 4.328 SNIP 1.465
Scopus rating (2004): SJR 4.227 SNIP 1.457
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 4.409 SNIP 1.484
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 4.302 SNIP 1.522
Scopus rating (2000): SJR 4.152 SNIP 1.518
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 4.568 SNIP 1.604
Original language: English
DOIs:
10.4049/jimmunol.1500210
Publication: Research - peer-review › Journal article – Annual report year: 2015
Necrotizing Enterocolitis in Preterm Pigs Is Associated with Increased Density of Intestinal Mucosa-Associated Bacteria Including Clostridium perfringens

Background: Necrotizing enterocolitis (NEC) is associated with changes in the luminal gut microbiota. It is not known whether the mucosa-associated microbiota is affected by NEC and stimulates inflammatory lesions. Objective: We hypothesized that the density of the mucosa-associated microbiota correlates with NEC severity in preterm pigs and that in vitro infection with increasing densities of Clostridium perfringens, which has been associated with NEC in preterm infants, would lead to a transcriptional response related to the inflammatory conditions of NEC. Methods: First, we determined the density of total bacteria and C. perfringens in the distal small intestinal mucosa of 58 NEC and healthy preterm pigs using quantitative PCR. Next, we analyzed in IPEC-J2 cells the effect of different infection densities of C. perfringens type A on the expression of genes related to intestinal function and immune response. Results: Total bacterial and C. perfringens densities were higher in NEC versus healthy pigs and correlated positively with NEC severity. In IPEC-J2 cells, expression levels of inflammation-related genes (CCL5, NFKBIA, IL8, IL1RN, and TNFAIP3) increased, while the expression of the sodium/glucose co-transporter (SLC5A1) decreased, with increasing density of C. perfringens. Conclusions: Total bacterial and C. perfringens densities were higher in NEC versus healthy pigs and correlated positively with NEC severity. In IPEC-J2 cells expression levels of inflammation-related genes (CCL5, NFKBIA, IL8, IL1RN, and TNFAIP3) increased, while the expression of the sodium/glucose co-transporter (SLC5A1) decreased, with increasing density of C. perfringens.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, University of Copenhagen
Authors: Støy, A. C. F. (Intern), Mølbak, L. (Intern), Delègue, C. L. (Ekstern), Thymann, T. (Ekstern), Sangild, P. T. (Ekstern), Heegaard, P. M. H. (Intern), Manurung, S. (Intern), Skovgaard, K. (Intern)
Pages: 188-195
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Neonatology
Volume: 108
Issue number: 3
ISSN (Print): 1661-7800
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.118 SJR 1.114 CiteScore 2.55
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 1.355 SNIP 1.262 CiteScore 2.47
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.501 SNIP 1.288 CiteScore 2.41
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.366 SNIP 1.223 CiteScore 2.26
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.423 SNIP 1.357 CiteScore 2.38
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.21 SNIP 1.325 CiteScore 2.46
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.231 SNIP 1.107 CiteScore 2.4
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.064 SNIP 1.089
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.901 SNIP 0.885
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.834 SNIP 0.843
Scopus rating (2007): SJR 0.712 SNIP 0.754
Scopus rating (2006): SJR 0.639 SNIP 0.769
Scopus rating (2005): SJR 0.52 SNIP 0.64
New filtration system for efficient recovery of waterborne Cryptosporidium oocysts and Giardia cysts

Aims
To develop a filtration unit for efficient recovery of waterborne Cryptosporidium oocysts and Giardia cysts ((oo-)cysts) in drinking water.

Methods and Results
This unit utilizes a metallic filter and an ultrasound transducer for eluting (oo-)cysts, with a fixed retentate backwash volume; approx. 400l. Changes in the viability was evaluated by seeding wild type (oo-)cysts (1x10(4)) followed by sonication for 5, 10, 20 or 40s (five replicates for each period). Flow cytometry analysis showed negligible increase in the mortality of (oo-)cysts exposed to 5-10s of sonication. Recovery rate was assessed by seeding ColorSeed (10 replicates) into the filter unit followed by air backwash to a glass slide and counting of (oo-)cysts by epifluorescent microscopy. High recovery rates (mean±SD) were found: 84.9±48 for Giardia cysts and 70%±65 for Cryptosporidium oocysts. DNA of seeded wild type (oo-)cysts (1x10(2); 10 replicates) was successfully amplified using real-time PCR. Conclusions
The use of a metallic filter, sonication and air backwash were key factors for creating a highly efficient system for recovery of apparently undamaged protozoa. Significance and Impact of the Study
This reagent-less system can be used for monitoring of parasite contamination in drinking water.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Grundfos Management A/S, University of Copenhagen
Number of pages: 10
Pages: 894-903
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Applied Microbiology
Volume: 119
Issue number: 3
ISSN (Print): 1364-5072
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.41
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.41
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.57
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.56
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.69
New neonatal porcine diarrhoea syndrome in Danish pigs. Characterisation of viral findings in diseased and healthy control animals

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Section for Bacteriology, Pathology and Parasitology, Pig Research Centre, Swedish University of Agricultural Sciences, Statens Serum Institut
Authors: Larsen, L. E. (Intern), Goecke, N. B. (Intern), Kongsted, H. (Ekstern), Boye, M. (Intern), Hjulsager, C. K. (Intern), Granberg, F. (Ekstern), Kølsen Fischer, T. (Ekstern), Midgley, S. (Ekstern)
Pages: 181-181
Publication date: 2015

Host publication information
Title of host publication: Proceedings of the 7th European Symposium of Porcine Health Management
Place of publication: Nantes, France
Article number: P108
Main Research Area: Technical/natural sciences
Conference: 7th European Symposium of Porcine Health Management, Nantes, France, 22/04/2015 - 22/04/2015
Source: PublicationPreSubmission
Source-ID: 119056709
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2015

New reassortant and enzootic European swine influenza 1 viruses transmits efficiently through direct contact in the ferret model

The reverse zoonotic events that introduced the 2009 pandemic influenza virus into pigs have drastically increased the diversity of swine influenza viruses in Europe. The pandemic potential of these novel reassortments is still unclear, necessitating enhanced surveillance of European pigs with additional focus on risk assessment of these new viruses. In this study, four European swine influenza viruses were assessed for their zoonotic potential. Two of the four viruses were
enzootic viruses of subtype H1N2 (with avian-like H1) and H3N2 and two were new reassortants, one with avian-like H1 and human-like N2 and one with 2009 pandemic H1 and swine-like N2. All viruses replicated to high titers in nasal wash- and nasal turbinate samples from inoculated ferrets and transmitted efficiently by direct contact. Only the H3N2 virus transmitted to naïve ferrets via the airborne route. Growth kinetics using a differentiated human bronchial epithelial cell line showed that all four viruses were able to replicate to high titers. Further, the viruses revealed preferential binding to the α2,6-sialylated glycans and investigation of the antiviral susceptibility of the viruses revealed that all were sensitive to neuraminidase inhibitors. These findings suggest that these viruses have the potential to infect humans and further underline the need for continued surveillance as well as biological characterization of new influenza A viruses.

**General information**
State: Published
Organisations: National Veterinary Institute, Section for Virology, Section for Bacteriology, Pathology and Parasitology, St. Jude Children’s Research Hospital
Authors: Fobian, K. (Intern), P. Fabrizio, T. (Ekstern), Yoon, S. (Ekstern), Hansen, M. S. (Intern), Webby, R. J. (Ekstern), Larsen, L. E. (Intern)
Pages: 1603-1612
Publication date: 2015
Main Research Area: Technical/natural sciences

**Publication information**
Journal: Journal of General Virology
Volume: 96
Issue number: 7
ISSN (Print): 0022-1317
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.877 SJR 1.325 CiteScore 2.68
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.93 SJR 1.544 SNIP 0.891
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.738 SNIP 0.998 CiteScore 3.26
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.69 SNIP 1.057 CiteScore 3.25
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.764 SNIP 1.154 CiteScore 3.64
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.525 SNIP 1.034 CiteScore 3.28
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.684 SNIP 1.145 CiteScore 3.6
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.678 SNIP 1.053
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.662 SNIP 1.127
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.648 SNIP 1.068
Next Generation Sequencing of Classical Swine Fever Virus

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Rasmussen, T. B. (Intern)
Pages: 14-14
Publication date: 2015

Host publication information
Title of host publication: Workshop of the African and Classical Swine Fever National Reference Laboratories (ASF and CSF) : Abstract book
Place of publication: Madrid, Spain
Main Research Area: Technical/natural sciences
Workshop: Workshop of the African and Classical Swine Fever National Reference Laboratories, Madrid, Spain, 09/06/2015 - 09/06/2015
Electronic versions:
WorkshopASF_CSF_AGENDA_and_ABSTRACTS.pdf
Source: PublicationPreSubmission
Source-ID: 116892819
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2015

Non-invasive assessment of in-vitro embryo quality to improve transfer success

Although IVF has been performed routinely for many years to help couples with fertility problems and in relation to modern breeding of farm animals, pregnancy rates after transfer to a recipient have not improved during the last decade. Early prediction of the viability of in-vitro developed embryos before the transfer to a recipient still remains challenging. Presently, the predominant non-invasive technique for selecting viable embryos is based on morphology, where parameters such as rates of cleavage and blastocyst formation as well as developmental kinetics are evaluated mostly subjectively. The simple morphological approach is, however, inadequate for the prediction of embryo quality, and several studies have focused on developing new non-invasive methods using molecular approaches based particularly on proteomics, metabolomics and most recently small non-coding RNA, including microRNA. This review outlines the potential of several non-invasive in-vitro methods based on analysis of spent embryo culture medium.
Non-random patterns in viral diversity

It is currently unclear whether changes in viral communities will ever be predictable. Here we investigate whether viral communities in wildlife are inherently structured (inferring predictability) by looking at whether communities are assembled through deterministic (often predictable) or stochastic (not predictable) processes. We sample macaque faeces across
nine sites in Bangladesh and use consensus PCR and sequencing to discover 184 viruses from 14 viral families. We then use network modelling and statistical null-hypothesis testing to show the presence of non-random deterministic patterns at different scales, between sites and within individuals. We show that the effects of determinism are not absolute however, as stochastic patterns are also observed. In showing that determinism is an important process in viral community assembly we conclude that it should be possible to forecast changes to some portion of a viral community, however there will always be some portion for which prediction will be unlikely.
Ny forskning optimerer overvågning af paratuberkulose

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology
Authors: Kirkeby, C. (Intern)
Pages: 20-21
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Bovilogisk
Issue number: September
ISSN (Print): 0906-009X
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Original language: Danish
Links:
http://www.bovilogisk.dk/artikel?id=86127
Publication: Communication › Journal article – Annual report year: 2015

Overvågning af aviær influenza i vilde fugle i Danmark 2014

real time RT-PCR der spezifisch detekterer HA-genet i H1N1pdm09 virus 3) Isolering af virus i MDCK celler 4) Subtypning af positive virusisolater ved sekvensanalyse (HA og NA generne) 5) Komplett genotyp karakterisering af udvalgte virusisolater. Der blev totalt i 2014 iværksat undersøgelse for influenza A virus på 1173 prøver fordelt på 538 indsendelser fra 422 besætninger. I alt var 435 (37 %) af prøvene positive og 239 (44 %) af indsendelserne havde minimum en positiv prøve fordelt på 199 forskellige besætninger. Indsendelserne fodelse sig over hele landet og over hele året. Der var flest indsendelser til undersøgelse i de kolde måneder, men influenza virus blev påvist med næsten samme hyppighed hele året. I alt blev influenza viruspositive indsendelser opdyrtet i MDCK celler. De dyrkede virusisolater blev undersøgt ved sekvensanalyse for at bestemme subtypen. Disse analyser viste, at de to mest almindelige subtyper i danske svin i 2014 var den danske variant af H1N2 og subtypen. Prævalensen af det almindelige svininfluenza virus “avian-like swine” H1N1 subtype er faldet drastisk og forekom i 2014 tilsyneladende mindre hyppigt end H1N1pdm09 subtypen.


Undersøgelserne har med stor sandsynlighed vist, at H1pdm09, som stadig må betragtes som en zoonose, nu er etableret i den danske svinepopulation, hvor den cirkulerer uafhængigt af den humane influenza virus sæson. Overvågningen har endvidere påvist adskillige nye virus reasortments, hvor gener fra H1pdm09 indgår, bl.a. tyder det på at H1N2 virus med interne gener fra H1pdm09 er etableret i den danske svine population. Der er global bevågenhed omkring svininfluenza virus med interne gener fra H1N1pdm09, da der i flere tilfælde er vist smitte med sådanne virus til mennesker, fx H3N2v i USA. Overvågningen har også bidraget til, at vi tidligt har påvist et nyt virus med zoonotisk potentiale som H3hu05N2sw. Dette betyder, at der kan foretages en nærmere genetisk og biologisk karakterisering af dette virus, hvilket kan danne evidens-baseret baggrundsviden for risikohåndteringen, i det tilfælde at der konstateres human smitte med dette virus. Den fremtidige overvågning vil bl.a. have fokus på at undersøge om dette virus bliver etableret i danske svin. Fra et veterinært synspunkt er det vigtigt at få fastlagt hvilke(n) subtype(r), der cirkulerer i besætningen, da valg af vaccine er afhængig af denne information. Det er derfor positivt, at der over de senere år er sket en stigning i antal indsendelser til influenzaafværk påvisning i Danmark, da det øger muligheden for at vaccinere korrekt og derved nedbringe risikoen for antibiotika krævende sekundære infektioner. Det er også positivt at det H1N2 subtype (med human-like HA-gen), der er dominerende i andre dele af Europa, stadig ikke findes i Danmark. Indtræden af dette virus kan frygtes at få epizootisk karakter, da immuniteten i populationen mod dette virus er meget lille. Det kan konkluderes, at den iværksatte overvågning har givet et godt indblik i hvilke influenza A virus, der cirkulerer i danske svin, og at denne information dagligt bruges proaktivt ved håndtering af sygdom i besætningerne. Overvågningen har endvidere vist, at virus med nye gen kombinationer er blevet etableret i danske svin, og der bør de kommende år holdes øje med, om disse virus smitter til mennesker.

**General information**

*State:* Published  
*Organisations:* National Veterinary Institute, Section for Virology  
*Authors:* Krog, J. S. (Intern), Hjulsager, C. K. (Intern), Larsen, L. E. (Intern)  
*Publication date:* 2015

**Publication information**

*Publisher:* DTU Veterinærinstitutet  
*Original language:* English  
*Main Research Area:* Technical/natural sciences  
*Electronic versions:*  
*Overvågning af influenza A virus i svin i 2014 ORBIT.pdf*  
*Source:* PublicationPreSubmission  
*Source-ID:* 112090824  
*Publication date:* Research - peer-review › Report – Annual report year: 2015

**Parasites and other infectious agents in marine finfish and shellfish species posing a hazard to human health (ToR b)**

Several parasites and other infectious agents frequently reported by the WGPDMO in the annual update of disease trends (ICES WGPDMO reports 1999–2015) have the potential to be harmful to human health if ingested in unprocessed or inadequate-ly/partly processed seafood. These include, but are not limited to, larval stages of the nematodes Anisakis simplex and Pseudoterranova decipiens. For them the risk to human health may occur in two ways: gastrointestinal infections with the possibility of sub-sequent peritonitis or the involvement of other sites in the body. Infections may also lead to allergic reactions to pathogen-related substances (e.g. secretory products) pre-sent in seafood. This review will
identify reported zoonotic agents in ICES-member countries in the period 1999–2014 and summarize risks and mitigation strategies based on existing literature. It will also highlight issues that require further research and solutions.

**General information**
State: Published
Organisations: National Veterinary Institute
Authors: Alfjorden, A. (Ekstern), Podolska, M. (Ekstern), Karaseva, T. (Ekstern), Madsen, L. (Intern)
Pages: 12-27
Publication date: 2015

**Host publication information**
Title of host publication: ICES WGPDMO REPORT 2015 : Report of the Working Group on Pathology and Diseases of Marine Organisms (WGPDMO)
Place of publication: Copenhagen V
Publisher: International Council for the Exploration of the Sea (ICES)
Chapter: 5.2
Main Research Area: Technical/natural sciences
Publication: Research - peer-review › Report chapter – Annual report year: 2016

PED - Porcin Epidemisk Diarré

**General information**
State: Published
Organisations: National Veterinary Institute
Authors: Bøtner, A. (Intern), Strandbygaard, B. (Intern)
Number of pages: 1
Pages: 40
Publication date: 2015
Main Research Area: Technical/natural sciences

**Publication information**
Journal: Dansk Veterinaertidsskrift
Issue number: 6
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
ISI indexed (2012): ISI indexed no
BFI (2011): BFI-level 1
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
BFI (2009): BFI-level 1
BFI (2008): BFI-level 1
Original language: English
Electronic versions:
PED_Nyt_fra_DTU_Veterin_instituttet_DVT_2015.pdf
Source: PublicationPreSubmission
Source-ID: 114805335
Publication: Communication › Comment/debate – Annual report year: 2015

Persistent Spatial Clusters of Prescribed Antimicrobials among Danish Pig Farms - A Register-Based Study
The emergence of pathogens resistant to antimicrobials has prompted political initiatives targeting a reduction in the use of veterinary antimicrobials in Denmark, especially for pigs. This study elucidates the tendency of pig farms with a significantly higher antimicrobial use to remain in clusters in certain geographical regions of Denmark. Animal Daily Doses/100 pigs/day were calculated for all three age groups of pigs (weaners, finishers and sows) for each quarter during 2012-13 in 6,143 commercial indoor pig producing farms. The data were split into four time periods of six months.
Repeated spatial cluster analyses were performed to identify persistent clusters, i.e. areas included in a significant cluster throughout all four time periods. Antimicrobials prescribed for weaners did not result in any persistent clusters. In contrast, antimicrobial use in finishers clustered persistently in two areas (157 farms), while those issued for sows clustered in one area (51 farms). A multivariate analysis including data on antimicrobial use for weaners, finishers and sows as three separate outcomes resulted in three persistent clusters (551 farms). Compared to farms outside the clusters during this period, weaners, finishers and sows on farms within these clusters had 19%, 104% and 4% higher use of antimicrobials, respectively. Production type, farm type and farm size seemed to have some bearing on the clustering effect. Adding these factors as categorical covariates one at a time in the multivariate analysis reduced the persistent clusters by 24.3%, 30.5% and 34.1%, respectively.

**General information**

**State:** Published

**Organisations:** National Food Institute, National Veterinary Institute, Section for Epidemiology, University of Prince Edward Island, University of Copenhagen

**Authors:** Fertner, M. E. (Intern), Sanchez, J. (Ekstern), Boklund, A. (Intern), Stryhn, H. (Ekstern), Dupont, N. (Ekstern), Toft, N. (Intern)

**Number of pages:** 13

**Publication date:** 2015

**Main Research Area:** Technical/natural sciences

**Publication information**

**Journal:** P L o S One

**Volume:** 10

**Issue number:** 8

**Article number:** e0136834

**ISSN (Print):** 1932-6203

**Ratings:**

- BFI (2018): BFI-level 1
- Web of Science (2018): Indexed yes
- BFI (2017): BFI-level 1
- Scopus rating (2017): CiteScore 3.01 SJR 1.164 SNIP 1.111
- Web of Science (2017): Indexed yes
- BFI (2016): BFI-level 1
- Scopus rating (2016): CiteScore 3.11 SJR 1.236 SNIP 1.101
- Web of Science (2016): Indexed yes
- BFI (2015): BFI-level 1
- Scopus rating (2015): SJR 1.427 SNIP 1.136 CiteScore 3.32
- Web of Science (2015): Indexed yes
- BFI (2014): BFI-level 1
- Scopus rating (2014): SJR 1.559 SNIP 1.148 CiteScore 3.54
- Web of Science (2014): Indexed yes
- BFI (2013): BFI-level 1
- Scopus rating (2013): SJR 1.772 SNIP 1.153 CiteScore 3.94
- ISI indexed (2013): ISI indexed yes
- Web of Science (2013): Indexed yes
- BFI (2012): BFI-level 1
- Scopus rating (2012): SJR 1.982 SNIP 1.156 CiteScore 4.15
- ISI indexed (2012): ISI indexed yes
- Web of Science (2012): Indexed yes
- BFI (2011): BFI-level 1
- Scopus rating (2011): SJR 2.425 SNIP 1.233 CiteScore 4.58
- ISI indexed (2011): ISI indexed no
- Web of Science (2011): Indexed yes
- BFI (2010): BFI-level 1
- Scopus rating (2010): SJR 2.705 SNIP 1.178
- Web of Science (2010): Indexed yes
- BFI (2009): BFI-level 1
- Scopus rating (2009): SJR 2.614 SNIP 1.046
Pharmacodynamic modelling of in vitro activity of tetracycline against a representative, naturally occurring population of porcine Escherichia coli

The complex relationship between drug concentrations and bacterial growth rates require not only the minimum inhibitory concentration but also other parameters to capture the dynamic nature of the relationship. To analyse this relationship between tetracycline concentration and growth of Escherichia coli representative of those found in the Danish pig population, we compared the growth of 50 randomly selected strains. The observed net growth rates were used to describe the in vitro pharmacodynamic relationship between drug concentration and net growth rate based on $E_{\text{max}}$ model with three parameters: maximum net growth rate ($\alpha_{\text{max}}$); concentration for a half-maximal response ($E_{\text{max}}$); and the Hill coefficient ($\gamma$). The net growth rate in the absence of antibiotic did not differ between susceptible and resistant isolates ($P = 0.97$). The net growth rate decreased with increasing tetracycline concentrations, and this decline was greater in susceptible strains than resistant strains. The lag phase, defined as the time needed for the strain to reach an OD600 value of 0.01, increased exponentially with increasing tetracycline concentration. The pharmacodynamic parameters confirmed that the [Formula: see text] between susceptible and resistant strains in the absence of a drug was not different. EC50 increased linearly with MIC on a log-log scale, and $\gamma$ was different between susceptible and resistant strains. The in vitro model parameters described the inhibition effect of tetracycline on E. coli when strains were exposed to a wide range of tetracycline concentrations. These parameters, along with in vivo pharmacokinetic data, may be useful in mathematical models to predict in vivo competitive growth of many different strains and for development of optimal dosing regimens for preventing selection of resistance.
Pharmacokinetic-Pharmacodynamic Model To Evaluate Intramuscular Tetracycline Treatment Protocols To Prevent Antimicrobial Resistance in Pigs

High instances of antimicrobial resistance are linked to both routine and excessive antimicrobial use, but excessive or inappropriate use represents an unnecessary risk. The competitive growth advantages of resistant bacteria may be amplified by the strain dynamics; in particular, the extent to which resistant strains outcompete susceptible strains under antimicrobial pressure may depend not only on the antimicrobial treatment strategies but also on the epidemiological parameters, such as the composition of the bacterial strains in a pig. This study evaluated how variation in the dosing...
protocol for intramuscular administration of tetracycline and the composition of bacterial strains in a pig affect the level of resistance in the intestine of a pig. Predictions were generated by a mathematical model of competitive growth of Escherichia coli strains in pigs under specified plasma concentration profiles of tetracycline. All dosing regimens result in a clear growth advantage for resistant strains. Short treatment duration was found to be preferable, since it allowed less time for resistant strains to outcompete the susceptible ones. Dosing frequency appeared to be ineffective at reducing the resistance levels. The number of competing strains had no apparent effect on the resistance level during treatment, but possession of fewer strains reduced the time to reach equilibrium after the end of treatment. To sum up, epidemiological parameters may have more profound influence on growth dynamics than dosing regimens and should be considered when designing improved treatment protocols.
Intestinal mononuclear phagocytes, comprising macrophages (Mφs) and dendritic cells (DCs), play important roles in the generation and the regulation of immune responses to intestinal antigens, and alterations in the development and/or the function of these cells are thought to contribute to the pathogenesis of inflammatory bowel disease. In this review, we discuss the role of tumor necrosis factor-α (TNF) in regulating multiple aspects of intestinal Mφ and DC physiology, including their differentiation, migration, maturation, survival and effector functions. In inflammatory bowel disease, TNF signaling has been implicated in reprogramming monocyte differentiation from the anti-inflammatory Mφ lineage towards the pro-inflammatory mononuclear phagocyte lineage. These cells become a major source of TNF and, thus, may contribute to the chronic inflammatory process. Finally, we highlight some of the important gaps in our current knowledge regarding the role of TNF in Mφ and DC physiology and suggest important directions for future research in this field.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Skåne University Hospital, Lund University
Authors: Rivollier, A. M. C. (Intern), Marsal, J. (Ekstern), Agace, W. W. (Intern)
Pages: 9-26
Publication date: 2015

Host publication information
Title of host publication: Anti-Tumor Necrosis Factor Therapy in Inflammatory Bowel Disease
Volume: 34
Publisher: Karger
Editors: Rogler, G., Herfarth, H., Hibi, T., Nielsen, O. H.
ISBN (Print): 978-3-318-05473-6
ISBN (Electronic): 978-3-318-05474-3
Series: Frontiers of Gastrointestinal Research
ISSN: 0302-0665
Main Research Area: Technical/natural sciences
DOIs:
Piscirickettsia salmonis infection in European sea bass - an emerging disease in Mediterranean mariculture

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Section for Bacteriology, Pathology and Parasitology, AquaPrI Innovation, Croatian Veterinary Institute
Authors: Zrncic, S. (Ekstern), Vendramin, N. (Intern), Boutrup, T. S. (Ekstern), Boye, M. (Intern), Bruun, M. S. (Intern), Brnic, D. (Ekstern), Oraic, D. (Ekstern)
Pages: 153-153
Publication date: 2015

Host publication information
Title of host publication: 17th International Conference on Diseases of Fish and Shellfish: Abstract book
Place of publication: Las Palmas
Publisher: European Association of Fish Pathologists
Article number: O-145
Main Research Area: Technical/natural sciences
Conference: 17th International Conference on Diseases of Fish and Shellfish, Las Palmas, Spain, 07/09/2015 - 07/09/2015
Electronic versions:
Book_of_abstracts_17th_International_conference_on_Diseases_of_Fish_and_Shellfish.pdf

Planning a cross-sectional study of antimicrobial resistance genes in Danish pig farms

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology
Authors: Birkegård, A. C. (Intern), Hisham Beshara Halasa, T. (Intern), Toft, N. (Intern)
Number of pages: 1
Publication date: 2015
Main Research Area: Technical/natural sciences
Electronic versions:
poster_AC_Birkeg_rd.pdf
Source: PublicationPreSubmission
Source-ID: 118950958

Planning a cross-sectional study of antimicrobial resistance genes in Danish pig farms

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology
Authors: Birkegård, A. C. (Intern), Hisham Beshara Halasa, T. (Intern), Toft, N. (Intern)
Number of pages: 1
Publication date: 2015
Main Research Area: Technical/natural sciences
Electronic versions:
Poster_Anna_Camilla_Birkeg_rd.pdf
Source: PublicationPreSubmission
Source-ID: 118950829

Population Viability Analysis of feral raccoon dog (Nyctereutes procyonoides) in Denmark
To assess the effects of actions implemented by the Danish Action Plan (DAP) for eradication of the raccoon dog, the population dynamics of the raccoon dog in Denmark was simulated. A population viability analysis (PVA) was generated with the stochastic simulation program, VORTEX, based on population parameters of raccoon dog in other European...
countries (Poland, Finland and Germany), combined with statistics on dead raccoon dogs reported to the Danish National Veterinary Institute between 2008 and 2012. Simulations showed that the present feral population of raccoon dogs would expand markedly and reach an assessed carrying capacity of 30,000 individuals with no intervention within 10 years. Simulations of the current culling strategy showed that the raccoon dog in Denmark would reach the carrying capacity with only a few years’ delay compared to simulations with no intervention. This indicates that more efficient and intensive actions are needed to reach the goal of the DAP, aiming at eradicating the breeding population of raccoon dogs in Denmark within 2015. Simulations suggested that around 950 individuals should be culled a year from 2012 to 2015. Sensitivity analysis that was performed showed that the only parameter that had a strong influence on the population dynamic was the first year mortality.

**General information**

State: Published
Organisations: National Veterinary Institute, Aarhus University, Aalborg University
Authors: Rømer, A. E. (Ekstern), Nørgaard, L. S. (Ekstern), Mikkelsen, D. M. G. (Ekstern), Chriél, M. (Intern), Elmerose, M. (Ekstern), Madsen, A. B. (Ekstern), Pertoldi, C. (Ekstern), Hammer Jensen, T. (Ekstern)
Pages: 111-117
Publication date: 2015
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Archives of Biological Sciences
Volume: 67
Issue number: 1
ISSN (Print): 0354-4664
Ratings:
Web of Science (2018): Indexed yes
Scopus rating (2017): SNIP 0.415 SJR 0.232 CiteScore 0.57
Web of Science (2017): Indexed Yes
Scopus rating (2016): SJR 0.204 SNIP 0.312 CiteScore 0.42
Scopus rating (2015): SJR 0.238 SNIP 0.395 CiteScore 0.46
Web of Science (2015): Indexed yes
Scopus rating (2014): SJR 0.301 SNIP 0.538 CiteScore 0.74
Scopus rating (2013): SJR 0.333 SNIP 0.593 CiteScore 0.75
ISI indexed (2013): ISI indexed yes
Scopus rating (2012): SJR 0.325 SNIP 0.494 CiteScore 0.68
ISI indexed (2012): ISI indexed yes
Scopus rating (2011): SJR 0.204 SNIP 0.402 CiteScore 0.42
ISI indexed (2011): ISI indexed no
Scopus rating (2010): SJR 0.18 SNIP 0.23
Scopus rating (2009): SJR 0.156 SNIP 0.079
Original language: English
Population viability, Analysis, VORTEX, Invasive species, Eradication, Nycterutes procyonoides, Raccoon dog

Electronic versions:
0354_46641400012R.pdf
DOI:
10.2298/ABS140905012R
Links:
Source: PublicationPreSubmission
Source-ID: 106565171
Publication: Research - peer-review › Journal article – Annual report year: 2015

**Preliminary data on the presence of bacteria in the uterus of pregnant cows**

Bacterial invasion of the uterus during the postpartum period has been well described. Recent papers using 16S rRNA gene sequencing techniques suggest that the nonpregnant uterus contains a diverse flora of bacteria that are not necessarily pathogenic. In contrast, the pregnant uterus has until now been considered a sterile environment. The aim of the present study was to investigate whether bacteria were present in the uteri of pregnant cows. Uteri from pregnant, slaughtered animals (n = 47) were sampled. The surface of the uterus was wiped with alcohol, flame sterilized, and cut open with sterile scissors. Samples were taken from the endometrium and from the placentalomes. The samples were embedded in paraffin, sectioned at 3 microns, and prepared for fluorescence in situ hybridization using a probe targeting the 16S rRNA of the domain bacteria, so that all bacteria regardless of species were visualised. Using fluorescence microscopy, the presence of bacteria within or on the surface of the endometrium and within the placentalomes was noted.
The stage of pregnancy was estimated to range from 26 to 263 days by measuring the size of the embryo or fetus. The endometrial samples from 85.1% (40/47) of pregnant cows contained bacteria. In 22 cows, the bacteria were localised within the endometrial tissue, whereas in the remaining 18 cows, the bacteria were on the epithelial surface. Placental samples were obtained from 43 cows, and 76.7% (33/43) of these contained bacteria. The presence of bacteria in the pregnant uterus may suggest that a cow can carry a pregnancy despite the presence of few potentially pathogenic bacteria or that normal flora exist in the uterus as in, for example, the vagina. In conclusion, bacteria were present in the endometrium and placentomes of pregnant cows. Further analyses using rRNA gene sequencing techniques will aim to confirm the presence of bacteria in the bovine pregnant uterus and to investigate which species of bacteria are present in the uterus during pregnancy.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Copenhagen
Authors: Pedersen, H. G. (Ekstern), Knudsen, L. R. V. (Intern), Agerholm, J. S. (Ekstern), Jensen, T. K. (Intern), Schou, K. K. (Intern), Karstrup, C. C. (Ekstern)
Pages: 165-166
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Reproduction, Fertility and Development
Volume: 28
Issue number: 2
ISSN (Print): 1031-3613
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.766 SJR 0.681 CiteScore 1.75
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.788 SNIP 0.895 CiteScore 1.88
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.852 SNIP 0.96 CiteScore 1.9
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.054 SNIP 1.101 CiteScore 2.45
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.917 SNIP 0.961 CiteScore 2.04
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.916 SNIP 1.032 CiteScore 2.27
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.845 SNIP 0.833 CiteScore 1.9
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.872 SNIP 0.925
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.896 SNIP 1.024
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.796 SNIP 0.794
Scopus rating (2007): SJR 0.883 SNIP 0.924
Scopus rating (2006): SJR 0.676 SNIP 0.839
Scopus rating (2005): SJR 0.499 SNIP 0.576
Scopus rating (2004): SJR 0.483 SNIP 0.638
Scopus rating (2003): SJR 0.454 SNIP 0.557
Scopus rating (2002): SJR 0.354 SNIP 0.515
Scopus rating (2001): SJR 0.423 SNIP 0.407
Scopus rating (2000): SJR 0.705 SNIP 0.799
Present status, actions taken and future considerations due to the findings of *E. multilocularis* in two Scandinavian countries

When *Echinococcus* (*E.*) *multilocularis* was first detected in mainland Scandinavia in Denmark in 2000, surveillance was initiated/intensified in Sweden, mainland Norway and Finland. After 10 years of surveillance these countries all fulfilled the requirements of freedom from *E. multilocularis* as defined by the EU, i.e. a prevalence in final hosts <1% with 95% confidence level. However, in 2011 *E. multilocularis* was detected in Sweden for the first time and surveillance was increased in all four countries. Finland and mainland Norway are currently considered free from *E. multilocularis*, whereas the prevalence in foxes in Sweden and Denmark is approximately 0.1% and 1.0%, respectively. *E. multilocularis* has been found in foxes from three different areas in Denmark: Copenhagen (2000), Hejer (2012–14) and Grindsted (2014). Unlike Sweden, Norway and Finland, human alveolar echinococcosis (AE) is not notifiable in Denmark, and the number of human cases is therefore unknown. In Sweden, *E. multilocularis* has been found in foxes in four counties, Västra Götaland, Södermanland, Dalarna (2011) and Småland (2014). *E. multilocularis* has also been found in an intermediate host in Södermanland (2014). Two cases of AE have been reported in humans (2012), both infected abroad. No cases of *E. multilocularis* or AE have been reported in Finland and Norway. Recommendations and future considerations are discussed further.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, National Veterinary Institute Sweden, Norwegian Veterinary Institute, Finnish Food Safety Authority
Pages: 172-181
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Veterinary Parasitology
Volume: 213
Issue number: 3-4
ISSN (Print): 0304-4017
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.215 SJR 1.275 CiteScore 2.55
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.49 SJR 1.228 SNIP 1.218
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.21 SNIP 1.309 CiteScore 2.46
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.324 SNIP 1.42 CiteScore 2.53
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.262 SNIP 1.437 CiteScore 2.63
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.163 SNIP 1.439 CiteScore 2.6
ISI indexed (2012): ISI indexed yes
Preterm Birth Reduces Nutrient Absorption With Limited Effect on Immune Gene Expression and Gut Colonization in Pigs

The primary risk factors for necrotizing enterocolitis (NEC) are preterm birth, enteral feeding, and gut colonization. It is unclear whether feeding and colonization induce excessive expression of immune genes that lead to NEC. Using a pig model, we hypothesized that reduced gestational age would upregulate immune-related genes and cause bacterial imbalance after birth. Preterm (85%-92% gestation, n=53) and near-term (95%-99% gestation, n=69) pigs were delivered by cesarean section and euthanized at birth or after 2 days of infant formula or bovine colostrum feeding. At birth, preterm delivery reduced 5 of 30 intestinal genes related to nutrient absorption and innate immunity, whereas 2 genes were upregulated. Preterm birth also reduced ex vivo intestinal glucose and leucine uptake (40%-50%), but failed to increase cytokine secretions from intestinal explants relative to near-term birth. After 2 days of formula feeding, NEC incidence was increased in preterm versus near-term pigs (47% vs 0%-13%). A total of 6 of the 30 genes related to immunity (TLR2, IL1B, and IL8), permeability (CLDN3, and OCLN), and absorption (SGLT) decreased in preterm pigs without affecting Gram-negative bacteria-related responses (TLR4, IKBA, NFKB1, TNFAIP3, and PAFA). Bacterial abundance tended to be higher in preterm versus near-term pigs (P=0.09), whereas the composition was unaffected. Preterm birth predisposes to NEC and reduces nutrient absorption but does not induce upregulation of immune-related genes or cause bacterial dyscolonization in the neonatal period. Excessive inflammation and bacterial overgrowth may occur relatively late in NEC progression in preterm neonates.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, University of Copenhagen
Pre-test habituation improves the reliability of a handheld test of mechanical nociceptive threshold in dairy cows

Mechanical nociceptive threshold (MNT) testing has been used to investigate aspects of painful states in bovine claws. We investigated a handheld tool, where the applied stimulation force was monitored continuously relative to a pre-encoded based target force. The effect on MNT of two pre-testing habituation procedures was performed in two different experiments comprising a total of 88 sound Holsteins dairy cows kept either inside or outside their home environment. MNT testing was performed using five consecutive mechanical nociceptive stimulations per cow per test at a fixed pre-encoded target rate of 2.1 N/s. The habituation procedure performed in dairy cows kept in their home environment led to lowered intra-individual coefficient of variation of MNT (P < 0.001), increased MNT (P < 0.001) and decreased the discrepancy between applied and target force during stimulations (P < 0.001). Pre-test habituation improved the reliability of the handheld tool when used in dairy cows kept in their home environment.

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, University of Copenhagen, Swedish University of Agricultural Sciences, Aarhus University, University of British Columbia
Authors: Raundal, P. M. (Ekstern), Andersen, P. H. (Ekstern), Toft, N. (Intern), Herskin, M. S. (Ekstern), Forkman, B. (Ekstern), Munksgaard, L. (Ekstern), de Passillé, A. M. (Ekstern), Rushen, J. (Ekstern)
Number of pages: 7
Pages: 189-195
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Research in Veterinary Science
Volume: 102
ISSN (Print): 0034-5288
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SJR 0.593 SNIP 0.941 CiteScore 1.82
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): SJR 0.646 SNIP 0.779 CiteScore 1.46
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 0.774 SNIP 0.933 CiteScore 1.57
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 0.687 SNIP 0.887 CiteScore 1.58
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 0.691 SNIP 0.945 CiteScore 1.62
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 0.633 SNIP 1.067 CiteScore 1.63
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 0.726 SNIP 1.054 CiteScore 1.65
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 2
Prevalence of salmonella in captive reptiles from Croatia

Salmonellosis transmitted by pet reptiles is an increasing public health issue worldwide. The aim of this study was to investigate the prevalence of Salmonella strains from captive reptiles in Croatia. From November 2009 to November 2011 a total of 292 skin, pharyngeal, cloacal, and fecal samples from 200 apparently healthy reptiles were tested for Salmonella excretions by bacteriologic culture and serotyping. These 200 individual reptiles included 31 lizards, 79 chelonians, and 90 snakes belonging to private owners or housed at the Zagreb Zoo, Croatia. Salmonella was detected in a total of 13% of the animals, among them 48.4% lizards, 8.9% snakes, and 3.8% turtles. Representatives of five of the six Salmonella enterica subspecies were identified with the following proportions in the total number of isolates: Salmonella enterica enterica 34.6%, Salmonella enterica houtenae 23.1%, Salmonella enterica arizonae 23.1%, Salmonella enterica diarizonae 15.4%, and Salmonella enterica salamae 3.8%. The 14 different serovars isolated included several rarely occurring serovars such as Salmonella Apapa, Salmonella Halle, Salmonella Kisarawe, and Salmonella Potengi. These findings confirm that the prevalence of Salmonella is considerable in captive reptiles in Croatia, indicating that these animals may harbor serovars not commonly seen in veterinary or human microbiologic practice. This should be addressed in the prevention and diagnostics of human reptile-transmitted infections.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Zagreb
Authors: Lukac, M. (Ekstern), Pedersen, K. (Intern), Prukner-Radovcic, E. (Ekstern)
Pages: 234-240
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Zoo and Wildlife Medicine
Volume: 46
Issue number: 2
ISSN (Print): 1042-7260
Ratings:
Prevalence, risk factors and spatial analysis of infections with liver flukes in Danish cattle herds

Liver fluke infection, also known as fasciolosis, is a world-wide prevalent zoonotic parasitic disease infecting a wide range of host species and is caused by Fasciola hepatica. Despite of the substantial economic and animal welfare effects of the disease, knowledge on its prevalence and the factors related to its occurrence and distribution are scarce in Denmark. A retrospective study was performed using liver inspection data of approximately 1.5 million cattle for the period 2011 to 2013. Spatial analysis was carried out to explore whether the data on F. hepatica infection was clustered in space as this could help understand whether or not the infection was driven by local environmental factors. Both global and local spatial autocorrelation techniques were used. Herd level and environmental risk factors were evaluated for their association with prevalence of F. hepatica infection using Generalized Estimating Equations.
Prevalence, risk factors and spatial analysis of liver fluke infections in Danish cattle herds

Background: Fasciola hepatica, a trematode parasite (liver fluke), infects a wide range of host species causing fasciolosis. The disease is prevalent world-wide and causes considerable economic losses to the livestock industry. Fasciolosis is regarded as an emerging food-borne zoonosis. To promote awareness among farmers and to implement strategies to control the infection, this study examined the prevalence, spatial distribution and risk factors for Fasciola hepatica infection in Danish cattle herds. Methods: A retrospective population based study was performed using meat inspection data of approximately 1.5 million cattle slaughtered in the period 2011 to 2013. Annual cumulative prevalence of recorded liver fluke findings was calculated for each year. Global and local spatial cluster analysis was used to identify and map spatial patterns of Fasciola hepatica positive and negative herds to explore environmental indicators of infection. Herd level, trade and environmental risk factors were evaluated for association with infection using logistic regression. Herd infection status as predicted from the final risk factor model was compared with the observed status using heat maps to assess how well the model fitted the observed spatial pattern. Results: During the investigated period (2011-2013), an increase in annual herd prevalence was noted (2011-25.6%; 2012-28.4%; 2013-29.3%). The spatial analysis suggested significant clustering of positive and negative herds. Presence of streams, wetlands and pastures on farms showed a significant association with the presence of infection in cattle herds. Buying animals from positive herds was a risk factor on conventional farms. Additionally, risk of being infected with Fasciola hepatica was higher in non-dairy herds of medium size (>= 30 and <100) when compared to dairy and large (>= 100) cattle herds. The observed spatial pattern could be reproduced by predictions of the risk factor model. Conclusions: This study showed an increase in annual herd level prevalence (2011 to 2013) indicating that an increasing proportion of herds are infected with Fasciola hepatica infection every year in Denmark. Fasciolosis was found to be associated with both herd and environmental factors where the infection was influenced by local factors that clustered geographically.
Preventing foot and mouth disease - how are the costs divided between the public authorities and the pig and cattle industries in Denmark?

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Danish Veterinary and Food Administration, Danish Agriculture and Food Council, University of Copenhagen
Authors: Christensen, T. (Ekstern), Denver, S. (Ekstern), Alban, L. (Ekstern), Boklund, A. (Intern), Houe, H. (Ekstern), Leth Hougaard, J. (Ekstern), Mortensen, S. (Ekstern), Rasmussen, S. D. (Ekstern), Tamstorf, T. V. (Ekstern), Toft, N. (Intern), Zobbe, H. (Ekstern)
Pages: 220-220
Publication date: 2015

Host publication information
Title of host publication: Proceedings of the 14th international symposium om veterinary epidemiology and economics
Place of publication: Merida, Yucatan, Mexico
Main Research Area: Technical/natural sciences
Conference: 14th Conference of the International Society for Veterinary Epidemiology and Economics, Mérida, Yucatan, Mexico, 03/11/2015 - 03/11/2015
Electronic versions: ISVEE_14_Proceedings.pdf
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2016

Prion-Specific Antibodies Produced in Wild-Type Mice
Peptide-specific antibodies produced against synthetic peptides are of high value in probing protein structure and function, especially when working with challenging proteins, including not readily available, non-immunogenic, toxic, and/or pathogenic proteins. Here, we present a straightforward method for production of mouse monoclonal antibodies (MAbs) against peptides representing two sites of interest in the bovine prion protein (boPrP), the causative agent of bovine
spongiform encephalopathy ("mad cow disease") and new variant Creutzfeldt-Jakob's disease (CJD) in humans, as well as a thorough characterization of their reactivity with a range of normal and pathogenic (misfolded) prion proteins. It is demonstrated that immunization of wild-type mice with ovalbumin-conjugated peptides formulated with Freund's adjuvant induces a good immune response, including high levels of specific anti-peptide antibodies, even against peptides very homologous to murine protein sequences. In general, using the strategies described here for selecting, synthesizing, and conjugating peptides and immunizing 4-5 mice with 2-3 different peptides, high-titered antibodies reacting with the target protein are routinely obtained with at least one of the peptides after three to four immunizations with incomplete Freund's adjuvant.
PRRSV type 1 detection in aerosols from three swine herds in Denmark

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Technical University of Denmark, Boehringer Ingelheim Danmark A/S, Boehringer Ingelheim Vetmedica, Inc., Svinevet Pig Practise
Authors: Priebe, A. (Ekstern), Rathkjen, P. H. (Ekstern), Larsen, L. E. (Intern), Kvisgaard, L. K. (Intern), Hjulsager, C. K. (Intern), Angulo, J. (Ekstern), Havn, K. (Ekstern)
Number of pages: 1
Publication date: 2015

Host publication information
Title of host publication: Proceedings of the 7th European Symposium of Porcine Health Management
Place of publication: Nantes, France
Article number: PO85
Main Research Area: Technical/natural sciences
Conference: 7th European Symposium of Porcine Health Management, Nantes, France, 22/04/2015 - 22/04/2015
Source: PublicationPreSubmission
Source-ID: 119056467
Publication: Research › Conference abstract in proceedings – Annual report year: 2015

PRRSV type 1 detection in aerosols inside a PRRSV-positive swine herd in Denmark

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Technical University of Denmark, Boehringer Ingelheim Danmark A/S, Boehringer Ingelheim Vetmedica, Inc., Svinevet Pig Practise
Authors: Priebe, A. (Ekstern), Rathkjen, P. H. (Ekstern), Larsen, L. E. (Intern), Kvisgaard, L. K. (Intern), Hjulsager, C. K. (Intern), Angulo, J. (Ekstern), Havn, K. (Ekstern)
Number of pages: 1
Publication date: 2015

Host publication information
Title of host publication: Proceedings of the 7th European Symposium of Porcine Health Management
Place of publication: Nantes, France
Article number: PO85
Main Research Area: Technical/natural sciences
Conference: 7th European Symposium of Porcine Health Management, Nantes, France, 22/04/2015 - 22/04/2015
Source: PublicationPreSubmission
Source-ID: 119056467
Publication: Research › Conference abstract in proceedings – Annual report year: 2015
Purified extracts from chicory (Cichorium intybus) inhibit Ascaris suum glutathione-S transferase activity and reduce survival of larvae in vitro

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Section for Immunology and Vaccinology, University of Copenhagen
Authors: Williams, A. (Ekstern), Pena-Espinoza, M. A. (Intern), Alstrup Hansen, T. (Ekstern), Boas, U. (Intern), Milan Thamsborg, S. (Ekstern)
Number of pages: 1
Pages: 142-142
Publication date: 2015

Host publication information
Title of host publication: 25th International Conference of the World Association for the Advancement of Veterinary Parasitology: Abstract Book
Place of publication: Liverpool, United Kingdom
Main Research Area: Technical/natural sciences
Conference: 25th International Conference of the World Association for the Advancement of Veterinary Parasitology, Liverpool, United Kingdom, 16/08/2015 - 16/08/2015
Electronic versions:
Williams_et_al_WAAVP2015.pdf
Source: PublicationPreSubmission
Source-ID: 117638549
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2015

Rabies 2014 - Rabies hos dyr

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Rasmussen, T. B. (Intern)
Number of pages: 3
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: E P I - Nyt
Issue number: Uge 14/15
ISSN (Print): 1602-4184
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Original language: Danish
Electronic versions:
Rabies_2014_Rabies_hos_dyr.pdf
Links:
Rapportering af diagnostiske undersøgelser af faldvildt 2015

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology
Authors: Chriél, M. (Intern), Hansen, M. S. (Intern), Larsen, G. (Intern), Holm, E. (Intern), Petersen, H. H. (Intern), Hjulsager, C. K. (Intern)
Number of pages: 27
Publication date: 2015

Publication information
Place of publication: Frederiksberg C
Publisher: Veterinarinstituttet, Danmarks Tekniske Universitet
Original language: Danish
Main Research Area: Technical/natural sciences
Electronic versions:
Rapportering_af_diagnostiske_unders_gelser_af_faldvildt_2015.pdf

Rationally designed chemokine-based toxin targeting the viral G protein-coupled receptor US28 potently inhibits cytomegalovirus infection in vivo

The use of receptor-ligand interactions to direct toxins to kill diseased cells selectively has shown considerable promise for treatment of a number of cancers and, more recently, autoimmune disease. Here we move the fusion toxin protein (FTP) technology beyond cancer/autoimmune therapeutics to target the human viral pathogen, human cytomegalovirus (HCMV), on the basis of its expression of the 7TM G protein-coupled chemokine receptor US28. The virus origin of US28 provides an exceptional chemokine-binding profile with high selectivity and improved binding for the CX3C chemokine, CX3CL1. Moreover, US28 is constitutively internalizing by nature, providing highly effective FTP delivery. We designed a synthetic CX3CL1 variant engineered to have ultra-high affinity for US28 and greater specificity for US28 than the natural sole receptor for CX3CL1, CX3CR1, and we fused the synthetic variant with the cytotoxic domain of Pseudomonas Exotoxin A. This novel strategy of a rationally designed FTP provided unparalleled anti-HCMV efficacy and potency in vitro and in vivo.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, INAGEN Aps, University of Copenhagen, Rutgers New Jersey Medical School, Xiamen University, Stanford University School of Medicine, University of Plymouth
Number of pages: 6
Pages: 8427-8432
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Proceedings of the National Academy of Sciences of the United States of America
Volume: 112
Issue number: 27
ISSN (Print): 0027-8424
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 8.59 SJR 6.092 SNIP 2.626
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Reappearance of Salmonella serovar Choleraesuis var. Kunzendorf in Danish pig herds
Salmonella enterica serovar Choleraesuis is a porcine adapted serovar which may cause serious outbreaks in pigs. Here we describe outbreaks of salmonellosis due to S. Choleraesuis in four Danish pig farms in 2012–2013 by clinic, serology, and microbiology and compare the isolates to those of a previous outbreak in 1999–2000. The infection was in some herds associated with high mortality and a moderate to high sero-prevalence was found. In 2012–2013 the disease contributed to increased mortality but occurred concomitant with other disease problems in the herds, which likely delayed the diagnosis by up to several months. Nine isolates from the four farms in 2012–2013 and 14 isolates obtained from the outbreak in Denmark in 1999–2000 were subjected to typing using pulsed-field gel electrophoresis (PFGE). Seven isolates were selected for whole genome sequencing (WGS). The PFGE results of 23 isolates displayed five different profiles. The isolates from 2012 to 2013 revealed two distinct profiles, both different from the isolates recovered in 1999–2000. Two of the 2012–2013 farms shared PFGE profiles and had also transported pigs between them. The profile found in the two other 2012–2013 farms was indistinguishable but no epidemiological connection between these farms was found. Analysis of the number of single nucleotide polymorphisms (SNPs) from the WGS data indicated that the isolates from the farms in 2012–2013 were more closely related to each other than to isolates from the outbreak in 1999. It was therefore concluded that the infection was a new introduction and not a persistent infection since the outbreak in 1999. It may further be suggested that there were two or three independent rather than a single introduction. The re-introduction of S. Choleraesuis in Denmark emphasizes the importance of strict hygiene measures in the herds. Further investigations using WGS are now in progress on a larger collection of isolates to study clonality at European level and trace the origin of the infections.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, National Food Institute, Division of Food Microbiology, Comparative Microbial Genomics, Division of Epidemiology and Microbial Genomics, Danish Agriculture and Food Council
Authors: Pedersen, K. (Intern), Sørensen, G. (Intern), Löfström, C. (Intern), Leekitcharoenphon, P. (Intern), Nielsen, B. (Ekstern), Wingstrand, A. (Intern), Aarestrup, F. M. (Intern), Hendriksen, R. S. (Intern), Baggesen, D. L. (Intern)
Pages: 282-291
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Veterinary Microbiology
Volume: 176
Issue number: 3-4
ISSN (Print): 0378-1135
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.7 SJR 1.175 SNIP 1.241
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.363 SNIP 1.206
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.413 SNIP 1.21 CiteScore 2.56
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.291 SNIP 1.256 CiteScore 2.54
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.459 SNIP 1.471 CiteScore 3
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.441 SNIP 1.569 CiteScore 3.18
ISI indexed (2012): ISI indexed yes
Reduced field efficacy of ivermectin against Ostertagia ostertagi and Cooperia oncophora in Danish cattle

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Copenhagen
Number of pages: 1
Pages: 265-265
Publication date: 2015

Host publication information
Title of host publication: 25th International Conference of the World Association for the Advancement of Veterinary Parasitology: Abstract Book
Place of publication: Liverpool, United Kingdom
Re-emergence of Streptococcus agalactiae: Cross-sectional investigation of a potential zoonosis in people and cattle

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology
Authors: Zadoks, R. (Ekstern), Lyhs, U. (Intern), Persson-Waller, J. (Ekstern)
Publication date: 2015
Event: Paper presented at 25th European Congress of Clinical Microbiology and Infectious Diseases, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Publication: Research - peer-review › Paper – Annual report year: 2015

Repeated examination of natural sapovirus infections in pig litters raised under experimental conditions

Porcine sapovirus, belonging to the family Caliciviridae, is an enteric virus that is widespread in the swine industry worldwide. A total of 14 sapovirus genogroups have been suggested and the most commonly found genogroup in swine is genogroup III (GIII). The goal of the present experiment was to examine the presence of sapovirus in 51 naturally infected pigs at two different time points. The pigs were kept under experimental conditions after weaning. Previous studies on sapovirus have primarily been of a cross sectional nature, typically prevalence studies performed on farms and abattoirs. In the present study, faecal samples, collected from each pig at 5½ weeks and 15-18 weeks of age, were analysed for sapovirus by reverse transcriptase polymerase chain reaction and positive findings were genotyped by sequencing. At 5½ weeks of age, sapovirus was detected in the majority of the pigs. Sequencing revealed four different strains in the 5½ week olds-belonging to genogroups GIII and GVII. Ten to 13 weeks later, the virus was no longer detectable from stools of infected pigs. However, at this time point 13 pigs were infected with another GIII sapovirus strain not previously detected in the pigs studied. This GIII strain was only found in pigs that, in the initial samples, were virus-negative or positive for GVII. At 5 weeks of age 74 % of the pigs were infected with sapovirus. At 15-18 weeks of age all pigs had cleared their initial infection, but a new sapovirus GIII strain was detected in 25 % of the pigs. None of the pigs initially infected with the first GIII strain were reinfected with this new GIII strain, which may indicate the presence of a genogroup-specific immunity.

General information
State: Published
Organisations: Section for Public sector service and commercial diagnostics, National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Section for Immunology and Vaccinology, State Serum Institute
Authors: Lauritsen, K. T. (Intern), Hansen, M. S. (Intern), Johnsen, C. K. (Ekstern), Jungersen, G. (Intern), Böttiger, B. (Ekstern)
Number of pages: 5
Publication date: 2015
Main Research Area: Technical/natural sciences
Publication information
Journal: Acta Veterinaria Scandinavica (Online)
Volume: 57
Issue number: 1
ISSN (Print): 0044-605X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.077 SJR 0.655 CiteScore 1.45
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.01 SJR 0.641 SNIP 0.826
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Retinoic acid signalling in thymocytes regulates T cell development

The Vitamin A derivative retinoic acid (RA) has emerged as an important regulator of peripheral T cell responses. However, whether there is endogenous retinoic acid receptor (RAR) signaling in developing thymocytes and the potential impact of such signals in thymocyte development remains unclear. Here, using a RA sensitive reporter mouse model, we demonstrate that endogenous RAR responses are induced in CD69+CD4+CD8lo and CD69+CD4+CD8+ thymocytes undergoing positive selection and lineage commitment, and continue to be present in both CD4+ and CD8+ single positive (SP) cells, with RA signaling further enhanced in recently generated CD69+CD4+ SP cells. To address the potential biological significance of RA signaling in developing thymocytes, we evaluated T cell development in CD4Cre-dnRAR
mice, where RA signaling is blocked in thymocytes from the CD4+CD8+ double positive (DP) stage onwards due to expression of a dominant-negative form of RAR. Interestingly, these mice displayed a marked reduction in all thymocyte subsets, with the exception of CD8⁺ SP cells but including ETP and DN2-4 subsets, suggesting that blocked RA signaling in DP thymocytes and their progeny indirectly impacts on thymocyte precursor entry and/or survival. Furthermore, CD4Cre-dnRAR mice showed a 4-fold reduction in CD4⁺/CD8⁺ SP ratio that was mainly due to enhanced accumulation of mature CD8⁺ SP cells, indicating that RA signaling may be directly involved in regulating thymic retention and/or post-selection expansion of this cell subset. Collectively, our data suggest a direct role for RA signaling in regulating thymocyte homeostasis and T cell development.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Lund University, University of Birmingham
Number of pages: 1
Publication date: 2015
Event: Abstract from 1st International Venice Thymus Meeting, San Servolo Island, Italy.
Main Research Area: Technical/natural sciences
Electronic versions:
Venice_abstract_2015.docx
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2015

Retinoic acid signalling in thymocytes regulates T cell development
The Vitamin A derivative retinoic acid (RA) works as a ligand for a family of nuclear RA receptors (RARα, RARβ and RARγ) which form heterodimers with retinoid X receptors (RXR). These complexes function as ligand-activated transcription factors, recognizing specific RA responsive elements in the regulatory regions of target genes. RA has been reported to play a direct role in regulating multiple aspects of peripheral T cell responses, while endogenous RA signalling occurs in developing thymocytes and the potential impact of such signals in regulating T cell development remains unclear. To address this question, we have crossed dnRARα mice, that carry a dominant-negative (dn) RARα transgene behind a floxed transcriptional STOP cassette, with CD4Cre mice. In the resulting dnRARα-CD4Cre⁺ mice, CD4-promotor driven Cre expression removes the STOP cassette and leads to constitutive expression of the dnRARα. This blocks RA signalling in developing thymocytes from the DN3/4 stage onwards and thus allows us to study the role of RA in T cell development.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Lund University, University of Birmingham
Number of pages: 1
Publication date: 2015
Event: Poster session presented at 1st International Venice Thymus Meeting, San Servolo Island, Italy.
Main Research Area: Technical/natural sciences
Electronic versions:
PosterVenice2015_KWendland_final.pdf
Publication: Research - peer-review › Poster – Annual report year: 2015

Retinoic acid signalling is required for the efficient differentiation of CD4+ T cells into pathogenic effector cells during the development of intestinal inflammation
Epidemiological studies of vitamin A deficient populations have illustrated the importance of the vitamin A metabolite retinoic acid (RA) in mucosal immune responses. However, RA seems to be a double-edge sword in CD4+ T cell biology. While it sustains the development of Foxp3+ regulatory T cells, it was also very recently reported to be essential for the stability of the Th1 lineage and to prevent transition to a Th17 program. Here we explored the role of RA signalling in CD4+ T cells during the development of intestinal inflammation in the T cell transfer colitis model. We found that RA signalling-deficient CD4+ T cells are less potent at inducing intestinal inflammation compared to their RA signalling-competent counterparts and exhibit a differentiation skewing towards more IFNγ-IL-17+, IL-17+IFNγ+ and Foxp3+ cells, while their capacity to differentiate into IL-17-IFNγ+ Th1 cells is compromised. In vitro studies confirm the inefficacy of RA signalling-deficient T cells to generate bona fide Th1 cells and demonstrate their aberrant increased RORγt expression while their differentiation into Th17 remains unaffected. Surprisingly, RA signalling-deficient CD45RB⁺ regulatory T cells (Tregs) are however as efficient as their RA signalling-competent counterparts to inhibit colitis development. Together our results indicate that RA, through its receptor RARα, negatively regulates the early expansion of CD4+ T cells.
during colitis and is necessary for the generation of colitogenic Th1/Th17 cells, while it is dispensable for the protective function of Treg cells. We are currently deciphering the mechanisms of these effects of RA on CD4+ T cells.

**General information**

State: Published

Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Lund University

Authors: Rivollier, A. M. C. (Intern), Pool, L. (Intern), Frising, U. (Ekstern), Wendland, K. (Ekstern), Agace, W. W. (Intern)

Number of pages: 1

Publication date: 2015

Event: Abstract from 17th International Congress of Mucosal Immunology , Berlin, Germany.

Main Research Area: Technical/natural sciences

Electronic versions:

2015_04_15_AbstractCMI2015.pdf

**Bibliographical note**

Oral presentation

Source: PublicationPreSubmission

Source-ID: 115438663

Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2015

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**Revisiting bovine pyometra-New insights into the disease using a culture-independent deep sequencing approach**

The bacteria present in the uterus during pyometra have previously been studied using bacteriological culturing. These studies identified Fusobacterium necrophorum and Trueperella pyogenes as the major contributors to the pathogenesis of pyometra. However, an increasing number of culture-independent studies have demonstrated that the bacterial diversity in most environments is underestimated in culture-based studies. Consequently, fastidious pyometra-associated pathogens may have been overlooked. Therefore, the primary purpose of this study was to investigate the diversity of bacteria in the uterus of cows with pyometra by using culture-independent 16S rRNA PCR combined with next generation sequencing. We investigated the microbial composition in the uterus of 21 cows with pyometra, which were obtained from a Danish slaughterhouse. Similar to the observations from the culture studies, Fusobacteriaceae, the family that F. necrophorum belongs to, was the operational taxonomic unit (OTU) observed in the largest quantities. By contrast, the Actinomycetaceae family, which includes T. pyogenes, constituted only 1% of the total number of reads. Thus we cannot confirm the previously reported role of species from this family in the pathogenesis of pyometra. Finally, we identified a large number of sequences representing three families of Gram-negative bacteria in the pyometra samples: Porphyromonadaceae, Mycoplasmataceae, and Pasteurellaceae. It is likely that these families comprise potential pathogenic species of a fastidious nature, which have been overlooked in previous studies. Our results increase the knowledge of the complexity of the pyometra microbiota and suggest that pathogens in addition to F. necrophorum may be involved in the pathogenesis of pyometra. (C) 2014 Elsevier B.V. All rights reserved.

**General information**

State: Published

Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Copenhagen

Authors: Knudsen, L. R. V. (Intern), Karstrup, C. C. (Ekstern), Pedersen, H. G. (Ekstern), Agerholm, J. S. (Ekstern), Jensen, T. K. (Intern), Schou, K. K. (Intern)

Number of pages: 6

Pages: 319-324

Publication date: 2015

Main Research Area: Technical/natural sciences

**Publication information**

Journal: Veterinary Microbiology

Volume: 175

Issue number: 2-4

ISSN (Print): 0378-1135

Ratings:

BFI (2018): BFI-level 2

Web of Science (2018): Indexed yes

BFI (2017): BFI-level 2

Scopus rating (2017): CiteScore 2.7 SJR 1.175 SNIP 1.241

Web of Science (2017): Indexed yes

BFI (2016): BFI-level 2

Scopus rating (2016): CiteScore 2.65 SJR 1.363 SNIP 1.206

Web of Science (2016): Indexed yes
Risk of entry and transmission for two Culicoides - borne diseases in horse: comparison of Africa n horse sickness and Equine encephalosis for France
Sampling and Pooling Methods for Capturing Herd Level Antibiotic Resistance in Swine Feces using qPCR and CFU Approaches

The aim of this article was to define the sampling level and method combination that captures antibiotic resistance at pig herd level utilizing qPCR antibiotic resistance gene quantification and culture-based quantification of antibiotic resistant coliform indicator bacteria. Fourteen qPCR assays for commonly detected antibiotic resistance genes were developed, and used to quantify antibiotic resistance genes in total DNA from swine fecal samples that were obtained using different sampling and pooling methods. In parallel, the number of antibiotic resistant coliform indicator bacteria was determined in the same swine fecal samples. The results showed that the qPCR assays were capable of detecting differences in antibiotic resistance levels in individual animals that the coliform bacteria colony forming units (CFU) could not. Also, the qPCR assays more accurately quantified antibiotic resistance genes when comparing individual sampling and pooling methods. qPCR on pooled samples was found to be a good representative for the general resistance level in a pig herd compared to the coliform CFU counts. It had significantly reduced relative standard deviations compared to coliform CFU counts in the same samples, and therefore differences in antibiotic resistance levels between samples were more readily detected. To our knowledge, this is the first study to describe sampling and pooling methods for qPCR quantification of antibiotic resistance genes in total DNA extracted from swine feces.
Selective Expression of the MAPK Phosphatase Dusp9/MKP-4 in Mouse Plasmacytoid Dendritic Cells and Regulation of IFN-beta Production

Plasmacytoid dendritic cells (pDCs) efficiently produce large amounts of type I IFN in response to TLR7 and TLR9 ligands, whereas conventional DCs (cDCs) predominantly secrete high levels of the cytokines IL-10 and IL-12. The molecular basis underlying this distinct phenotype is not well understood. In this study, we identified the MAPK phosphatase Dusp9/MKP-4 by transcriptome analysis as selectively expressed in pDCs, but not cDCs. We confirmed the constitutive expression of Dusp9 at the protein level in pDCs generated in vitro by culture with Flt3 ligand and ex vivo in sorted splenic pDCs. Dusp9 expression was low in B220(-) bone marrow precursors and was upregulated during pDC differentiation, concomitant with established pDC markers. Higher expression of Dusp9 in pDCs correlated with impaired phosphorylation of the MAPK ERK1/2 upon TLR9 stimulation. Notably, Dusp9 was not expressed at detectable levels in human pDCs, although these displayed similarly impaired activation of ERK1/2 MAPK compared with cDCs. Enforced retroviral expression of Dusp9 in mouse GM-CSF-induced cDCs increased the expression of TLR9-induced IL-12p40 and IFN-beta, but not of IL-10. Conditional deletion of Dusp9 in pDCs was effectively achieved in Dusp9(flox/flox); CD11c-Cre mice at the mRNA and protein levels. However, the lack of Dusp9 in pDC did not restore ERK1/2 activation after TLR9 stimulation and only weakly affected IFN-beta and IL-12p40 production. Taken together, our results suggest that expression of Dusp9 is sufficient to impair ERK1/2 activation and enhance IFN-beta expression. However, despite selective expression in pDCs, Dusp9 is not essential for high-level IFN-beta production by these cells.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Sensor detection of parasite eggs and (oo-)cysts - possibilities and challenges

To secure the safety and quality of food and water presence of pathogens including parasites must be controlled. This relies among other things on implementation of sensitive and specific tests which are able to rule out the occurrence of parasites. Worldwide environmentally resistant oocysts and cysts ((oo-)cysts) of the protozoan genera Cryptosporidium and Giardia are major causes of waterborne outbreaks of diarrhea. Methods for routine recovery and detection of waterborne Giardia and/or Cryptosporidium include filtration, immunomagnetic separation and detection by microscopy of immunofluorescence stained (oo-)cysts. These methods have low recovery rates, are time consuming, costly, and require well equipped laboratory facilities. Likewise, microscopy is the universal diagnostic method for detection of helminth eggs and protozoa in food and feed despite low sensitivity, difficulties to maintain quality control and common misdiagnosis. Novel optical techniques for high-resolution imaging and image transfer over data networks may offer solutions to these problems.

This presentation focus on results and experiences obtained from use of the FluidScopeTM technology for online, real-time sensor detection of Cryptosporidium and Giardia in drinking water. This novel optical technique, in combination with advanced data analysis, yields a measure for the protozoal content present in a sample. High sensitivity of the system is acquired through a combination of a new, patented filtration system and ultrasound to obtain high recovery rates of apparently undamaged protozoa: 84.9% (Standard deviation (±) 4.8) for Giardia cysts and 70% (± 6.5) for Cryptosporidium oocysts. Ultrasound in the current system is tuned into a useful tool for enhanced elution of filtered (oo-)cysts. The combined use of a metallic filter, sonication and "air backwash" are key factors in the creation of this highly efficient and robust system which can be used continuously for extended time with minimal maintenance requirements. Sample acquisition and analysis is performed in real-time where objects in suspension are differentiated into e.g. Cryptosporidium spp., Giardia spp., organic and inorganic subgroups. Subsequently (oo-)cysts passing through the system are collected on a filter and may be used for further molecular characterization. The detection system is a compact, low power, reagentless device and thus ideal for applications where relatively long service intervals and remote operation are important. The applications envisioned for this environmentally friendly system includes early warning of source water contamination e.g. water plants/water distribution networks, filtration systems (water purification), commercial buildings, swimming pools, and industry in general.

Development of highly specific algorithms for detection of Cryptosporidium and Giardia pose some challenges which will be discussed. For comparison newly developed, vision based systems for detection of helminth eggs in clinical samples and liquid suspensions will also be presented. These techniques, although not yet commercially available, offer promising options for future detection of parasites in food, feed and water even if further development is still needed before they can be used routinely.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology
Authors: Enemark, H. (Intern)
Number of pages: 1
Pages: 30-30
Publication date: 2015

Host publication information
Title of host publication: Abstract book of the 10th Conference RME2015
Place of publication: The Netherlands
Main Research Area: Technical/natural sciences
Conference: 10th Conference RME2015, Netherlands, 20/04/2015 - 20/04/2015
Electronic versions:
Sensor_detection_of_eggs_oo_cysts_1.pdf
Source: PublicationPreSubmission
Source-ID: 108239798
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2015
Sesquiterpene lactone-containing extracts from two chicory cultivars show different anthelmintic activity in vitro against Ostertagia ostertagi

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Section for Immunology and Vaccinology, University of Copenhagen
Authors: Pena-Espinoza, M. A. (Intern), Boas, U. (Intern), Williams, A. (Ekstern), Thamsborg, S. M. (Ekstern), Enemark, H. (Intern)
Number of pages: 1
Pages: 298-298
Publication date: 2015

Host publication information
Title of host publication: 25th International Conference of the World Association for the Advancement of Veterinary Parasitology : Abstract Book
Place of publication: Liverpool, United Kingdom
Main Research Area: Technical/natural sciences
Conference: 25th International Conference of the World Association for the Advancement of Veterinary Parasitology, Liverpool, United Kingdom, 16/08/2015 - 16/08/2015
Electronic versions:
Pe_a_Espinoza_et_al_in_vitro_WAAVP2015.pdf
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2015

Sesquiterpene lactone containing extracts from two cultivars of forage chicory (Cichorium intybus) show distinctive chemical profiles and in vitro activity against Ostertagia ostertagi

The study investigated direct anthelmintic effects of sesquiterpene lactones (SL)-containing extracts from forage chicory against free-living and parasitic stages of Ostertagia ostertagi. Freeze-dried leaves from chicory cultivars ‘Spadona’ and ‘Puna II’ were extracted using methanol/water. Total SL were further fractionated by solid-phase extraction and resulting extracts were characterised by high-performance liquid chromatography (HPLC). O. ostertagi eggs from faeces of mono-infected calves were hatched and L1 were used in a larval feeding inhibition assay (LFIA), while cultured L3 were used in a larval exsheathment inhibition assay (LEIA). Adult worms were immediately recovered after slaughter and used for motility inhibition assays (AMIA). Electron microscopy (EM) was performed on adult O. ostertagi exposed to 1000 μg extract mL−1 of both chicory cultivars. In all assays, decreasing concentrations of SL-containing extracts in PBS (1% DMSO) were tested in replicates with 1% DMSO in PBS as negative controls. HPLC demonstrated similar concentrations of most SL in both extracts. However, Spadona-extract contained significantly higher concentrations of 11, 13-dihydro-8-deoxy lactucin (P = 0.01), while Puna II-extract had increased levels of 11, 13-dihydro lactucin (P < 0.0001). In the LFIA, both extracts reduced larval feeding at increasing concentrations, but Spadona-extract showed higher potency confirmed by significantly lower EC50 (P < 0.0001). In the LEIA, neither of the two extracts interfered with the exsheathment of L3 (P > 0.05). In the AMIA, both SL-containing extracts induced a dose-dependent effect but Spadona-extract showed greater activity and exerted faster worm paralysis than Puna II-extract with significantly lower EC50 (P < 0.0001). No cuticular damage was observed by EM in worms exposed to any of the extracts. We have demonstrated that SL-containing extracts from forage chicory can inhibit feeding of free-living larvae and exert direct effects against parasitic stages of O. ostertagi. Our results may contribute to the identification of natural anti-parasitic compounds and to interpret the in vivo anthelmintic effects of forage chicory.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Section for Immunology and Vaccinology, University of Copenhagen
Authors: Pena-Espinoza, M. A. (Intern), Boas, U. (Intern), Williams, A. (Ekstern), Thamsborg, S. M. (Ekstern), Simonsen, H. T. (Intern), Enemark, H. (Intern)
Pages: 191-200
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: International Journal for Parasitology: Drugs and Drug Resistance
Volume: 5
Issue number: 3
ISSN (Print): 2211-3207
Ratings:
Web of Science (2018): Indexed yes
Significance of Timing on Effect of Metaphylactic Toltrazuril Treatment against Eimeriosis in Calves

In this multicentric, randomised, blinded and placebo-controlled field study, the effect of treatment with toltrazuril (Baycox® Bovis, Bayer) on oocyst excretion, diarrhoea score and weight gain was studied in Danish dairy herds with confirmed history of eimeriosis (coccidiosis) and prevalence of Eimeria bovis and Eimeria zuernii. Three commercial herds and a total of 71 calves, aged 48 – 135 days, were included. Treatment with a single oral dose of toltrazuril (15 mg/kg) was given after relocation to common pens and one week before expected outbreak of eimeriosis. The effect of treatment was followed by weekly faecal sampling and weighing initially and at the end of a study period of 8 weeks. In Herd 2 and 3 toltrazuril treated calves gained on average 7.95 kg more than placebo treated calves (p = 0.007), and both oocyst excretion and prevalence of Eimeria spp. were significantly reduced the first weeks post treatment. In Herd 1, by contrast, the farmer made some unforeseen changes in the management which entailed relocation to large deep-litter pens 3 – 6 weeks post treatment. In addition, many calves were not treated metaphylactically while few calves excreted oocysts when the trial was initiated. Thus, no significant difference in weight gain was found between toltrazuril and placebo treated calves (p = 0.523), and the oocyst excretion of toltrazuril treated calves was significantly higher during week 7 and 8. Significant differences in faecal scores were observed between the herds (p

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Jan Dahl Consult, Bayer HealthCare
Authors: Enemark, H. (Intern), Dahl, J. (Ekstern), Enemark, J. M. D. (Ekstern)
Number of pages: 12
Pages: 201-212
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Parasitology Research
Volume: 114
Issue number: 1
ISSN (Print): 0932-0113
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.46 SJR 0.991 SNIP 1.001
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.2 SJR 0.94 SNIP 0.967
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.967 SNIP 0.988 CiteScore 2.07
Web of Science (2015): Indexed yes
Simulating Spread of Antimicrobial Resistant Bacteria in the Pig Pen: try our online tool

General information
State: Published
Organisations: Department of Applied Mathematics and Computer Science, National Veterinary Institute, Section for Epidemiology, Dynamical Systems, University of Copenhagen
Authors: Græsbøll, K. (Intern), Nielsen, S. S. (Ekstern), Toft, N. (Intern), Christiansen, L. E. (Intern)
Number of pages: 1
Publication date: 2015
Event: Poster session presented at Annual Conference of The Society for Veterinary Epidemiology and Preventive Medicine, Ghent, Belgium.
Main Research Area: Technical/natural sciences
Electronic versions:
SVEPM4.pdf
Source: PublicationPreSubmission
Source-ID: 110923815
Publication: Research - peer-review » Poster – Annual report year: 2015
Simulating Spread of Antimicrobial Resistant Bacteria in the Pig Pen: try our online tool

General information
State: Published
Organisations: Department of Applied Mathematics and Computer Science, National Veterinary Institute, Section for Epidemiology, Dynamical Systems, University of Copenhagen
Authors: Græsbøll, K. (Intern), Nielsen, S. S. (Ekstern), Toft, N. (Intern), Christiansen, L. E. (Intern)
Number of pages: 1
Publication date: 2015
Event: Poster session presented at 14th Conference of the International Society for Veterinary Epidemiology and Economics, Mérida, Yucatan, Mexico.
Main Research Area: Technical/natural sciences
Electronic versions:
kagr_ISVEE14.pdf
Publication: Research - peer-review › Poster – Annual report year: 2015

Simulering af kontrolforanstaltninger til bekæmpelse af plasmacytose i minkfarne

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Copenhagen Fur
Authors: Boklund, A. (Intern), Hisham Beshara Halasa, T. (Intern), Chriél, M. (Intern), Struve, T. (Ekstern), Østergaard, J. (Ekstern), Clausen, J. (Ekstern)
Publication date: 2015
Main Research Area: Technical/natural sciences
Publication information
Journal: Dansk Veterinaertidsskrift
Issue number: 6
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Simulering af tiltag til bekæmpelse af plasmacytose i mink

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology
Authors: Boklund, A. (Intern), Hisham Beshara Halasa, T. (Intern), Struve, T. (Ekstern), Østergaard, J. (Ekstern), Clausen, J. (Ekstern), Chriél, M. (Intern)
Pages: 117-123
Publication date: 2015

Host publication information
Title of host publication: Faglig Årsberetning 2014
Place of publication: Aarhus N
Publisher: Kopenhagen Fur
Main Research Area: Technical/natural sciences
Publication: Research › Book chapter – Annual report year: 2015

Simultaneous vaccination with PRRS mlv against both PRRSV type 1 and type 2: duration of viraemia and level of clinical protection

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Technical University of Denmark, Danish Pig Production
Authors: Kristensen, C. S. (Ekstern), Kvisgaard, L. K. (Intern), Pawlowski, M. (Ekstern), Holmgard Carlsen, S. (Ekstern), Hjulsager, C. K. (Intern), Larsen, L. E. (Intern)
Number of pages: 1
Publication date: 2015
Event: Abstract from 7th International Symposium on Emerging and Re-emerging Pig Diseases, Kyoto, Japan.
Main Research Area: Technical/natural sciences
Electronic versions:
ISERPD2015_abstract_Lindholm_final.pdf
Source: PublicationPreSubmission
Source-ID: 119057308
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2015

Spatial analysis and temporal trends of porcine reproductive and respiratory syndrome in Denmark from 2007 to 2010 based on laboratory submission data
Porcine reproductive and respiratory syndrome (PRRS) has been a cause for great concern to the Danish pig industry since it was first diagnosed in 1992. The causative agent of PRRS is an RNA virus which is divided into different genotypes. The clinical signs, as well as its morbidity and mortality, is highly variable between herds and regions. Two
different genotypes of PRRS virus (PRRSV) are found in Denmark: type 1 and type 2. Approximately 40 % of Danish swine herds are seropositive for one or both PRRSV types. The objective of this study was to describe the temporal trend and spatial distribution of PRRSV in Danish swine herds from 2007 to 2010, based on type-specific serological tests from the PRRS surveillance and control program in Denmark using the results stored in the information management system at the National Veterinary Institute, Technical University of Denmark (DTU Vet). The average monthly seroprevalence of PRRSV type 1 was 9 % (minimum of 5 %; maximum of 13 %) in breeding herds, and 20 % (minimum of 14 %; maximum of 26 %) in production herds; PRRSV type 2 had an average seroprevalence of 3 % (minimum of 1 %; maximum of 9 %) in breeding herds and of 9 % (minimum of 5 %; maximum of 13 %) within production herds. The seroconversion rate followed a similar and consistent pattern, being higher for type 1 than for type 2 for both PRRSV types. Regarding the spatiotemporal results, the relative risk distribution maps changed over time as a consequence of the changes in PRRSV seroprevalence, suggesting a general decline in the extent of areas with higher relative risk for both type 1 and 2. Local spatial analysis results demonstrated the existence of statistically significant clusters in areas where the relative risk was higher for both herds. PRRSV type 1 seroprevalence was constantly higher than for PRRSV type 2 in both herd types. Significant spatial clusters were consistently found in Denmark, suggesting that PRRSV is endemic in these areas. Furthermore, relative risk distribution maps revealed different patterns over time as a consequence of the changes in seroprevalence.
Strain-specific serological response after simultaneous vaccination with PRRS MLV against

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Technical University of Denmark, Danish Pig Production
Authors: Kristensen, C. S. (Ekstern), Kvisgaard, L. K. (Intern), Pawlowski, M. (Ekstern), Carlsen, S. H. (Ekstern), Hjulsager, C. K. (Intern), Larsen, L. E. (Intern)
Number of pages: 1
Publication date: 2015
Event: Abstract from International Porcine Reproductive And Respiratory Syndrome Congress, Ghent, Belgium.
Main Research Area: Technical/natural sciences
Electronic versions:
Sonnes_abstract.pdf
Source: PublicationPreSubmission
Source-ID: 119057138
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2015

Structure and Function of a Nonruminant Gut: A Porcine Model

In many aspects, the anatomical, physiological, and microbial diversity features of the ruminant gut are different from that of the monogastric animals. Thus, the main aim of this chapter is to give a comparative overview of the structure and function of the gastrointestinal tract of a nonruminant monogastric animal, and here it is represented by a pig model. In this chapter, we describe and discuss (i) microbial diversity in different parts of the porcine gut; (ii) differences between the ruminant and nonruminant gut; (iii) main events during colonization and succession of microbiota in the porcine gut; (iv) effects of various feed additives including antibiotics, phages, probiotics, and prebiotics on pigs; and (v) the use of the porcine model in translational medicine.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, National Agriculture and Food Research Organization
Authors: Tajima, K. (Ekstern), Aminov, R. (Intern)
Number of pages: 29
Publication date: 2015
Host publication information
Title of host publication: Rumen Microbiology: From Evolution to Revolution
Publisher: Springer
Editors: Puniya, A. K., Singh, R., Kamra, D. N.
ISBN (Print): 978-81-322-2400-6
Chapter: 5
Main Research Area: Technical/natural sciences
DOIs:
10.1007/978-81-322-2401-3_5
Source: PublicationPreSubmission
Source-ID: 110892196
Publication: Research - peer-review › Book chapter – Annual report year: 2015
Swine influenza viruses in circulation in European pigs exhibit an increasing genetic diversity since last pandemic 2009

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, University Paris-Est Anses, Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia, IDT-Biologika GmbH, Friedrich Loeffler Institute, National Veterinary Research Institute, Finnish Food Safety Authority, University of Thessaly, Central Veterinary Institute
Authors: Simon, G. (Ekstern), Larsen, L. E. (Intern), Dürrwald, R. (Ekstern), Foni, E. (Ekstern), Harder, T. (Ekstern), Markowska-Daniel, I. (Ekstern), Dan, A. (Ekstern), Maldonaldo, J. (Ekstern), Huovilainen, A. (Ekstern), Billinis, C. (Ekstern), Davidson, I. (Ekstern), Reid, S. M. (Ekstern), Brown, I. H. (Ekstern), Loeffen, W. (Ekstern)
Pages: 80-80
Publication date: 2015

Host publication information
Title of host publication: Proceedings of the 7th European Symposium of Porcine Health Management
Place of publication: Nantes, France
Article number: 014
Main Research Area: Technical/natural sciences
Conference: 7th European Symposium of Porcine Health Management, Nantes, France, 22/04/2015 - 22/04/2015
Electronic versions:
Source: PublicationPreSubmission
Source-ID: 119056233
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2015

Swine plasma immunoglobulins for prevention and treatment of post-weaning diarrhoea: Safety and Preliminary results

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Department of Chemical and Biochemical Engineering, Center for BioProcess Engineering, Section for Bacteriology, Pathology and Parasitology, Section for Virology, Upfront Chromatography A/S, Upfront Chromatography A/S
Authors: Hedegaard, C. J. (Intern), Strube, M. L. (Intern), Bendix Hansen, M. (Ekstern), Kjær Lindved, B. (Ekstern), Larsen, L. E. (Intern), Lihme, A. (Ekstern), Boye, M. (Intern), Heegaard, P. M. H. (Intern)
Publication date: 2015
Event: Poster session presented at 5th European Veterinary Immunology Workshop, Vienna, Austria.
Main Research Area: Technical/natural sciences
Electronic versions:
POSTER_EVIW_2015_CJHE.pdf

Relations
Activities:
5th European Veterinary Immunology Workshop
Publication: Research › Poster – Annual report year: 2015

Swine plasma immunoglobulins for prevention and treatment of post-weaning diarrhoea: Safety and Preliminary results
Post-weaning diarrhoea (PWD) is a common condition in intensive swine production, resulting in reduced welfare of weaners and economic losses for the farmer as a result of illness, death, and treatment costs. It is also one of the main causes of antibiotics- and zinc use in the pig production industry. We aim at developing a sustainable product for protection against PWD based on natural antibodies (immunoglobulins) derived directly from inexpensive raw materials. The availability of such an inexpensive and highly active immunoglobulin product would allow swine producers to reduce expenses and minimize the on antibiotics and zinc usage. Swine immunoglobulins were isolated directly from slaughterhouse swine plasma-waste by expanded bed chromatography. It was shown that the isolated Immunoglobulin fraction bound enterotoxigenic Escherichia coli (ETEC) and Salmonella spp. and inhibited their adhesion to porcine epithelial cells in vitro. As the immunoglobulin fraction is intended for oral use as a feed supplement, we also tested the safety of feeding 4 grams of natural immunoglobulins to 4-5 week old weaner piglets for 14 days and observed no adverse effects. In an experimental model of E. coli F4+ induced PWD, we observed that piglets given IgG as a feed supplement cleared the E. coli infection significantly faster than control weaner piglets not receiving an immunoglobulin feed supplement. Furthermore, deep sequencing of the ileal microbiota showed a significantly lowered colonization of the family Enterobactericea in immunoglobulin fed piglets as compared to the control group. Thus pig slaughterhouse plasma is indicated as a potential source resource of antibodies for the control of PWD.
Swine production on Maio Island, Cape Verde: a household survey

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology
Authors: Lopes Antunes, A. C. (Intern), Vieira, S. (Ekstern), Malta, M. (Ekstern), Nunes, T. (Ekstern), Vaz, Y. (Ekstern)
Pages: 155-159
Publication date: 2015
Main Research Area: Technical/natural sciences
Publication information
Journal: Revista Portuguesa de Ciencias Veterinarias
Volume: 110
Issue number: 595-596
ISSN (Print): 0035-0389
Ratings:
Web of Science (2018): Indexed yes
Web of Science (2015): Indexed yes
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Original language: English
Electronic versions:
antunes.pdf
Source: PublicationPreSubmission
Source-ID: 122906559
Publication: Research - peer-review › Journal article – Annual report year: 2016

Sygdom og sundhed

General information
State: Published
Organisations: Section for Virology, National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Dansk Akvakultur, University of Copenhagen
Authors: Henriksen, N. H. (Ekstern), Buchmann, K. (Ekstern), Olesen, N. J. (Intern), Dalsgaard, I. (Intern), Madsen, L. (Intern), Bruun, M. S. (Intern), Boultrup, T. S. (Intern)
Number of pages: 39
Pages: 56-94
Publication date: 2015
Host publication information
Title of host publication: Akvakultur
Publisher: Landbrugsforlaget
Chapter: 5
Main Research Area: Technical/natural sciences
Links:
Temperature as a predictor of fouling and diarrhea in Slaughter pigs

The PigIT Project aims at improving welfare and production of slaughter pigs by integration of various sensor systems for alarm purposes. Here we present an exploratory analysis to assess the predictive value of temperature sensor data with respect to pen fouling and diarrhea. We recorded the temperature at four locations in two double-pens (by the drinking nipples and by the corridor) between November 2013 and December 2014. Logistic regression models were made to express the probability of fouling and diarrhea per day, and were reduced via backwards elimination. Furthermore, fitting the models was attempted with the raw temperature data as well as data averaged over 10, 15, 30 and 60 minutes. The predictive performances were evaluated with Matthews Correlation Coefficient (MCC). For diarrhea, the minimal and maximal temperatures at the water nipple and the corridor, as well as the maximal rate of temperature decrease, were found to be either significant or borderline significant. The same factors, with the addition of maximum rate in temperature increase, were found to be significant or borderline significant predictors for pen fouling. Both conditions were consistently detected at better than randomly (MCC between 0.422 and 0.557 for diarrhea, and between 0.386 and 0.560 for fouling). Thus, temperature information seems to contain predictive value in relation to fouling and diarrhea, but not enough to stand alone. It would thus be meaningful to combine this information with other available data to achieve an optimal predictive power.

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, University of Copenhagen
Authors: Jensen, D. (Ekstern), Toft, N. (Intern), Kristensen, A. K. (Ekstern)
Number of pages: 1
Pages: 20-20
Publication date: 2015

Host publication information
Title of host publication: Programme & Abstracts : PhD Day
Place of publication: Copenhagen N
Publisher: Copenhagen University
Main Research Area: Technical/natural sciences
Conference: PhD Day at Copenhagen University, Copenhagen, Denmark, 21/05/2015 - 21/05/2015
Electronic versions:
ku_2015_05_11.pdf
Source: FindIt
Source-ID: 2281472673
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2015

Temperature as a predictor of fouling and diarrhea in Slaughter pigs

Understanding the underlying pleiotropic relationships among quantitative traits is integral to predict correlated responses to artificial selection. The availability of large-scale next-generation sequence data in cattle has provided an opportunity to examine whether pleiotropy is responsible for overlapping QTLs in multiple economic traits. In the present study, we examined QTLs effecting cattle stillbirth, calf size, and adult stature located in the same genomic region. A genome scan with whole sequence variants revealed one QTL with large effects on the service sire calving index (SCI), and body conformation index (BCI) at the same location (~39 Mb) on chromosome 6 in Nordic Red cattle. The targeted region was analyzed for SCI and BCI component traits. The QTL peak included LCORL/NCAPG genes, which were earlier reported to influence fetal growth, and adult stature in several species. The QTL exhibited large effects on calf size and stature in Nordic Red cattle. Two deviant haplotype ypes (HAP1 and HAP2) were resolved, which increased calf size at birth, and effected adult body conformation. However, the haplotypes also resulted in increased calving difficulties and calf mortality due to increased calf size at birth. Haplotype locations overlapped, however linkage disequilibrium (LD) between the sites was low, suggesting two independent mutations responsible for similar effects. The difference in prevalence between the two haplotypes in Nordic Red subpopulations suggested independent origins in different populations. Results of our study identified QTLs with large effects on body conformation, and service sire calving traits on chromosome 6 in cattle. We present robust evidence that variation at the LCORL/NCAPG locus effects calf size at birth and adult stature. We suggest the two deviant haplotypes within the QTL were due to two independent mutations.

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, University of Copenhagen
Authors: Jensen, D. B. (Ekstern), Toft, N. (Intern), Kristensen, A. R. (Ekstern)
Number of pages: 1
**The Danish National Veterinary Institute and disease surveillance**

The National Veterinary Institute at the Technical University of Denmark, DTU-Vet, conducts research in infectious diseases in livestock, wildlife and fish, and diagnoses diseased animals. We give advice to public authorities and cooperate with these on the Danish veterinary contingency plan. The research at DTU-Vet covers methods for detection, control and prevention of many infectious diseases in animals, including use of animal disease models for comparative studies of human diseases. However, our main focus is on notifiable diseases, as well as other severe infectious diseases that affect farm livestock.

Veterinarians can submit samples from diseased animals for diagnosis. For notifiable diseases the diagnosis is free, whereas we diagnose other diseases on commercial terms. All our diagnostic services are based on accredited or quality-assured analysis methods.

DTU-Vet is responsible for the laboratory component of the Danish veterinary contingency plan, which puts emergency procedures into action in the event of suspected or actual outbreaks of serious infectious animal diseases. The contingency plan is supported by our activities in conjunction with a range of national monitoring programs on animal diseases and zoonoses.

We will give a general overview of the activities of DTU-Vet with focus on participation in serological disease surveillance and on two selected examples from the laboratories:

Porcine Epidemic Diarrhea (PED) was first identified in Europe in 1971, and PED virus (PEDV) was detected as etiologic agent in 1978. Later, this virus was reported in Asia during the 1980s. The outbreaks in this part of the world were more severe than in Europe and became increasingly problematic. In May 2013, PED was identified for the first time in the central Iowa of the United States. The PEDV strain, circulating in North America, showed a close similarity with 99.5% nucleotide identity to a Chinese strain from 2012. Since September 2014 outbreaks of PED with strains similar to the strains circulating in North America has been observed in Europe.

Since 1988 the PEDV has been grown in cell culture and this has led to the development of a blocking ELISA based on whole virus antigen. With introduction of the new PEDV strains from America to Europe it is of crucial importance to test the sensitivity and specificity of this test in the context of these new strains.

The Danish surveillance on Salmonella antibodies in hen eggs is performed by DTU-Vet, and has been one of several important tools for paving the road for the achievement of Danish EU special status on importation of eggs in 2012. When testing serum and egg yolk, a mix-ELISA is used, based on S. typhimurium and S. enteritidis antigens. 2009-2012 the mix-ELISA produced an unacceptably large amount of seropositive findings that could not be confirmed by subsequent confirmatory bacteriological sampling. Therefore we enhanced the specificity of the ELISA, without losing sensitivity, by refining the antigens. This example will be given to illustrate the way that laboratories sometimes have to keep optimizing and validating tests currently used, in order to adapt to the scope of the surveillance.
The diet of Danish red foxes (Vulpes vulpes) in relation to a changing agricultural ecosystem. A historical perspective

Rodents and especially voles (Microtus agrestis or arvalis) make up the basic diet of foxes (Vulpes vulpes) in Denmark. As the abundance of voles and mice may have decreased as a result of modern agricultural procedures, this study investigates potential changes in the diet of Danish red foxes over the past 4 decades in relation to a changing agricultural landscape. Our study compares the stomach contents of foxes collected in Jutland during the years 2012–2014 with a similar study from 1965 to 1970. The results show that small rodents occur in the stomachs of foxes with the same frequencies today (73 %) as 40–50 years ago (67 %), while the frequency of European brown hare (Lepus europaeus) has decreased from 7 to 3 % and the frequency of roe deer (Capreolus capreolus) has increased from 3 to 18 %. The changes in the occurrence of brown hare and roe deer in the diet of foxes during the past 40 years most probably reflect changes in the populations of the two species. By comparing digitised orthophotos of six agricultural areas (3.5×3.5 km) of the past 1974/1975 and present landscapes, it was revealed that the total area of crop fields, small natural habitats, hedgerows and grasslands have remained almost unchanged. However, mean field size has increased by 48 %, and the mean size of small natural habitats has increased by 15 %; meaning that the length of field boundaries and the number of small natural habitats have decreased by 65 and 33 %, respectively. The distance between natural habitats in the cultivated areas has become larger during the past 40 years. Overall, the areas of natural biotopes have remained the same in Denmark during the past 40 years. Field boundaries on the other hand which are known to be important vole habitats have become fewer in the cultivated areas. Despite this, small rodents still occur in high frequencies in the diet of nowadays foxes. As voles are sensitive to fragmentation, narrow stipes of permanent grass should be maintained or even re-established in the cultivated areas to improve life conditions for small rodents and other wildlife.

General information
State: Published
Organisations: National Food Institute, National Veterinary Institute, FO-Aarhus, Aarhus University, Danish Hunters Association
Authors: Pagh, S. (Ekstern), Tjørnløv, R. S. (Ekstern), Olesen, C. R. (Ekstern), Chriél, M. (Intern)
Number of pages: 11
Pages: 319-329
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Mammal Research
Volume: 60
Issue number: 4
ISSN (Print): 2199-241x
Ratings:
Web of Science (2018): Indexed yes
Scopus rating (2017): SNIP 0.816 SJR 0.7 CiteScore 1.4
Web of Science (2017): Indexed Yes
Scopus rating (2016): CiteScore 1.1 SJR 0.611 SNIP 0.891
Scopus rating (2015): SJR 0.547 SNIP 0.621
Web of Science (2015): Indexed yes
Scopus rating (2014): SJR 0.51 SNIP 0.894
Scopus rating (2013): SJR 0.476 SNIP 0.842
Scopus rating (2012): SJR 0.466 SNIP 0.793
Scopus rating (2011): SJR 0.373 SNIP 0.66
Scopus rating (2010): SJR 0.425 SNIP 0.718
Scopus rating (2009): SJR 0.48 SNIP 0.873
Scopus rating (2008): SJR 0.711 SNIP 0.772
Scopus rating (2007): SJR 0.402 SNIP 0.776
Scopus rating (2006): SJR 0.306 SNIP 0.496
Scopus rating (2005): SJR 0.356 SNIP 0.6
Scopus rating (2004): SJR 0.378 SNIP 0.829
Scopus rating (2003): SJR 0.544 SNIP 0.949
Scopus rating (2002): SJR 0.611 SNIP 1.106
Scopus rating (2001): SJR 0.478 SNIP 0.679
Scopus rating (2000): SJR 0.716 SNIP 0.693
The dog and cat population on Maio Island, Cape Verde: characterisation and prediction based on household survey and remotely sensed imagery

The objective was to estimate and characterise the dog and cat population on Maio Island, Cape Verde. Remotely sensed imagery was used to document the number of houses across the island and a household survey was carried out in six administrative areas recording the location of each animal using a global positioning system instrument. Linear statistical models were applied to predict the dog and cat populations based on the number of houses found and according to various levels of data aggregation. In the surveyed localities, a total of 457 dogs and 306 cats were found. The majority of animals had owners and only a few had free access to outdoor activities. The estimated population size was 531 dogs [95% confidence interval (CI): 453-609] and 354 cats (95% CI: 275-431). Stray animals were not a concern on the island in contrast to the rest of the country.

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology
Number of pages: 5
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Geospatial Health
Volume: 10
Issue number: 2
ISSN (Print): 1827-1987
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.51 SJR 0.554 CiteScore 1.38
Web of Science (2017): Indexed Yes
Scopus rating (2016): SJR 0.812 SNIP 0.745 CiteScore 1.48
Scopus rating (2015): SJR 0.682 SNIP 0.723 CiteScore 1.41
Web of Science (2015): Indexed yes
Scopus rating (2014): SJR 0.65 SNIP 0.804 CiteScore 1.51
Scopus rating (2013): SJR 0.728 SNIP 1.026 CiteScore 1.85
Scopus rating (2012): SJR 0.615 SNIP 0.973 CiteScore 1.9
Scopus rating (2011): SJR 0.974 SNIP 0.888 CiteScore 3.07
Scopus rating (2010): SJR 1.023 SNIP 1.105
Scopus rating (2009): SJR 0.659 SNIP 0.449
Scopus rating (2008): SJR 0.446
Scopus rating (2007): SJR 0.171

Dog, Cat Household survey, Remote sensing, Maio Island

Electronic versions:
386_1262_2_PB.pdf
DOIs:
10.4081/gh.2015.386
Links:
The immunity raised by recent European subtype 1 PRRSV strains allows a better replication of East European subtype 3 PRRSV strain Lena than the immunity raised by an older strain -increased risk for spatial expansion of PRRSV Lena-like strains

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Ghent University
Authors: Trus, I. (Ekstern), Frydas, I. S. (Ekstern), Reddy, V. R. A. P. (Ekstern), Bonckaert, C. (Ekstern), Li, Y. (Ekstern), Kvisgaard, L. K. (Intern), Larsen, L. E. (Intern), Nauwynck, H. J. (Ekstern)
Number of pages: 1
Publication date: 2015
Event: Abstract from International Porcine Reproductive And Respiratory Syndrome Congress, Ghent, Belgium.
Main Research Area: Technical/natural sciences
Electronic versions:
Ivan_Trus_abstract.pdf
Source: PublicationPreSubmission
Source-ID: 119057016
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2015

The impact of a decade of research on vector borne diseases

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology
Number of pages: 131
Publication date: 2015

Publication information
Publisher: CIRAD
Original language: English
Main Research Area: Technical/natural sciences
Electronic versions:
EDENEXT_BOOK_Final_Pages_Basse_def.pdf
DOIs:
10.13140/RG.2.1.4382.6400

Bibliographical note
Not complete author list
Source: PublicationPreSubmission
Source-ID: 115475584
Publication: Research - peer-review › Book – Annual report year: 2015

The joint risk score for vector-borne diseases used for early detection

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Utrecht University, INRA Institut National de La Recherche Agronomique, Friedrich Loeffler Institute, National Veterinary Institute Sweden
Authors: Fischer, E. A. J. (Ekstern), Andersson, M. G. (Ekstern), Faverjon, C. (Ekstern), Leblond, A. (Ekstern), Gussmann, M. (Ekstern), Gethmann, J. (Ekstern), Bäder, R. (Intern)
Number of pages: 1
Publication date: 2015
The pig as a large animal model for influenza A virus infection

It is increasingly realized that large animal models like the pig are exceptionally human-like and serve as an excellent model for disease and inflammation. Pigs are fully susceptible to human influenza, share many similarities with humans regarding lung physiology and innate immune cell infiltration of the respiratory system.

This study aimed at providing a better understanding of the involvement of innate immune factors and non-coding RNA in blood leukocytes during influenza A virus infection. By using the pig as a model we were able to perform highly controlled experimental infections and study early clinical signs of disease, viral titer, and transcriptional response of coding and non-coding RNA. This was completed during the first two weeks after experimental viral infection, generating information that would be difficult to obtain from human patients.

Expression of a wide range of immune factors including several genes known to be centrally involved in the viral defence was quantified by high throughput qPCR (BioMark, Fluidigm). Likewise, miRNAs were quantified using the BioMark (Fluidigm) as well as by MiRCURY LNATM (Exiqon).

During the first 24 hours of infection we found the expression of several antiviral genes, including interferon and interferon-related genes, to mimic key findings from human studies. Finally, several circulating miRNAs isolated from blood leukocytes was found to hold great potential as biomarkers for progression of viral lung infection. These results further consolidate the pig as a valuable model for influenza A virus infection.

General information

State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Section for Virology, Technical University of Denmark, IDT-Biologika GmbH
Authors: Skovgaard, K. (Intern), Brogaard, L. (Intern), Larsen, L. E. (Intern), Mortensen, S. (Ekstern), Dürrwald, R. (Ekstern), Schengel, M. (Ekstern), Heegaard, P. M. H. (Intern)
Number of pages: 1
Publication date: 2015
Main Research Area: Technical/natural sciences
Electronic versions:

Source: PublicationPreSubmission
Source-ID: 122152951
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2016

The pig as a model for therapeutic human anti-cancer vaccine development, elucidating the T-cell reactivity against IDO and RhoC

Immunotherapy against cancer has shown increased overall survival of metastatic cancer patients and is a promising new vaccine target. For this to succeed, appropriate tailoring of vaccine formulations to mount in vivo cytotoxic T cell (CTL) responses towards co-delivered cancer antigens is important. Previous development of therapeutic cancer vaccines has largely been based on studies in mice and the majority of these candidate vaccines failed to establish therapeutic responses in subsequent human clinical trials. Since the porcine immunome is more closely related to the human counterpart, we here introduce pigs as a superior large animal model for human cancer vaccine development via the use of our unique technology for swine leukocyte antigen (SLA) production. IDO and RhoC, both known to be important in human cancer development and progression, were used as vaccine targets. Pigs were immunized with overlapping 20-mer peptides spanning the entire porcine IDO and RhoC sequences formulated in a panel of CTL-inducing adjuvants. 198 candidate IDO- and RhoC-derived 9-11mer peptides potentially binding to SLA- 1*04:01, -1*07:02, -2*04:01, -2*05:02 and/or -3*04:01 were identified in silico, and peptide-SLA complex stability measurements revealed 89 stable (t½ ≥ 0.5 hour) complexes. Vaccine-induced peptide-specific CTL responses were monitored using IFN-γ release as a read out. We found responses to IDO- and RhoC-derived peptides across all groups; surprisingly non-stably binding peptides also induced responses. None of the adjuvants was found to be superior as they were all capable of generating CTL responses to IDO and RhoC hence supporting the further use of pigs as a large animal model for vaccine development against human cancer.

General information
The Proteolytically Stable Peptidomimetic Pam-(Lys-βNSSpe)₆-NH₂ Selectively Inhibits Human Neutrophil Activation via Formyl Peptide Receptor 2

Immunomodulatory host defense peptides (HDPs) are considered to be lead compounds for novel anti-sepsis and anti-inflammatory agents. However, development of drugs based on HDPs has been hampered by problems with toxicity and low bioavailability due to in vivo proteolysis. Here, a subclass of proteolytically stable HDP mimics consisting of lipidated α-peptide/β-peptoid oligomers was investigated for their effect on neutrophil function. The most promising compound, Pam-(Lys-βNSSpe)₆-NH₂, was shown to inhibit formyl peptide receptor 2 (FPR2) agonist-induced neutrophil granule mobilization and release of reactive oxygen species. The potency of Pam-(Lys-βNSSpe)₆-NH₂ was comparable to that of PBP10, the most potent FPR2-selective inhibitor known. The immunomodulatory effects of structural analogues of Pam-(Lys-βNSSpe)₆-NH₂ emphasized the importance of both the lipid and peptidomimetic parts. By using imaging flow cytometry in primary neutrophils and FPR-transfected cell lines we found that a fluorescently labelled analogue of Pam-(Lys-βNSSpe)₆-NH₂ interacted selectively with FPR2. Furthermore, the interaction between Pam-(Lys-βNSSpe)₆-NH₂ and FPR2 was found to prevent binding of the FPR2-specific activating peptide agonist Cy5-WKYMWM, while the binding of a FPR1-selective agonist was not inhibited. To our knowledge, Pam-(Lys-βNSSpe)₆-NH₂ is the first HDP mimic found to inhibit activation of human neutrophils via direct interaction with FPR2. Hence, we consider Pam-(Lys-βNSSpe)₆-NH₂ to be a convenient tool in the further dissection of the role of FPR2 in inflammation and homeostasis as well as for investigation of the importance of neutrophil stimulation in anti-infective therapy involving HDPs.
Thermostability enhancement of an endo-1,4-β-galactanase from Talaromyces stipitatus by site-directed mutagenesis

Enzymatic conversion of pectinaceous biomasses such as potato and sugar beet pulp at high temperatures is advantageous as it gives rise to lower substrate viscosity, easier mixing, and increased substrate solubility and lowers the risk of contamination. Such high-temperature processing requires development of thermostable enzymes. Talaromyces stipitatus was found to secrete endo-1,4-β-galactanase when grown on sugar beet pectin as sole carbon source. The mature protein contained 353 AA and the MW was estimated to 36.5 kDa. It was subjected to codon optimization and produced in Pichia pastoris in 2 l scale yielding 5.3 g. The optimal reaction condition for the endo-1,4-β-galactanase was determined to be 46 °C at pH 4.5 at which the specific activity was estimated to be 6.93 μmol/min/mg enzyme with half-lives of 13 and 2 min at 55 and 60 °C, respectively. For enhancement of the half-life of TSGAL, nine single amino acid residues were selected for site-directed mutagenesis on the basis of semi-rational design. Of these nine mutants, G305A showed half-lives of 114 min at 55 °C and 15 min at 60 °C, respectively. This is 8.6-fold higher than that of the TSGAL at 55 °C, whereas the other mutants displayed moderate positive to negative changes in their half-lives.
The SimSpay-Student Perceptions of a Low-Cost Build-It-Yourself Model for Novice Training of Surgical Skills in Canine Ovariohysterectomy

Practical and ethical considerations have led to an increased use of artificial substitutes for live animals in veterinary surgical skills training. However, commercially produced models are expensive and homemade models often require full-time staff to produce enough models for training large groups of students. In the Department of Veterinary Clinical and Animal Sciences of the University of Copenhagen, a low-cost build-it-yourself model, the SimSpay, was developed for novice training of surgical skills in canine ovariohysterectomy. The model did not require the use of trained technical staff or costly, hard-to-source supplies. The SimSpay was developed and implemented in the clinical veterinary curriculum in 2013. In 2014, 54 students participated in a questionnaire study to investigate their perception of the usefulness of the SimSpay as a learning tool. On a five-point Likert-type scale, students were asked to rate their perceived levels of competence, confidence, and anatomic knowledge before and after SimSpay training. Results demonstrate a strongly significant (p < .0001) increase in all three areas after training on the SimSpay. By increasing students' perceived levels of competence, confidence, and anatomic knowledge, the low-fidelity Sim Spay is a useful, low-cost learning tool for teaching ovariohysterectomy.

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology
Authors: Langebæk, R. (Ekstern), Toft, N. (Intern), Eriksen, T. (Ekstern)
Number of pages: 6
Pages: 166-171
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Veterinary Medical Education
Volume: 42
Issue number: 2
ISSN (Print): 0748-321X
Ratings:
  BFI (2018): BFI-level 1
  Web of Science (2018): Indexed yes
  BFI (2017): BFI-level 1
  Scopus rating (2017): SNIP 0.775 SJR 0.353 CiteScore 0.89
  Web of Science (2017): Indexed Yes
  BFI (2016): BFI-level 1
  Scopus rating (2016): SJR 0.332 SNIP 0.583 CiteScore 0.49
  BFI (2015): BFI-level 1
  Scopus rating (2015): SJR 0.421 SNIP 0.722 CiteScore 0.96
  Web of Science (2015): Indexed yes
  BFI (2014): BFI-level 1
  Scopus rating (2014): SJR 0.426 SNIP 0.858 CiteScore 0.86
  BFI (2013): BFI-level 1
  Scopus rating (2013): SJR 0.298 SNIP 0.698 CiteScore 0.76
  ISI indexed (2013): ISI indexed yes
  BFI (2012): BFI-level 1
  Scopus rating (2012): SJR 0.285 SNIP 0.492 CiteScore 0.5
  ISI indexed (2012): ISI indexed yes
  Web of Science (2012): Indexed yes
Thymic and lymph node mesenchymal subsets can be derived from PDGFRα/β⁺Gp38⁺CD34⁺ICAM1⁻ vascular adventitial precursors

While discrete Gp38⁻ and Gp38⁺ mesenchymal populations have previously been described in the lymph nodes (LNs) and in the thymus the putative relationship between LN and thymic mesenchymal cells remains unclear. Here, using transcriptome profiling as well as phenotypic and localization studies we comprehensively assessed the mesenchymal cell subset composition of the LNs and the thymus. We find that while LNs selectively harbored a BP3⁺ PDGFRα⁺Gp38⁺ compartment consisting of CCL21-producing fibroblastic reticular cells (FRC), MAdCAM⁺ marginal reticular cells (MRC) and CR1₂⁺ follicular dendritic cells (FDC), both organs were populated by two corresponding subsets of BP3⁻ PDGFRβ⁺ cells, PDGFRα⁻Gp38⁻ITGA7⁺ pericytes and PDGFRα⁻Gp38⁻ CD34⁺ cells localized in the vascular adventitia and in the capsule. Focusing on the thymus as a model organ we obtain evidence that the latter two subsets initially developed from a common PDGFRα/β⁺ Gp38⁺ CD34⁺ICAM1⁻ embryonic precursor population. Notably, precursor-progeny studies involving transfer of adult thymus- and adipose tissue-derived BP3⁺Gp38⁺ PDGFRα⁺ CD34⁺ICAM1⁻ cells into thymic and LN re-aggregate organ grafts uncovered a precursor activity towards not only pericytes but also BP3⁺ FRC, MRC and FDC and provided evidence of local environmental imprinting of BP3⁺Gp38⁺ cells with organ-specific features. Finally, we demonstrate that BP3⁻Gp38⁺ mesenchymal cell maintenance/maturatio in the thymus requires LTβR signaling while this pathway appeared dispensable for pericyte differentiation. These findings bring novel insights to the understanding of lymphoid mesenchymal cell heterogeneity and implicate an unforeseen role of the vascular adventitia in lymphoid stroma turnover/regeneration.

General information
State: Published
Organizations: National Veterinary Institute, Section for Immunology and Vaccinology, Lund University, University of Birmingham
Number of pages: 1
Publication date: 2015
Event: Abstract from 1st International Venice Thymus Meeting, San Servolo Island, Italy.
Main Research Area: Technical/natural sciences
Electronic versions:
Katarzyna_Sitnik_abstract.docx
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2015

Transmission dynamics of foodborne parasites in pork (pig and wild boar)
Two Virus-Induced MicroRNAs Known Only from Teleost Fishes Are Orthologues of MicroRNAs Involved in Cell Cycle Control in Humans

MicroRNAs (miRNAs) are similar to 22 base pair-long non-coding RNAs which regulate gene expression in the cytoplasm of eukaryotic cells by binding to specific target regions in mRNAs to mediate transcriptional blocking or mRNA cleavage. Through their fundamental roles in cellular pathways, gene regulation mediated by miRNAs has been shown to be involved in almost all biological phenomena, including development, metabolism, cell cycle, tumor formation, and host-pathogen interactions. To address the latter in a primitive vertebrate host, we here used an array platform to analyze the miRNA response in rainbow trout (Oncorhynchus mykiss) following inoculation with the virulent fish rhabdovirus Viral hemorrhagic septicaemia virus. Two clustered miRNAs, miR-462 and miR-731 (herein referred to as miR-462 cluster), described only in teleost fishes, were found to be strongly upregulated, indicating their involvement in fish-virus interactions. We searched for homologues of the two teleost miRNAs in other vertebrate species and investigated whether findings related to ours have been reported for these homologues. Gene synteny analysis along with gene sequence conservation suggested that the teleost fish miR-462 and miR-731 had evolved from the ancestral miR-191 and miR-425 (herein called miR-191 cluster), respectively. Whereas the miR-462 cluster locus is found between two protein-coding genes (intergenic) in teleost fish genomes, the miR-191 cluster locus is found within an intron of a protein-coding gene (intragenic) in the human genome. Interferon (IFN)-inducible and immune-related promoter elements found upstream of the teleost miR-462 cluster locus suggested roles in immune responses to viral pathogens in fish, while in humans, the miR-191 cluster functionally associated with cell cycle regulation. Stimulation of fish cell cultures with the IFN inducer poly I:C accordingly upregulated the expression of miR-462 and miR-731, while no stimulatory effect on miR-191 and miR-425 expression was observed in human cell lines. Despite high sequence conservation, evolution has thus resulted in different regulation and presumably also different functional roles of these orthologous miRNA clusters in different vertebrate lineages.
Typebestemmelse af de danske M. bovis stammer

Mycoplasma bovis er en af de mest betydningsfulde mykoplasma i kvægbruget på verdensplan. Bakterien findes oftest i forbindelse med mastitis, lunge- og ledbetændelse, men andre kliniske manifestationer kan også forekomme. Der findes ikke præcise, nyere beregninger over konsekvenser af M. bovis relateret sygdomme, men det anses, at infektionen hvert år globalt pålægger en økonomisk byrde til kvægbruget i en multimillion skala.


I de seneste fire år blev M. bovis isoleret ved DTU-VET fra led, lunge, mellemøre, mælk og yver fra klinisk syge dyr samt næsesvaber og øjensvaber fra dyr uden kliniske symptomer i besætninger fra Jylland, Fyn, Sjælland, Lolland og Bornholm. De opsamlede stammer blev undersøgt for variation i hele bakteriens arvemassen ved fuldgenomsekventering med henblik på at kortlægge genomisk diversitet i de nyere danske population af M. bovis. Desuden blev disse også sammenlignet med de ældre danske isolater med henblik på at identificere eventuel tilstedeværelse af stabile klonale linjer over en længere tidsperiode.


For at fastslå beslægtedenheden af G1 og G2 klonal linjer med de globalt kendte M. bovis typer har vi analyseret et udvalg af "husholdnings" gener som indgår i typning skemaet (1). Undersøgelsen viste at stammer tilhørende G1 og G2 klonal linjer repræsenterer hidtil ukendte typer som hører til et såkaldt "Clonal Complex 2".

Vores resultater viser entydigt at de seneste års udbrud af M. bovis relaterede sygdomme i kvægbesætninger over hele landet hovedsageligt skyldes infektion med en enkelt klonal linje af bakterien. Denne klonal linje har tilsyneladende ingen præferencer til et bestemt organ og er i stand til at forårsage forskellige kliniske manifestationer. Desuden er denne klonal linje aldrig før blevet påvist hverken i Danmark eller i udlandet, og så er den genetisk ganske forskellig fra de gamle danske stammer isoleret før 2001.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology
Authors: Kokotovic, B. (Intern)
Number of pages: 1
Publication date: 2015
Event: Abstract from Kvegkonference 2015, Billund, Denmark.
Main Research Area: Technical/natural sciences
Electronic versions:
kv_g.pdf
Source: PublicationPreSubmission
Source-ID: 115272833
Publication: Research › peer-review › Conference abstract for conference – Annual report year: 2015

Udbrud af klinisk salmonellose hos æglæggende høns

General information
State: Published
Organisations: Department of Systems Biology, National Food Institute, Research Group for Diagnostic Engineering, National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Landbrugets Veterinære Konsulcntjeneste
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Pages: 52-54
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Dansk Erhvervsfjerkrae
Volume: 44
Issue number: 8
ISSN (Print): 0045-9607
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Original language: English
Source: PublicationPreSubmission
Source-ID: 115102454
Publication: Communication › Journal article – Annual report year: 2015

Urea and thiourea modified polypropyleneimine dendrimers clear intracellular α-synuclein aggregates in a human cell line
Synucleinopathies are neurodegenerative pathologies in which disease progression is closely correlated to brain accumulation of insoluble α-synuclein, a small protein abundantly expressed in neural tissue. Here, two types of modified
polypropyleneimine (PPI) dendrimers having either urea or methylthiourea (MTU) surface functional groups were investigated in a cellular model of synucleinopathy. Dendrimers are synthetic macromolecules that may be produced in a range of well-defined molecular sizes. Using cellomics array scan high-content screening, we show that both types of dendrimers are able to significantly reduce intracellular levels of α-synuclein aggregates dependent on the concentration, the type and molecular size of the dendrimer with the bigger size MTU-dendrimers having the highest potency. The intracellular clearance of α-synuclein aggregates by dendrimers was achieved at noncytotoxic concentrations. (Figure Presented).

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Department of Systems Biology, H. Lundbeck A/S
Authors: Laumann, K. (Intern), Boas, U. (Intern), Larsen, H. M. (Intern), Heegaard, P. M. H. (Intern), Bergström, A. (Ekstern)
Number of pages: 9
Pages: 116-124
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Biomacromolecules
Volume: 16
Issue number: 1
ISSN (Print): 1525-7797
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 1.339 SJR 1.95 CiteScore 5.89
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 5.74 SJR 1.98 SNIP 1.323
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 2.105 SNIP 1.434 CiteScore 6.05
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 2.207 SNIP 1.642 CiteScore 6.38
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 2.09 SNIP 1.593 CiteScore 6.07
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 2.316 SNIP 1.661 CiteScore 5.72
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 2.222 SNIP 1.759 CiteScore 5.74
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.347 SNIP 1.652
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 2.29 SNIP 1.582
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Use of recombinant capsid proteins in the development of a vaccine against foot-and-mouth disease virus (FMDV).

Foot-and-mouth disease remains one of the world's most economically important diseases of livestock. It is caused by foot-and-mouth disease virus, a member of the picornavirus family. The virus replicates very rapidly and can be efficiently transmitted between hosts by a variety of routes. The disease has been effectively controlled in some parts of the world but remains endemic in many others, thus there is a constant risk of introduction of the disease into areas that are normally free of foot-and-mouth disease with potentially huge economic consequences. To reduce the need for large-scale culling of infected, and potentially infected, animals there has been significant effort to develop new vaccines against this disease which avoid some, or all, of the deficiencies of current vaccines. A major focus has been on the use of systems that express the structural proteins of the virus that self-assemble to generate "empty capsid" particles which share many features with the intact virus but lack the ribonucleic acid genome and are therefore non-infectious. Such particles can be "designed" to improve their stability or modify their antigenicity and can be produced without "high containment" facilities. The development and use of such improved vaccines should assist in the global efforts to control this important disease.
Vaccination of pigs with attenuated Lawsonia intracellularis induced acute phase protein responses and primed cell-mediated immunity without reduction in bacterial shedding after challenge

Nomically important diseases in modern pig production worldwide. The Enterisol®Ileitis vaccine have been shown to reduce clinical disease and to increase weight gain, however, while the natural infection with L. intracellularis can provide complete protection against re-infection, this has not been achieved by this vaccine. We therefore undertook a detailed characterization of immune responses to L. intracellularis infection in vaccinated pigs (VAC) compared to previously infected pigs (RE) in order to pinpoint immunological determinants of protection. Results: The VAC pigs shed L. intracellularis to the same extent as non-vaccinated pigs after challenge, however less L. intracellularis in ileum and lymph nodes was seen post mortem. In the RE group, challenged did not lead to L. intracellularis shedding and no challenge bacteria were found post mortem. In both VAC and RE the acute phase haptoglobin response was diminished and L. intracellularis specific IgG responses were delayed and reduced compared to non-vaccinated pigs. On the other hand L. intracellularis specific IFN- responses tended to develop faster in the VAC group compared to controls. Conclusion: Although vaccinated and non-vaccinated pigs shed L. intracellularis at similar levels after challenge, a lower number of intestinal L. intracellularis was observed in the vaccinated pigs at postmortem inspection. This might be due to the observed faster CMI responses upon challenge in vaccinated pigs. Complete protection against infection without L. intracellularis shedding, however, was only seen after a previous infection resulting in IFN- production predominantly by CD8+ and CD4+CD8+ cells. Improved protective vaccines against L. intracellularis should therefore target stimulation of these T cell subsets.
Vaccination with peptides of Mycobacterium avium subsp. paratuberculosis (MAP) reduces MAP burden of infected goats

Mycobacterium avium subsp. paratuberculosis (Map) is the cause of paratuberculosis, a chronic enteritis of ruminants that is widespread worldwide. We investigated the effect of post-exposure vaccination with Map specific peptides in a goat model aiming at developing a Map vaccine that will neither interfere with diagnosis of paratuberculosis nor bovine tuberculosis.

Peptides were initially selected by two strategies 1) in silico selection of unique Map peptides (compared to other Mycobacteria) (n =51) and with predicted binding to 5 known bovine MHC class II molecules or 2) hydrophobic peptides...
unique to Map from selected proteins (n =68).

For vaccination, 23 MAP peptides (20 µg each) were selected and formulated with Montanide ISA 61 VG adjuvant. At age three weeks 10 goats were orally inoculated with 4x10E9 live Map and assigned to two groups of 5 goats each: 5 vaccinated (V) at 14 and 18 weeks post inoculation (PI) and 5 unvaccinated (C). At termination 32 weeks PI, Map burdens in 15 intestinal tissues and lymph nodes were determined by IS900 qPCR.

Of the 75 tissue samples from the 5 C goats only 5 samples were IS900 qPCR negative. In contrast, only 9 samples in total from 5 V goats were IS900 positive. All V goats responded with strong IFN-γ responses to peptides after vaccination while C goats were unresponsive. IFN-γ responses to PPDj were low in all goats at all times, except for one V goat that responded from 26 weeks PI and onwards. A single goat in the C group seroconverted in ID Screen ELISA at last sampling.

The results indicate that a peptide vaccine against Map can induce a protective immune response against paratuberculosis.
Flavobacterium psychrophilum, Characterization, VNTR, Genotyping, PCA, Salmonid, Wild, Farmed

Electronic versions:
art_3A10.1186_2Fs12917_015_0469_7.pdf

DOIs:
10.1186/s12917-015-0469-7
Source: Findit
Source-ID: 275531899
Publication: Research - peer-review › Journal article – Annual report year: 2015

Vascular gene expression in diet-induced atherosclerotic göttingen minipigs

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Technical University of Denmark
Authors: Blom, L. (Ekstern), Skovgaard, K. (Intern), Ludvigsen, T. (Ekstern), Kirk, R. (Ekstern), Christoffersen, B. Ø. (Ekstern), Pedersen, H. D. (Ekstern), Heegaard, P. M. H. (Intern), Olsen, L. H. (Ekstern)
Number of pages: 1
Vector optimization and needle-free intradermal application of a broadly protective polyvalent influenza A DNA vaccine for pigs and humans

The threat posed by the 2009 pandemic H1N1 virus emphasized the need for new influenza A virus vaccines inducing a broad cross-protective immune response for use in both humans and pigs. An effective and broad influenza vaccine for pigs would greatly benefit the pork industry and contribute to public health by diminishing the risk of emerging highly pathogenic reassortants. Current inactivated protein vaccines against swine influenza produce only short-lived immunity and have no efficacy against heterologous strains. DNA vaccines are a potential alternative with advantages such as the induction of cellular and humoral immunity, inherent safety and rapid production time. We have previously developed a DNA vaccine encoding selected influenza proteins of pandemic origin and demonstrated broad protective immune responses in ferrets and pigs. In this study, we evaluated our DNA vaccine expressed by next-generation vectors. These new vectors can improve gene expression, but they are also efficiently produced on large scales and comply with regulatory guidelines by avoiding antibiotic resistance genes. In addition, a new needle-free delivery of the vaccine, convenient for mass vaccinations, was compared with intradermal needle injection followed by electroporation. We report that when our DNA vaccine is expressed by the new vectors and delivered to the skin with the needle-free device in the rabbit model, it can elicit an antibody response with the same titers as a conventional vector with intradermal electroporation. The needle-free delivery is already in use for traditional protein vaccines in pigs but should be considered as a practical alternative for the mass administration of broadly protective influenza DNA vaccines.

General information
State: Published
Organisations: National Veterinary Institute, Statens Serum Institut, Nature Technology Corporation
Authors: Borggren, M. (Ekstern), Nielsen, J. (Ekstern), Bragstad, K. (Ekstern), Karlsson, I. (Ekstern), Krog, J. S. (Intern), Williams, J. A. (Ekstern), Fomsgaard, A. (Ekstern)
Pages: 1983-1990
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Human Vaccines & Immunotherapeutics
Volume: 11
Issue number: 8
ISSN (Print): 2164-5515
Ratings:
Web of Science (2018): Indexed yes
Scopus rating (2017): SNIP 0.764 SJR 0.984 CiteScore 1.96
Web of Science (2017): Indexed Yes
Scopus rating (2016): SJR 0.957 SNIP 0.688 CiteScore 1.87
Scopus rating (2015): SJR 0.973 SNIP 0.636 CiteScore 1.7
Web of Science (2015): Indexed yes
Scopus rating (2014): SJR 0.924 SNIP 0.687 CiteScore 1.77
Scopus rating (2013): SJR 0.676 SNIP 0.574 CiteScore 1.28
Scopus rating (2012): SJR 0.916 SNIP 0.968
Scopus rating (2011): SJR 1.027 SNIP 0.918
Scopus rating (2010): SJR 0.857 SNIP 0.693
Scopus rating (2009): SJR 0.751 SNIP 0.706
Scopus rating (2008): SJR 0.811 SNIP 0.771
Scopus rating (2007): SJR 0.588 SNIP 0.485
Scopus rating (2006): SJR 0.235
Original language: English
DOIs: 10.1080/21645515.2015.1011987
Source: PublicationPreSubmission
Source-ID: 112091497
Publication: Research - peer-review › Journal article – Annual report year: 2015
**VHS virus - present situation**

Geographic distribution: VHSV can be divided into 4 genotypes and at least 8 subtypes and there is a close linkage between genotypes, geographic range and affected fish species. VHS is still only reported from the Northern hemisphere and while countries like Denmark, Norway and England have freed themselves for VHS, several countries are still struggling with the disease. An update on the recent VHS outbreaks in rainbow trout in Iran, in olive flounder in Korea, in wrasse in Scotland, in turbot in Turkey, in a number of fish species in the great lakes in USA and Canada, and a general overview of the worldwide distribution of the disease will be given. Virus evolution: Recent studies indicate that only a few amino acid changes in the structural proteins of VHSV can change the virulence patterns significantly, thereby coming closer to assessing the risk of none to low virulent viruses becoming high virulent. Virulence factors both depend on the ability of VHSV to enter a cell and on the speed and efficiency of virus replication in the cells. Apparently the viral nucleocapsid protein plays a very important role for the later and seems to be the target for determination of a virulence marker.
GAS manifested increased virulence in C4BPxFH mice: higher organism burdens and greater elevations of pro-inflammatory cytokines and they died earlier than single transgenic or wt controls. The effects of hu-C4BP and hu-FH were specific for GAS strains that bound these inhibitors because strains that did not bind the inhibitors showed reduced virulence in the 'double' tg mice compared to strains that did bind; mortality was also similar in wild-type and C4BPxFH mice infected by non-binding GAS. Our findings emphasize the importance of binding of complement inhibitors to GAS that results in impaired opsonization and phagocytic killing, which translates to enhanced virulence in a humanized whole animal model. This novel hu-C4BPxFH tg model may prove invaluable in studies of GAS pathogenesis and for developing vaccines and therapeutics that rely on human complement activation for efficacy.
Weaner production with low antimicrobial usage: a descriptive study

Background: Health, productivity and antimicrobial use in the production of pigs are expected to be interrelated to some extent. Previous studies on register-based data have investigated these correlations with a subsequent large variation residing at the farm level. In order to study such farm factors in more detail we designed an elaborate interview-guide. By in-depth interviews of farmers with well-managed 7-30 kg (weaner) productions we sought to describe a set of common key-factors characterizing their management practices. Identification of such common practices could be used in follow-up projects, investigating whether identified factors really are characteristic for good-practicing farmers.

Results: Eleven farms were selected for a farm visit and in-depth interview. Participating farms used less antimicrobials than the national median (8.2 animal daily doses/100 weaners/day), had a mortality below the national average (2.9%) and an average daily weight gain above the national average (443 g/day). Similarities were observed among participating farms, including the sectioning of farms, use of all-in-all-out procedures with subsequent cleaning, purchasing 7 kg weaners from only one source, as well as active participation in management by a committed farm owner. Most farmers had a specific point of focus in their management, and were convinced that this was the reason for their success. This included; feeding, treatment strategy, refurbishment of facilities and presence in the shed.

Conclusion: According to register data, participating farms were alike; in the good league regarding use of antimicrobials, mortality and daily growth. However, on-farm interviews elucidated more heterogeneity among farmers than expected. Most of the farmers had a specific point of focus, which they considered to be crucial for their good results. These results indicate the importance of non-registerable factors, highlighting the value of qualitative study techniques in the understanding of human actions. Further studies on the effect of various farmer types are recommended.
Whole Genome Sequencing and Phylogenetic Analysis of a Historical Collection of Bacillus anthracis Strains from Danish Cattle

Bacillus anthracis, the causative agent of anthrax, is known as one of the most genetically monomorphic species. Canonical single-nucleotide polymorphism (SNP) typing and whole-genome sequencing were used to investigate the molecular diversity of eleven B. anthracis strains isolated from cattle in Denmark between 1935 and 1988. Danish strains were assigned into five canSNP groups or lineages, i.e., A.Br.001/002 (n = 4), A.Br.Ames (n = 2), A.Br.008/011 (n = 2), A.Br.005/006 (n = 2) and A.Br.Aust94 (n = 1). The match with the A.Br.Ames lineage is of particular interest as the occurrence of such lineage in Europe is demonstrated for the first time, filling an historical gap within the phylogeography of the lineage. Comparative genome analyses of these strains with 41 isolates from other parts of the world revealed that the two Danish A.Br.008/011 strains were related to the heroin-associated strains responsible for outbreaks of injection...
anthrax in drug users in Europe. Eight novel diagnostic SNPs that specifically discriminate the different sub-groups of Danish strains were identified and developed into PCR-based genotyping assays.

**General information**

**State:** Published

**Organisations:** National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University Paris-Est Anses

**Authors:** Derzelle, S. (Ekstern), Girault, G. (Ekstern), Kokotovic, B. (Intern), Angen, Ø. (Intern)

**Number of pages:** 11

**Publication date:** 2015

**Main Research Area:** Technical/natural sciences

**Publication information**

**Journal:** P L o S One

**Volume:** 10

**Issue number:** 8

**Article number:** e0134699

**ISSN (Print):** 1932-6203

**Ratings:**

- BFI (2018): BFI-level 1
- Web of Science (2018): Indexed yes
- BFI (2017): BFI-level 1
- Scopus rating (2017): CiteScore 3.01 SJR 1.164 SNIP 1.111
- Web of Science (2017): Indexed yes
- BFI (2016): BFI-level 1
- Scopus rating (2016): CiteScore 3.11 SJR 1.236 SNIP 1.101
- Web of Science (2016): Indexed yes
- BFI (2015): BFI-level 1
- Scopus rating (2015): SJR 1.427 SNIP 1.136 CiteScore 3.32
- Web of Science (2015): Indexed yes
- BFI (2014): BFI-level 1
- Scopus rating (2014): SJR 1.559 SNIP 1.148 CiteScore 3.54
- Web of Science (2014): Indexed yes
- BFI (2013): BFI-level 1
- Scopus rating (2013): SJR 1.772 SNIP 1.153 CiteScore 3.94
- ISI indexed (2013): ISI indexed yes
- Web of Science (2013): Indexed yes
- BFI (2012): BFI-level 1
- Scopus rating (2012): SJR 1.982 SNIP 1.156 CiteScore 4.15
- ISI indexed (2012): ISI indexed yes
- Web of Science (2012): Indexed yes
- BFI (2011): BFI-level 1
- Scopus rating (2011): SJR 2.425 SNIP 1.233 CiteScore 4.58
- ISI indexed (2011): ISI indexed no
- Web of Science (2011): Indexed yes
- BFI (2010): BFI-level 1
- Scopus rating (2010): SJR 2.705 SNIP 1.178
- Web of Science (2010): Indexed yes
- BFI (2009): BFI-level 1
- Scopus rating (2009): SJR 2.614 SNIP 1.046
- Web of Science (2009): Indexed yes
- BFI (2008): BFI-level 1
- Scopus rating (2008): SJR 2.506 SNIP 1.006
- Web of Science (2008): Indexed yes
- Scopus rating (2007): SJR 1.379 SNIP 0.537
- Web of Science (2007): Indexed yes

**Original language:** English
Within- and between-herd prevalence variation of Mycobacterium avium subsp. paratuberculosis infection among control programme herds in Denmark (2011-2013)

This study aimed to estimate the between- (HTP) and within- (TP) herd true prevalence distribution of Mycobacterium avium subsp. paratuberculosis (MAP) infection in dairy cattle herds participating in the Danish MAP control programme. All herds enrolled in the programme between 2011 and 2013 were included in the analysis, and one annual milk-ELISA test of all lactating cows present in such herds was considered. A Bayesian latent class model was used to obtain HTP and TP posterior distributions for each year. The model adjusts for uncertainty in age-specific test sensitivity and prior prevalence estimates. Bayesian posterior probabilities were computed in order to compare prevalence between the years. A total of 665,700 samples were included in the study, from 221,914, 224,040, and 220,466 cows sourced from 1138, 1112, and 1059 herds in years 2011, 2012, and 2013, respectively. In that period, HTP estimates of 0.92 (95% posterior probability interval (PPI), 0.87-0.96), 0.78 (95% PPI, 0.74-0.83), and 0.75 (95% PPI, 0.71-0.78) were recorded, respectively. Low TP were observed, with population mean estimates of 0.08 (95% PPI, 0.07-0.08), 0.07 (95% PPI, 0.07-0.08), and 0.07 (95% PPI, 0.06-0.07) for the three consecutive years. Statistically-important differences were recorded for HTP and population mean TP estimates between years, indicating a trend for a decreasing level of MAP infection at both herd and animal level. Model results showed that MAP infection was widespread among the Dairy cattle herds participating in the Danish control programme, though in general it was kept at very low levels.

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, University of Copenhagen
Authors: Verdugo, C. (Ekstern), Toft, N. (Intern), Nielsen, S. (Ekstern)
Number of pages: 6
Pages: 282-287
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Preventive Veterinary Medicine
Volume: 121
Issue number: 3-4
ISSN (Print): 0167-5877
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 1.31 SJR 1.144 CiteScore 2.26
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.2 SJR 1.249 SNIP 1.361
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.282 SNIP 1.177 CiteScore 2.1
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.27 SNIP 1.407 CiteScore 2.37
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.264 SNIP 1.529 CiteScore 2.49
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.265 SNIP 1.436 CiteScore 2.45
Low-dose antibiotics: current status and outlook for the future

Antimicrobial therapy is a key factor in our success against pathogens poised to ravage at risk or infected individuals. However, we are currently at a watershed point as we face a growing crisis of antibiotic resistance among diverse pathogens. One area of intense interest is the impact of the application of antibiotics for uses other than the treatment of patients and the association with such utilization with emerging drug resistance. This Research Topic “Low-dose antibiotics: current status and outlook for the future” in Frontiers in Microbiology: Antimicrobials, Resistance and Chemotherapy details various aspects of the wide ranging effects of antimicrobial therapy from areas such as the regulation of host responses to modulation of bacterial virulence factors to acquisition of antibiotic resistance genes.

General information

State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Yeshiva University, University of Tennessee, Parnell Pharmaceuticals
Authors: Nosanchuk, J. D. (ed.) (Ekstern), Lin, J. (ed.) (Ekstern), Hunter, R. P. (ed.) (Ekstern), Aminov, R. (ed.) (Intern)
Number of pages: 167
Publication date: Dec 2014
Overvågning af aviær influenza i vilde fugle i Danmark 2013

Overvågningen af aviær influenza (AI) virus i vilde fugle i Danmark i 2013 blev udført i samarbejde mellem Fødevarestyrelsen (FVST), Veterinærinstituttet, Danmarks Tekniske Universitet (DTU-VET) og Statens Naturhistoriske Museum, Københavns Universitet (SNM) i henhold til ”Aftale mellem Fødevarestyrelsen og Veterinærinstituttet om overvågning af aviær influenza i vilde fugle i Danmark i 2013” (bilag 4).

Overvågning af AI på EU niveau går tilbage til 2002, og Danmark er underlagt EU kommissionens bestemmelser for udføring af overvågningen, der dog har skiftet gennem årene i takt med indhøstede erfaringer.

I 2013 blev der udført passiv overvågning af døde vilde fugle, der blev fundet i naturen. Der blev testet 10 fugle, og ingen af disse var positive for AI virus. Tre blev indsendt af Veterinærafdeling Øst, de øvrige var indsendt faldvildt fra private indsamlere.

General information
State: Published
Organisations: National Veterinary Institute, Section for Public sector service and commercial diagnostics, Section for Virology, Natural History Museum of Denmark
Authors: Hjulsager, C. K. (Intern), Krog, J. S. (Intern), Madsen, J. J. (Ekster), Thorup, K. (Ekster), Larsen, L. E. (Intern)
Publication date: 15 Mar 2014

Secret mission of microscopic drones revealed
Vaccinations of cattle and sheep against insect-borne diseases cost society millions each year. Danish researcher sheds new light on how the little bloodsucking creatures spread disease.

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology
Authors: Kirkeby, C. (Intern)
Publication date: 8 Jan 2014
Main Research Area: Technical/natural sciences

Mikroskopiske droners hemmelige mission afsløret
Samfundet har i de senere år brugt millioner på vaccination af kvæg og får mod insektbårne sygdomme. Nu afslører ny forskning hvor de små blodsugende insekter flyver hen.
3 PRRS-stabile sohold leverede hver 10 hold PRRS-fri smågrise
I tre besætninger var det muligt at producere 10 PRRS-fri hold af smågrise i hver besætning over tid, selvom soholdet var PRRS-positivt. Dette var muligt på trods af forskelle i produktionsmønstre, karantæneniveau og PRRS-vaccinationsstrategier.

I undersøgelsen indgik tre besætninger. Besætningerne var deklareret PRRS-positive, hvilket betyder at der var påvist antistoffer mod PRRS i søernes blod, men besætningsejerne formodede, at de havde et PRRS-stabilt sohold (ingen cirkulation af PRRS-virus blandt søerne), så grisene var PRRS-fri (grise uden PRRS-virus) ved 30 kg. I hver besætning blev der taget blodprover af 10 hold grise ved 30 kg.

A Comparison between Two Simulation Models for Spread of Foot-and-Mouth Disease
Two widely used simulation models of foot-and-mouth disease (FMD) were used in order to compare the models’ predictions in term of disease spread, consequence, and the ranking of the applied control strategies, and to discuss the effect of the way disease spread is modeled on the predicted outcomes of each model. The DTU-DADS (version 0.100), and ISP (version 2.001.11) were used to simulate a hypothetical spread of FMD in Denmark. Actual herd type, movements, and location data in the period 1st October 2006 and 30th September 2007 was used. The models simulated the spread of FMD using 3 different control scenarios: 1) A basic scenario representing EU and Danish control strategies, 2) pre-emptive depopulation of susceptible herds within a 500 meters radius around the detected herds, and 3) suppressive vaccination of susceptible herds within a 1,000 meters radius around the detected herds. Depopulation and vaccination started 14 days following the detection of the first infected herd. Five thousand index herds were selected randomly, of which there were 1,000 cattle herds located in high density cattle areas and 1,000 in low density cattle areas, 1,000 swine herds located in high density swine areas and 1,000 in low density swine areas, and 1,000 sheep herds. Generally, DTU-DADS predicted larger, longer duration and costlier epidemics than ISP, except when epidemics started in cattle located in high density cattle areas. ISP supported suppressive vaccination rather than pre-emptive depopulation, while DTU-DADS was indifferent to the alternative control strategies. Nonetheless, the absolute differences between control strategies were small making the choice of control strategy during an outbreak to be most likely based on practical reasons.

A Comparison between Two Simulation Models for Spread of Foot-and-Mouth Disease
Two widely used simulation models of foot-and-mouth disease (FMD) were used in order to compare the models’ predictions in term of disease spread, consequence, and the ranking of the applied control strategies, and to discuss the effect of the way disease spread is modeled on the predicted outcomes of each model. The DTU-DADS (version 0.100), and ISP (version 2.001.11) were used to simulate a hypothetical spread of FMD in Denmark. Actual herd type, movements, and location data in the period 1st October 2006 and 30th September 2007 was used. The models simulated the spread of FMD using 3 different control scenarios: 1) A basic scenario representing EU and Danish control strategies, 2) pre-emptive depopulation of susceptible herds within a 500 meters radius around the detected herds, and 3) suppressive vaccination of susceptible herds within a 1,000 meters radius around the detected herds. Depopulation and vaccination started 14 days following the detection of the first infected herd. Five thousand index herds were selected randomly, of which there were 1,000 cattle herds located in high density cattle areas and 1,000 in low density cattle areas, 1,000 swine herds located in high density swine areas and 1,000 in low density swine areas, and 1,000 sheep herds. Generally, DTU-DADS predicted larger, longer duration and costlier epidemics than ISP, except when epidemics started in cattle located in high density cattle areas. ISP supported suppressive vaccination rather than pre-emptive depopulation, while DTU-DADS was indifferent to the alternative control strategies. Nonetheless, the absolute differences between control strategies were small making the choice of control strategy during an outbreak to be most likely based on practical reasons.
Actions taken and future considerations due to findings of Echinococcus multilocularis in two Scandinavian countries

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, National Veterinary Institute Sweden, Norwegian Defence Research Institute, Finnish Food Safety Authority
Publication date: 2014
Event: Abstract from ESCCAP Echinococcus Event, Vilnius, Lithuania.
Main Research Area: Technical/natural sciences
Electronic versions:
14.10_ESCCAP2014_Echinococcus_Vilnius.pdf
Source: PublicationPreSubmission
Source-ID: 102865154
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2014

Activities preceding a decline in the paratuberculosis test prevalence

A voluntary control programme on Mycobacterium avium subsp. paratuberculosis (MAP) was initiated in Denmark in 2006 and has since 2007 included 25-28% of the dairy herds and 35-40% of the dairy cows. The programme was complemented with activities aimed to reduce the MAP infection prevalence. A challenge in evaluation of activities in a national programme is essentially a sample size of one without a control group. Therefore, the apparent effect of activities on programme level can only be descriptive. Our objective was to describe the decline in the test-prevalence along with the activities preceding this decline. The cohort of herds enrolled in 2006-2007 had an average estimated within-herd test-prevalence of 10% at start. By January 2014 this had declined to 2%. The test-prevalence in the cohort of herds enrolled in 2008-2010 started at approximately 6% and by January 2014 was reduced to about 3%. In addition to these data, a “sampling error” in August 2011 resulted in the availability of a sample of 99 herds that were not enrolled in the programme. They had a median test-prevalence of 5.5% compared to 3.1% in 268 herds from the 2006-2007 cohort tested in the same month. This sample and associated estimates were used to validate that a test prevalence reduction was due to the programme. The decline in test-prevalence has been statistically associated to herd-level factors such as low level of livestock purchases and culling of cows deemed to be infectious, but not really to other management factors. On national level, the first initiatives included training of herd health advisors, information campaigns including various sources of information material and farmer’s meetings. In the last approximately 5 years, the programme has run routinely with few specific extraordinary activities, except for a “continuous” flow of diagnostic test information four times annually in each herd. This information can be used for detection and management of infectious animals and for prevalence monitoring.

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, University of Copenhagen
Authors: Nielsen, S. S. (Ekstern), Toft, N. (Intern)
Number of pages: 1
Publication date: 2014
Event: Abstract from 12th International Colloquium on Paratuberculosis, Parma, Italy.
Main Research Area: Technical/natural sciences
Source: FindIt
Source-ID: 2193127546
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2015

Alaria alata - en "ny" parasitær zoonose?

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Section for Public sector service and commercial diagnostics, University of Copenhagen
Authors: Enemark, H. L. (Intern), Al-Sabi, M. N. S. (Intern), Takeuchi-Storm, N. (Intern), Thamsborg, S. M. (Forskerdatabase), Chriél, M. (Intern)
Alaria alata - en "ny" parasitær zoonose?

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Section for Public sector service and commercial diagnostics, University of Copenhagen
Authors: Enemark, H. L. (Intern), Al-Sabi, M. N. S. (Intern), Takeuchi-Storm, N. (Intern), Thamsborg, S. M. (Ekstern), Chriél, M. (Intern)
Pages: 1519
Publication date: 2014
Main Research Area: Technical/natural sciences

Publication information
Journal: Svensk Veterinaertidning
Volume: 66
ISSN (Print): 0346-2250
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Original language: Danish
Links:
http://svf.se/sv/Tidningen/
Publication: Research - peer-review » Journal article – Annual report year: 2014

Alaria alata - en "ny" parasitær zoonose?

General information
State: Published
A multiplexed immunoassay for detection of antibodies to Actinobacillus pleuropneumoniae (App) in pigs

The bacterium Actinobacillus pleuropneumoniae (App) is the causative agent of porcine pleuropneumonia, a contagious and severe respiratory disease in pigs. Based on capsular antigens, 15 App serovars have been described, and the
prevalence and morbidity of these serovars vary with geographic regions (1). In Denmark, the most important serovars are considered to be App 1, 2, 5, 6, 7, 10 and 12. As part of the Danish surveillance program for App, the Danish Veterinary Institute uses ELISAs and complement fixation tests (CFT) to test for porcine anti-App antibodies (2-7). In an effort to improve our diagnostic tools, we are currently developing a novel indirect fluorescent microsphere immunoassay that can facilitate simultaneous detection of antibodies towards multiple App serovars within a single serum sample volume. The multiplex immunoassay is based on Luminex technology (8) and has several benefits compared to ELISA and CFT, including reduced serum sample volumes, lowered amount of labor and faster acquisition of results.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology
Authors: Berger, S. S. (Intern), Boas, U. (Intern), Andresen, L. O. (Intern), Lauritsen, K. T. (Intern), Klausen, J. (Intern)
Number of pages: 1
Publication date: 2014

Host publication information
Title of host publication: Abstract Book and Final Programme- 3rd European EAVLD Congress
Article number: 01
Main Research Area: Technical/natural sciences
Conference: 3rd European Association of Veterinary Laboratory Diagnosticians, Pisa, Italy, 12/10/2014 - 12/10/2014
Multiplexed immunoassay, Actinobacillus pleuropneumoniae, Lipopolysaccharide
Electronic versions:
Multiplex_abstract_2014_1_.pdf
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2014

Analysis of ORF5 and Full-Length Genome Sequences of Porcine Reproductive and Respiratory Syndrome Virus Isolates of Genotypes 1 and 2 Retrieved Worldwide Provides Evidence that Recombination Is a Common Phenomenon and May Produce Mosaic Isolates
Recombination is currently recognized as a factor for high genetic diversity, but the frequency of such recombination events and the genome segments involved are not well known. In the present study, we initially focused on the detection of recombinant porcine reproductive and respiratory syndrome virus (PRRSV) isolates by examining previously published data sets of ORF5 sequences (genotypes 1 and 2) obtained worldwide. We then examined full-length genome sequences in order to determine potential recombination breakpoints along the viral genome. For ORF5, 11 sets of genotype 1 sequences from different geographical areas, including 2 Asian, 1 American, and 7 European regions, and three sets of genotype 2, including sets from China, Mexico, and the United States, were analyzed separately. Potential recombination breakpoints were detected in 10/11 genotype 1 sets, including 9 cases in which the clustering of at least one isolate was different before and after the breakpoints. In genotype 2, potential breakpoints and different tree clustering of at least one strain before and after the breakpoint were observed in 2 out of 3 sets. The results indicated that most of the ORF5 data sets contained at least one recombinant sequence. When the full-length genome sequences were examined, both genotype 1 and 2 sets presented breakpoints (10 and 9, respectively), resulting in significantly different topologies before and after the breakpoints. Mosaic genomes were detected in genotype 1 sequences. These results may have significant implications for the understanding of the molecular epidemiology of PRRSV. IMPORTANCE PRRSV is one of the most important viruses affecting swine production worldwide, causing big economic losses and sanitary problems. One of the key questions on PRRSV arises from its genetic diversity, which is thought to have a direct impact on immunobiology, epidemiology, diagnosis, and vaccine efficacy. One of the causes of this genetic diversity is recombination among strains. This study provides evidence that recombinant PRRSV isolates are common in most of the countries with significant swine production, especially PRRSV genotype 1. This observation has implications in the proper characterization of PRRSV strains, in the future development of phylogenetic studies, and in the development of new PRRSV control strategies. Moreover, the present paper emphasizes the need for a deeper understanding of the mechanisms and circumstances involved in the generation of genetic diversity of PRRSV.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Universidad Autonoma de Barcelona, The Pirbright Institute, Centro de Investigacion en Alimentacion y Desarrollo
Authors: Martín-Valls, G. E. (Ekstern), Kvisgaard, L. K. (Intern), Tello, M. (Forskerdatabase), Darwich, L. (Ekstern), Cortey, M. (Ekstern), Burgara-Estrella, A. J. (Ekstern), Hernández, J. (Forskerdatabase), Larsen, L. E. (Intern), Mateu, E. (Ekstern)
Pages: 3170-3181
Publication date: 2014
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Virology
Volume: 88
Issue number: 6
An oligonucleotide-tagged microarray for routine diagnostics of colon cancer by genotyping KRAS mutations

Colorectal cancer (CRC) is one of the most prevalent types of cancer, causing significant morbidity and mortality worldwide. CRC is curable if diagnosed at an early stage. Mutations in the oncogene KRAS play a critical role in early development of CRC. Detection of activated KRAS is of diagnostic and therapeutic importance. In this study, KRAS gene fragments containing mutations in codon 12 were amplified by multiplex PCR using a 5’-Cy5-labeled reverse primer in combination with 3’-mutation-specific forward primers that were linked with four unique nucleotide-sequence tags at the 5’-end. The Cy5-labeled reverse primer was extended under PCR amplification to the 5’-end of the mutation-specific forward primers and thus included the complimentary sequence of the tag. PCR products were hybridized to tag-probes immobilized on various substrates and detected by a scanner. Our results indicate that all mutations at codon 12 of KRAS derived from cancer cells and clinical samples could be unambiguously detected. KRAS mutations were accurately detected when the mutant DNA was present only in 10% of the starting mixed materials including wild-type genomic DNA, which was isolated from either cancer cells or spiked fecal samples. The immobilized tag-probes were stable under multiple thermal cycling treatments, allowing re-use of the tag-microarray and further optimization to solid PCR. Our results demonstrated that a novel oligonucleotide-tagged microarray system has been developed which would be suitable to be used for detection of KRAS mutations and clinical diagnosis of CRC.
Anthelmintic effects of forage chicory against parasitic nematodes in cattle

BACKGROUND: Chicory (Cichorium intybus) has potential as a natural anthelmintic in livestock, however evidence of efficacy against cattle nematodes is lacking. Here, we investigated anthelmintic effects of chicory in stalled calves.

METHODS: Jersey male calves (2-4 months) were stratified by live weight and allocated randomly to 2 groups: chicory (CHI, n=9) and control (CON, n=6). CHI and CON calves were fed with forage chicory silage (cv. Spadona) and hay ad libitum, resp., for 8 weeks. After 2 weeks, calves were infected with 10,000 Ostertagia ostertagi and 65,000 Cooperia oncophora larvae. Fecal egg counts (FEC) and live weights were assessed weekly. Six weeks after infection, calves were slaughtered for worm recovery. In parallel, total sesquiterpene lactone (SL)-extracts from forage chicory (Spadona and cv. Puna II) were prepared and incubated with first-stage larvae (L1) of O. ostertagi. L1 viability was evaluated after 12 hours incubation.

RESULTS: Mean FECs (corrected for faecal dry matter) were not different between groups (p=0.14), but weight gains were higher in CHI calves (+ 35%; p<0.05). Mean worm counts for O. ostertagi adults were 1599 and 3752 in CHI and CON, respectively (p<0.01). Worm counting of C. oncophora is ongoing. SL extracts from forage chicory were toxic to O. ostertagi L1 in vitro, with a mortality of 99% at concentrations ≥ 500 mg/mL (EC50 =132.8 mg/mL). Puna II-SL extracts induced a L1 mortality of only 37% at the highest concentration tested (2000 mg/mL). CONCLUSIONS: Based on these preliminary results, chicory silage (Spadona) has significant in vivo anthelmintic effects against O. ostertagi, possibly mediated by SL, and marked differences exist in the anti-parasitic activity of SL extracts from two different chicory cultivars.
Antibiotics modulate intestinal immunity and prevent necrotizing enterocolitis in preterm neonatal piglets

Preterm birth, bacterial colonization, and formula feeding predispose to necrotizing enterocolitis (NEC). Antibiotics are commonly administered to prevent sepsis in preterm infants, but it is not known whether this affects intestinal immunity and NEC resistance. We hypothesized that broad-spectrum antibiotic treatment improves NEC resistance and intestinal structure, function, and immunity in neonates. Caesarean-delivered preterm pigs were fed 3 days of parenteral nutrition followed by 2 days of enteral formula. Immediately after birth, they were assigned to receive either antibiotics (oral and parenteral doses of gentamycin, ampicillin, and metronidazole, ANTI, n = 11) or saline in the control group (CON, n = 13), given twice daily. NEC lesions and intestinal structure, function, microbiology, and immunity markers were recorded. None of the ANTI but 85% of the CON pigs developed NEC lesions by day 5 (0/11 vs. 11/13, P <0.05). ANTI pigs had higher intestinal villi (+60%), digestive enzyme activities (+53–73%), and goblet cell densities (+110%) and lower myeloperoxidase (−51%) and colonic microbial density (105 vs. 1010 colony-forming units, all P <0.05). Microarray transcriptomics showed strong downregulation of genes related to inflammation and innate immune response to microbiota and marked upregulation of genes related to amino acid metabolism, in particular threonine, glucose transport systems, and cell cycle in 5-day-old ANTI pigs. In a follow-up experiment, 5 days of antibiotics prevented NEC at least until day 10. Neonatal prophylactic antibiotics effectively reduced gut bacterial load, prevented NEC, intestinal atrophy, dysfunction, and inflammation and enhanced expression of genes related to gut metabolism and immunity in preterm pigs.
Obesity-associated type 2 diabetes (T2D) is characterized by a state of chronic, low-grade inflammation with an excessive secretion of pro-inflammatory mediators, such as IL-6, TNF-α, and leptin from the adipose tissue and decrease in the anti-inflammatory adipokine adiponectin. T2D is accompanied with a set of metabolic abnormalities comprising the metabolic syndrome, such as hypertension, dyslipidemia, and insulin resistance. Although the exact causes for the onset of clinical disease remain largely unknown, emerging evidence seems to suggest that obesity-induced inflammation, especially in the adipose tissue, is involved in the metabolic dysregulation and therefore plays an important role in the pathogenesis of this deteriorating disease. Bariatric surgery, including the Roux-en Y gastric bypass (RYGB), is one of the most effective treatments for severe obesity. In addition to weight loss, the RYGB procedure is associated with immediate improvement in glycemic control and insulin secretion. The exact mechanisms for the immediate and long-term positive effect of RYGB on glucose metabolism and obesity related co-morbidities remain unclear. Changes in inflammatory cellular and molecular mediators have been found following RYGB, suggesting one potential mechanism by which bariatric surgery re-establishes insulin sensitivity. RYGB also enhances circulating levels of certain gastrointestinal-derived hormones, particularly the postprandial secretion of glucagon-like peptide 1 (GLP-1). A growing body of literature reports anti-inflammatory and other immunological effects of GLP-1 in animals and in humans suggesting that GLP-1 acts beyond purely glucoregulatory mechanisms. The exaggerated postprandial GLP-1 secretion following RYGB may thus be involved in the beneficial metabolic effects both directly via the classical glucoregulatory pathways and indirectly via anti-inflammatory and immune-regulatory mechanisms. The findings of a direct GLP-1-mediated effect on lymphocyte subpopulations in vitro and in vivo and the few but interesting case reports on clinical improvements in psoriasis patients treated with GLP-1 receptor agonists have supported immune-regulatory actions of GLP-1. The main aim of this thesis was to explore potential anti-inflammatory and immunoregulatory effects of GLP-1 on immune system parameters to increase the mechanistic understanding of the effects observed in the clinic and to provide new aspect on the interplay between metabolism, obesity and inflammation. The in vitro work and animal study, and the three manuscripts constituting this
thesis describe different approaches in studying GLP-1 effects on immune system parameters. In **Study I**, the functionality of human expanded Tregs in the presence of GLP-1 was examined *in vitro*. **Study II** investigated antiinflammatory effect of GLP-1 *in vivo* in the PMA-induced ear inflammation model. Three human studies were conducted that generated the three manuscripts in the thesis; two RYGB studies (**Study III, Manuscript I and Study IV, Manuscript II**) and one study in obese T2D subjects commencing liraglutide therapy (**Study V, Manuscript III**), to evaluate immunological changes either after surgery (1 week, 3 months, and 1 year) or after 12 weeks of GLP-1 therapy.

**General information**

State: Published

Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Zealand Pharma A/S

Authors: Bovbjerg, K. K. L. (Intern), Heegaard, P. M. H. (Intern), Steensberg, A. (Ekstern), Mosolff Mathiesen, J. (Ekstern)

Number of pages: 156

Publication date: 2014

**Publication information**

Place of publication: Kgs. Lyngby

Publisher: Technical University of Denmark (DTU)

Original language: English

Main Research Area: Technical/natural sciences

Electronic versions:

FINAL_PhD_Thesis_Kirsten_Bovbjerg..PDF

Publication: Research › Ph.D. thesis – Annual report year: 2015

**Anti-parasitic effects of plant secondary metabolites on swine nematodes**

Organic production presents challenges to animal health and productivity. In organic pig production, animals must have access to outdoor pastures which increases exposure to gastrointestinal parasites. Moreover, the routine use of synthetic anti-parasitic drugs is not allowed. Thus, novel parasite-control options are required. We present results from a comprehensive in vitro screen of plant secondary metabolites (PSM) from diverse plant sources on the economically important pig parasites *Ascaris chlamydiae* and *Oesophagostomum dentatum*. We focused on two PSM classes commonly found in natural diets – condensed tannins (CT) and sesquiterpene lactones (SL). Different CT-types were purified from various plant sources to reflect their diversity; SL were purified from forage chicory. These PSM were tested in inhibition assays of worm motility and migratory ability. CT had potent activity against *A. suum*, with substantial inhibition of migration of in vitro hatched larvae (EC 50 values ranging from 40 to 120 μg/ml). In contrast, migratory ability of *O. dentatum* larvae was not significantly affected. However, the motility of adult *O. dentatum* was reduced after in vitro incubation with CT. The purified chicory extract showed potent inhibition of *A. suum* larval migration (EC50 value of 42 μg/ml) and was also active against larval and adult stages of *O. dentatum*. Electron microscopy demonstrated significant structural damage to the cuticle and digestive tissues in nematodes exposed to PSM. Plants rich in PSM such as CT and SL show promise as natural anthelmintics against two highly prevalent swine parasites. Experiments to determine in vivo efficacy and mechanisms of nematocidal action are on-going.

**General information**

State: Published

Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Copenhagen, University of Reading

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Publication date: 2014

Event: Abstract from 65th Annual meeting of the European Federation of Animal Science, Copenhagen, Denmark.

Main Research Area: Technical/natural sciences

Electronic versions:

14.08_EAAP_Copenhagen_2014.pdf

**Bibliographical note**

p. 250

Source: PublicationPreSubmission

Source-ID: 100629936

Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2014

**Anti-parasitic effects of plant secondary metabolites on swine nematodes**

Organic production presents challenges to animal health and productivity. In organic pig production, animals must have access to outdoor pastures which increases exposure to gastrointestinal parasites. Moreover, the routine use of synthetic anti-parasitic drugs is not allowed. Thus, novel parasite-control options are required. We present results from a comprehensive in vitro screen of plant secondary metabolites (PSM) from diverse plant sources on the economically important pig parasites *Ascaris chlamydiae* and *Oesophagostomum dentatum*. We focused on two PSM classes commonly found in natural diets – condensed tannins (CT) and sesquiterpene lactones (SL). Different CT-types were
purified from various plant sources to reflect their diversity; SL were purified from forage chicory. These PSM were tested in inhibition assays of worm motility and migratory ability. CT had potent activity against A. suum, with substantial inhibition of migration of in vitro hatched larvae (EC 50 values ranging from 40 to 120 μg/ml). In contrast, migratory ability of O. dentatum larvae was not significantly affected. However, the motility of adult O. dentatum was reduced after in vitro incubation with CT. The purified chicory extract showed potent inhibition of A. suum larval migration (EC 50 value of 42 μg/ml) and was also active against larval and adult stages of O. dentatum. Electron microscopy demonstrated significant structural damage to the cuticle and digestive tissues in nematodes exposed to PSM. Plants rich in PSM such as CT and SL show promise as natural anthelmintics against two highly prevalent swine parasites. Experiments to determine in vivo efficacy and mechanisms of nematocidal action are on-going.

A serological survey for antibodies against foot-and-mouth disease virus (FMDV) in domestic pigs during outbreaks in Kenya

Foot-and-mouth disease (FMD) is endemic in Kenya and has been well studied in cattle, but not in pigs, yet the role of pigs is recognised in FMD-free areas. This study investigated the presence of antibodies against FMD virus (FMDV) in pigs sampled during a countrywide random survey for FMD in cattle coinciding with SAT 1 FMDV outbreaks in cattle. A total of 191 serum samples were collected from clinically healthy pigs in 17 districts. Forty-two of the 191 sera were from pigs vaccinated against serotypes O/A/SAT 2 FMDV. Antibodies against FMDV non-structural proteins were found in sera from 30 vaccinated and 71 non-vaccinated pigs, altogether 101/191 sera (53 %), and 91 % of these (92/101) also had antibodies measurable by serotype-specific ELISAs, predominantly directed against SAT 1 with titres of 10–320. However, only five high titres against SAT 1 in vaccinated pigs were confirmed by virus neutralisation test (VNT). Due to high degree of agreement between the two ELISAs, it was concluded that positive pigs had been infected with FMDV. Implications of these results for the role of pigs in the epidemiology of FMD in Kenya are discussed, and in-depth studies are recommended.
A Single Amino Acid Mutation (I1012F) of the RNA Polymerase of Marine Viral Hemorrhagic Septicemia Virus Changes In Vitro Virulence to Rainbow Trout Gill Epithelial Cells

Viral hemorrhagic septicemia virus (VHSV) is separated into four different genotypes (I to IV) with different sublineages (K. Einer-Jensen, P. Ahrens, R. Forsberg, and N. Lorenzen, J. Gen. Virol. 85: 1167-1179, 2004; K. Einer-Jensen, J. Winton, and N. Lorenzen, Vet. Microbiol. 106: 167-178, 2005). European marine VHSV strains (of genotypes I to III) are, in general, nonpathogenic or have very low pathogenicity to rainbow trout after a waterborne challenge, and here we also show that genotype IVa is nonpathogenic to trout. Despite several attempts, it has not been possible to link genomic variation to in vivo virulence. In vitro virulence to gill epithelial cells (GECs) has been used as a proxy for in vivo virulence, and here we extend these studies further with the purpose of identifying residues associated with in vitro virulence. Genotype Ia (DK-3592B) and III (NO/650/07) isolates, which are pathogenic to rainbow trout (O. B. Dale, I. Orpetveit, T. M. Lyngstad, S. Kahns, H. F. Skall, N. J. Olesen, and B. H. Dannevig, Dis. Aquat. Organ. 85: 93-103, 2009), were compared to two marine strains that are nonpathogenic to trout, genotypes Ib (strain 1p8 [H. F. Mortensen, O. E. Heuer, N. Lorenzen, L. Otte, and N. J. Olesen, Virus Res. 63: 95-106, 1999]) and IVa (JF-09). DK-3592 and NO/650/07 were pathogenic to GECs, while marine strains 1p8 and JF-09 were nonpathogenic to GECs. Eight conserved amino acid substitutions contrasting high-and low-virulence strains were identified, and reverse genetics was used in a gain-of-virulence approach based on the JF-09 backbone. Mutations were introduced into the G, NV, and L genes, and seven different virus clones were obtained. For the first time, we show that a single amino acid mutation in conserved region IV of the L protein, I1012F, rendered the virus able to replicate and induce a cytopathic effect in trout GECs. The other six mutated variants remained nonpathogenic.
A single or multistage mycobacterium avium subsp. paratuberculosis subunit vaccine

The present invention provides one or more immunogenic polypeptides for use in a preventive or therapeutic vaccine against latent or active infection in a human or animal caused by a Mycobacterium species, e.g. Mycobacterium avium subsp. paratuberculosis. Furthermore a single or multi-phase vaccine comprising the one or more immunogenic polypeptides is provided for administration for the prevention or treatment of infection with a Mycobacterium species, e.g. Mycobacterium avium subsp. paratuberculosis. Additionally, nucleic acid vaccines, capable of in vivo expression of the multi-phase vaccine comprising the one or more immunogenic polypeptides, is provided for prevention or treatment of infection with a Mycobacterium species, e.g. Mycobacterium avium subsp. paratuberculosis.

General information
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Publication date: 2014

Assessment of zoonotic potential of four European swine influenza viruses in the ferret model

The reverse zoonotic events that introduced the 2009 pandemic influenza virus into swine herds have drastically increased the diversity of reassortants throughout Europe. The pandemic potential of these novel reassortants is unknown, hence necessitating enhanced surveillance of European swine herds and enhanced focus on risk assessment of these new viruses. In this study, four European swine influenza viruses were assessed for their zoonotic potential. Of the four viruses, two were enzootic viruses of subtype H1N2 (with avian-like H1) and H3N2 and two were new reassortants, one with avian-like H1 and human-like N2 and one with pandemic H1 and swine-like N2. All viruses replicated to high viral titers in nasal wash- and nasal turbinate samples from inoculated ferrets and transmitted efficiently by direct contact. Only the H3N2 virus transmitted to naïve ferrets via respiratory droplets. Growth kinetics using human bronchial cells showed that all four viruses were able to replicate to high titers. Further, the viruses revealed preferential binding to the α2,6-sialylated glycans and investigation of the antiviral susceptibility of the viruses revealed that they were all sensitive to neuraminidase inhibitors. These findings suggest that the investigated viruses have the potential to infect humans and further underline the need for continued surveillance as well as pandemic and zoonotic assessment of new influenza reassortants.

General information
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Association of MAP specific ELISA-responses and productive parameters in 314 Danish dairy farms

General information
State: Published
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Number of pages: 1
Publication date: 2014
Event: Poster session presented at 12th International Colloquium on Paratuberculosis, Parma, Italy.
Main Research Area: Technical/natural sciences
Electronic versions: icp14_poster_v3.pdf
Source: PublicationPreSubmission
Source-ID: 97569852
Publication: Research - peer-review › Poster – Annual report year: 2014

Association of map specific ELISA-responses and productive parameters in 367 danish dairy farms

General information
State: Published
Organisations: Department of Applied Mathematics and Computer Science, Dynamical Systems, National Veterinary Institute, Section for Epidemiology, University of Copenhagen
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Pages: 139-141
Publication date: 2014
Event: Poster session presented at 12th International Colloquium on Paratuberculosis, Parma, Italy.
Main Research Area: Technical/natural sciences
Electronic versions: 12icp.pdf
Source: PublicationPreSubmission
Source-ID: 97569852
Publication: Research - peer-review › Poster – Annual report year: 2014

Bactericidal Antibiotics Increase Hydroxyphenyl Fluorescein Signal by Altering Cell Morphology

It was recently proposed that for bactericidal antibiotics a common killing mechanism contributes to lethality involving indirect stimulation of hydroxyl radical (OH center dot) formation. Flow cytometric detection of OH center dot by hydroxyphenyl fluorescein (HPF) probe oxidation was used to support this hypothesis. Here we show that increased HPF signals in antibiotics-exposed bacterial cells are explained by fluorescence associated with increased cell size, and do not reflect reactive oxygen species (ROS) concentration. Independently of antibiotics, increased fluorescence was seen for elongated cells expressing the oxidative insensitive green fluorescent protein (GFP). Although our data question the role of ROS in lethality of antibiotics other research approaches point to important interplays between basic bacterial metabolism and antibiotic susceptibility. To underpin such relationships, methods for detecting bacterial metabolites at a cellular level are needed.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Copenhagen
Bacteriological investigations of skin ulcers in a Swedish pig herd

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Swedish Animal Health Service, National Veterinary Institute Sweden, Uppsala University, Lund University
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Number of pages: 1
Publication date: 2014
Event: Poster session presented at 6th European Symposium of Porcine Health Management (ESPHM 2014), Italy.
Main Research Area: Technical/natural sciences
Electronic versions:
Poster_ESPHM_2014.pdf
Source: PublicationPreSubmission
Source-ID: 99798058
Publication date: 2014

Biocide and antibiotic susceptibility of Salmonella isolates obtained before and after cleaning at six Danish pig slaughterhouses

Salmonella sp. continues to be one of the most important foodborne pathogens. Control measures in terms of cleaning and disinfection on food production plants are very important for limiting the risk of contaminated food products to reach the consumer. In the last decade concern has arisen that bacteria exposed to disinfectants can develop resistance toward disinfectants and can have a higher risk of developing antibiotic resistance. The objectives of this study were to examine the prevalence of biocide resistant Salmonella sp. in Danish pig slaughterhouses, to evaluate if there was a correlation between susceptibilities to biocides and antibiotics, and to examine if cleaning and disinfection select isolates with changed susceptibility toward biocides or antibiotics. Salmonella sp. was isolated from the environment in Danish pig slaughterhouses before and after cleaning and disinfection. The susceptibility toward three different biocides, triclosan and two commercial disinfection products: Desinfect Maxi, a quaternary ammonium compound, and Incimaxx DES, an acetic compound, was determined. We found no resistance toward the biocides tested, but we did find that isolates obtained after cleaning had higher minimum inhibitory concentration (MIC) values toward one of the disinfectants (Incimaxx DES) compared to isolates obtained before cleaning and disinfection. This could indicate selection of strains that are more tolerant, due to the cleaning and disinfection. Furthermore, we found that there was a weak statistical correlation between MICs toward the biocides and some antibiotics, but no difference in log(MIC)s toward antibiotics between isolates obtained before and after cleaning, nor did we find any difference in the number of resistances of isolates obtained before and after cleaning and disinfection.

General information
State: Published
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Number of pages: 7
Pages: 53-59
Publication date: 2014
Main Research Area: Technical/natural sciences

Publication information
Journal: International Journal of Food Microbiology
Volume: 181
ISSN (Print): 0168-1605
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SJR 1.366 SNIP 1.436 CiteScore 3.76
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.97 SJR 1.481 SNIP 1.553
Web of Science (2016): Indexed yes
Bovine colostrum improves intestinal function following formula-induced gut inflammation in preterm pigs

Background & aims
Only few hours of formula feeding may induce proinflammatory responses and predispose to necrotizing enterocolitis
(NEC) in preterm pigs. We hypothesized that bovine colostrum, rich in bioactive factors, would improve intestinal function in preterm pigs following an initial exposure to formula feeding after some days of total parenteral nutrition (TPN).

Methods
After receiving TPN for 2 days, preterm pigs were fed formula (FORM, n = 14), bovine colostrum (COLOS, n = 6), or formula (6 h) followed by bovine colostrum (FCOLOS, n = 14). Intestinal lesions, function, and structure, abundance and location of bacteria, and inflammation markers were investigated.

Results
NEC severity and interleukins (IL)-1β and -8 protein concentrations were lower, while villus height, galactose absorption, and brush-border enzyme activities were increased in the distal small intestine in COLOS and FCOLOS pigs, relative to FORM pigs. Intestinal gene expression of serum amyloid A, IL-1β, -6 and -8, and bacterial abundance, correlated positively with NEC severity of the distal small intestine.

Conclusions
Bovine colostrum restores intestinal function after initial formula-induced inflammation in preterm pigs. Further studies are required to test if bovine colostrum may also benefit preterm infants during the challenging transition from total parenteral nutrition to enteral nutrition, when human milk is unavailable.
Bulk tank milk ELISA for detection of antibodies to Mycobacterium avium subsp. paratuberculosis: Correlation between repeated tests and within-herd antibody-prevalence

Detection of bulk tank milk (BTM) antibodies using ELISA (BTM-ELISA) may constitute an inexpensive test for surveillance of Mycobacterium avium subsp. paratuberculosis (MAP) infection in dairy cattle herds provided that the test is accurate and consistent. The objectives of this study were to determine: (a) the correlation between repeated BTM reactions; and (b) the association between the BTM antibody ELISA-level and the within-herd prevalence of antibody-positive cows. Eight BTM samples per herd and approximately four milk samples per lactating cow per herd were collected from each of 108 Danish Holstein herds over a period of one year. All samples were tested using a commercial indirect ELISA for detection of MAP specific antibodies. The individual cow's results were dichotomised and used to estimate the within-herd antibody prevalence at each test-date. These prevalences were then combined with the ELISA reading on the BTM test-date closest to the cow-level test-date. A mixed-effect analysis of covariance with autoregressive type 1 correlation structure was carried out using the log-transformed BTM-ELISA results as outcome. This model was used to assess the correlation between repeated tests with and without correction for within-herd antibody prevalence. The repeated BTM-recordings were highly correlated with a correlation of 0.80 between samples collected 1.5 months apart. The within-herd antibody prevalence significantly influenced this estimate (p <0.0001), which dropped to 0.60 when corrected for the within-herd antibody prevalence. Although the test-results were relatively consistent and correlated with the within-herd prevalence, the magnitude of the test-values makes it difficult to use the BTM-ELISA for surveillance of MAP infections in practice.
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.2 SJR 1.249 SNIP 1.361
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.282 SNIP 1.177 CiteScore 2.1
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.27 SNIP 1.407 CiteScore 2.37
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.264 SNIP 1.529 CiteScore 2.49
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.265 SNIP 1.436 CiteScore 2.45
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.194 SNIP 1.295 CiteScore 2.24
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.156 SNIP 1.284
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.032 SNIP 1.338
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.056 SNIP 1.258
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.009 SNIP 1.353
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.06 SNIP 1.277
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.931 SNIP 1.414
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.812 SNIP 1.146
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.846 SNIP 1.323
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.857 SNIP 1.427
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 1.045 SNIP 1.48
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 0.623 SNIP 1.261
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 0.647 SNIP 1.005
Original language: English
DOIs:
10.1016/j.prevetmed.2013.10.013
Source: FindIt
Source-ID: 255703792
Publication: Research - peer-review › Journal article – Annual report year: 2014
Characteristics of a foot-and-mouth disease virus with a partial VP1 G-H loop deletion in experimentally infected cattle

Previous work in cattle illustrated the protective efficacy and negative marker potential of an A serotype foot-and-mouth disease virus (FMDV) vaccine prepared from a virus lacking a significant portion of the VP1 G-H loop (termed A(−)). Since this deletion also includes the arginine-glycine-aspartate (RGD) motif required for virus attachment to the host cell in vivo, it was hypothesised that this virus would be attenuated in naturally susceptible animals. The A(−) virus was passaged three times in cattle via needle inoculation of virus suspension delivered into the intradermal space of the tongue (intradermolingual: IDL). Included in the study were three direct contact cattle, two of which were used for the third cattle passage (by inoculation) after direct contact exposure for three days. Cattle were monitored for clinical signs and samples were collected for sequencing as well as antibody and viral genome detection by ELISA and qRT-PCR. Following needle inoculation with the A(−) virus, naïve cattle developed typical clinical signs of FMDV infection, diagnostic assays also provided positive serological and virological results. However, the contact cattle did not develop clinical signs or generate serological or virological markers indicative of FMDV infection even when the cattle were subsequently needle inoculated with 105 TCID50 A(−) FMDV delivered IDL following three days of direct contact exposure. The results suggest that the A(−) virus is not attenuated in cattle when inoculated IDL. This virus could be useful as a tool to understand further the natural pathogenesis, receptor usage and internalisation pathways of FMDV.

General information
State: Published
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Pages: 58-66
Publication date: 2014
Main Research Area: Technical/natural sciences

Publication information
Journal: Veterinary Microbiology
Volume: 169
Issue number: 1-2
ISSN (Print): 0378-1135
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.7 SJR 1.175 SNIP 1.241
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.363 SNIP 1.206
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.413 SNIP 1.21 CiteScore 2.56
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.291 SNIP 1.256 CiteScore 2.54
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.459 SNIP 1.471 CiteScore 3
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.441 SNIP 1.569 CiteScore 3.18
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.56 SNIP 1.729 CiteScore 3.27
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Characterization of the bacterial gut microbiota in new neonatal porcine diarrhoea

During the last decade farmers and veterinarians have reported the emergence of a new neonatal porcine diarrhoea (NNPD) affecting piglets up to 7 days old. Routine laboratory testing for common pathogens are inconclusive and vaccination and treatment with antibiotics or alternative zootechnical interventions have limited effect. NNPD is not associated with an increased mortality, but have been reported to cause significant morbidity within herds and litters. Piglets born to gilts are in particularly affected by NNPD. NNPD impairs the welfare of the piglets, and results in decreased weight gain which is of economic importance to the farmer. Despite the limited effect of antibiotics, farmers often treat affected piglets with antibiotics to prevent secondary infections to NNPD resulting in increased consumption of antibiotics. Thus, there are several encouraging reasons for identifying the aetiology behind NNPD. Consequently an interdisciplinary project called: “New neonatal porcine diarrhoea in Denmark. Elucidation of aetiology, diagnostics, and effect of treatments” (freely translated) was initiated. The project enrolled three PhD students with different approaches and hypotheses. The aim of this project was to investigate whether the aetiology to NNPD could be identified in the bacterial gut microbial changes.

In order to be able to characterize the bacterial gut microbiota of numerous samples simultaneously the Gut Microbiotassay was developed. This is an assembly of 24 different primer sets targeting 16S or 23S rRNA genes of the major bacterial groups constituting the gut microbiota. This approach was applied due to the limited number of intestinal bacteria that currently can be cultivated. Primers were found in published literature, tested in silico and modified or designed if necessary. The Gut Microbiotassay was optimized for the high-throughput quantitative real-time PCR-based 48.48 Access Array™ Integrated Fluidic Circuit (Fluidigm). The efficiency and sensitivity of the primer sets were tested against 15 different pure-cultured bacterial strains. Finally the Gut Microbiotassay was tested on DNA extracted from ileal or colonic contents from piglets with or without NNPD and verified via 454 next generation sequencing of the PCR amplicons. Bioinformatics was conducted using BION-meta customized for this specific setup.

With the Gut Microbiotassay in place gut microbial profiles of ileal and colonic contents of 50 control piglets and 52 case piglets from four Danish pig farms affected by NNPD were obtained and deeper taxonomic insight was acquired by sequencing the PCR amplicons. Statistic results from qPCR data revealed that the gut microbiota of NNPD-affected piglets differed from that of control piglets by a depletion of the phyla Firmicutes, Bacteroidetes, and Actinobacteria, while the numbers of genus Enterococcus and the class Beta- and Gammaproteobacteria (including family Enterobacteriaceae...
and species Escherichia coli), but also phylum Fusobacteria were elevated. Moreover, piglet born to gilts possessed more members from family Enterobacteriaceae including species E. coli and a reduced number of bacteria from phylum Firmicutes. Piglets born to gilts were estimated to have 25 higher odds of being affected by NNPD. Sequence results revealed genus Enterococcus to be comprised of high read numbers of species Enterococcus hirae but also Enterococcus durans. Conversely, particularly Lactobacillus acidophilus was scarcely represented in piglets suffering from NNPD. As part of one of the other enrolled PhD projects a NNPD-infection model was established by inoculating healthy neonate piglets with intestinal NNPD-material (case piglets) or healthy intestinal material (control piglets), while some piglets not were inoculated. Diarrhoea was successfully reproduced in case piglets while control piglets remained healthy. In order to assess whether the diarrhoea was characterized by similar gut microbial changes as detected for field cases of NNPD, ileal and colonic intestinal contents from 49 case piglets (13 un-inoculated) and 32 control piglets (18 un-inoculated) were analyzed using the Gut Microbiot assay. The corresponding regulation of selected intestinal genes involved in diarrhoea was examined for a subset of piglets by qPCR using the 96.96 Dynamic Array™ Integrated Fluidic Circuits (Fluidigm). Similar to NNPD-field cases the gut microbiota of case piglets were characterized by reduced numbers of the phyla Firmicutes, Bacteroidetes, and Actinobacteria. Furthermore, they were inhabited by increased numbers of genus Enterococcus as well as class Beta- and Gammaproteobacteria including species E. coli. The expression of several genes involved in recognition of pathogen-associated molecular patterns, inflammation, and intestinal barrier function were significantly up- or down-regulated reflecting the complex immunological response to being inoculated and/or infected with NNPD-material. Finally, a high abundance of genus Enterococcus (characteristic of case piglets) was associated with high expressions of several transcripts involved in epithelial integrity. Altogether, the results of the studies included in this thesis reveal that NNPD is associated with a disturbed gut microbial composition, and all points towards members from the genus Enterococcus are involved in the pathogenesis of NNPD.

General information
State: Published
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Number of pages: 184
Publication date: 2014

Publication information
Place of publication: Kgs. Lyngby
Publisher: Technical University of Denmark (DTU)
Original language: English
Main Research Area: Technical/natural sciences
Electronic versions:
Ph.d._afhandling_Marie_Louise_Hermann_Bank.pdf
Publication: Research › Ph.D. thesis – Annual report year: 2015

Characterization of the Emerging Salmonella 4,[5],12:i:- in Danish Animal Production.
Abstract The monophasic Salmonella variant with the antigenic formula Salmonella 4,[5],12:i:- has emerged in the last decade as one of the main serotypes related to human salmonellosis. In the present study, a collection of 94 isolates of the S. 4,12:i:- and S. 4,5,12:i:- coming from Danish farm animals, swine (86), cattle (7), and poultry (1), with well-defined identification was further typed by polymerase chain reaction serotyping, phage typing, and molecular typing (polymerase chain reaction and multilocus variable-number tandem-repeat analysis [MLVA]). Moreover, the determination of antimicrobial resistance pattern of each isolate was tested. In 68 of the isolates the fljB gene was absent (i.e., they were true monophasic strains), whereas in 26 isolates, the gene was present despite the fact that the isolates did not express it. The results clustered the isolates in three main pulse-types. The predominant cluster was compatible with the previously described pattern STYMXB.0131. All the isolates included in this cluster lacked the fljB gene, and all the isolates except one belonged to phage type DT 193 with the AMP-STR-SMX-TET resistance pattern. MLVA analysis divided the clusters in several MLVA profiles previously reported by other studies. Finally, antimicrobial resistance and multiresistance was frequent, although no resistance was detected in critical compounds: fluoroquinolones and cephalosporins. The present study demonstrates the presence of monophasic Salmonella Typhimurium-like strains in Danish food animal production with well-characterized clones that are described by previous studies, demonstrating the emergence and spread of this serotype in Denmark.

General information
State: Published
Organisations: National Food Institute, Division of Food Microbiology, National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of León
Authors: Argüello, H. (Ekstern), Sørensen, G. (Intern), Carvajal, A. (Ekstern), Baggesen, D. L. (Intern), Rubio, P. (Ekstern), Pedersen, K. (Intern)
Number of pages: 7
Pages: 366-372
Publication date: 2014
Main Research Area: Technical/natural sciences
Clinical characterization of a type 2 PRRSV causing significant clinical disease in the field in Denmark

General information
State: Published
Color test for selective detection of secondary amines on resin and in solution.

Resins for solid-phase synthesis give orange to red-brown resin beads selectively when secondary amines are present on the resin when treated with a solution of acetaldehyde and an Fmoc-amino acid in NMP. The method shows good specificity and gives colorless beads when exposed to a variety of other functional groups. Furthermore, the acetaldehyde/Fmoc amino acid method can be used as a selective colorimetric test for secondary amines in solution.
Comparative analysis of sequences from PT 2013

Every year The European reference Laboratory offers two proficiency tests for all national Reference Laboratories in Europe as well as any other country that wants to participate. In 2013 43 laboratories participated in at least one of the two proficiency tests that cover all the listed fish diseases in Europe.

As part of the EU Reference Laboratory proficiency test for fish diseases it is required to sequence any RANA virus isolates found in any of the samples. It is also highly recommended to sequence the ISA virus to determine whether it be HPRΔ or HPR0.

Furthermore, it is recommended that any VHSV and IHNV isolates be genotyped.

As part of the evaluation of the proficiency results it was decided this year to look into the quality and similarity of the sequence results for selected viruses.

Ampoule III in the proficiency test 2013 contained an EHNV isolate. The EU Reference Laboratory received 43 sequences from 41 laboratories. All but one sequence mapped to the MCP gene while the last sequence mapped to the Neurofilament gene. Approx. half of the sequences contained no errors while the rest differed with 88-99 percent similarity with most having 99% similarity. One sequence, when BLASTed, showed most similarity to European Sheatfish and not EHNV. Generally, mistakes occurred at the ends of the sequences. This can be due to several factors. One is that the sequence has not been trimmed of the sequence primer sites. Another is the lack of quality control of the chromatogram. Finally, sequencing in just one direction can result in unclear determination of nucleotides at places with a bad quality score. This talk will present some of the problems that can occur with sequencing as well as discuss potential pitfalls.

General information

State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Mikkelsen, S. S. (Intern)
Publication date: 2014
Event: Abstract from 18th Annual Workshop of the National Reference Laboratories for Fish Diseases, Frederiksborg C, Denmark.
Comparative pathogenicity study of ten different betanodavirus strains in experimentally infected European sea bass, *Dicentrarchus labrax* (L.)

Viral encephalopathy and retinopathy (VER), otherwise known as viral nervous necrosis (VNN), is a severe pathological condition caused by RNA viruses belonging to the Nodaviridae family, genus Betanodavirus. The disease, described in more than 50 fish species worldwide, is considered as the most serious viral threat affecting marine farmed species in the Mediterranean region, thus representing one of the bottlenecks for further development of the aquaculture industry. To date, four different genotypes have been identified, namely red-spotted grouper nervous necrosis virus (RGNNV), striped jack nervous necrosis virus (SJNNV), tiger puffer nervous necrosis virus and barfin flounder nervous necrosis virus, with the RGNNV genotype appearing as the most widespread in the Mediterranean region, although SJNNV-type strains and reassortant viruses have also been reported. The existence of these genetically different strains could be the reason for the differences in mortality observed in the field. However, very little experimental data are available on the pathogenicity of these viruses in farmed fish. Therefore, in this study, the pathogenicity of 10 isolates has been assessed with an in vivo trial. The investigation was conducted using the European sea bass, the first target fish species for the disease in the Mediterranean basin. Naive fish were challenged by immersion and clinical signs and mortality were recorded for 68 days; furthermore, samples collected at selected time points were analysed to evaluate the development of the infection. Finally, survivors were weighed to estimate the growth reduction. The statistically supported results obtained in this study demonstrated different pathogenicity patterns, underlined the potential risk represented by different strains in the transmission of the infection to highly susceptible species and highlighted the indirect damage caused by a clinical outbreak of VER/VNN.

**General information**

State: Published
Organisations: National Veterinary Institute, Section for Virology, Instituto Zooprofilattico Sperimentale delle Venezie
Authors: Vendramin, N. (Intern), Toffan, A. (Ekstern), Mancin, M. (Ekstern), Cappellozza, E. (Ekstern), Panzarin, V. (Ekstern), Cattoli, G. (Ekstern), Capua, I. (Ekstern), Terregino, C. (Ekstern)
Pages: 371-383
Publication date: 2014
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Journal of Fish Diseases
Volume: 37
Issue number: 4
ISSN (Print): 0140-7775
Ratings:
- BFI (2018): BFI-level 1
- Web of Science (2018): Indexed yes
- BFI (2017): BFI-level 1
- Scopus rating (2017): CiteScore 1.82
- Web of Science (2017): Indexed yes
- BFI (2016): BFI-level 1
- Scopus rating (2016): CiteScore 2.12
- Web of Science (2016): Indexed yes
- BFI (2015): BFI-level 1
- Scopus rating (2015): CiteScore 1.71
- Web of Science (2015): Indexed yes
- BFI (2014): BFI-level 1
- Scopus rating (2014): CiteScore 1.99
- Web of Science (2014): Indexed yes
- BFI (2013): BFI-level 1
- Scopus rating (2013): CiteScore 1.74
- ISI indexed (2013): ISI indexed yes
- Web of Science (2013): Indexed yes
Comparison of two real-time RT-PCR assays for differentiation of C-strain vaccinated from classical swine fever infected pigs and wild boars

Classical swine fever is one of the most important infectious diseases for the pig industry worldwide due to its economic impact. Vaccination is an effective means to control disease, however within the EU its regular use is banned owing to the inability to differentiate infected and vaccinated animals, the so called DIVA principle. This inability complicates monitoring of disease and stops international trade thereby limiting use of the vaccine in many regions. The C-strain vaccine is safe to use and gives good protection. It is licensed for emergency vaccination in the EU in event of an outbreak. Two genetic assays that can distinguish between wild type virus and C-strain vaccines have recently been developed. Here the results from a comparison of these two real-time RT-PCR assays in an interlaboratory exercise are presented. Both assays showed similar performance.

General information
State: Published
Organisations: National Veterinary Institute, National Veterinary Institute Sweden, Animal Health and Veterinary Laboratories Agency, Friedrich Loeffler Institute, Centro de Investigación en Sanidad Animal, Veterinary and Agrochemical Research Centre
Authors: Widén, F. (Ekstern), Everett, H. (Ekstern), Blome, S. (Ekstern), Fernandez Pinero, J. (Ekstern), Utenthal, Å. (Intern), Cortey, M. (Ekstern), von Rosen, T. (Intern), Tignon, M. (Ekstern), Liu, L. (Ekstern)
Number of pages: 3
Pages: 455-457
Publication date: 2014
Main Research Area: Technical/natural sciences

Publication information
Journal: Research in Veterinary Science
Volume: 97
Issue number: 2
ISSN (Print): 0034-5288
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
The complete genome sequence of the genotype 3 border disease virus strain Gifhorn has been determined; this strain was originally isolated from pigs. This represents the consensus sequence for the virus used to produce the bacterial artificial chromosome (BAC) cDNA clone pBeloGif3, which yields a virus that is severely attenuated in cell culture.
Complete Genome Sequence of Classical Swine Fever Virus Genotype 2.2 Strain Bergen
The complete genome sequence of the genotype 2.2 classical swine fever virus strain Bergen has been determined; this strain was originally isolated from persistently infected domestic pigs in the Netherlands and is characterized to be of low virulence.

General information
State: Published
Organisations: Molecular Evolution, National Veterinary Institute, Section for Virology, Friedrich Loeffler Institute
Authors: Fahnøe, U. (Intern), Höper, D. (Ekstern), Beer, M. (Ekstern), Rasmussen, T. B. (Intern)
Number of pages: 2
Publication date: 2014
Main Research Area: Technical/natural sciences

Publication information
Journal: Genome Announcements
Volume: 2
Issue number: 3
ISSN (Print): 2169-8287
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.407 SJR 0.553 CiteScore 1.01
Scopus rating (2016): CiteScore 0.41 SJR 0.583 SNIP 0.469
Web of Science (2016): Indexed yes
Scopus rating (2015): SJR 0.591 SNIP 0.398
Scopus rating (2014): SJR 0.539 SNIP 0.344
ISI indexed (2013): ISI indexed no
Original language: English
Electronic versions:
Fahnøe et al 2014 GenomeA BDV Gifhorn.pdf
DOIs:
10.1128/genomeA.01142-13
Links:
http://genomea.asm.org/content/2/1/e01142-13.full

Bibliographical note
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Source: dtu
Source-ID: u::10447
Publication: Research - peer-review › Journal article – Annual report year: 2014
Correlation between real-time qPCR and development of strongyle eggs from cattle

Differentiation of veterinary important parasitic strongyle eggs is time-consuming, because morphologically distinct third-stage larvae (L3) must be cultured for species/genus identification. A recently published qPCR technique provides a non-labour intensive method for detection and quantification of the two most important nematode eggs in cattle faeces. However, as quantification correlates with DNA content, quantification of copy numbers of the second internal transcribed spacer (ITS2) region is problematic as DNA content increases during egg development. The aim of this study was to assess the impact of oxygen availability and temperature on the multiplication of ITS2 copy numbers in O. ostertagi eggs. Fresh eggs were recovered from cattle faeces by sieving, flotation and entrapment in nylon-mesh filters and subsequently deposited in aliquots (n=18) of 5 ml distilled water with air circulation. To test the effect of oxygen deprivation, fresh faecal samples (n=18) were vacuum packed. A total of 36 aliquots were stored at temperatures of 4°C or 25°C for up to 336 hours. Morphological changes were observed, and DNA content was measured at nine time points throughout the study period. Preliminary morphological analysis demonstrated developmental progression. In waterdeposited eggs, first-stage larvae (L1) were observed after 336 hours at 4°C and after 24 hours at 25°C. An additional 24 hour study showed formation of L1 already after 12 hours incubation at 25°C. In oxygendeprived eggs, no development was observed neither at 4°C nor at 25°C throughout the 336 hours study. Thus, the importance of oxygen and temperature as regulators of egg development was verified. Ongoing studies will quantify ITS2 copy numbers by qPCR. The results will allow us to correlate observed developmental progression with ITS2 copy numbers, and thereby provide knowledge on optimal storage conditions and sources of errors for data interpretation of this diagnostic molecular technique.
the rapid accumulation of a second site substitution within the 2A sequence (L2P) that also blocked VP1/2A cleavage suggesting a linkage between the E83K change in VP1 and cleavage of the VP1/2A junction. In a serotype A background, the K210E substitution in VP1 rapidly reverted to wild type. However, introduction of the 2A L2P substitution alone, or with the VP1 K210E change, into this virus resulted in the production of viable viruses. Cells infected with viruses containing the VP1 K210E and/or the 2A L2P substitutions contained the uncleaved VP1-2A protein; the 2A L2P substitution rendered the VP1/2A junction totally resistant to cleavage by 3C protease. The basis for the linkage between amino acid substitutions that are well separated on the surface of the virus particle will be discussed.

Cross-infection of virulent Dichelobacter nodosus between sheep and co-grazing cattle

Dichelobacter nodosus is the main aetiological agent of ovine footrot and the bacterium has also been associated with interdigital dermatitis in cattle. The aim of this study was to investigate possible cross-infection of virulent D. nodosus between sheep and co-grazing cattle. Five farms, where sheep previously diagnosed with virulent D. nodosus were co-grazing with cattle for different periods of time, were included. The study sample consisted of 200 cows and 50 sheep. All cows were examined for the presence of interdigital dermatitis, and ten ewes, preferably with symptoms of footrot, had the footrot scores recorded. On each farm, the same ten ewes and ten cows were chosen for bacterial analyses. Swabs were analysed for D. nodosus by PCR and culturing. D. nodosus isolates were virulence-tested and assigned to serogroups by fimA variant determination. Biopsies were evaluated histopathologically and analysed by fluorescent in situ hybridization for D. nodosus, Treponema spp. and Fusobacterium necrophorum. D. nodosus defined as virulent by the gelatin gel test were isolated from 16 sheep from four farms and from five cows from two of the same farms. All five cows had interdigital dermatitis. Two of the cows stayed infected for at least eight months. By pulsed-field gel electrophoresis (PFGE), the isolates from the five cows were found to be genetically indistinguishable or closely related to isolates from sheep from the same farm. This indicates that cross-infection between sheep and cows have occurred.
Cryptosporidiosis - an occupational risk and a disregarded zoonosis in Estonia

Background
Cases of cryptosporidiosis have not been officially reported in Estonia after the year 2000, and the disease appears to be either under-diagnosed or under-reported.
Findings
Based on a human case of cryptosporidiosis contracted during faecal sampling in dairy farms, cattle considered to be sources of infection were analysed for Cryptosporidium spp. by a modified Ziehl Neelsen technique and molecular typing. C. parvum subtype IIA16G1R1 was detected from the human case and from calves from one of nine farms enrolled in the study providing strong circumstantial evidence of zoonotic transmission from calves to humans.

Conclusion
Cryptosporidiosis presents an occupational risk to people with cattle contact, and may also be a risk to the human population in general. Thus increased public and medical awareness is warranted.
Culicoides (Avaritia) gornostaevae Mirzaeva, 1984 (Diptera: Ceratopogonidae) a possible vector species of the Obsoletus group new to the European fauna.

Culicoides gornostaevae Mirzaeva, 1984, known previously only from Siberia, is a boreal species included into the Obsoletus group of Culicoides sg. Avaritia. Members of the subgenus can act as vectors of various diseases. In Europe they are involved in the transmission of the Schmallenberg virus and bluetongue virus. Culicoides gornostaevae Mirzaeva, 1984 is reported for the first time in Europe with new country records from Norway, Poland and Sweden. Culicoides gornostaevae Mirzaeva, 1984 has not been previously mentioned from Europe, even though there has been an extensive monitoring of Culicoides species during the last decades. Most probably this species has been notoriously overlooked in the materials, because of the problems with identification of the females of the subgenus Avaritia. Similar to other species of the Obsoletus group, C. gornostaevae should be regarded as a possible vector for Schmallenberg and bluetongue virus.

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, University of Gdansk
Authors: Kirkeby, C. (Intern), Dominiak, P. (Ekstern)
Number of pages: 10
Publication date: 2014
Main Research Area: Technical/natural sciences

Publication information
Journal: Parasites & Vectors
Volume: 7
Issue number: 445
ISSN (Print): 1756-3305
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SJR 1.702 SNIP 1.295 CiteScore 3.29
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.23 SJR 1.534 SNIP 1.313
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Cytokine gene expression profiles in chicken spleen and intestinal tissues during Ascaridia galli infection

In the poultry production industry, chickens with access to outdoor areas are exposed to a wide range of parasites e.g. the helminth Ascaridia galli. By real-time quantitative RT-PCR, the relative gene expression of the T helper 1 (Th1) cytokine IFN-gamma, the T helper 2 (Th2) cytokine IL-13, the anti-inflammatory cytokines IL-10 and TGF-beta 4 and the proinflammatory cytokine IL-17F were determined over a period of 3 weeks in A. galli and non-A. galli-infected chickens. A characteristic Th2 response was observed in the jejunum of A. galli-infected chickens with increased expression of IL-13 and decreased expression of IFN-gamma from day 14 post infection. At the putative time of larvae invasion into the intestinal mucosa (day 7), an increased expression of IFN-gamma, IL-10, and TGF-beta 4 was observed in the spleen. At the putative onset of the innate immune response (day 10), a decreased expression of jejunal IFN-gamma and IL-13 was observed. Finally, at the expected period of an adaptive immune response (days 14-21) a general decreased expression of IFN-gamma and TGF-beta 4 in spleen and IFN-gamma in jejunum was followed by a decreased expression of IFN-gamma and IL-10 at day 21 in caecal tonsils. (C) 2014 Elsevier B.V. All rights reserved.
Main Research Area: Technical/natural sciences

Publication information
Journal: Veterinary Parasitology
Volume: 206
Issue number: 3-4
ISSN (Print): 0304-4017
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 1.215 SJR 1.275 CiteScore 2.55
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.49 SJR 1.228 SNIP 1.218
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.21 SNIP 1.309 CiteScore 2.46
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.324 SNIP 1.42 CiteScore 2.53
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.262 SNIP 1.437 CiteScore 2.63
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.163 SNIP 1.439 CiteScore 2.6
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.233 SNIP 1.429 CiteScore 2.61
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.254 SNIP 1.347
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.138 SNIP 1.414
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.117 SNIP 1.21
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.007 SNIP 1.421
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.932 SNIP 1.442
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.846 SNIP 1.437
Scopus rating (2004): SJR 0.883 SNIP 1.168
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.81 SNIP 1.233
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.919 SNIP 1.146
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.61 SNIP 1.123
Scopus rating (2000): SJR 0.841 SNIP 1.183
Web of Science (2000): Indexed yes
Demonstration of persistent contamination of a cooked egg product production facility with Salmonella enterica serovar Tennessee and characterization of the persistent strain

Aims: The aim of this study was to investigate whether continuous contamination of light pasteurized egg products with Salmonella enterica serovar Tennessee (S. Tennessee) at a large European producer of industrial egg products was caused by persistent contamination of the production facility and to characterize the persistent strains. Methods and Results: Seventy-three S. Tennessee isolates collected from products over a 3-year period with intermittent contamination, and 15 control strains were compared by pulsed field gel electrophoresis (PFGE) using two enzymes. Forty-five case isolates distributed throughout the full period were shown to belong to one profile type. Isolates representing different PFGE profiles were all assigned to ST 319 by multilocus sequence typing (MLST). The case isolates did not show a higher ability to form biofilm on a plastic surface than noncase isolates. Characteristically, members of the persistent clone were weak producers of H2S in laboratory medium. S. Tennessee isolated from the case was able to grow better in pasteurized egg product compared with other serovars investigated. Conclusions: It was concluded that the contamination was caused by a persistent strain in the production facility and that this strain apparently had adapted to grow in the relevant egg product. Significance and Impact of the Study: S. Tennessee has previously been associated with persistence in hatching facilities. This is the first report of persistent contamination of an egg production facility with this serovar.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Copenhagen
Authors: Jakociune, D. (Ekstern), Bisgaard, M. (Ekstern), Pedersen, K. (Intern), Olsen, J. E. (Ekstern)
Pages: 547-553
Publication date: 2014
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Applied Microbiology
Volume: 117
Issue number: 2
ISSN (Print): 1364-5072
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.41
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.41
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.57
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.56
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.69
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.51
Dendritic cell subsets in mucosal immune responses

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Lund University
Authors: Agace, W. W. (Intern)
Number of pages: 1
Pages: 21
Publication date: 2014
Conference: BSI Congress 2014: Annual Congress of the British Society for Immunology, Brighton, United Kingdom, 01/12/2014 - 01/12/2014
Main Research Area: Technical/natural sciences

Publication information
Journal: Immunology
Volume: 143
Issue number: SI
Article number: 148
ISSN (Print): 0019-2805
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.72 SJR 1.69 SNIP 0.938
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.74 SJR 1.964 SNIP 0.965
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Dendritic cell subsets in the regulation of intestinal immune responses

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Ghent University, Lund University
Authors: Luda, K. (Ekstern), Persson, E. (Ekstern), Joeris, T. (Intern), Lambrecht, B. (Ekstern), Agace, W. W. (Intern)
Number of pages: 1
Pages: 6
Publication date: 2014
Conference: 9th European Mucosal Immunology Group Meeting, Glasgow, United Kingdom, 09/10/2014 - 09/10/2014
Main Research Area: Technical/natural sciences
Detection and Quantification of Flavobacterium psychrophilum-Specific Bacteriophages In Vivo in Rainbow Trout upon Oral Administration: Implications for Disease Control in Aquaculture.

The use of bacteriophages in the treatment and prevention of infections by the fish pathogen Flavobacterium psychrophilum has attracted increased attention in recent years. It has been shown recently that phage delivery via the parenteral route resulted in immediate distribution of phages to the circulatory system and the different organs. However, little is known about phage dispersal and survival in vivo in rainbow trout after delivery via the oral route. Here we examined the dispersal and survival of F. psychrophilum phage FpV-9 in vivo in juvenile rainbow trout after administration by three different methods-bath, oral intubation into the stomach, and phage-coated feed-with special emphasis on the oral route of delivery. Phages could be detected in all the organs investigated (intestine, spleen, brain, and kidney) 0.5 h postadministration, reaching concentrations as high as ~10(5) PFU mg intestine(-1) and ~10(3) PFU mg spleen(-1) within the first 24 h following the bath and ~10(7) PFU mg intestine(-1) and ~10(4) PFU mg spleen(-1) within the first 24 h following oral intubation. The phages were most persistent in the organs for the first 24 h and then decreased exponentially; no phages were detected after 83 h in the organs investigated. Phage administration via feed resulted in the detection of phages in the intestine, spleen, and kidney 1 h after feeding. Average concentrations of ~10(4) PFU mg intestine(-1) and ~10(1) PFU mg spleen(-1) were found throughout the experimental period (200 h) following continuous delivery of phages with feed. These experiments clearly demonstrate the ability of the phages to survive passage through the fish stomach and to penetrate the intestinal barrier and enter the circulatory system after oral delivery, although the quantity of phages found in the spleen was 100- to 1,000-fold lower than that in the intestine. It was also shown that phages could tolerate long periods of desiccation on the feed pellets, with 60% survival after storage at -80°C, and 10% survival after storage at 5°C, for ~8 months. Continuous delivery of phages via coated feed pellets constitutes a promising method of treatment and especially prevention of rainbow trout fry syndrome.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Copenhagen, BioMar A/S
Authors: Christiansen, R. H. (Intern), Dalsgaard, I. (Intern), Middelboe, M. (Ekstern), Lauritsen, A. H. (Ekstern), Madsen, L. (Intern)
Pages: 7683-7693
Publication date: 2014
Main Research Area: Technical/natural sciences

Publication information
Journal: Applied and Environmental Microbiology
Volume: 80
Issue number: 24
ISSN (Print): 0099-2240
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 3.99
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 4.08
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.891 SNIP 1.308 CiteScore 4.14
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.857 SNIP 1.384 CiteScore 4.02
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.899 SNIP 1.414 CiteScore 4.25
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
Detection of European bat lyssavirus type 2 in Danish Daubenton’s bats

European bat lyssavirus (EBLV) is considered to be endemic in the Danish bat populations, but limited information exists about the types of EBLV strains currently in circulation. EBLV type 1 (EBLV-1) is seen as the predominant type in the Serotine bats (Eptesicus serotinus) with the latest case identified in 2009.

General information

State: Published
Organisations: National Veterinary Institute, Section for Virology, University of Copenhagen, Central Veterinary Institute
Authors: Rasmussen, T. B. (Intern), Chriél, M. (Intern), Baagøe, H. J. (Ekstern), Fjederholt, E. (Ekstern), Kooi, E. A. (Ekstern), Belsham, G. (Intern), Betner, A. (Intern)
Publication date: 2014
Event: Abstract from 8th Annual Meeting of Epizone, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Electronic versions:
EPIZONE_Abstract_Rasmussen_EBLV_2_in_DK.pdf
Detection of polytreponemal infection in three cases of porcine ulcerative stomatitis by Fluorescent in situ hybridization

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Veterinary Extension Services, University of Veterinary Medicine
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Publication date: 2014
Event: Abstract from Cutting Edge Pathology, Berlin, Germany.
Main Research Area: Technical/natural sciences

Detection of virus level in tissues of rainbow trout, Oncorhynhicus mykiss in clinical stage of viral hemorrhagic septicemia
In order to detecting VHS virus titer in various tissues in clinical stage of VHS disease, rainbow trout, Oncorhynhicus mykiss, were exposed to virus by bath. The experiments were carried out with 140 fish obtained from rainbow trout farm. The fish were divided into two equal groups in 120 liter tanks containing 70 fish. Group one was considered as control and group two infected by bath challenge with 103 TCID50 ml-1 of a VHS virus strain serologically similar to reference strain F1 with high pathogenicity in rainbow trout. At days 12, 13 and 14 post infection the organs including kidney, spleen, heart, skin, liver, pyloric caeca and brain were sampled from dead fish with appropriate clinical signs of VHS separately. Each sample was placed in vials adding 1 ml transport medium to assess virus titer in various tissues. Results of the study, showed that significant difference between virus loads in various organs (p≤ 0.05). The highest virus titer belongs to the heart while it is in minimum amount in the skin. According to the virus quantity the experimental tissues can be divided in three categories, respectively. Heart and kidney performed the highest amount of virus quantities while liver, gill, pyloric caeca and skin showed the lowest with brain and spleen lying in between. These results point out that the significant levels of VHS virus found in rainbow trout tissues are relevant for the biosecurity in VHS-free areas mainly when fish are displayed and retained as whole fish.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, University of Kurdistan
Authors: Ghiasi, F. (Ekstern), Olesen, N. J. (Intern)
Number of pages: 4
Pages: 3-6
Publication date: 2014
Main Research Area: Technical/natural sciences

Publication information
Journal: Brazilian Journal of Veterinary Pathology
Volume: 7
Issue number: 1
ISSN (Print): 1983-0246
Ratings:
Web of Science (2018): Indexed yes
Scopus rating (2017): SNIP 0.51 SJR 0.162 CiteScore 0.39
Scopus rating (2016): SJR 0.206 SNIP 0.587 CiteScore 0.53
Scopus rating (2015): SJR 0.141 SNIP 0.201 CiteScore 0.22
Scopus rating (2014): SJR 0.227 SNIP 0.522 CiteScore 0.35
Web of Science (2014): Indexed yes
Scopus rating (2013): SJR 0.209 SNIP 0.378 CiteScore 0.39
Scopus rating (2012): SJR 0.144 SNIP 0.208 CiteScore 0.32
Scopus rating (2011): SJR 0.112 SNIP 0.271 CiteScore 0.15
Original language: English
Veterinary (miscellaneous), Rainbow trout, Tropism, VHS virus
**Development of Methods for Genetic Assessment of Antibiotic Resistance In Animal Herds**

Antibiotic drugs are important in treating bacterial infectious diseases in humans and animals. There are severe consequences when infectious bacteria become resistant to antibiotics such as treatment failure and even death. Since antibiotics were discovered, their use has been associated with a parallel selection for resistant bacteria. Since the hazards related to antibiotic resistance development have been recognized, the prudent use of antibiotics has been in focus, especially concerning their use in animal production. For many years antibiotics have been, and still are, recklessly used in the animal production especially in the form of growth promoters. Due to the associated risks of resistant zoonotic bacteria transmission from animals to humans, it is of interest to keep antibiotic use and antibiotic resistance under strict surveillance. This PhD study was based on the development of real-time PCR (qPCR) assays that supply an easy and rapid method for quantifying antibiotic resistance levels in animal herds. The pig production is accountable for a large portion of the antibiotics used for food producing animals in Denmark. Therefore, the antibiotic resistance genes included in this study had previously been described in association with pig herds, and they encoded resistance to antibiotics used in the Danish pig production. The **first objective** had emphasis on the qPCR assays’ design and development. The goal was to design 10-15 qPCR assays representing different antibiotic classes that ultimately would be tested in a swine herd. A total of 14 assays were developed, representing the following antibiotic classes: Tetracycline (tet(A), tet(B), tet(C), tet(M), tet(O), tet(W)), β-lactam (blaCTX-M-1 group, blaSHV family, and vanA), sulphonamide (sulI, sulII), macrolide, lincosamide, and streptogramin B (ermB, ermF), and glycopeptide (vanA). The glycopeptide vanA gene was included as a follow-up to the avoparcin growth promoter ban implemented in Denmark in 1995. Besides the 14 antibiotic resistance gene qPCR assays, a 16S rDNA assay was also included. Manuscript I was an investigation of the affects PCR conditions had on the diversity and prevalence of antibiotic resistance genes detected in swine manure. This work was carried out in Dr. Zhongtang Yu’s laboratory at The Department of Animal Science, The Ohio State University, Columbus, Ohio. At this point of the first objective, decisions were being made concerning qPCR chemistry (probe vs. DNA-binding dye) and mastermix composition. In this study, three cycle numbers and 4 MgCl₂ concentrations were evaluated for their effect on the diversity and prevalence of ribosomal protection proteins (RPPs) in a 3 x 4 factorial design. Significant differences in genetic diversity and prevalence of tet genes were found amongst the cycle number and MgCl₂ combinations, and suggested that 35 PCR cycles and 7 mM MgCl₂ enabled optimal detection of RPP genes in swine manure using the Ribo2_new_FW/Ribo2_RV primer pair. The results emphasized the importance of the PCR conditions when performing studies involving tet gene prevalence, and when results are interpreted. Upon completion of the qPCR assay development and optimization the project progressed to the **second objective**. The second objective was to establish if the qPCR assays could quantify antibiotic resistance genes in swine herds by comparing this principle to culture dependent antibiotic resistance detection. In order to do so, fecal samples in a swine herd were collected using different sampling methods that were also pooled at different levels. The antibiotic resistance levels were then determined both by the qPCR assays and coliform colony forming unit (CFU) estimates. The different sampling and pooling methods were evaluated. This established the qPCR assays’ capacity to quantify antibiotic resistance genes in a swine herd (Manuscript II) where significant differences in qPCR gene copy number estimates between pens were found (p<0.05 for ermB, tet(C), tet(W); p<0.0001 for ermF and tet(O)), while other antibiotic resistance genes were not detected in any samples during sampling 1 and sampling 2 (blaCTX-M-1 group, blaSHV family, and vanA). On the other hand, the coliform CFU counts differed significantly between pens for ampicillin and 8 tetracycline or erythromycin. This emphasizes the major shortcomings of both methods, namely that the CFU counts only represent the coliform bacteria while the qPCR assays only detect the pre-defined genes. However, the qPCR gene copy numbers had lower relative standard deviations compared to the coliform CFU counts meaning that there is less variation in the qPCR gene copy estimates compared to the colony CFU counts (Manuscript II). The variation in the coliform CFU counts consequently complicated the comparison of different sampling methods using coliform CFU counts (Manuscript III). In order to compare the qPCR principle of antibiotic resistance quantification, 20 of the individually sampled animals were randomly selected and analyzed by qPCR, coliform CFU counts, and colony hybridization using probes that correspond to the fragments amplified by the qPCR assays’ primers (Manuscript III). This study showed that it is important to define which bacterial population is relevant in achieving the specific goal of the antibiotic resistance quantification, and the method chosen for antibiotic resistance quantification has a large influence on the results obtained. This is exemplified by the higher level of tetracycline resistance observed in the coliform bacteria CFU counts compared to the colony hybridization (p<0.0001) (Manuscript III) despite the smaller bacterial fraction represented in the coliform estimates compared to the colony hybridization. This suggests that the majority of the tetracycline resistant bacteria were not detected by colony hybridization because they do not carry the specific genes that were used as probes. The first and second objectives established that the qPCR assays could be utilized in quantifying antibiotic resistance genes in total DNA extracted from swine feces. It was also confirmed that qPCR and culture dependent antibiotic resistance estimates represent two completely different populations, and cannot be compared directly. This was perceived by the lack of correlation between the total coliform CFU counts and the total number of bacteria in the population represented by the 16S copy number (R² =0.1) (Manuscript III), and by the differences in resistance estimates obtained by qPCR, coliform bacteria CFU counts, and colony hybridization (Manuscript III). Furthermore, pen floor sampling (pooled at stable level or not pooled), shoe cover samples (not pooled), and slurry tank samples were evaluated and are promising sampling methods when determining antibiotic resistance at herd level. The **third objective** involved the application of the qPCR assays in an animal population.
that was completely distant from the Danish pig production. Fecal samples from wildlife and Massai cattle in Tanzania were screened for the presence of the 14 antibiotic resistance genes using the qPCR assays. The wildlife and cattle samples were collected in the Ngorongoro Conservational Area (NCA) (wildlife and cattle interaction), and wildlife samples from the Mikumi National Park (MNP) (cattle are prohibited). Antibiotic resistant coliform bacteria estimates were also determined. This study constitutes Manuscript IV and the findings were surprising. The antibiotic resistance genes that were found in the wildlife were also detected in the wildlife samples, regardless of the sampling site. Eight of the antibiotic resistance genes were detected in the samples, the most prevalent being tet(W) and blaCMY-2. Due to the nature of the blaCMY-2 antibiotic resistance spectrum, and the finding of this gene in 10 of 12 screened samples gives rise to concern. However, the finding of the blaCMY-2 gene in the wildlife further substantiates the qPCR assay as this gene was not detected in any of the pig samples collected and described in Manuscript II. Nevertheless, further studies should be conducted to study the antibiotic resistance gene pool among the wildlife in northern Tanzania. In conclusion, the 14 qPCR assays developed here successfully quantified antibiotic resistance in pig herds, where pen floor sampling (pooled at stable level or non-pooled), shoe cover sampling (non-pooled), and slurry tank sampling are promising sampling collection methods. To our knowledge, Manuscript II is the first study to describe sampling and pooling methods for qPCR quantification of antibiotic resistance genes in total DNA extracted from swine feces. The qPCR assays were also capable of detecting antibiotic resistance genes in Tanzanian wildlife and cattle samples representing a completely different population than the Danish pig production. Also, a gene not detected in the Danish pigs was detected in the Tanzanian wildlife and cattle samples further validating the qPCR assay. Generally, our results indicate that there is a large variation in the antibiotic gene abundance, regardless of animal species or sampling method. Furthermore, the present study highlights how different methods for antibiotic resistance detection (resistance coliform counts, colony hybridization on MacConkey and BA (anaerobic), and qPCR gene copy number estimates) reflect antibiotic resistance levels in different bacterial populations (Manuscript III). This emphasizes the importance of defining which bacterial population is relevant in the specific goal of antibiotic resistance quantification. When the aim is to monitor and quantify antibiotic resistance at herd level, using a method where few chosen indicator bacteria represent the resistance in the intestinal bacterial population let alone the herds’ is not optimal due to the large portion of neglected bacteria. When using qPCR for antibiotic resistance quantification the complete gene pool of the bacterial community is reflected. Besides being rapid and having minimal processing requirements, qPCR also enables precise measurement of small differences in DNA levels between samples, while detecting antibiotic resistance in viable and non-viable bacteria. However, qPCR only enables detection of the chosen genes, it is subject to inhibition, and results can be biased. It is therefore critical to assess qPCR assay parameters in order to establish the optimal conditions to accurately depict the antibiotic resistance levels. Additional studies evaluating the sampling methods in several animal herds should be tested in order to assist in understanding the antibiotic resistance gene variation. This study illustrates the immensity of the antibiotic resistance problem and the necessity for systematic surveillance of antibiotic consumption and resistance development at global, national, and local scales.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, University of Copenhagen
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Number of pages: 175
Publication date: 2014

Publication information
Place of publication: Kgs. Lyngby
Publisher: Technical University of Denmark (DTU)
Original language: English
Main Research Area: Technical/natural sciences
Electronic versions: PhD_Thesis_Gunilla_Veslem_y_Schmidt.pdf
Publication: Research › Ph.D. thesis – Annual report year: 2015

Development of tailored real-time RT-PCR assays for the detection and differentiation of serotype O, A and Asia-1 foot-and-mouth disease virus lineages circulating in the Middle East

Rapid and accurate diagnosis is essential for effective control of foot-and-mouth disease (FMD). In countries where FMD is endemic, identification of the serotypes of the causative virus strains is important for vaccine selection and tracing the source of outbreaks. In this study, real-time reverse transcription polymerase chain reaction (rRT-PCR) assays using primer/probe sets designed from the VP1 coding region of the virus genomes were developed for the specific detection of serotype O, A and Asia-1 FMD viruses (FMDVs) circulating in the Middle East. These assays were evaluated using representative field samples of serotype O strains belonging exclusively to the PanAsia-2 lineage, serotype A strains of the Iran-05 lineage and serotype Asia-1 viruses from three relevant sub-groups. When RNA extracted from archival and contemporary field strains was tested using one- or two-step rRT-PCR assays, all three primer/probe sets detected the RNA from homotypic viruses and no cross-reactivity was observed with heterotypic viruses. Similar results were obtained using both single- and multiplex assay formats. Using plasmid standards, the minimum detection level of these tests was found to be lower than two copies. The results illustrate the potential of tailored rRT-PCR tools for the detection and categorization of viruses circulating in the Middle East belonging to distinct subgroups of serotypes O, A and Asia-1.
These assays can also overcome the problem of serotyping samples which are found positive by the generic rRT-PCR diagnostic assays but negative by virus isolation and antigen-detection ELISA which would otherwise have to be serotyped by nucleotide sequencing. A similar approach could be used to develop serotyping assays for FMDV strains circulating in other regions of the world.

**General information**

State: Published  
Organisations: National Veterinary Institute, Section for Virology, The Pirbright Institute  
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Pages: 146-153  
Publication date: 2014  
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Journal of Virological Methods  
Volume: 207  
ISSN (Print): 0166-0934  
Ratings:  
BFI (2018): BFI-level 1  
Web of Science (2018): Indexed yes  
BFI (2017): BFI-level 1  
Scopus rating (2017): SNIP 0.817 SJR 0.858 CiteScore 1.82  
Web of Science (2017): Indexed Yes  
BFI (2016): BFI-level 1  
Scopus rating (2016): SJR 0.873 SNIP 0.729 CiteScore 1.78  
Web of Science (2016): Indexed yes  
BFI (2015): BFI-level 1  
Scopus rating (2015): SJR 0.87 SNIP 0.802 CiteScore 1.68  
BFI (2014): BFI-level 1  
Scopus rating (2014): SJR 0.898 SNIP 0.933 CiteScore 1.87  
Web of Science (2014): Indexed yes  
BFI (2013): BFI-level 1  
Scopus rating (2013): SJR 0.866 SNIP 0.9 CiteScore 1.99  
ISI indexed (2013): ISI indexed yes  
Web of Science (2013): Indexed yes  
BFI (2012): BFI-level 1  
Scopus rating (2012): SJR 0.873 SNIP 0.929 CiteScore 2.08  
ISI indexed (2012): ISI indexed yes  
Web of Science (2012): Indexed yes  
BFI (2011): BFI-level 1  
Scopus rating (2011): SJR 0.908 SNIP 0.987 CiteScore 2.23  
ISI indexed (2011): ISI indexed yes  
Web of Science (2011): Indexed yes  
BFI (2010): BFI-level 1  
Scopus rating (2010): SJR 0.91 SNIP 1.001  
Web of Science (2010): Indexed yes  
BFI (2009): BFI-level 1  
Scopus rating (2009): SJR 0.973 SNIP 1.059  
Web of Science (2009): Indexed yes  
BFI (2008): BFI-level 1  
Scopus rating (2008): SJR 0.926 SNIP 1.072  
Web of Science (2008): Indexed yes  
Scopus rating (2007): SJR 0.963 SNIP 1.025  
Web of Science (2007): Indexed yes  
Scopus rating (2006): SJR 0.886 SNIP 1.073  
Web of Science (2006): Indexed yes
Foot-and-mouth disease virus, FMDV serotyping, FMDV real-time serotyping RT-PCR assay, FMDV multiplex real-time serotyping RT-PCR assay

Diet type dictates the gut microbiota and the immune response against Yersinia ruckeri in rainbow trout (Oncorhynchus mykiss)

This study investigated the influence of the rainbow trout (Oncorhynchus mykiss) commensal intestinal microbiota in connection to an experimental Yersina ruckeri infection, the causative agent of enteric redmouth disease. One marine and one plant diet was administrated to two different groups of rainbow trout. The plant-based diet gave rise to an intestinal microbiota dominated by the genera Streptococcus, Leuconostoc and Weissella from phylum Firmicutes whereas phylum Proteobacteria/Bacteroidetes/Actinobacteria dominated the community in the marine fed fish. In connection to the Y. ruckeri bath challenge there was no effect of the diet type on the cumulative survival, but the number of Y. ruckeri positive fish as measured by plate count and the number of fish with a 'high' number of reads belonging to genus Yersinia as measured by 16S rRNA next-generation sequencing was higher for marine diet fed fish. Furthermore, the two experimental groups of fish showed a differential immune response, where Y. ruckeri challenged marine fed fish had a higher transcription of IL-1β and MBL-2 relative to challenged plant diet fed fish. The data suggest that the plant diet gave rise to a prebiotic effect favouring the presence of bacterial taxons proving protective in connection to bath challenge by Y. ruckeri.
The bacteria associated with the infectious claw disease bovine digital dermatitis (DD) are spirochetes of the genus Treponema; however, their environmental reservoir remains unknown. To our knowledge, the current study is the first report of the discovery and phylogenetic characterization of rRNA gene sequences from DD-associated treponemes in the dairy herd environment. Although the spread of DD appears to be facilitated by wet floors covered with slurry, no DD-associated treponemes have been isolated from this environment previously. Consequently, there is a lack of knowledge about the spread of this disease among cows within a herd as well as between herds. To address the issue of DD infection reservoirs, we searched for evidence of DD-associated treponemes in fresh feces, in slurry, and in hoof lesions by deep sequencing of the V3 and V4 hypervariable regions of the 16S rRNA gene coupled with identification at the operational-taxonomic-unit level. Using treponeme-specific primers in this high-throughput approach, we identified small amounts of DNA (on average 0.6% of the total amount of sequence reads) from DD-associated treponemes in 43 of 64 samples from slurry and cow feces collected from six geographically dispersed dairy herds. Species belonging to the Treponema denticola/Treponema pedis-like and Treponema phagedenis-like phylogenetic clusters were among the most prevalent treponemes in both the dairy herd environment and the DD lesions. By the high-throughput approach presented here, we have demonstrated that cow feces and environmental slurry are possible reservoirs of DD-associated treponemes. This method should enable further clarification of the etiopathogenesis of DD.
Dissektionen af kaskelothvalerne på Henne Strand

I februar strandede to voksne han-kaskelothvaler på Henne Strand nord for Esbjerg. Herefter begyndte tre dages intenst arbejde med at dissekere hvalerne. En mulig dødsårsag blev fundet hos den ene af dem, men det er fortsat en gåde, hvorfor kaskeloter undertiden strander i fløkke.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Aalborg University
DIVA vaccine properties of the live chimeric pestivirus strain CP7_E2gif

Live modified vaccines to protect against classical swine fever virus (CSFV), based on chimeric pestiviruses, have been developed to enable serological Differentiation of Infected from Vaccinated Animals (DIVA). In this context, the chimeric virus CP7_E2gif vaccine candidate is unique as it does not include any CSFV components. In the present study, the DIVA vaccine properties of CP7_E2gif were evaluated in comparison to the conventional live attenuated Riemser C-strain vaccine. Sera and tonsil samples obtained from pigs immunised with these two vaccines were analysed. No viral RNA was found in serum after vaccination with CP7_E2gif, whereas some serum samples from C-strain vaccinated animals were positive. In both vaccinated groups, individual viral RNA-positive tonsil samples were detected in animals euthanised between 7 and 21 days post vaccination. Furthermore, serum samples from these animals, together with archival samples from pigs vaccinated with CP7_E2gif and subsequently CSFV challenged, were analysed for specific antibodies using ELISAs and for homologous neutralising antibodies. In animals vaccinated with CP7_E2gif, neutralising antibodies were detected from day 10. However, the sera remained negative for anti-CSFV E2-specific antibodies whereas pigs vaccinated with Cstrain seroconverted against CSFV by 14 days after vaccination, as determined by a CSFVE2 specific blocking ELISA. One week after subsequent CSFV challenge, a strong anti-CSFV E2 reaction was detected in CP7_E2gif vaccinated pigs and anti-Erns antibodies were detected from 10 days after infection. In conclusion, CP7_E2gif has the potential to be used as a DIVA vaccine in combination with detection of anti-CSFV E2-specific antibodies.
Diversity and Geographical Distribution of *Flavobacterium psychrophilum* Isolates and Their Phages: Patterns of Susceptibility to Phage Infection and Phage Host Range

*Flavobacterium psychrophilum* is an important fish pathogen worldwide that causes cold water disease (CWD) or rainbow trout fry syndrome (RTFS). Phage therapy has been suggested as an alternative method for the control of this pathogen in aquaculture. However, effective use of bacteriophages in disease control requires detailed knowledge about the diversity and dynamics of host susceptibility to phage infection. For this reason, we examined the genetic diversity of 49 *F. psychrophilum* strains isolated in three different areas (Chile, Denmark, and USA) through direct genome restriction enzyme analysis (DGREA) and their susceptibility to 33 bacteriophages isolated in Chile and Denmark, thus covering large geographical (>12,000 km) and temporal (>60 years) scales of isolation. An additional 40 phage-resistant isolates obtained from culture experiments after exposure to specific phages were examined for changes in phage susceptibility against the 33 phages. The *F. psychrophilum* and phage populations isolated from Chile and Denmark clustered into geographically distinct groups with respect to DGREA profile and host range, respectively. However, cross infection between Chilean phage isolates and Danish host isolates and vice versa was observed. Development of resistance to certain bacteriophages led to susceptibility to other phages suggesting that "enhanced infection" is potentially an important cost of resistance in *F. psychrophilum*, possibly contributing to the observed co-existence of phage-sensitive *F. psychrophilum* strains and lytic phages across local and global scales. Overall, our results showed that despite the identification of local communities of phages and hosts, some key properties determining phage infection patterns seem to be globally distributed.
Draft Genome Sequences of Six Ruminant Coxiella burnetii Isolates of European Origin

Coxiella burnetii is responsible for Q fever, a worldwide zoonosis attributed to the inhalation of aerosols contaminated by livestock birth products. Six draft genome sequences of European C. burnetii isolates from ruminants are presented here. The availability of these genomes will help in understanding the potential host specificity and pathogenicity and in identifying pertinent markers for surveillance and tracing.

General information
State: Published
Organisations: National Veterinary Institute, Agence nationale de la sécurité sanitaire, alimentation, environnement et travail, Animal Health and Veterinary Laboratories Agency, National Veterinary Institute Sweden
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Publication date: 2014
Main Research Area: Technical/natural sciences

Publication information
Journal: Genome Announcements
Volume: 2
Issue number: 3
Article number: e00285-14
ISSN (Print): 2169-8287
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.407 SJR 0.553 CiteScore 1.01
Scopus rating (2016): CiteScore 0.41 SJR 0.583 SNIP 0.469
Web of Science (2016): Indexed yes
Scopus rating (2015): SJR 0.591 SNIP 0.398
Scopus rating (2014): SJR 0.539 SNIP 0.344
ISI indexed (2013): ISI indexed no
Dynamic monitoring of weight data at the pen vs at the individual level
The PigIT project, led by the University of Copenhagen, aims at improving welfare and productivity in growing pigs using ICT methods. Automatically and manually recorded data are currently being collected in a production herd. One of the first steps of the project is to make use of the manually recorded weight data from finisher pigs. Data are collected at insertion and at the exit of the first pigs in the pen, and in few pens, the weight is recorded weekly. Dynamic linear models are fitted on the weight data, at the pig level (univariate), at the double pen level using averaged weight (univariate) and using individual pig values as parameters in a hierarchical (multivariate) model including section, double pen, and individual level. Variance components of the different models are estimated using the Expectation Maximization algorithm. The difference of information obtained at the individual vs pen level is thereafter assessed. Whereas weight data is usually monitored after a batch is being sent to the slaughter house, this method provides weekly updating of the data. Perspectives of application include dynamic monitoring of weight data in relation to events such as diarrhoea, tail biting and fouling in order to assess whether it is possible to detect deviations of patterns before or during the occurrence of these events.

Effect of mild streptozotocin/nicotinamide-induced diabetes on aortic plaque area in new minipig model of atherosclerosis

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, University of Copenhagen, Novo Nordisk A/S
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Pages: e236-e237
Publication date: 2014
Main Research Area: Technical/natural sciences
Effect of subinhibitory concentrations of four commonly used biocides on the conjugative transfer of Tn916 in Bacillus subtilis

Objectives Large amounts of biocides are used to reduce and control bacterial growth in the healthcare sector, food production and agriculture. This work explores the effect of subinhibitory concentrations of four commonly used biocides (ethanol, hydrogen peroxide, chlorhexidine digluconate and sodium hypochlorite) on the conjugative transposition of the mobile genetic element Tn916.

Methods Conjugation assays were carried out between Bacillus subtilis strains. The donor containing Tn916 was pre-exposed to subinhibitory concentrations of each biocide for a defined length of time, which was determined by an analysis of the transcriptional response of the promoter upstream of tet(M) using β-glucuronidase reporter assays.

Results Ethanol significantly (P = 0.01) increased the transfer of Tn916 by 5-fold, whereas hydrogen peroxide, chlorhexidine digluconate and sodium hypochlorite did not significantly affect the transfer frequency.

Conclusions These results suggest that exposure to subinhibitory concentrations of ethanol may induce the transfer of Tn916-like elements and any resistance genes they contain.
Effects of level of social contact on dairy calf behavior and health

Housing preweaned dairy calves in pairs rather than individually has been found to positively affect behavioral responses in novel social and environmental situations, but concerns have been raised that close contact among very young animals may impair their health. In previous studies, the level of social contact permitted in individual housing has been auditory, visual, or physical contact. It is unclear how these various levels of social contact compare with each other and to pair housing, when their effects on behavior and health are considered, and whether the timing of pair housing has an effect.

To investigate this, 110 Holstein calves (50 males, 60 females) in 11 blocks were paired according to birth date. Within 60 h of birth, each pair of calves was allocated to 1 of 5 treatments: individual housing with auditory contact (I), individual housing with auditory and visual contact (V), individual housing with auditory, visual, and tactile contact (T), pair housing (P), or individual housing with auditory and visual contact the first 2 wk followed by pair housing (VP). At 6 wk of age, calves were subjected to a social test and a novel environment test. In the social test, all pair-housed calves (P and VP) had a shorter latency to sniff an unfamiliar calf than did individually housed calves (I, V; and T), whereas calves with physical contact (T, P, and VP) sniffed the unfamiliar calf for longer than calves on the remaining treatments (I and V). In the novel environment test, calves with physical contact (T, P, and VP) had a lower heart rate, and more of these calves vocalized during the test compared with calves without physical contact (I and V). No effect of treatment was found for clinical scores, levels of the 5 most common pathogens in feces, or in development of serum antibodies against the 3 most common respiratory pathogens. Calves housed individually are more fearful of unfamiliar calves than are pair-housed calves. Contrary to common belief, the allowance of physical contact and pair housing had no effects on the health of the calves.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Aarhus University
Authors: Jensen, M. B. (Ekstern), Larsen, L. E. (Intern)
Pages: 5035-5044
Publication date: 2014
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Dairy Science
Volume: 97
Issue number: 8
ISSN (Print): 0022-0302
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SNIP 1.491 SJR 1.35 CiteScore 2.84
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.66 SJR 1.331 SNIP 1.484
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.479 SNIP 1.488 CiteScore 2.63
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.434 SNIP 1.504 CiteScore 2.78
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.411 SNIP 1.589 CiteScore 2.82
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.443 SNIP 1.717 CiteScore 2.79
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
In the last decade, many porcine epidemic diarrhoea (PED) outbreaks have been reported by several countries in Asia whereas only a few Member States of the European Union (EU) have reported PED clinical cases and/or PED virus (PEDV)-seropositive animals. This alphacoronavirus was first reported in the USA in May 2013, followed by rapid spread throughout the country and outbreaks reported by several countries in the Americas. The recent PEDV-EU isolates have high level of sequence identity to PEDV-Am isolates. Based on nucleotide sequencing, multiple variants of PEDV are circulating in Europe, the Americas and Asia but any difference in virulence and antigenicity is currently unknown. Serological cross-reactivity has been reported between PEDV isolated in Europe and in the Americas; however no data regarding cross-protection are available. The impact of different PEDV strains is difficult to compare between one country and another, since impact is dependent not only on pathogenicity but also on factors such as biosecurity, farm management, sanitary status or herd immune status. However, the clinical signs of PEDV infections in naive pigs are similar in different countries with mortalities up to 100% in naive newborn piglets. The impact of recently reported PED outbreaks in Asia and the USA seems to be more severe than what has been described in Europe. Infected animals, faeces, feed and objects contaminated with faeces are matrices that have been reported to transmit PEDV between farms. Infectious PEDV has been detected in spray-dried porcine plasma (SDPP) in one study but the origin of the infectious PEDV in SDPP is not clear. Detection of porcine deltacoronavirus (PDCoV) has been reported in a few countries but only limited testing has been done. Based on the currently available information, it seems that PDCoV would have a lower impact than PEDV.
EFSA (European Food Safety Authority) and ECDC (European Centre for Disease Prevention and Control), 2014. The European Union Summary Report on Trends and Sources of Zoonoses, Zoonotic Agents and Food-borne Outbreaks in 2012

Zoonoses are infections and diseases that are naturally transmissible, directly or indirectly, for example via contaminated foodstuffs, between animals and humans. The severity of these diseases in humans varies from subclinical infection or mild symptoms to life-threatening conditions. In order to prevent zoonoses from occurring, it is important to identify which animals and foodstuffs are the main sources of infection. For this purpose information aimed at protecting human health is collected and analysed from all European Union Member States.

In 2012, 27 Member States submitted information on the occurrence of zoonoses, zoonotic agents and food-borne outbreaks to the European Commission and the European Food Safety Authority. Furthermore, information on cases of zoonoses reported in humans was provided by the European Centre for Disease Prevention and Control. In addition, three European countries that were not European Union Member States provided information. The European Food Safety Authority and the European Centre for Disease Prevention and Control jointly analysed the data, the results of which are published in this annual European Union Summary Report, which covers 15 zoonoses and food-borne outbreaks.

In 2012, the notification rate and confirmed number of cases of human campylobacteriosis in the European Union decreased compared with 2011. Human campylobacteriosis, however, continued to be the most commonly reported zoonosis with 214,268 confirmed cases. The number of confirmed cases of campylobacteriosis in the European Union has followed a significant increasing trend in the last five years (2008-2012), along with a clear seasonal trend. The proportion of Campylobacter-positive food and animal samples remained mainly at levels similar to previous years, with the occurrence of Campylobacter continuing to be high in broiler meat.

The number of salmonellosis cases in humans decreased by 4.7 % compared with 2011. A statistically significant increasing trend in the European Union was observed over the period 2008-2012. In total, 91,034 confirmed human cases were reported in 2012. It is assumed that the observed reduction in salmonellosis cases is mainly a result of the successful Salmonella control programmes in poultry populations. Most Member States met their Salmonella reduction targets for poultry, and Salmonella is declining in these animal populations. In foodstuffs, Salmonella was most often detected in fresh broiler meat. The food categories with the highest proportion of products not complying with the European Union Salmonella criteria were minced meat and meat preparations, meat products, as well as live bivalve molluscs.

The number of listeriosis cases in humans increased slightly compared with 2011, and 1,642 confirmed human cases were reported in 2012. A statistically significant increasing trend in the European Union was observed over the period 2008-2012, though only slowly increasing, along with a seasonal pattern. As in previous years, a high fatality rate (17.8 %) was reported among the cases. A total of 198 deaths due to listeriosis were reported by 18 Member States in 2012, which was the highest number of fatal cases reported since 2006. Listeria monocytogenes was seldom detected above the legal safety limit from ready-to-eat foods at point of retail. Samples exceeding this limit were most often found in fishery products.
A total of 5,671 confirmed verocytotoxigenic Escherichia coli infections were reported in 2012, which was a decrease of 40 % compared with 2011. Of those cases in which the serogroup was known, most were caused by serogroup O157, followed by O26 and O91. There was an increasing European Union trend of confirmed human verocytotoxigenic Escherichia coli infections in 2008–2012. Even without the 2011 data the European Union trend for verocytotoxigenic Escherichia coli infections during 2008–2010 was significantly increasing. Human pathogenic verocytotoxigenic Escherichia coli strains were detected by the reporting Member States from fresh bovine meat occasionally and at low levels. The human pathogenic verocytotoxigenic Escherichia coli serogroups isolated from the bovine meat and cattle samples included VTEC O157, O26, O91, O103 and O145.

The number of confirmed human tuberculosis cases due to Mycobacterium bovis in the European Union in 2012 was 125. This was a decrease compared with 2011, with a few Member States accounting for the majority of the reported cases. The reported prevalence of bovine tuberculosis in cattle increased slightly at European Union level, but remained at a very low level. This slight increase was, however, due to one Member State that reported an increase in prevalence of bovine tuberculosis for the fourth consecutive year.

The number of confirmed brucellosis cases in humans was 328 at European Union level, which was almost the same as in 2011. The number of brucellosis-positive cattle, and sheep and goat herds continued to decrease, although marginally compared with 2011.

Trichinella caused 301 confirmed human cases in the European Union. Although the number of cases was slightly higher in 2012 than in 2011, human trichinellosis cases remained at a low level in the European Union compared with 2009 and previous years. In 2012, the prevalence of Trichinella in pigs was similar to that observed in 2011. The parasite was more prevalent in wildlife than in farmed animals. However, seven out of the nine strong-evidence outbreaks reported were due to consumption of pig meat.

Toxoplasma was reported by the Member States from pigs, sheep, goats, hunted wild boar and hunted deer, in 2011 and 2012. In addition, positive findings were detected in cats (the natural hosts), cattle and dogs as well as several other animal species, indicating the wide distribution of the parasite among different animal and wildlife species.

One domestically acquired human case and one imported human case of rabies were reported in the European Union in 2012. The general decreasing trend in the total number of rabies cases in animals observed in previous years was reversed in 2012, as there was an increase in the rabies cases reported in animals. In the European Union, the number of cases reported in farm animals and foxes increased.

In 2012, a total of 643 confirmed cases of Q fever in humans were reported in the European Union. There was an overall 15.3 % decrease in the number of reported confirmed cases compared with 2011 (759 cases). All 22 reporting Member States, except one, found animals positive for Coxiella burnetii, the causative agent of Q fever, which demonstrates that the pathogen is widely distributed in the European Union. Positive findings were detected in cattle, sheep as well as goats.

A total of 232 cases of West Nile fever in humans were reported in the European Union. There was an overall 75.8 % increase in the number of reported cases compared with 2011 (132 cases), but a 33.5 % decrease compared with 2010 (349 cases). 2012 was the first year in which Member States were specifically invited to report data on West Nile virus in animals. Most data were from solipeds, notably horses, and less information was received from birds and other animal species. Test-positive solipeds were reported by Southern European countries but few test-positive horses were also reported by Central and Western European Member States.

A total of 5,363 food-borne outbreaks were reported in the European Union, resulting in 55,453 human cases, 5,118 hospitalisations and 41 deaths. Most of the reported outbreaks were caused by Salmonella, bacterial toxins, viruses and Campylobacter. The most important food sources of the outbreaks were eggs and egg products, followed by mixed food and fish and fish products. Overall, 16 waterborne outbreaks were reported in 2012, caused by calicivirus, verocytotoxigenic E. coli, Cryptosporidium parvum and rotavirus.

General information
State: Published
Organisations: National Food Institute, Division of Risk Assessment and Nutrition, National Veterinary Institute, Epidemiology, Research Group for Genomic Epidemiology
Authors: EFSA Journal
Number of pages: 312
Publication date: 2014

Publication information
Place of publication: Parma, Italy
Publisher: European Food Safety Authority
Original language: English
Series: The EFSA Journal
Volume: 12(2)
Ascaridia galli infection influences the development of both humoral and cell-mediated immunity after Newcastle Disease vaccination in chickens

Potent vaccine efficiency is crucial for disease control in both human and livestock vaccination programmes. Free range chickens and chickens with access to outdoor areas have a high risk of infection with parasites including Ascaridia galli, a gastrointestinal nematode with a potential influence on the immunological response to vaccination against other infectious diseases. The purpose of this study was to investigate whether A. galli infection influences vaccine-induced immunity to Newcastle Disease (ND) in chickens from an MHC-characterized inbred line. Chickens were experimentally infected with A. galli at 4 weeks of age or left as non-parasitized controls. At 10 and 13 weeks of age half of the chickens were ND-vaccinated and at 16 weeks of age, all chickens were challenged with a lentogenic strain of Newcastle disease virus (NDV). A. galli infection influenced both humoral and cell-mediated immune responses after ND vaccination. Thus, significantly lower NDV serum titres were found in the A. galli-infected group as compared to the non-parasitized group early after vaccination. In addition, the A. galli-infected chickens showed significantly lower frequencies of NDV-specific T cells in peripheral blood three weeks after the first ND vaccination as compared to non-parasitized chickens. Finally, A. galli significantly increased local mRNA expression of IL-4 and IL-13 and significantly decreased TGF-ß4 expression in the jejunum two weeks after infection with A. galli. At the time of vaccination (six and nine weeks after A. galli infection) the local expression in the jejunum of both IFN-? and IL-10 was significantly decreased in A. galli-infected chickens. Upon challenge with the NDV LaSota strain, viral genomes persisted in the oral cavity for a slightly longer period of time in A. galli-infected vaccinees as compared to non-parasitized vaccinees. However, more work is needed in order to determine if vaccine-induced protective immunity is impaired in A. galli-infected chickens.

General information
State: Published
Organisations: National Food Institute, Division of Industrial Food Research, Communications and Management Secretariat, National Veterinary Institute, Section for Immunology and Vaccinology, Aarhus University, DHI Denmark
Pages: 383–392
Publication date: 2014
Main Research Area: Technical/natural sciences

Publication information
Journal: Vaccine
Volume: 32
Issue number: 3
ISSN (Print): 0264-410X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.19 SJR 1.863 SNIP 1.124
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.33 SJR 1.985 SNIP 1.142
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.073 SNIP 1.248 CiteScore 3.45
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.105 SNIP 1.218 CiteScore 3.57
Web of Science (2014): Indexed yes
Enteric porcine viruses in farmed shellfish in Denmark

Bivalve shellfish are at constant risk of being exposed to pathogens as a consequence of contamination of the shellfish beds with human or animal waste originating from sewage treatment plants or slurry fertilized fields. Consumption of contaminated oysters and mussels are frequently reported as causes of disease outbreaks caused by norovirus or hepatitis A virus. Other zoonotic pathogens such as hepatitis E virus (HEV), rotavirus (RV) and Salmonella from livestock may also be transmitted to shellfish via this route. In this study, 29 pooled samples from commercial Danish blue mussels were tested for porcine pathogens and indicator bacteria Escherichia coli (E. coli). All samples tested negative for HEV, RV and Salmonella, whereas E. coli and the highly stable porcine circovirus type 2 (PCV2) were detected in eight and 12 samples, respectively. This is the first study to report the detection of PCV2 in clean areas with low prevalence of the normally applied fecal indicator E. coli, testing for PCV2 may be a more sensitive and robust specific porcine waste indicator in shellfish harvesting areas.

General information

State: Published
Organisations: National Veterinary Institute, Section for Virology, National Food Institute, Division of Food Microbiology
Authors: Krog, J. S. (Intern), Larsen, L. E. (Intern), Schultz, A. C. (Intern)
Pages: 105-109
Publication date: 2014
Main Research Area: Technical/natural sciences

Publication information

Journal: International Journal of Food Microbiology
Volume: 186
ISSN (Print): 0168-1605
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SJR 1.366 SNIP 1.436 CiteScore 3.76
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 3.97 SJR 1.481 SNIP 1.553
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.614 SNIP 1.683 CiteScore 4.02
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.493 SNIP 1.695 CiteScore 3.62
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.612 SNIP 1.841 CiteScore 3.8
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.603 SNIP 1.705 CiteScore 3.7
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Erratum: Apparent prevalence of beef carcasses contaminated with mycobacterium avium subsp. paratuberculosis sampled from danish slaughter cattle (Veterinary Medicine International)

A tabulation error appeared in Table 1. The fecal contamination data for Age <2 years and >2 years were incorrectly recorded into the table. Whereas the numbers in the table were transposed incorrectly, the actual statistical analyses remain correct. The revised table is reproduced below.
Establishment of the West Nile virus vector, *Culex modestus*, in a residential area in Denmark

**General information**

**State:** Published

**Organisations:** National Veterinary Institute, Section for Epidemiology, Technical University of Denmark

**Authors:** Bødker, R. (Intern), Klitgard, K. (Ekstern), Byriel, D. B. (Ekstern), Kristensen, B. (Intern)

**Number of pages:** 3

**Publication date:** 2014

**Main Research Area:** Technical/natural sciences

**Publication information**

**Journal:** Journal of Vector Ecology

**Volume:** 39

**Issue number:** 2

**ISSN (Print):** 1081-1710

**Ratings:**

- BFI (2018): BFI-level 1
- Web of Science (2018): Indexed yes
- BFI (2017): BFI-level 1
- Scopus rating (2017): SNIP 0.66 SJR 0.785 CiteScore 1.39
- BFI (2016): BFI-level 1
- Scopus rating (2016): CiteScore 1.23 SNIP 0.632 SJR 0.7
- BFI (2015): BFI-level 1
- Scopus rating (2015): CiteScore 1.16 SNIP 0.671 SJR 0.683
- BFI (2014): BFI-level 1
- Scopus rating (2014): CiteScore 1.42 SNIP 0.821 SJR 0.729
- BFI (2013): BFI-level 1
- Scopus rating (2013): CiteScore 1.56 SNIP 0.866 SJR 0.856
- ISI indexed (2013): ISI indexed no
- BFI (2012): BFI-level 1
- Scopus rating (2012): CiteScore 1.45 SNIP 0.847 SJR 0.671
European Surveillance Network for Influenza in Pigs: Surveillance Programs, Diagnostic Tools and Swine Influenza Virus Subtypes Identified in 14 European Countries from 2010 to 2013

Swine influenza causes concern for global veterinary and public health officials. In continuing two previous networks that initiated the surveillance of swine influenza viruses (SIVs) circulating in European pigs between 2001 and 2008, a third European Surveillance Network for Influenza in Pigs (ESNIP3, 2010-2013) aimed to expand widely the knowledge of the epidemiology of European SIVs. ESNIP3 stimulated programs of harmonized SIV surveillance in European countries and supported the coordination of appropriate diagnostic tools and subtyping methods. Thus, an extensive virological monitoring, mainly conducted through passive surveillance programs, resulted in the examination of more than 9,000 herds in 17 countries. Influenza A viruses were detected in 31% of herds examined from which 1887 viruses were preliminary characterized. The dominating subtypes were the three European enzootic SIVs: avian-like swine H1N1 (53.6%), human-like reassortant swine H1N2 (13%) and human-like reassortant swine H3N2 (9.1%), as well as pandemic A/H1N1 2009 (H1N1pdm) virus (10.3%). Viruses from these four lineages co-circulated in several countries but with very different relative levels of incidence. For instance, the H3N2 subtype was not detected at all in some geographic areas.
whereas it was still prevalent in other parts of Europe. Interestingly, H3N2-free areas were those that exhibited highest frequencies of circulating H1N2 viruses. H1N1pdm viruses were isolated at an increasing incidence in some countries from 2010 to 2013, indicating that this subtype has become established in the European pig population. Finally, 13.9% of the viruses represented reassortants between these four lineages, especially between previous enzootic SIVs and H1N1pdm. These novel viruses were detected at the same time in several countries, with increasing prevalence. Some of them might become established in pig herds, causing implications for zoonotic infections.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Number of pages: 21
Publication date: 2014
Main Research Area: Technical/natural sciences

Publication information
Journal: PLOS ONE
Volume: 9
Issue number: 12
Article number: PMC4277368
ISSN (Print): 1932-6203
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.01 SJR 1.164 SNIP 1.111
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.11 SJR 1.236 SNIP 1.101
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.427 SNIP 1.136 CiteScore 3.32
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.559 SNIP 1.148 CiteScore 3.54
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.772 SNIP 1.153 CiteScore 3.94
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.982 SNIP 1.156 CiteScore 4.15
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 2.425 SNIP 1.233 CiteScore 4.58
ISI indexed (2011): ISI indexed no
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.705 SNIP 1.178
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 2.614 SNIP 1.046
Web of Science (2009): (Indexed yes)
Evaluation of feed safety aspects in feeding organic layers with fresh house fly larvae (Musca domestica) reared in poultry manure

General information
State: Published
Organisations: National Food Institute, Division of Food Microbiology, National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Danish Technological Institute, University of Copenhagen
Authors: Nordentoft, S. (Intern), Fischer, C. (Ekstern), Hald, B. (Intern), Enemark, H. (Intern), Thapa, S. (Ekstern), Bjerrum, L. (Ekstern)
Number of pages: 1
Publication date: 2014

Host publication information
Title of host publication: Insects to Feed The World : Abstract book
Main Research Area: Technical/natural sciences
Conference: International Conference Insects to Feed the World, Ede, Netherlands, 14/05/2014 - 14/05/2014
Electronic versions:
Source: PublicationPreSubmission
Source-ID: 99594930
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2014

Evaluation of MAP-specific peptides following vaccination of goats

Our aim is to develop a subunit MAP vaccine not interfering with the diagnosis of paratuberculosis or bovine tuberculosis. This study’s objective was to evaluate MAP-specific peptides defined by in silico analysis.

Peptides were picked by 1) comparing MAP genomes to that of other mycobacterium species or 2) selected based on "experience". Peptides predicted to bind bovine MHC II by in silico analysis were included in further studies, resulting in two panels 1) genome-based and 2) selected. Initially, two groups of 15 healthy goats were vaccinated with one of the two panels (50 µg/peptide in CAF01 adjuvant/CAF04 for boosting). Four MAP-infected goats were also vaccinated. In a second vaccination trail, groups of 8 healthy goat kids were vaccinated with genome-based peptides, selected peptides or selected peptides linked together in a recombinant protein (20 µg/peptide or 50 µg protein in Montanide ISA61 adjuvant). IFN-γ responses were measured by ELISA and ELISPOT upon stimulation with peptide pools or individual peptides. T cell lines were made by cultivating CD4+ cells in the presence of antigen, feeder cells plus cytokines, and used to evaluate responses to peptide pools and individual peptides.

IFN-γ responses in healthy goats after the first vaccination were low, but testing of T cell lines from MAP-infected goats identified peptides inducing strong proliferative responses. Peptides for a second vaccination were selected by combining results from this study with a parallel cattle study. In the second trial, goats in the genome-based and the selected peptide group had solid IFN-γ responses while goats in the protein group had modest responses. Only a moderate boosting effect was seen in the second trial. The genome-based pool induced the strongest CD4+ T cell line responses and had the highest number of immunogenic peptides.

This study shows 1) that detection of immunogenic antigens using in silico predictions and T cell lines work, and 2) the identified MAP-specific peptides show potential for use in a subunit vaccine.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Statens Serum Institut
Evolutionary dynamics and genetic diversity from three genes of Anguillid rhabdovirus

Wild freshwater eel populations have dramatically declined in recent past decades in Europe and America, partially through the impact of several factors including the widespread of infectious diseases. The anguillid rhabdoviruses eel virus European X (EVEX) and eel virus American (EVA) potentially play a role in this decline, even if their real contribution is still unclear. In this study, we investigate the evolutionary dynamics and genetic diversity of anguillid rhabdoviruses by analysing sequences from the glycoprotein, nucleoprotein and phosphoprotein (P) genes of 57 viral strains collected from seven countries over 40 years using maximum-likelihood and Bayesian approaches. Phylogenetic trees from the three genes are congruent and allow two monophyletic groups, European and American, to be clearly distinguished. Results of nucleotide substitution rates per site per year indicate that the P gene is expected to evolve most rapidly. The nucleotide diversity observed is low (2-3 %) for the three genes, with a significantly higher variability within the P gene, which encodes multiple proteins from a single genomic RNA sequence, particularly a small C protein. This putative C protein is a potential molecular marker suitable for characterization of distinct genotypes within anguillid rhabdoviruses. This study provides, to our knowledge, the first molecular characterization of EVA, brings new insights to the evolutionary dynamics of two genotypes of Anguillid rhabdovirus, and is a baseline for further investigations on the tracking of its spread.
African swine fever virus (ASFV) causes a severe hemorrhagic fever in domestic pigs. The disease was introduced from the African continent to Georgia in 2007 and has since spread throughout the Caucasus and the Russian Federation. ASF is now established in Eastern Europe and outbreaks have occurred in domestic pigs and wild boar in Poland and the Baltic countries in 2014. Therefore, there is an increased risk of further transmission across Europe. The present study investigates the properties and the effect of the circulating ASF virus strain in Danish pregnant sows.
Experimental infection of sheep with ovine and bovine Dichelobacter nodosus isolates

The aim of this study was, under experimental conditions, to investigate infection of Norwegian White sheep with ovine and bovine isolates of Dichelobacter nodosus of varying virulence. In addition, the efficacy of gamithromycin as a treatment for the experimentally induced infections was examined. The study was performed as a single foot inoculation using a boot. Four groups, each with six lambs, were inoculated with four different challenge strains (Group 1: benign bovine strain; Group 2: virulent bovine strain; Group 3: benign ovine strain; Group 4: virulent ovine strain). The main criterion to determine that infection was transferred was that D. nodosus isolate was obtained by culture. After the trial all lambs were treated with gamithromycin. Clinical symptoms of footrot developed in all groups, and when removing the boots two weeks after challenge, D. nodosus was isolated from 5 of 24 experimental lambs. All lambs tested negative for D. nodosus by PCR within six weeks after treatment with gamithromycin. This study strongly indicates that D. nodosus isolates from both sheep and cattle can be transferred to sheep under experimental conditions. The study also indicates that gamithromycin may be effective against D. nodosus.
Expression studies of six human obesity-related genes in seven tissues from divergent pig breeds

Obesity has reached epidemic proportions globally and has become the cause of several major health risks worldwide. Presently, more than 100 loci have been related to obesity and metabolic traits in humans by genome-wide association studies. The complex genetic architecture behind obesity has triggered a need for the development of better animal models than rodents. The pig has emerged as a very promising biomedical model to study human obesity traits. In this study, we have characterized the expression patterns of six obesity-related genes, leptin (LEP), leptin receptor (LEPR), melanocortin 4 receptor (MC4R), fat mass and obesity associated (FTO), neuronal growth regulator 1 (NEGR)1 and adiponectin (ADIPOQ), in seven obesity-relevant tissues (liver; muscle; pancreas; hypothalamus; and retroperitoneal, subcutaneous and mesenteric adipose tissues) in two pig breeds (production pigs and Göttingen minipigs) that deviate phenotypically and genetically from each other with respect to obesity traits. We observe significant differential expression for LEP, LEPR and ADIPOQ in muscle and in all three adipose tissues. Interestingly, in pancreas, LEP expression is only detected in the fat minipigs. FTO shows significant differential expression in all tissues analyzed, and NEGR1 shows significant differential expression in muscle, pancreas, hypothalamus and subcutaneous adipose tissue. The MC4R transcript can be detected only in hypothalamus. In general, the expression profiles of the investigated genes are in accordance with those observed in human studies. Our study shows that both the differences between the investigated breeds and the phenotypic state with respect to obesity/leanness play a large role for differential expression of the obesity-related genes.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, University of Copenhagen, Novo Nordisk A/S
Authors: Cirera, S. (Ekstern), Jensen, M. S. (Ekstern), Elbrønd, V. S. (Ekstern), Moesgaard, S. G. (Ekstern), Christoffersen, B. Ø. (Ekstern), Kadmideen, H. N. (Ekstern), Skovgaard, K. (Intern), Bruun, C. V. (Ekstern), Karlov-Mortensen, P. (Ekstern), Jørgensen, C. B. (Ekstern), Fredholm, M. (Ekstern)
Pages: 59–66
Publication date: 2014
Main Research Area: Technical/natural sciences
Extensive changes in innate immune gene expression in obese Göttingen minipigs do not lead to changes in concentrations of circulating cytokines and acute phase proteins

The usefulness of Göttingen minipigs as models for obesity and obesity-related pathologies is well established. The low-grade inflammation associated with obesity involves a range of innate immune factors; however, to our knowledge, the impact of obesity on innate immune factor expression has not been studied in Göttingen minipigs. Therefore, we studied the expression of innate immune genes in liver and adipose tissues as well as serum concentrations of cytokines and acute phase proteins in obese vs. lean Göttingen minipigs. In the liver, of 35 investigated genes, the expression of nine was significantly different in obese pigs (three up-regulated, six down-regulated). Of 33 genes in adipose tissues, obesity was associated with changed expression of 12 genes in the visceral adipose tissue (VAT) (three up-regulated), 11 in the abdominal retroperitoneal adipose tissue (RPAT) (seven of these up-regulated) and eight in the subcutaneous adipose
tissue (SAT) from the neck (five of which were up-regulated). Obesity-associated expression changes were observed for three genes in all adipose tissues, namely chemokine (C-C motif) ligand 3-like 1 (up-regulated), CD200 molecule (down-regulated) and interleukin 1 receptor antagonist (up-regulated) with interleukin 1 receptor antagonist being the most highly regulated gene in both VAT and RPAT. Looking at patterns of expression across the three types of adipose tissues, obesity was associated with an increased number of acute phase proteins differentially expressed between adipose tissues and a decreased tissue-specific expression of cytokines and chemokines. In contrast to obese humans, no changes in serum concentrations of haptoglobin, C-reactive protein, serum amyloid A, tumor necrosis factor-a and interleukin 6 were found in obese Göttingen minipigs.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Novo Nordisk A/S, University of Copenhagen
Authors: Højbøge, T. R. (Intern), Skovgaard, K. (Intern), Moesgaard, S. G. (Ekstern), Cirera, S. (Ekstern), Christoffersen, B. Ø. (Ekstern), Heegaard, P. M. H. (Intern)
Pages: 67–73
Publication date: 2014
Main Research Area: Technical/natural sciences

Publication information
Journal: Animal Genetics
Volume: 45
Issue number: 1
ISSN (Print): 0268-9146
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): SNIP 0.977 SJR 0.83 CiteScore 1.73
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.64 SJR 0.786 SNIP 0.798
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.931 SNIP 1.012 CiteScore 1.8
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.934 SNIP 1.131 CiteScore 2.12
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.018 SNIP 1.126 CiteScore 2.33
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.009 SNIP 1.104 CiteScore 2.19
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.99 SNIP 1.016 CiteScore 2
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.89 SNIP 0.916
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 0.953 SNIP 1.145
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.761 SNIP 0.725
Scopus rating (2007): SJR 0.658 SNIP 0.673
Scopus rating (2006): SJR 0.495 SNIP 0.706
Scopus rating (2005): SJR 0.638 SNIP 0.766
Scopus rating (2004): SJR 0.715 SNIP 0.809
Scopus rating (2003): SJR 0.581 SNIP 0.795
Faldvild undersøgelser på DTU Veterinærinstituttet i 2013


General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology
Authors: Hansen, M. S. (Intern), Larsen, G. (Intern), Holm, E. (Intern), Jensen, T. K. (Intern), Al-Sabi, M. N. S. (Intern), Chriél, M. (Intern)
Number of pages: 1
Publication date: 2014
Event: Poster session presented at Temadag om Forskningsbaseret forvaltning af fugle og pattedyr, Aarhus, Denmark.
Main Research Area: Technical/natural sciences
Electronic versions:
Source: PublicationPreSubmission
Source-ID: 103299708
Publication: Research - peer-review › Poster – Annual report year: 2014

Fibre måske et alternativ til antibiotika

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology
Authors: Strube, M. L. (Intern)
Pages: 38-40
Publication date: 2014
Main Research Area: Technical/natural sciences

Publication information
Journal: Hyologisk
Issue number: September
ISSN (Print): 0906-0995
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Original language: Danish
Source: PublicationPreSubmission
Source-ID: 105563092
Publication: Research › Journal article – Annual report year: 2015

Projects:
Disease databases
The general purpose of the project is to explore the potential use and value of different data sources as a monitoring tool for detection of diseases in Danish swine herds. The project is a continuation of the PhD project "Veterinary Epidemiology with the focus on monitoring livestock disease using diagnostic databases", in which different databases and monitoring methods were explored in the context of endemic diseases.
As a starting point, the project will be focused on methods to detect changes in mortality and to find possible links among diseases occurrence, antibiotic usage, and other data streams (such as meat inspection and laboratory diagnostic data).

Animal Influenza Viruses - Impacts of influenza virus in Danish swine herds

Financing sources
Source: Internal funding (public)
Name of research programme: Samfinansierede - Virksomhed
Project: PhD

Porcine coronavirus - pathogenesis and control

National Veterinary Institute
Period: 01/09/2016 → 13/06/2020
Number of participants: 4
Phd Student:
Lazov, Christina Marie (Intern)
Supervisor: Belsham, Graham (Intern)
Identification of virulence markers in two Novirhabdoviruses causing serious diseases in fish

National Veterinary Institute
Period: 15/07/2016 → 14/07/2019
Number of participants: 4
Phd Student:
Alencar, Anna Luiza Farias (Intern)
Supervisor:
Bremont, Michel (Ekstern)
Rasmussen, Thomas Bruun (Intern)
Main Supervisor:
Olesen, Niels Jørgen (Intern)

Financing sources
Source: Internal funding (public)
Name of research programme: Institut stipendie (DTU)
Project: PhD

Bovine abortions revisited

Every month, approximately 700 bovine abortions are registered in the national Danish “Kvægdatabasen” but the number is estimated to be significantly higher as abortion-registration is deficient. Our knowledge on the causes of bovine abortion is very limited and prophylactic measures are scarce. Out of more than 100 abortion cases analysed at DTU Vet during 2014, 35% were found to have an infectious cause (bacterial infections and neosporosis). In 44% of submissions, histopathologic lesions in the placenta and/or the foetus were found, that indicate infection however, no infectious agent was detected by routine diagnostic methods. In 22% of the submitted foetuses no specific pathological findings were made.

The aim of this project is to gain in-depth knowledge on the possible bacterial and viral infections of the bovine foetus and placenta by use of state of the art molecular methods for culture-independent identification of bacteria and viruses. Furthermore, placental and foetal infection is to be verified by in situ hybridization of the agents.
On the basis of the project’s results, knowledge will be gained on bacterial and viral infections as causes of bovine abortions in Denmark. For example will the relevance of *Chlamydia* and *Chlamydia*-like bacteria be assessed, since those have lately been shown to play a role in swine production. The results of this study will complement knowledge-based counselling and prophylactic measures on herd-level.

National Veterinary Institute
Section for Bacteriology, Pathology and Parasitology
University of Copenhagen
Period: 01/04/2016 → 31/03/2019
Number of participants: 3
Phd Student:
Wolf-Jäckel, Godelind (Intern)
Supervisor:
Schou, Kirstine Kilgaard (Intern)
Main Supervisor:
Jensen, Tim Kåre (Intern)

**Bovine Abortions Revisited**
National Veterinary Institute
Period: 01/04/2016 → 31/03/2019
Number of participants: 4
Phd Student:
Wolf-Jäckel, Godelind (Intern)
Supervisor:
Agerholm, Jørgen Steen (Ekstern)
Strube, Mikael Lenz (Intern)
Main Supervisor:
Jensen, Tim Kåre (Intern)

**Financing sources**
Source: Internal funding (public)
Name of research programme: Samfinansieret - Andet
Project: PhD

**Sundhed i vækstperioden - årsager til sygdom, diagnostik og forbrug af medicin - delprojekt om coccidiose hos mink**
National Veterinary Institute
Bacteriology & Parasitology
Period: 01/03/2016 → 31/12/2016
Number of participants: 1
Project participant:
Petersen, Heidi Huus (Intern)

**Annual Report on Zoonoses in Denmark**
National Food Institute
Division of Risk Assessment and Nutrition
Division of Food Production Engineering
Section for Diagnostics and Scientific Advice
Division of Toxicology and Risk Assessment
Fødevarestyrelsen
Landbrug og Fødevarer
SEGES Cattle
Investigation of the Added Value of using Differential Cell Count in Addition to Existing Parameters Measured in Milk to Diagnose Intramammary Infection

National Veterinary Institute
Period: 01/01/2016 → 30/11/2017
Number of participants: 5
Phd Student: Zervens, Lisa Marie-Louise (Intern)
Supervisor:
Hisham Beshara Halasa, Tariq (Intern)
Nielsen, Søren Saxmose (Ekstern)
Schwarz, Daniel (Ekstern)
Main Supervisor:
Toft, Nils (Intern)

Financing sources
Source: Internal funding (public)
Name of research programme: Samfinansieret - Andet
Project: PhD

Effective Monitoring and Control of Mastitis

National Veterinary Institute
Section for Epidemiology

FOSS
Period: 01/11/2015 → 01/11/2018
Number of participants: 1
Acronym: EMCoMAST
Number of related Ph.D. students: 1
Project participant:
Kirkeby, Carsten Thure (Intern)

AquaExcel II

National Veterinary Institute
Section for Virology

Period: 01/10/2015 → 01/10/2020
Number of participants: 1
Project participant:
Mikkelsen, Susie Sommer (Intern)

FMDV capsid assembly

National Veterinary Institute
Period: 01/10/2015 → 30/09/2018
Number of participants: 3
Phd Student:
Mass spectrometry imaging (MSI) based investigation on interdependent agent-host responses

National Veterinary Institute
Section for Bacteriology, Pathology and Parasitology
Period: 01/09/2015 → 01/09/2018
Number of participants: 1
Project participant:
Nonnemann, Bettina (Intern)

Investigation og the genetic basis for virus tropism and virulence of classical swine fever virus

National Veterinary Institute
Period: 15/08/2015 → 14/08/2018
Number of participants: 4
Phd Student:
Johnston, Camille Melissa (Intern)
Supervisor:
Belsham, Graham (Intern)
Pedersen, Anders Gorm (Intern)
Main Supervisor:
Rasmussen, Thomas Bruun (Intern)

Investigation of transmission dynamics and virulence of new African Swine Fever Virus strains

Section for Public sector service and commercial diagnostics
National Veterinary Institute
Section for Virology
Section for Epidemiology
Period: 01/08/2015 → 31/07/2018
Number of participants: 4
Phd Student:
Olesen, Ann Sofie (Intern)
Supervisor:
Bøtner, Anette (Intern)
Boklund, Anette (Intern)
Main Supervisor:
Rasmussen, Thomas Bruun (Intern)

Host range selection, virulence determinants and pathogenesis of influenza A viruses: Towards the identification of new antiviral drugs and vaccines
National Veterinary Institute
Period: 01/08/2015 → 31/12/2018
Number of participants: 3
Phd Student:
Andersen, Malene Rask (Intern)
Supervisor:
Kvisgaard, Lise Kirstine (Intern)
Main Supervisor:
Larsen, Lars Erik (Intern)

Financing sources
Source: Internal funding (public)
Name of research programme: Institut stipendie (DTU)
Project: PhD

Investigation of transmission dynamics and virulence of new European African Swine Fever Virus strains
National Veterinary Institute
Period: 01/08/2015 → 31/07/2018
Number of participants: 4
Phd Student:
Olesen, Ann Sofie (Intern)
Supervisor:
Boklund, Anette (Intern)
Bøtner, Anette (Intern)
Main Supervisor:
Rasmussen, Thomas Bruun (Intern)

Financing sources
Source: Internal funding (public)
Name of research programme: Samfinansieret - Andet
Project: PhD

Development of a herd- and cow-specific decision support tool for control of mastitis
National Veterinary Institute
Period: 01/07/2015 → 30/06/2018
Number of participants: 7
Phd Student:
Gussmann, Maya Katrin (Intern)
Supervisor:
Christiansen, Lasse Engbo (Intern)
Toft, Nils (Intern)
Main Supervisor:
Hisham Beshara Halasa, Tariq (Intern)
Examiner:
Boklund, Anette (Intern)
Denwood, Matthew (Ekstern)
Rajaia-Schultz, Päivi (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Samfinansieret - Andet
Project: PhD

Simulation modeling of LA-MRSA dispersal and control between swine herds
National Veterinary Institute
Period: 01/05/2015 → 20/10/2018
Number of participants: 4
Phd Student:
ParaFish Control

National Veterinary Institute

Section for Virology
Period: 01/04/2015 → 01/04/2020
Number of participants: 1
Project participant:
Mikkelsen, Susie Sommer (Intern)

The spread and control of LA-MRSA within Danish pig herds

National Veterinary Institute
Period: 01/04/2015 → 20/06/2018
Number of participants: 8
Phd Student:
Serensen, Anna Irene Vedel (Intern)
Supervisor:
Boklund, Anette (Intern)
Larsen, Jesper (Ekstern)
Toft, Nils (Intern)
Main Supervisor:
Hisham Beshara Halasa, Tariq (Intern)
Examiner:
Kirkeby, Carsten Thure (Intern)
Mortensen, Sten (Ekstern)
Wagenaar, Jaap A. (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Offentlig finansiering
Project: PhD

Relations
Publications:
Spread and control of livestock-associated methicillin-resistant Staphylococcus aureus (LA-MRSA) in Danish pig herds

Novel methods for applied spatio-temporal risk assessment models of endemic and emerging vector borne diseases

National Veterinary Institute
Period: 15/02/2015 → 15/06/2018
Number of participants: 7
Phd Student:
Cuellar, Ana Carolina (Intern)
Supervisor:
Kjær, Lene Jung (Intern)
Toft, Nils (Intern)
Main Supervisor:
Veterinary Epidemiology - biological models of vector borne diseases

National Veterinary Institute
Period: 15/02/2015 → 13/08/2018
Number of participants: 4
PhD Student:
Haider, Najmul (Intern)
Supervisor:
Kjær, Lene Jung (Intern)
Toft, Nils (Intern)
Main Supervisor:
Bødker, Rene (Intern)

Financing sources
Source: Internal funding (public)
Name of research programme: Institut stipendie (DTU)
Project: PhD

Mutated sequences as targets for immune-reactivity against cancer – and their potential use in personalized therapy
PhD project

National Veterinary Institute
Section for Immunology and Vaccinology
Period: 07/01/2015 → 06/01/2018
Number of participants: 2
Project participant:
Ramskov, Sofie (Intern)
Main Supervisor:
Hadrup, Sine Reker (Intern)

Optimeret sygdomsforebyggelse i slægtesvinesæætninger

National Veterinary Institute
Diagnostic & Development
Virology
Innate Immunology
SEGES Pig Research Center
Period: 01/01/2015 → 31/12/2017
Number of participants: 5
Number of related Ph.D. students: 1
Project participant:
Larsen, Lars Erik (Intern)
Hjulsager, Charlotte Kristiane (Intern)
Skovgaard, Kerstin (Intern)
PhD Student:
Goecke, Nicole Bakkegård (Intern)
Project Manager, academic: Jorsal, Sven Erik Lind (Intern)

Financing sources
Source: Private funding (private)
Name of research programme: Svineafgiftsfonden
Amount: 1,776,000.00 Danish Kroner
Year of approval: 2014
Documents: Optimeret sygdomsforebyggelse i slagtesvinebesætninger

Diagnostic methods for veterinary pathogens
National Veterinary Institute
Period: 15/12/2014 → 16/05/2018
Number of participants: 7
Phd Student: Goecke, Nicole Bakkegård (Intern)
Supervisor: Hjulsager, Charlotte Kristiane (Intern)
Skovgaard, Kerstin (Intern)
Main Supervisor: Larsen, Lars Erik (Intern)
Examiner: Bøtner, Anette (Intern)
Salicio, Susanna Cirera (Ekstern)
Simon, Gaëlle (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Samfinansieret - Andet
Project: PhD

Genome sequencing of important animal pathogenic bacteria
National Veterinary Institute
Period: 15/12/2014 → 18/04/2018
Number of participants: 6
Phd Student: Ronco, Troels (Intern)
Supervisor: Aarestrup, Frank Møller (Intern)
Main Supervisor: Pedersen, Karl (Intern)
Examiner: Schou, Kirstine Klitgaard (Intern)
Damborg, Peter Panduro (Ekstern)
Van Immerseel, Filip (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Institut stipendie (DTU)

Relations
Publications: Whole-genome sequencing of veterinary pathogens
Project: PhD

Methicillin resistant Staphylococcus aureus in pig production
Molecular biology of foot-and-mouth disease virus

National Veterinary Institute
Period: 15/12/2014 → 20/06/2018
Number of participants: 6
Phd Student:
Kjær, Jonas (Intern)
Supervisor:
Rasmussen, Thomas Bruun (Intern)
Main Supervisor:
Belsham, Graham (Intern)
Examiner:
Larsen, Lars Erik (Intern)
Bukh, Jens (Ekstern)
Ryan, Martin Denis (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Offentlig finansiering

Relations
Publications:
Conserved elements within the genome of foot-and-mouth disease virus; their influence on viral replication
Project: PhD
**Accelerating development of vaccines against cancer with pigs as a large animal model**

Accelerating development of vaccines against cancer with pigs as a large animal model (CANVACPIG)

This project runs July 1st 2014 and until December 31st 2017. It is budgeted for 5.7 million DKK and is financed by the Danish Council for Independent Research, ID: DFF – 4005-00428.

**Current project participants**
- Professor Gregers Jungersen, DTU National Veterinary Institute
- Postdoc Thomas March Fresig, DTU National Veterinary Institute
- PhD student Nana Haahr Overgaard, DTU National Veterinary Institute
- Master’s thesis student Rikke Selbeck Andersen, DTU National Veterinary Institute
- Postdoc Maria Rathmann Sørensen, DTU National Veterinary Institute
- Professor Søren Buus, University of Copenhagen
- Professor Mads Hald Andersen, Center for Cancer Immune Therapy, Herlev Hospital

**Former project participants**
- Master’s thesis student Zina Al-Shatrawi, DTU National Veterinary Institute
- Master’s thesis student Mette Ilsøe, DTU National Veterinary Institute

The project

Development of vaccines against cancer requires the use of animal models before new vaccines can be used in patients. The mouse is most often used, but there are large differences in the immune system between humans and mice. The immune system of the pig on contrary resembles the human one in several ways, and we aim therefore to accelerate the development of cancer vaccines by using pigs as an animal model for the correct activation of the immune system by vaccination. The goal is to identify the optimal vaccine composition for stimulation of the immune system and the generation of killer cells specifically attacking the cancer cells.

Vaccines, consisting of cancer-related molecules (peptides) and the combination with different immune-activating substances will be tried in healthy pigs. By using luminescent tissue type molecules in the laboratory we can monitor the development of killer cells after the vaccination, specifically recognizing the cell surface of the cancer cells.

National Veterinary Institute

Section for Immunology and Vaccinology

University of Copenhagen

University Hospital Herlev

Period: 01/07/2014 → 31/12/2017

Number of participants: 4

cancer, animal model, immunology, T cells, MHC multimer

Acronym: CANVACPIG

Project ID: 23217

Number of related Ph.D. students: 1

Project participant:
- Fresig, Thomas March (Intern)
- Overgaard, Nana Haahr (Intern)
- Jungersen, Gregers (Intern)
- Sørensen, Maria Rathmann (Intern)

**COST Action ES1403: New and emerging challenges and opportunities in wastewater reuse**

Wastewater reuse is currently considered globally as the most critical element of sustainable water management. Water scarcity, foreseen to aggravate, pushes for maximum utilization of non-conventional water. Although reuse is accompanied by a number of benefits, several potential drawbacks still puzzle scientists. The applied treatments fail to completely remove microcontaminants, antibiotic-resistant bacteria and/or their genes (ARB&Gs). Knowledge on the actual effects of reuse with regard to these aspects is currently not consolidated. This Action will answer critical questions through a European multidisciplinary network, structured in interactive Working Groups (WGs), to achieve: a) identification of the microbiome and mobile antibiotic resistome in treated wastewater, b) assessment of the potential for uptake/transmission of microcontaminants and ARB&Gs in crops, c) determination of effect-based bioassays required for
wastewater reuse, d) identification of efficient/economically viable technologies able to meet the current challenges and, e) development of a relevant risk assessment and policy framework. The Action will establish criteria on technologies/assessment methods for wastewater treatment and suggest new effluent quality criteria to overcome current barriers and safeguard the reuse practice. The Action will have a major impact on the enhancement of sustainable wastewater reuse in light of current challenges at technological, economical and societal level.

National Veterinary Institute

Section for Bacteriology, Pathology and Parasitology

Period: 14/05/2014 – 13/05/2018
Number of participants: 1
Acronym: NEREUS
Project Manager, academic: Aminov, Rustam (Intern)

Financing sources

Source: EU research programme (public)
Name of research programme: COST (European Cooperation in Science and Technology)
Web address: http://www.cost.eu/
Documents: ES1403 MoU

New possibilities for growth and robustness in organic aquaculture (ROBUSTFISH) (39159)

Main aim:
To support the credibility, growth and robustness in the production of healthy and stress resilient Danish organic rainbow trout, considering environmental, ethical as well as economic aspects.

Sub goals:
1) Develop methods for selecting robust fry.
2) Investigating how sustainable non-fish based feed given early in the development affect the robustness of the fry.
3) Include welfare and environmental aspects in relation to water treatment procedures.
4) Improve economic competitiveness of Danish organic aquaculture.

The project is coordinated by DTU Aqua.

This project is funded by Organic RDD 2 Programme, which is coordinated by the International Centre for Research in Organic Food Systems (ICROFS). It has received grants from the Danish Ministry of Food, Agriculture and Fisheries through the Green Growth and Development Programme (GUDP).

National Veterinary Institute

National Institute of Aquatic Resources

Section for Aquaculture

Danish Aquaculture Association

University of Copenhagen

Aalborg University

Period: 01/04/2014 – 31/12/2017
Number of participants: 6
Research areas: Aquaculture & Fisheries Management
Project participant:
Gesto, Manuel (Intern)
Pedersen, Lars-Flemming (Intern)
Skov, Peter Vilhelm (Intern)
Larsen, Erling (Intern)
Lazado, Carlo Cabacang (Intern)
Project Coordinator:
Jokumsen, Alfred (Intern)
A plant-produced immunoenhanced pig vaccine against PRRS

National Veterinary Institute
Section for Immunology and Vaccinology
Section for Virology
Center for Electron Nanoscopy
Aarhus University
Boehringer Ingelheim Vetmedica, Inc.
Period: 01/01/2014 → 31/12/2018
Number of participants: 3
Acronym: Pigvac
Project participant:
Sørensen, Maria Rathmann (Intern)
Larsen, Lars Erik (Intern)
Approving authority:
Jungersen, Gregers (Intern)

Veterinary Epidemiology with focus on monitoring livestock disease using diagnostic databases

National Veterinary Institute
Period: 15/12/2013 → 26/04/2017
Number of participants: 6
Phd Student:
Lopes Antunes, Ana Carolina (Intern)
Supervisor:
Hisham Beshara Halasa, Tariq (Intern)
Main Supervisor:
Toft, Nils (Intern)
 Examiner:
Jensen, Vibeke Frækjaer (Intern)
Mortensen, Sten (Ekstern)
Revie, Crawford W. (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Offentlig finansiering

Relations
Publications:
Monitoring diseases based on register data: Methods and application in the Danish swine production
Project: PhD

Optimizing Infectious Disease Control Though Bayesian Modeling - Exemplified by Mycoplasma bovis in Danish Cattle

National Veterinary Institute
Period: 01/12/2013 → 31/12/2016
Number of participants: 4
Phd Student:
Nielsen, Per Kantsø (Intern)
Supervisor:
Hisham Beshara Halasa, Tariq (Intern)
Nielsen, Liza Rosenbaum (Ekstern)
Main Supervisor:
Toft, Nils (Intern)

Financing sources
Source: Internal funding (public)
Name of research programme: Samfinansieret - Andet
**Veterinary epidemiology with emphasis on the association between spatial proximity, contact structures, antibiotic consumption and antibiotic resistance**

National Veterinary Institute  
**Period:** 01/12/2013 → 20/12/2017  
**Number of participants:** 6  
**PhD Student:** Birkegård, Anna Camilla (Intern)  
**Supervisor:** Hisham Beshara Halasa, Tariq (Intern)  
**Main Supervisor:** Toft, Nils (Intern)  
**Examiner:** Boklund, Anette (Intern)  
**Dewulf, Jeroen (Ekstern)**  
**Nielsen, Søren Saxmose (Ekstern)**  

**Financing sources**  
**Source:** Internal funding (public)  
**Name of research programme:** Samfinansieret - Andet  

**Relations**  
**Publications:**  
Antimicrobial resistance in Danish pigs: A cross sectional study of the association between antimicrobial resistance and geography, exposure to antimicrobials, and trade  
**Project:** PhD  

**Non-invasive screening of embryo culture miRNA for predicting embryo developmental success**

National Veterinary Institute  
**Section for Immunology and Vaccinology**  
**Aarhus University**  
**University of Gothenburg**  
**Period:** 01/11/2013 → 31/10/2016  
**Number of participants:** 5  
**Project participant:** Højbege, Tina Rødgaard (Intern)  
**Heegaard, Peter Mikael Helweg (Intern)**  
**Skovgaard, Kerstin (Intern)**  
**Callesen, Henrik (Ekstern)**  
**Valadi, Hadi (Ekstern)**  

**iCull**  
Herd-specific economic decision tool for farmers.  
**National Veterinary Institute**  
**Section for Epidemiology**  
**Section for Veterinary Epidemiology and public sector consultancy**  
**Department of Applied Mathematics and Computer Science**  
**Dynamical Systems**  
**Period:** 01/11/2013 → 31/10/2015  
**Number of participants:** 6  
**Acronym:** iCull  
**Project ID:** 23176
Molecular characterization of Mycoplasma bovis
National Veterinary Institute
Period: 01/10/2013 → 31/05/2016
Number of participants: 5
Phd Student:
Shukla, Ankit (Intern)
Supervisor:
Lund, Ole (Intern)
Pilo, Paula (Ekstern)
Schou, Kirstine Kiltgaard (Intern)
Main Supervisor:
Lyhs, Ulrike (Intern)

Financing sources
Source: Internal funding (public)
Name of research programme: Eksternt finansieret virksomhed
Project: PhD

Functional analysis of replication determinants in classical swine fever virus
National Veterinary Institute
Period: 01/09/2013 → 05/04/2017
Number of participants: 6
Phd Student:
Hadsbjerg, Johanne (Intern)
Supervisor:
Rasmussen, Thomas Bruun (Intern)
Main Supervisor:
Belsham, Graham (Intern)
Examiner:
Larsen, Lars Erik (Intern)
Becher, Paul (Ekstern)
Knudsen, Charlotte Rohde (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Institut stipendie (DTU)

Relations
Publications:
Functional analysis of replication determinants in classical swine fever virus
Tailored Design of Innovative Vaccine against PRRSV
National Veterinary Institute
Period: 01/09/2013 → 20/12/2017
Number of participants: 7
Phd Student: Welner, Simon (Intern)
Supervisor: Jungersen, Gregers (Intern)
Lund, Ole (Intern)
Main Supervisor: Larsen, Lars Erik (Intern)
Examiner: Rasmussen, Thomas Bruun (Intern)
Graham, Simon Paul (Ekstern)
Lundegaard, Claus (Intern)

Financing sources
Source: Internal funding (public)
Name of research programme: Institut stipendie (DTU)

Relations
Publications:
Design, development and experimental trial of a tailored cytotoxic T-cell vaccine against Porcine Reproductive and Respiratory Syndrome Virus-2
Project: PhD

New dendrimer-based immunomodulators
National Veterinary Institute
Period: 15/08/2013 → 01/12/2016
Number of participants: 6
Phd Student: Mirsharghi, Sahar (Intern)
Supervisor: Heegaard, Peter Mikael Helweg (Intern)
Main Supervisor: Boas, Ulrik (Intern)
Examiner: Almdal, Kristoffer (Intern)
Christensen, Jørn B. (Ekstern)
Malkoch, Michael (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Institut stipendie (DTU)

Relations
Publications:
Design, synthesis and characterization of polylysine dendrones for biomedical applications
Project: PhD

Non-coding RNA mediated gene regulation during influenza infection
National Veterinary Institute
Period: 15/07/2013 → 31/01/2018
Number of participants: 6
Phd Student: Brogaard, Louise (Intern)
Vector-borne threats in northern Europe
Evaluation of future vector-borne threats in northern Europe.

International CoVetLab project, project ID: 23143.
National Veterinary Institute
Section for Epidemiology
Period: 01/01/2013 → 31/10/2013
Number of participants: 1
Vector-borne diseases, Emerging diseases
Project ID: 23143
Project participant:
Kirkeby, Carsten Thure (Intern)

Relations
Activities:
Vector-borne Threats in northern Europe
Press / Media items:
Researcher discovered Siberian midge on Sweden trip
Project

Evaluation of current and future strategies for risk-based early warning and detection of known and unknown vector-borne threats
Club 5 Joint Research 2012

Over the past 5 years, emerging infections caused by vector-borne pathogens have increasingly become a challenge for the EU, with examples such as bluetongue virus, Schmallenberg virus as well as the zoonotic Crimean-Congo Haemorrhagic Fever virus and West Nile virus.

A common experience is that these emerging situations have become apparent first at the stage where they are clinically manifested in livestock and wild fauna, at a fairly late stage after the initial introduction. An improved ability to detect aberrations, such as changes in pathogen or vector levels, indicative of a threat at an earlier stage or detection of emerging pathogens in vectors before clinically manifest in the livestock host, would give more time to assess the situation and to prepare for any necessary interventions or developments.

In the light of an emerging threat, basic epidemiological data on prevalence of the pathogen in hosts and vectors as well as evidence of exposure are usually needed with short notice, together with information on vector densities and frequency of interactions between vector and host populations. However, experiences have shown that surveillance data for the assessment of vector-borne threats is typically scarce or unavailable at the time when they are first needed.

Consequently, there is a substantial need for a generic and systematic approach to surveillance of vector-borne disease, including the harmonisation of underlying risk assessment frameworks as well as relevant indicators across diseases and countries.

The focus of this project is the early detection of emerging vector-borne disease threats, including both previously defined and undefined diseases. The project will review available approaches and how surveillance for vector-borne disease is currently carried out in CoVetLab institute countries and provide recommendations for a future systematic approach to risk-based early warning surveillance and investigations of emerging vector-borne disease, including the identification and prioritisation of joint developmental needs within CoVetLab institutes. There are necessary steps in setting up a more long-
term, sustainable surveillance of vector-borne disease and for a better preparedness for future threats in this area which will facilitate prevention, earlier detection and effective control of these conditions.

National Veterinary Institute
Division of Veterinary Diagnostics and Research
Section for Veterinary Epidemiology and public sector consultancy
National Veterinary Institute Sweden
Animal Health and Veterinary Laboratories Agency
CVI Lelystad
Agence nationale de la sécurité sanitaire, alimentation, environnement et travail
Period: 01/12/2012 → 31/12/2013
Number of participants: 1
Project ID: 22532
Project participant:
Enøe, Claes (Intern)

Swine plasma immunoglobulins against post-weaning diarrhoea
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Innate Immunology
Virology
Section for Immunology and Vaccinology
KiBif ApS
Videncenter for Svineproduktion, Landbrug & Fødevarer
Period: 01/10/2012 → 30/09/2015
Number of participants: 3
Project ID: 22619
Project participant:
Larsen, Lars Erik (Intern)
Hedegaard, Chris Juul (Intern)
Project applicant:
Heegaard, Peter Mikael Helweg (Intern)

Financing sources
Source: Public research council
Name of research programme: GUDP - Projekt. Udviklings- og demonstrationsprojekt med forskningsandel
Amount: 5,017,193.00 Danish Kroner
Year of approval: 2012

Relations
Activities:
10th International Veterinary Immunology Symposium
Mucosal Vaccines, Adjuvants & Delivery
15th International Conference on Production Diseases in Farm Animals
10th Workshop in Protein.DTU
5th European Veterinary Immunology Workshop
2nd international symposium on alternatives to antibiotics (ATA)
11th International Veterinary Immunology Symposium

Anthelmintic resistance in parasitic nematodes of Danish cattle: Detection and control with special focus on Bioactive Plants
National Veterinary Institute  
Period: 01/10/2012 → 29/09/2016  
Number of participants: 7  
Phd Student:  
Pena-Espinoza, Miguel Angel (Intern)  
Supervisor:  
Enemark, Heidi (Intern)  
Thamsborg, Stig Milan (Ekstern)  
Main Supervisor:  
Boas, Ulrik (Intern)  
Examiner:  
Jungersen, Gregers (Intern)  
Hoste, Hervé (Ekstern)  
Morgan, Eric René (Ekstern)  

Financing sources  
Source: Internal funding (public)  
Name of research programme: Institut stipendie (DTU) Samf.

Relations  
Publications:  
Anthelmintic activity of forage chicory (Cichorium intybus) and field efficacy of ivermectin against gastrointestinal nematodes in Danish cattle  
Project: PhD

Bayesian statistical analysis to assess serological testing strategies for avian influenza surveillance in Europe  
Club 5 Joint Research 2012  
National Veterinary Institute  
Division of Veterinary Diagnostics and Research  
Virology  
Animal Health and Veterinary Laboratories Agency  
CVI Lelystad  
National Veterinary Institute Sweden  
Period: 01/10/2012 → 31/10/2013  
Number of participants: 1  
Project ID: 22531  
Project participant:  
Larsen, Lars Erik (Intern)  

Prevention disease caused by Aeromonas salmonicida  
National Veterinary Institute  
Period: 01/08/2012 → 30/06/2016  
Number of participants: 6  
Phd Student:  
Bartkova, Simona (Intern)  
Supervisor:  
Kokotovic, Branko (Intern)  
Main Supervisor:  
Dalsgaard, Inger (Intern)  
Examiner:  
Pedersen, Karl (Intern)  
Bojesen, Anders Miki (Ekstern)  
Colquhoun, Duncan John (Ekstern)  

Financing sources
**Relations**

**Publications:**
Aeromonas salmonicida - Epidemiology, whole genome sequencing, detection and in vivo imaging

**Project:** PhD

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**Prebiotika til hindring af tarmsygdomme hos svin**

National Veterinary Institute
**Period:** 01/07/2012 → 25/11/2015
**Number of participants:** 6

**Phd Student:**
Strube, Mikael Lenz (Intern)

**Supervisor:**
Meyer, Anne S. (Intern)

**Main Supervisor:**
Boye, Mette (Intern)

**Examiner:**
Licht, Tine Rask (Intern)

Hotchkiss, Jr., Arland Tillotson (Ekstern)

Thymann, Thomas (Ekstern)

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**Financing sources**

Source: Internal funding (public)

Name of research programme: Institut stipendie (DTU)

Project: PhD

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**Functional characterization of protective immunity following DNA vaccination against a lethal viral disease in fish**

National Veterinary Institute
**Period:** 01/06/2012 → 31/07/2013
**Number of participants:** 3

**Phd Student:**
Sepulveda Araneda, Dagoberto Andres (Intern)

**Supervisor:**
Olesen, Niels Jørgen (Intern)

**Main Supervisor:**
Lorenzen, Niels (Intern)

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**Financing sources**

Source: Internal funding (public)

Name of research programme: Stipendie fra udlandet

Project: PhD

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**Akvakulturuddannelse**

National Veterinary Institute

Section for Virology

National Institute of Aquatic Resources

Dansk Akvakultur

Danmarks Miljøundersøgelser

University of Copenhagen
**Period:** 01/05/2012 → 10/06/2014
**Number of participants:** 1

**Project participant:**
Boutrup, Torsten Snogdal (Intern)
Molecular Tracing of Viral Pathogens in Aquaculture

National Veterinary Institute
Section for Virology
National Veterinary Institute
Agence nationale de la sécurité sanitaire, alimentation, environnement et travail

IFREMER
IRD

Friedrich Loeffler Institute
Period: 01/04/2012 → 31/03/2015
Number of participants: 1
Acronym: MOLTRAQ
Project participant: Mikkelsen, Susie Sommer (Intern)

Relations
Activities:
MOLTRAQ Workshop
Workshop: Molecular tracing of viral diseases in aquaculture

Coping with Anthelmintic Resistance in ruminants

The objective is to provide sustainable strategies for Coping with Anthelmintic RESistance in ruminants (CARES). We will investigate:
- methods of early and sensitive detection of AR (WP1)
- the use of plants with AH properties as a promising alternative control option (WP2)
- reversion of AR by plant compounds (WP3)
- the combination of bioactive forages with best-use options, e.g. grazing management and TST on-farm (WP4)

Expected results and their exploitation
Our collaboration will yield novel synergies which can dramatically improve the sustainability of parasite control and livestock production, and result in:
- better AR detection for early intervention and decreased spread of AR and consequent economic losses;
- guidelines for use of AH plants in GIN control, including against AR nematodes;
- better/reduced use of existing drugs, reversion of existing AR, and reduced chemical residues in food;
- evidence-based advice for herd management for GIN control and for limiting AR;
- on-farm demonstration of novel, sustainable and economical means of GIN control;
- and international and national dissemination of findings.

The aims of the project, the expected results and their exploitation agree closely with the EMIDA-aims of new tools for detection of AR and effective GIN control by herd management and alternative medication while limiting AR.

The success and the performance of the project relies on several synergetic aspects:
(i) its novelty in the context of sustainable agronomic systems
(ii) the use of complementary approaches ranging from molecular tools and field management practices and
(iii) the recent development of novel cellular and molecular tools that are available in the laboratories involved in the project, to study resistance mechanisms in nematodes. The extensive experience of most partners with field work and on-farm contacts will secure exploitation and successful dissemination to the livestock industry.
Vector-borne infections: risk based and cost effective surveillance systems
EMIDA ERA-Net Application

The overall aim is to develop a fully functional framework for a dynamic risk-based surveillance for VBD according to EMIDAs specific topic A5. The potential risk of outbreaks of VBD and consequently the spread within the population at risk will be continuously estimated. This will permit 1) active surveillance to be focused on specific periods and areas of elevated risk and 2) active surveillance activities to be fitted to the available resources at EU and national level.

The proposed surveillance system will be based on computer models scanning and interpreting risk parameters already collected for other purposes (weather data, environmental data, import data, syndromes) and costs may therefore be very low. Only during time periods and in areas of elevated risk will costly active surveillance activities gradually be suggested based on cost-effectiveness estimates and the desired sensitivity.

This framework for continuous risk based surveillance will be based on three independent pillars: (1) risk of introduction, (2) potential for spread if introduced and (3) syndrome surveillance. The sensitivity of the system will be evaluated with scenario trees. The surveillance system will be built on present knowledge of disease biology and vector ecology. The surveillance system will be modular allowing for easy and continuous updating of the underlying models whenever new or more precise information becomes available.

Using selected VBD we will demonstrate how risk and hence the need for active surveillance can be communicated as dynamic maps of risk displayed on the internet at a weekly resolution. We will also demonstrate the surveillance system on historic data for a 30-year period to determine the average risk and hence cost of surveillance. This will assist decision makers at national and EU level to estimate long-term expenses for surveillance in various regions. Furthermore we will make spatially specific 50-year prognoses based on existing climate change predictions.
**Targeting the genetic complexity within adapting RNA virus populations**

National Veterinary Institute  
Period: 15/12/2011 → 27/05/2015  
Number of participants: 6  
PhD Student: Fahnøe, Ulrik (Intern)  
Supervisor: Pedersen, Anders Gorm (Intern)  
Main Supervisor: Rasmussen, Thomas Bruun (Intern)  
Examiner: Polacek, Charlotte (Intern)  
Ruggli, Nicolas (Ekstern)  
Vignuzzi, Marco (Ekstern)

**Financing sources**  
Source: Internal funding (public)  
Name of research programme: Institut stipendie (DTU) Samf.  
Project: PhD

**Udvikling af mikrofluidic system til aktivering og måling af antigen specifik cellemedieret immun respons**

National Veterinary Institute  
Period: 15/12/2011 → 02/06/2016  
Number of participants: 7  
PhD Student: Hartmann, Sofie Bruun (Intern)  
Supervisor: Emnéus, Jenny (Intern)  
Wolff, Anders (Intern)  
Main Supervisor: Jungersen, Gregers (Intern)  
Examiner: Larsen, Niels Bent (Intern)  
Bailey, Mick (Ekstern)  
Eugen-Olsen, Jesper (Ekstern)

**Financing sources**  
Source: Internal funding (public)  
Name of research programme: Institut stipendie (DTU) Samf.

**Relations**  
Publications:  
A three-dimensional approach to in vitro culture of immune-related cells  
Project: PhD

**Undersøgelse af sammenhænge mellem sundhed, velfærd og antibiotikaforbrug hos danske husdyr**

National Veterinary Institute  
Period: 15/12/2011 → 17/11/2016  
Number of participants: 8  
PhD Student: Fertner, Mette Ely (Intern)  
Supervisor: Boklund, Anette (Intern)  
Christiansen, Lasse Engbo (Intern)
Improved farming technology to optimize production, water quality and disease prevention in model trout farms (FOOP) (38950)
The aim of the project was to identify water quality parameters of significance to production traits and disease resistance in rainbow trout; specifically ammonia nitrogen, nitrite nitrogen, carbon dioxide, oxygen and nitrogen gas.

The project further aimed to pinpoint where in the model trout farm changes in water quality occurs. From these findings the project will attempt various rectifying actions to improve water quality. Finally, a series of experiments in collaboration with DTU Vet will clarify the importance of water quality parameters on disease resistance.

Examination of operational conditions at a number of different model trout farms showed that supersaturation with nitrogen gases was a chronic problem, and that dissolved CO2 levels were generally 2-3 fold higher than equilibrium conditions. Nitrogen supersaturation did however not occur at levels that negatively influenced production parameters (feed intake, feed conversion, and growth), however, CO2 levels were shown in laboratory experiments to negatively influence production at the observed levels. Ammonia and nitrogen levels were all within safe thresholds as verified by growth studies performed in the laboratory.

Fixed bed and moving bed biofilters each have their advantages and shortcomings. Hydraulic conditions in fixed bed biofilters caused a reduction in N turnover efficiency; however under laboratory conditions (optimal hydraulic conditions) fixed bed biofilters outperform moving bed. In site observations shown that fixed bed biofilters are also more resilient to variations in operational conditions, and are better at removing chemical therapeutants, possibly due to a higher load of organic material within the filter.

Biofilter performance was shown to be sensitive to both dissolved oxygen levels and alkalinity, but not at levels relevant for daily operation.

The project was coordinated by DTU Aqua.

This project was funded by the Danish Ministry of Food, Agriculture and Fisheries and the European Fisheries Fund (EFF).

National Veterinary Institute
National Institute of Aquatic Resources
Section for Aquaculture
Dansk Akvakultur

Model trout farms
Period: 01/10/2011 → 01/10/2013
Number of participants: 3
Research area: Aquaculture
Project participant:
Pedersen, Lars-Flemming (Intern)
Pedersen, Per Bovbjerg (Intern)

Project Coordinator:
Skov, Peter Vilhelm (Intern)
Selection of protective antigens in Lawsonia intracellularis by reverse vaccinology

National Veterinary Institute
Section for Immunology and Vaccinology
Period: 01/10/2011 → 31/03/2015
Number of participants: 2
Project participant:
Sørensen, Maria Rathmann (Intern)
Approving authority:
Jungersen, Gregers (Intern)

Antibiotikaresistens hos bakterier i dansk fiskeopdræt

National Veterinary Institute
Division of Veterinary Diagnostics and Research
Bacteriology & Pathology
Period: 01/10/2011 → 31/03/2013
Number of participants: 2
Project participant:
Dalsgaard, Inger (Intern)
Madsen, Lone (Intern)

Forbedret Opdrætsteknologi til Optimering af Produktion, vandkvalitet og sygdomsforebyggelse i modeldambrug

National Veterinary Institute
Section for Virology
National Institute of Aquatic Resources
Section for Aquaculture
Dansk Akvakultur
Period: 01/10/2011 → 01/05/2013
Number of participants: 2
Acronym: FOOP
Project participant:
Boutrup, Torsten Snogdal (Intern)
Project Coordinator:
Skov, Peter Vilhelm (Intern)

Multiple detections of epizootic and zoonotic pathogens in ticks. Development of low density DNA microarrays used as new epidemiologic investigative tools

Club 5 project

A third of tick-borne pathogens (bacteria, parasites, virus) are the causative agents of zoonosis. A better understanding of their epidemiologies, requires multiplex of pathogens in one sample (tick or pool of ticks). To this end, we propose to develop low density DNA microarrays that will be used as new epidemiologic investigative tools. Based on chip technology called BioMarkTM dynamic arrays, we will detect 48 pathogens in 48 samples with few nanoliters of sample. Besides to save money and time, these arrays will permit to perform large scala studies on epidemiology of tick-borne pathogens.

National Veterinary Institute
Division of Veterinary Diagnostics and Research
Section for Veterinary Epidemiology and public sector consultancy
Agence nationale de la sécurité sanitaire, alimentation, environnement et travail

National Veterinary Institute Sweden

CVI Lelystad
Period: 01/10/2011 → 31/03/2013
Number of participants: 1
Club 5 Flåter
Project ID: 11/04545
Project participant:
Bødker, Rene (Intern)
Project

Selection of protective antigens in Lawsonia intracellularis by reverse vaccinology

National Veterinary Institute
Division of Veterinary Diagnostics and Research
Adaptive Immunology & Parasitology
Center for Biological Sequence Analysis
Period: 01/10/2011 → 30/09/2014
Number of participants: 5
Lawsonia
Acronym: Lawsonia antigens
Project ID: 22502
Project participant:
Riber, Ulla (Intern)
Hvass, Henriette Cordes (Intern)
Vadekær, Dorte Fink (Intern)
Lundegaard, Claus (Intern)
Project applicant:
Jungersen, Gregers (Intern)
Project

Quality Assurance Exercises and Networking on the Detection of Highly Infectious Pathogens
EU-Projekt Application for a Joint Action 19. March 2010 - including 30 european partners

National Veterinary Institute
Division of Veterinary Diagnostics and Research
Bacteriology & Pathology
Period: 02/09/2011 → 31/07/2014
Number of participants: 2
QUANDHIP
Acronym: QUANDHIP
Project ID: 22501
Project participant:
Angen, Øystein (Intern)
Project applicant:
Grunow, Roland (Ekstern)
Documents:
Ansøgning_QUANDHIP
Project

Cooperative refining of the BioChip microarray into a routine investigative tool to address emerging viral diseases
Club 5 project

In two previous projects, UK BioChip and EU NoE project Epizone, we have established micro-array principles to detect rare or newly emerging viruses. In the UK BioChip project we established the technology and successfully provided evidence for its feasibility (Gurrala et al., 2009). In the latter, we extended the approach and adopted the technology to in situ synthesis printing for its punctuality, higher density and lower background.
The key aim of the proposes project is to refine the microarray probe coverage for transfer into a regular investigatative tool, particularly addressing avian diseases. The array will also be used to investigate several Diagnosis Not Reached (DNR) cases where multiple infections or emerging/novem viruses are suspected.

National Veterinary Institute
Division of Veterinary Diagnostics and Research
Virology
Animal Health and Veterinary Laboratories Agency
CVI Lelystad
Agence nationale de la sécurité sanitaire, alimentation, environnement et travail
Period: 01/09/2011 → 30/09/2012
Number of participants: 1
Club5 Microarray virus
Project ID: 22523
Project participant:
Larsen, Lars Erik (Intern)

Molecular Characterization of Endometritis in Dairy Cattle
National Veterinary Institute
Period: 01/09/2011 → 26/01/2015
Number of participants: 7
Phd Student:
Knudsen, Lif Rødtness Vesterby (Intern)
Supervisor:
Angen, Øystein (Intern)
Jensen, Tim Kåre (Intern)
Main Supervisor:
Schou, Kirstine Kiltgaard (Intern)
Examiner:
Boye, Mette (Intern)
Bojesen, Anders Miki (Ekstern)
Sheldon, Iain Martin (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Institut stipendie (DTU) Samf.
Project: PhD

Endometritis hos malkekvæg: årsager og behandling
National Veterinary Institute
University of Copenhagen
Period: 01/08/2011 → 31/12/2014
Number of participants: 2
Project ID: 22474
Contact person:
Agerholm, Jørgen S. (Ekstern)
Project Manager, organisational:
Jensen, Tim Kåre (Intern)

Financing sources
Source: Forsk. Private danske - Fonde
Name of research programme: Forsk. Private danske - Fonde
Amount: 445,000.00 Danish Kroner
Project
Minimering af antibiotikaforbrug i akvakultur gennem stikvaccinering af små fisk

National Veterinary Institute
Division of Veterinary Diagnostics and Research
Bacteriology & Pathology

Period: 01/07/2011 → 31/12/2014
Number of participants: 6

STIKVACC
Acronym: STIKVACC
Project ID: 22498
Project participant:
Dalsgaard, Inger (Intern)
Priess, Morten (Ekstern)
Red, Torben (Ekstern)
Clausen, Thomas (Ekstern)
Buchmann, Kurt (Intern)

Project applicant:
Henriksen, Niels Henrik (Intern)

Fiskesygdomskurser - Udvikling af kursustilbud til akvakulturbrugere om fiskesygdomme, med primær fokus på forebygelse og behandling samt reduktion af negative miljøeffekter

National Veterinary Institute
Division of Veterinary Diagnostics and Research
Bacteriology & Pathology
Dansk Akvakultur

University of Copenhagen
Period: 01/07/2011 → 31/12/2012
Number of participants: 1

Fiskesygdomskurser
Project ID: 22513
Project participant:
Dalsgaard, Inger (Intern)

Documents:
Ans_gning_Fiskesygdomskurser_maj_2011_Final.pdf

Assessment of relationship between antibiotic resistance and treatment strategies in swine herds

National Veterinary Institute

Period: 01/06/2011 → 22/09/2015
Number of participants: 4
Phd Student:
Mellerup, Anders (Intern)
Supervisor:
Angen, Øystein (Intern)
Olsen, John Elmerdahl (Ekstern)
Main Supervisor:
Folkesson, Anders (Intern)

Financing sources
Source: Internal funding (public)
Name of research programme: Institut stipendie (DTU) Samf.
Project: PhD

Investigation of inflammatory aspects of diabetes and obesity with special emphasis on the effects of incretins
Control Flavobacteriaceae infections in European fish farms

Project aims:
To improve the control of Fp and Tm infections, data at both the epidemiological and molecular levels are urgently needed. This project aims at filling this scientific gap and immediately investing the acquired knowledge to provide the fish-farming community with new tools for diagnostic and prophylactic methods.

National Veterinary Institute
Division of Veterinary Diagnostics and Research
Bacteriology & Pathology
INRA Institut National de La Recherche Agronomique
Instituto Zooprofilattico Sperimentale delle Venezie
PHARMAQ AS
National Fish Disease Laboratory
Phylogene SA

Præventiv behandling af spædgrisediarre i Danmark

Microbial Ecology
Division of Veterinary Diagnostics and Research
National Veterinary Institute
Arla Foods

Period: 01/04/2011 → 03/12/2014
Number of participants: 7
PhD Student:
Bovbjerg, Kirsten Katrine Lindegaard (Intern)
Supervisor:
Mathiesen, Jesper M. (Ekstern)
Steensberg, Adam (Ekstern)
Main Supervisor:
Heegaard, Peter Mikael Helweg (Intern)
Examiner:
Schøller, Jørgen (Intern)
Knop, Filip Krag (Ekstern)
Spee, Pieter (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: ErhvervsPhD-ordningen VTU
Project: PhD

Control Flavobacteriaceae infections in European fish farms

Project aims:
To improve the control of Fp and Tm infections, data at both the epidemiological and molecular levels are urgently needed. This project aims at filling this scientific gap and immediately investing the acquired knowledge to provide the fish-farming community with new tools for diagnostic and prophylactic methods.

National Veterinary Institute
Division of Veterinary Diagnostics and Research
Bacteriology & Pathology
INRA Institut National de La Recherche Agronomique
Instituto Zooprofilattico Sperimentale delle Venezie
PHARMAQ AS
National Fish Disease Laboratory
Phylogene SA

Præventiv behandling af spædgrisediarre i Danmark

Microbial Ecology
Division of Veterinary Diagnostics and Research
National Veterinary Institute
Arla Foods

Period: 01/03/2011 → 28/02/2014
Number of participants: 1
Acronym: PathoFish
Project ID: 22479
Project participant:
Dalsgaard, Inger (Intern)
Project
Project participant:
Hinrichsen, Torben (Ekstern)
Hvid, Claus (Ekstern)
Project Manager, organisational:
Mølbak, Lars (Intern)

Financing sources
Source: Forskningsprojekter - Fødevareministeriet
Name of research programme: Forskningsprojekter - Fødevareministeriet
Amount: 3,110,000.00 Danish Kroner

Project
Expression of rhabdovirus-induced fish-specific microribonucleic acids in rainbow trout (Oncorhynchus mykiss)
National Veterinary Institute
Period: 01/02/2011 → 26/09/2014
Number of participants: 6
Phd Student:
Bela-Ong, Dennis (Intern)
Supervisor:
Schyth, Brian Dall (Intern)
Main Supervisor:
Lorenzen, Niels (Intern)
Examiner:
Skovgaard, Kerstin (Intern)
Mikkelsen, Jacob Giehm (Ekstern)
Wiegertjes, Geert (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Institut stipendie (DTU) Samf.

Project: PhD

Treponema spp. in porcine skin ulcers, clinical aspects
PhD projekt, Frida Karlsson.
Medvejleder: Tim K. Jensen
National Veterinary Institute
Section for Bacteriology, Pathology and Parasitology
Period: 01/01/2011 → 15/05/2014
Number of participants: 1
Supervisor:
Jensen, Tim Kåre (Intern)
Documents:
F. Karlsson SLU

Biology and control of vector-borne infections in Europe
The EDENext project (Biology and control of vector-borne diseases in Europe) builds on the concepts, methods, tools and results of the FP6 EDEN project (Emerging diseases in a changing European environment). We adopt here the same general approach of understanding and explaining the biological, ecological and epidemiological processes in order to develop a set of state-of-the-art methods and tools to improve prevention, surveillance and control of vector populations, and vector-borne diseases (VBD). The EDEN project has been focusing on the effects of environmental changes on the emergence of VBD.
Here, we want to explain and model the processes leading to the introduction, establishment, and spread of vectors and/or vector-borne diseases, and assess the possible control strategies to break the epidemiological cycles of vector-borne diseases. The project structure follows that of EDEN that was so conspicuously successful, with a set of vertical disease related activities linked by horizontal themes providing integrated technical input to all vertical groups, thereby minimising duplication and ensuring a coordinated approach throughout the project.

National Veterinary Institute
Division of Veterinary Diagnostics and Research

Section for Veterinary Epidemiology and public sector consultancy
Period: 01/01/2011 → 31/12/2015
Number of participants: 1

EDENext
Acronym: EDENext
Project ID: 22484
Project participant:
Bødker, Rene (Intern)

Relations
Publications:
A Unifying Model for the Analysis of Phenotypic, Genetic and Geographic Data
The range of attraction for light traps catching Culicoides biting midges (Diptera: Ceratopogonidae)
Simulating spread of Bluetongue Virus by flying vectors between hosts on pasture

Documents:
Ansøgning_EDENext Biology and control of vector-borne infections in Europe

Control Flavobacteriaceae infections in European fish farms
Project Aims: To improve the control of Fp and Tm infections, data at both the epidemiological and molecular levels are urgently needed. This project aims at filling this scientific gap and immediately investing the acquired knowledge to provide the fish-farming community with new tools for diagnostic and prophylatic methods.

Division of Veterinary Diagnostics and Research
National Veterinary Institute
INRA Institut National de La Recherche Agronomique
Instituto Zooprofilattico Sperimentale delle Venezie
Åbo Akademi University
National Veterinary Institute
PHARMAQ AS
Phylogene SA

National Fish Disease Laboratory
Period: 01/01/2011 → 28/02/2014
Number of participants: 9
Acronym: PathoFish
Project ID: 22479
Project participant:
Nielsen, Hanne Katrine (Ekstern)
Dalsgaard, Inger (Intern)
Skorski, Gilbert (Ekstern)
Whali, Thomas (Ekstern)
Duchaud, Eric (Ekstern)
Nicolas, Pierre (Ekstern)
Amedeo, Manfrin (Ekstern)
Wiklund, Tom (Ekstern)
Brudeseth, Erik (Ekstern)

Financing sources
Source: Forsk. EU - Andre EU-midler
Name of research programme: Forsk. EU - Andre EU-midler
Amount: 3,046,455.00 Danish Kroner

Project
Interaction between gut bacteria and host tissue in a newborn compromised intestine

Microbial Ecology
Division of Veterinary Diagnostics and Research
National Veterinary Institute
University of Copenhagen
University of Memphis
Children's Hospital of Pittsburgh and University of Pittsburgh School of Medicine
Period: 01/01/2011 → 31/12/2013
Number of participants: 5
Project ID: 22475
Contact person:
Boye, Mette (Intern)
Sangild, Per T (Ekstern)
Buddington, Randal Kent (Ekstern)
Hackam, David J (Ekstern)
Project Manager, organisational:
Cilieborg, Malene Skovsted (Intern)

Financing sources
Source: Forskningsrådene - Andre
Name of research programme: Forskningsrådene - Andre
Amount: 3,349,440.00 Danish Kroner

Phagocytosis and macropinocytosis in antigen presenting cells - importance for immune response development
The objective of the project is to establish the role of phagocytosis and micropinocytosis of microorganisms by antigen presenting cells in the immune response against the microorganism. Moreover, the project aims at identifying factors of importance for the initiation of phagocytosis and macropinocytosis, and elucidating cellular regulation pathways of importance for initiation and regulation of the response. Such basis mechanisms may be of importance for our understanding of why some infections lead to a strong and efficient elimination, whereas other may lead to chronic inflammation or tolerance.

National Veterinary Institute
University of Copenhagen
Period: 01/01/2011 → 31/12/2013
Number of participants: 2
Phagocytosis
Project ID: 22477
Contact person:
Boye, Mette (Ekstern)
Project Manager, organisational:
Frøkiær, Hanne (Ekstern)

Financing sources
Source: Forskningsrådene - Andre
Name of research programme: Forskningsrådene - Andre
Amount: 127,191.00 Danish Kroner

Development of a novel subunit vaccine against Mycobacterium avium subspecies paratuberculosis that does not interfere with bovine TB diagnostic
Paratuberculosis is a chronic granulomatous enteritis of ruminants caused by Mycobacterium avium subsp. paratuberculosis (MAP). The disease leads to substantial economic losses and poor animal welfare. The currently available vaccines against paratuberculosis consist of variations of whole bacteria with adjuvants. These vaccines have shown various efficacies in field studies and seem to diminish the clinical symptoms, but they cannot prevent the animals from becoming bacterial shedders. Another major problem of the current vaccines is their interference with surveillance programs and diagnosis of bovine tuberculosis. Animals vaccinated with whole cell paratuberculosis vaccine will produce false-positive test results in screening programs for bovine TB. For these reasons vaccination against paratuberculosis with current vaccines is either not allowed or greatly restricted in many countries. MAP has also been linked to Crohn's disease in humans and enhanced control of paratuberculosis is therefore likely to have a positive impact on consumer
trust in animal products and possibly human health. It is therefore desirable to develop vaccines that prevent spreading of MAP, prevent MAP entering the human food chain and which do not confound diagnostic tests for bovine tuberculosis. One strategy for development of new vaccines is to use different antigens in the vaccines and the diagnostic tests, so called DIVA (Differentiation between Infected and Vaccinated Animals) strategy. We suggest exploiting the DIVA principle to develop a new vaccine for MAP that does not interfere with the current bovine TB surveillance program in place in most countries. Furthermore such a vaccine can potentially be used in combination with control program for paratuberculosis. Rather than use full length proteins we suggest using pools of shorter peptides that are specific for MAP. This is done because we can select a much larger number of sequence differences between the two genomes if we identify short (15-18 aminoacids) peptide rather than full length proteins that are unique to MAP. The aim of this project is thus to develop a novel vaccine against paratuberculosis that does not interfere with diagnostic tests for bovine TB and paratuberculosis. To achieve this we will identify potential peptide vaccine candidates using two completely different complementary approaches; in silico mining and MAP derived specific T-cell clones to screen a MAP expression library. Cocktails of specific peptides will be formulated in liposomes with the aim of obtaining maximal peptide absorption or entrapment inside the liposomes. The vaccine candidates will be tested for immunogenicity in mice followed by vaccination and challenge studies in calves. The effect of the vaccine candidates on bovine TB infection and diagnostic tests for bovine TB and paratuberculosis will be assessed. At the end of the study we aim to have a vaccine candidate that can go on to field evaluation.

Adaptive Immunology & Parasitology
Division of Veterinary Diagnostics and Research
National Veterinary Institute
Agri-Foods and Biosciences Institute
Statens Serum Institut
Period: 01/11/2010 → 31/12/2013
Number of participants: 4
Acronym: ParaTBVaccine
Project ID: 22473
Project Manager, organisational:
Olsen, Ingrid (Ekstern)
Strain, Sam (Ekstern)
Andersen, Peter (Ekstern)
Jungersen, Gregers (Intern)

Financing sources
Source: Forsk. EU - Andre EU-midler
Name of research programme: Forsk. EU - Andre EU-midler
Amount: 2,263,680.00 Danish Kroner

European Surveillance Network for Influenza in Pigs 3
This “European surveillance network for influenza in pigs 3 (ESNIP 3)” is in part a continuation of a surveillance network that was established during a previous EC concerted action (ESNIP 2, SSPE-022749). This second co-ordination action, which ran from 2005 until 2008, sought to achieve a better understanding of the epidemiology of swine influenza in Europe. Ten partners from eight different European countries (Belgium, The Netherlands, Italy, France, Germany, Spain, Bulgaria and UK) were involved including two industrial partners. Seven of these ESNIP 2 partners are members of the current ESNIP 3 consortium. ESNIP 3 will build upon the achievements of ESNIP 1 and 2 which were:
1) The standardisation of protocols for swine influenza (SI) virus (SIV) isolation, serology, antigenic and genetic typing of SIV isolates.
2) The selection and production of reference virus strains and (hyperimmune) sera. These were made available to all participants for preliminary sub typing of SIV isolates.
3) The establishment of a central SIV bank with a collection of recent isolates from various geographical areas in Europe.
4) The establishment of an electronic database with relevant information on the SIV isolates that were obtained in different countries during the life of the network.
5) The antigenic and genetic characterisation of a number of recent H1N1, H3N2 and H1N2 SIV isolates from different European countries.
6) The organisation of a serological survey to obtain preliminary data on the prevalence of different SIV subtypes in various European countries.

National Veterinary Institute
Period: 01/08/2010 → 09/03/2015
Number of participants: 6
Phd Student:
Jonach, Beata Renata (Intern)
Supervisor:
Boyce, Mette (Intern)
Main Supervisor:
Jensen, Tim Kåre (Intern)
Examiner:
Pedersen, Karl (Intern)
Duhamel, Gerald E. (Ekstern)
Thymann, Thomas (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Institut stipendie (DTU) Samf.
Project: PhD

Optimizing the bulk milk tank surveillance in Danish dairy cattle

National Veterinary Institute
Period: 01/07/2010 → 09/03/2015
Number of participants: 7
Phd Student:
Foddai, Alessandro (Intern)
Supervisor:
Hisham Beshara Halasa, Tariq (Intern)
Utenthal, Åse (Intern)
Main Supervisor:
Lind, Peter (Intern)
Examiner:
Larsen, Lars Erik (Intern)
Houe, Hans (Ekstern)
Lindberg, Ann (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Institut, samfinansiering
Project: PhD

Porcine Reproductive and respiratory Syndrome Virus (PRRSV)

National Veterinary Institute
Period: 01/07/2010 → 30/09/2013
Number of participants: 6
Phd Student:
Kvisgaard, Lise Kirstine (Intern)
Supervisor:
Hjulsager, Charlotte Kristiane (Intern)
Main Supervisor:
Larsen, Lars Erik (Intern)
Examiner:
Rasmussen, Thomas Bruun (Intern)
Bækbo, Poul (Ekstern)
Stadejek, Tomasz (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Anden EU-finansiering
Project: PhD

The establishment of the microbiota in piglets
National Veterinary Institute
Period: 01/07/2010 → 01/04/2015
Number of participants: 7
Phd Student:
Hermann-Bank, Marie Louise (Intern)
Supervisor:
Boyé, Mette (Intern)
Mølbak, Lars (Intern)
Main Supervisor:
Skovgaard, Kerstin (Intern)
Examiner:
Schou, Kirstine Klitgaard (Intern)
Jacobson, Magdalena (Ekstern)
Nielsen, Dennis Sandris (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Institut stipendie (DTU) Samf.
Project: PhD

Flavobacterium psychrophilum, forebyggelse og immunforsvar
National Veterinary Institute
Period: 15/06/2010 → 26/02/2014
Number of participants: 8
Phd Student:
Henriksen, Maya Maria Mihályi (Intern)
Supervisor:
Buchmann, Kurt (Ekstern)
Kania, Per (Ekstern)
Lorenzen, Niels (Intern)
Main Supervisor:
Dalsgaard, Inger (Intern)
Examiner:
Olesen, Niels Jørgen (Intern)
Aasted, Bent (Ekstern)
Wiklund, Tom Christer Oskar (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Institut stipendie (DTU) Samf.
Project: PhD
Animale influenza virus
National Veterinary Institute
Period: 01/06/2010 → 05/11/2014
Number of participants: 6
Phd Student:
Fobian, Kristina (Intern)
Supervisor:
Breum, Solvej Østergaard (Intern)
Main Supervisor:
Larsen, Lars Erik (Intern)
Examiner:
Belsham, Graham (Intern)
Bragstad, Karoline (Ekstern)
Harder, Timm Clemens (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Institut stipendie (DTU) Samf.
Project: PhD

Anvendelse af bakteriofagterapi til behandling af fiskesygdomme i akvakultur
Section for Veterinary Diagnostics
Division of Veterinary Diagnostics and Research
National Veterinary Institute
University of Copenhagen
BioMar A/S
Chr. Hansen A/S
Aquasearch farm ApS
Dansk Akvakultur
Period: 01/06/2010 → 31/05/2013
Number of participants: 7
Project ID: 22462
Contact person:
Larsen, Anne Hjørngaard (Ekstern)
Johansen, Eric (Ekstern)
Nielsen, Torben (Ekstern)
Henriksen, Niels Henrik (Ekstern)
Project participant:
Dalsgaard, Inger (Intern)
Madsen, Lone (Intern)
Project Manager, organisational:
Middelboe, Mathias (Ekstern)

Financing sources
Source: Forskningsprojekter - Fødevareministeriet
Name of research programme: Forskningsprojekter - Fødevareministeriet
Amount: 1,442,125.00 Danish Kroner
Project

Hepatitis E virus i svin
National Veterinary Institute
Period: 01/06/2010 → 30/09/2013
Number of participants: 6
Phd Student:
Krog, Jesper Schak (Intern)
Supervisor:
Breum, Solvej Østergaard (Intern)
Schultz, Anna Charlotte (Intern)
Main Supervisor:
Larsen, Lars Erik (Intern)
Examiner:
Ethelberg, Steen (Ekstern)
Poel, Wim H. M. Van der (Ekstern)

**Financing sources**
Source: Internal funding (public)
Name of research programme: Institut stipendie (DTU) Samf.
Project: PhD

**Genetic assessment of antibiotic resistance in animal herds**
National Veterinary Institute
Period: 15/04/2010 → 26/01/2015
Number of participants: 7
Phd Student:
Schmidt, Gunilla Veslemøy (Intern)
Supervisor:
Angen, Øystein (Intern)
Olsen, John Elmerdahl (Ekstern)
Main Supervisor:
Folkesson, Anders (Intern)
Examiner:
Pedersen, Karl (Intern)
Börjesson, Stefan (Ekstern)
Damborg, Peter Panduro (Ekstern)

**Financing sources**
Source: Internal funding (public)
Name of research programme: Programbevilling
Project: PhD

**Udvikling af metoder til at vurdere resistensudvikling i husdyrbesætninger**
Section for Veterinary Diagnostics
Division of Veterinary Diagnostics and Research
National Veterinary Institute
University of Copenhagen
Period: 01/04/2010 → 01/03/2013
Number of participants: 2
Project ID: 22423
Project Manager, organisational:
Angen, Øystein (Intern)
Olsen, John Elmerdahl (Ekstern)

**Financing sources**
Source: Forskningsprojekter - Fødevareministeriet
Name of research programme: Forskningsprojekter - Fødevareministeriet
Amount: 2,311,000.00 Danish Kroner
Project

**Occurrence and fate of Cryptosporidium in Danish, organic pigs and animal waste**
CamVac: Campylobacter vaccination of poultry
The main objective of this project is to develop a cost-effective vaccination strategy for the poultry production, hereby reducing the colonization of Campylobacter in both parental and broiler flocks. Vaccination is one of the few measures that can be applied to reduce the colonization of Campylobacter in free range organic poultry. The project aims to identify a vaccination strategy based on reduction, since risk assessment studies have shown that a 2 log reduction of colonization in poultry can reduce the risk of human infection by 30 times.
CamCon: Campylobacter control - Novel approaches in primary poultry production
Publications:
Campylobacter vaccination of poultry: Clinical trials, quantitative microbiological methods and decision support tools for the control of Campylobacter in poultry
Towards a best practice for Campylobacter prevention at farm and house level
Design and data analysis of experimental trials to test vaccine candidates against zoonotic pathogens in animals: the case of a clinical trial against campylobacter in broilers
Estimation of the variation that can be attributed to different levels in a clinical trial of a vaccine
Direct Quantification of Campylobacter jejuni in Chicken Fecal Samples Using Real-Time PCR: Evaluation of Six Rapid DNA Extraction Methods
Low-cost monitoring of campylobacter in poultry houses by air sampling and quantitative PCR.
The use of probabilistic graphical models (PGMs) to develop a cost-effective vaccination strategy against Campylobacter in poultry
Quantitative microbiological data analysis of a Campylobacter vaccination trial
Integration of Epidemiological Evidence in a Decision Support Model for the Control of Campylobacter in Poultry Production
Intestinal colonization of broiler chickens by Campylobacter spp. in an experimental infection study
Estimation of the variation that can be attributed to different levels in a clinical trial of a vaccine against Campylobacter in broilers

Short range modelling of Culicoides dispersal
National Veterinary Institute
Period: 01/02/2010 → 29/05/2013
Number of participants: 6
Phd Student:
Kirkeby, Carsten Thure (Intern)
Supervisor:
Bødker, Rene (Intern)
Stockmarr, Anders (Intern)
Main Supervisor:
Lind, Peter (Intern)
Examiner:
Ersbøll, Bjarne Kjær (Intern)
Chirico, Jan C. F. (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Institut stipendie (DTU) Samf.
Project: PhD

Identification of the determinants of efficient pestivirus replication
National Veterinary Institute
Period: 01/01/2010 → 18/12/2013
Number of participants: 6
Phd Student:
Risager, Peter Christian (Intern)
Supervisor:
Rasmussen, Thomas Bruun (Intern)
Main Supervisor:
Belsham, Graham (Intern)
Examiner:
Larsen, Lars Erik (Intern)
Becher, Paul (Ekstern)
Lindberg, Michael (Ekstern)
Financing sources
Source: Internal funding (public)
Name of research programme: Institut, samfinansiering
Project: PhD

New tools and approaches to control Porcine Reproductive and Respiratory Syndrome in the EU and Asia

Virology

Division of Veterinary Diagnostics and Research
National Veterinary Institute
Ghent University
Consejo Superior de Investigaciones Cientificas
Centre de Recerca en Sanitat Animal
Parco Technologico Padano
Eidgenossisches Volkswirtschaftsdepartement
Panstwowy Instytut Weterynaryjny
University of Edinburgh
Secretary of State for Environment, Food and Rural Affairs
Stichting Dienst Landbouwkundig Onderzoek
Chinese Academy of Agricultural Sciences
Ministry of Agriculture and Rural Development
Boehringer Ingelheim Vetmedica, Inc.
Period: 01/01/2010 → 31/12/2014
Number of participants: 24
Contact person:
Rodrigo, Rafael (Ekstern)
Sanchez-Serrano, Jose Juan (Ekstern)
Domingo, Mariano (Ekstern)
Taranzi, Luigi (Ekstern)
Piatti, Giancarlo (Ekstern)
Griot, Christian (Ekstern)
Summermatter, Kathrin (Ekstern)
Wijaszka, Tadeusz (Ekstern)
Kotelba, Barbara (Ekstern)
Waddell, Derek (Ekstern)
Campbell, Fiona (Ekstern)
Boriello, Peter (Ekstern)
Thorns, Christopher (Ekstern)
Bianchi, Andre (Ekstern)
vn Zijderveld, Fred (Ekstern)
Tong, Guangzhi (Ekstern)
Lin, Jiaojiau (Ekstern)
Bui, Quang Anh (Ekstern)
Hoang, Van Nam (Ekstern)
Seidler, Randolph (Ekstern)
Papp, Hubert (Ekstern)

Project participant:
Trebbien, Ramona (Intern)

Project Manager, organisational:
Nauwynck, Hans (Ekstern)
Nordic Climate Change Atlas. An atlas of climatic and environmental determinants of present and future veterinary and zoonotic diseases in the Nordic area

Develop a geographical information system (GIS) which includes major geographical, husbandry and biological spatial parameters relevant to the distribution of veterinary and zoonotic diseases, temperature and rainfall from the last 10 years and future temperature and rainfall based on internationally recognised climate scenarios. • Make the GIS available to Nordic researchers or alternatively describe data and provide scripts which will allow users to transform data obtained directly from data owners into the chosen GIS format. This will allow joint Nordic analysis of the impact of climate and environmental change on climate and environment driven disease e.g. vector borne diseases.

Section for Veterinary Epidemiology and public sector consultancy

Division of Veterinary Diagnostics and Research

National Veterinary Institute

Period: 01/01/2010 → 31/12/2010

Number of participants: 1

Project Manager, organisational:

Bødker, Rene (Intern)

Financing sources

Source: Forsk. EU - Rammeprogram
Name of research programme: Forsk. EU - Rammeprogram
Amount: 1,921 Danish Kroner

Ny spædgrisediarre i Danmark. Afklaring af årsagsforhold og diagnostik samt effekt af behandlinger.

Division of Veterinary Diagnostics and Research

Videncenter for Svineproduktion, Landbrug & Fødevarer

Period: 01/01/2010 → 31/12/2013

Number of participants: 7

Project ID: 22438

Project Manager, organisational:

Angen, Øystein (Intern)
Jensen, Tim Kåre (Intern)
Mølbak, Lars (Intern)
Kokotovic, Branko (Intern)
Larsen, Lars Erik (Intern)
Jorsal, Sven Erik Lind (Intern)
Bækbo, Poul (Ekstern)

Financing sources

Source: Forskningsprojekter - Fødevareministeriet
Name of research programme: Forskningsprojekter - Fødevareministeriet
Amount: 3,867,668.00 Danish Kroner

Optimering af sygdomsovervågning i kvægbruget

Section for Veterinary Epidemiology and public sector consultancy

Division of Veterinary Diagnostics and Research
National Veterinary Institute

Dansk Landbrugsrådgivning
Period: 01/01/2010 → 31/12/2012
Number of participants: 2
Project ID: 22463
Contact person:
Rattenborg, Erik (Ekstern)
Project Manager, organisational:
Enøe, Claes (Intern)

Financing sources
Source: Forskningsprojekter - Fødevareministeriet
Name of research programme: Forskningsprojekter - Fødevareministeriet
Amount: 2,974,078.00 Danish Kroner

Project

Reagentless online and real-time sensors for the detection of Cryptosporidium and Giardia parasites in drinking water
Adaptive Immunology & Parasitology
Division of Veterinary Diagnostics and Research
National Veterinary Institute
Grundfos Management A/S
Unisensor A/S
Center for Medicinsk Parasitologi, Klinisk Mikrobiologisk Afdeling
Period: 01/01/2010 → 31/12/2012
Number of participants: 4
Project ID: 22439
Contact person:
Bentien, Anders (Ekstern)
Olesen, Tom (Ekstern)
Kurtzhals, Jørgen (Ekstern)
Enemark, Heidi (Intern)

Financing sources
Source: Forsk. Andre statslige danske i øvrigt
Name of research programme: Forsk. Andre statslige danske i øvrigt
Amount: 1,504,800.00 Danish Kroner

Project

Third generation DIVA vaccines towards classical swine fever virus
National Veterinary Institute
Period: 01/01/2010 → 24/04/2013
Number of participants: 5
Phd Student:
Rangelova, Desislava Yordanova (Intern)
Main Supervisor:
Uttenthal, Åse (Intern)
Examiner:
Jungersen, Gregers (Intern)
Loeffen, Willie (Ekstern)
Schjønning Nielsen, Henriette (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: 1/3 FUU, 1/3 inst 1/3 Andet
Project: PhD
Zoonotiske aspekter af Hepatitis E i Danmark
Virology
Division of Veterinary Diagnostics and Research
National Veterinary Institute
National Food Institute
FoodDTU
Statens Seruminstitute
Period: 01/01/2010 → 31/12/2012
Number of participants: 4
Project ID: 22442
Project participant:
Christensen, Laurids Siig (Intern)
Böttiger, Blenda (Ekstern)
Larsen, Hans Henrik (Ekstern)
Project Manager, organisational:
Larsen, Lars Erik (Intern)

Financing sources
Source: Forskningsprojekter - Fødevareministeriet
Name of research programme: Forskningsprojekter - Fødevareministeriet
Amount: 917,000.00 Danish Kroner

A symbiotic feed for piglets
National Veterinary Institute
Period: 01/12/2009 → 06/02/2013
Number of participants: 7
Phd Student:
Manurung, Sarmauli (Intern)
Supervisor:
Jensen, Bent Borg (Ekstern)
Mølbak, Lars (Intern)
Main Supervisor:
Boye, Mette (Intern)
Examiner:
Licht, Tine Rask (Intern)
Smidt, Hauke (Ekstern)
Thymann, Thomas (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Institut stipendie (DTU) Samf.
Project: PhD

Delivery f small interfering RNAs (soRNAs) for treatment of viral disease in fish aquaculture
National Veterinary Institute
Period: 01/11/2009 → 29/01/2014
Number of participants: 7
Phd Student:
Larashati, Sekar (Intern)
Supervisor:
Rasmussen, Jesper Skou (Intern)
Schyth, Brian Dall (Intern)
Main Supervisor:
Lorenzen, Niels (Intern)
Examiner:
Heegaard, Peter Mikael Helweg (Intern)
Collet, Bertrand (Ekstern)
Pedersen, Finn Skou (Ekstern)

**Financing sources**
Source: Internal funding (public)
Name of research programme: Stipendie fra udlandet
Project: PhD

**Development of a Multi-Stage Vaccine against Paratuberculosis in Cattle**
National Veterinary Institute
Period: 01/11/2009 → 28/02/2013
Number of participants: 6
Phd Student:
Thakur, Aneesh (Intern)
Supervisor:
Aagaard, Claus Sindbjerg (Ekstern)
Main Supervisor:
Jungersen, Gregers (Intern)
Examiner:
Angen, Øystein (Intern)
Koets, Ad (Ekstern)
Lindenstrøm, Thomas (Ekstern)

**Financing sources**
Source: Internal funding (public)
Name of research programme: Forskningsrådsfinansiering
Project: PhD

**T cell reactive tetramers for virus infections in pigs**
National Veterinary Institute
Period: 01/11/2009 → 27/03/2013
Number of participants: 7
Phd Student:
Pedersen, Lasse Eggers (Intern)
Supervisor:
Buus, Søren (Ekstern)
Golde, William T. (Ekstern)
Main Supervisor:
Jungersen, Gregers (Intern)
Examiner:
Heegaard, Peter Mikael Helweg (Intern)
Saalmüller, Armin (Ekstern)
Skov, Søren (Ekstern)

**Financing sources**
Source: Internal funding (public)
Name of research programme: Forskningsrådsfinansiering
Project: PhD

**Inaktivering af virus i gødning på tørre overflader**
Section of Swine fever etc.
Division of Virology
National Veterinary Institute
**A symbiotic feed for post weaned piglets**

National Veterinary Institute

Ministry of Food, Agriculture and Fisheries

Period: 01/08/2009 → 31/12/2012

Number of participants: 1

Project Manager, organisational:

Mølbak, Lars (Intern)

Financing sources

Source: Forskningsprojekter - Fødevareministeriet

Amount: 4,000,000.00 Danish Kroner

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**T Cell Reactive Tetramers for Virus Infections in Pigs**

Virus infections in livestock are constant threats to animal welfare and productivity all over the world. In this project we will deliver new advanced technological reagents for measurement of the cytotoxic cells of the immune system with activity against virus infected cells in pigs. This will be an extremely important tool in the development of new efficacious vaccines against diseases like foot- and mouth disease and influenza. All cells in the body exhibit small fragments of their contents on the cell surface. A virus infected cell will therefore display fragments of virus proteins which, like a key in a lock on the cytotoxic cell, will activate killing of the infected cell. This will stop replication of the virus and this cell-mediated immunity is therefore a crucial part of the host defence against virus infections. The virus-key is made up of host tissue-type molecules displaying a small virus peptide (a chain of 8 to 11 amino acids). We will produce luminescent recombinant virus-keys, MHC class I tetramers, for pigs, which will enable us to directly stain and identify host cell with cytotoxic activity against virus. With these tetramers we can determine exactly which peptides in the virus proteins that mediate the desired immune response, and thereby which virus components that can be used in new targeted vaccines. Furthermore, we will be able to measure if vaccines have induced the desired cytotoxic effector cells, and we can develop computer models to predict peptide antigens of new viruses. The project group consists of scientists from Technical University of Denmark, Copenhagen University and leading American scientists in virus infections and MHC molecules in pigs.

Adaptive Immunology & Parasitology

Division of Veterinary Diagnostics and Research

National Veterinary Institute

Center for Biological Sequence Analysis

Department of Systems Biology

University of Copenhagen

University of Copenhagen

United States Department of Agriculture

Period: 01/07/2009 → 31/12/2012

Number of participants: 5

Project ID: 22380 X-1

Project participant:

Pedersen, Lasse Eggers (Intern)

Nielsen, Morten (Intern)
The Network of Animal Disease Infectiology Research Facility

NADIR aims to facilitate the development of Europe’s high level bio-containment facilities for which there is a strong demand from both the public and private sectors in the field of medical and veterinarian research, which have to respond to upgraded ethical and safety regulations whilst providing reliable answers in term of physiopathology for emerging infectious diseases (diagnosis, transmission conditions, risk analysis, therapeutic targets) or for vaccines and therapeutic trials.

National Veterinary Institute
Section for Virology
Period: 01/05/2009 → 30/04/2013
Number of participants: 1
Acronym: NADIR
Project participant:
Boutrup, Torsten Snogdal (Intern)

Bluetongue distribution and the impact of climate change in the Nordic countries

The project will use climate driven mathematical models to predict the potential spread of bluetongue and other vector borne diseases. The project is supplemented with a detailed analysis of bluetongue which emerged in the Nordic area in 2007. This detailed analysis involves joint Nordic field work. The project: • will identify and rank the vector borne zoonoses and vector borne infections in domestic animals most likely to emerge in the Nordic countries as a result of climate change. • will model the geographical distribution in the Nordic countries for the diseases that are most likely to emerge in the area. These models will be based on internationally recognised climatic scenarios for the coming 20 years (2030). • will facilitate Nordic exchange of entomological bluetongue surveillance data. • will facilitate joint presentations and interpretations of bluetongue surveillance date. • will analyse climatic determinants of bluetongue vector free periods in the Scandinavian region. • model bluetongue transmission in various parts of Scandinavia. • model potential impact on bluetongue of exceptional warm periods in the very near future. • model the risk that biting midges may become established on Iceland. • the project will hold a Nordic workshop to communicate the results, identify important gaps in present knowledge and discuss future Nordic veterinary surveillance and control strategies.

Section for Veterinary Epidemiology and public sector consultancy
Division of Veterinary Diagnostics and Research
National Veterinary Institute
National Veterinary Institute Sweden
Aarhus University
Period: 01/05/2009 → 31/12/2009
Number of participants: 4
Project ID: 22373
Contact person:
Chirico, Jan (Ekstern)
Sviland, Ståle (Ekstern)
Skovgård, Henrik (Ekstern)
Project Manager, organisational:
Bødker, Rene (Intern)

Project
Climate change, globalisation and vector borne diseases in the Nordic countries. The future distribution of vector borne diseases.

1. The project will identify and rank the vector borne zoonoses and vector borne infections in domestic animals most likely to emerge in the Nordic countries as a result of climate change. 2. The project will model the geographical distribution in the Nordic countries for the diseases that are most likely to emerge in the area. These models will be based on internationally recognised climatic scenarios for the coming 20 years (2030). 3. The project will hold a workshop to communicate the results, identify important gaps in present knowledge and discuss future Nordic veterinary surveillance and control strategies.

Section for Veterinary Epidemiology and public sector consultancy
Division of Veterinary Diagnostics and Research
National Veterinary Institute

Fødevarestyrelsen
Period: 01/05/2009 → 31/12/2009
Number of participants: 2
Project ID: 22376
Contact person:
Henriksen, Birgit (Ekstern)
Project Manager, organisational:
Bødker, Rene (Intern)

Financing sources
Source: Forsk. Andre offentlige og private - Nordiske
Name of research programme: Forsk. Andre offentlige og private - Nordiske
Amount: 300,000.00 Danish Kroner

Påvisning af Coxiella burnetii bakterier i komælk vha. PCR-metoden
Division of Veterinary Diagnostics and Research
National Veterinary Institute

University of Copenhagen
Period: 01/05/2009 → 31/01/2010
Number of participants: 4
Project ID: 22369
Project participant:
Christoffersen, Anna-Bodil (Intern)
Agerholm, Jørgen (Ekstern)
Agger, Jens Frederik (Ekstern)
Project Manager, organisational:
Angen, Øystein (Intern)

Financing sources
Source: Forsk. Private danske - Fonde
Name of research programme: Forsk. Private danske - Fonde
Amount: 99,600.00 Danish Kroner

The Network of Animal Disease Infectiology Research Facilities
NADIR is a project funded by the Europe Commission under the 7th framework programme. It gathers the major European experimental animal facilities with capacity to undertake research on zoonoses, emerging diseases and other animal infectious diseases requiring bio-containment at level 3 (L3). Its objective is to realise the potential European leadership in animal disease research.

Division of Virology
National Veterinary Institute
Detection of Campylobacter in manure, soil and water

National Veterinary Institute
Period: 01/04/2009 → 23/05/2012
Number of participants: 5
PhD Student:
Bui, Xuan Thanh (Intern)
Main Supervisor:
Bang, Dang Duong (Intern)
Examiner:
Lind, Peter (Intern)
Alter, Thomas (Ekstern)
Ingmer, Hanne (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: 1/3 DTU-stip, 2/3 FUR/andet
Project: PhD

Development, enhancement and complementation of animal-sparing, foot-an-mouth disease vaccine-based control strategies for free and endemic regions

Foot-and-mouth disease (FMD) is one of the world's most infectious diseases of livestock and continues to pose a significant threat to endemic and free regions alike. The impact of FMD on society and international trade is high, thereby demanding stringent prevention, surveillance and control plans taken up in crisis preparedness plans. On the other hand, there is a global increased demand for animal welfare and ethical considerations necessitating a decreased reliance on eradication of animals to control FMD virus (FMDV) spread, and on the use of animals for the regulatory testing of veterinary products. The project seeks to balance these apparently contracting viewpoints by addressing specific gaps in our knowledge on all aspects of FMD control to enable implementation of enhanced animal-sparing vaccine-based control strategies tailored to the needs of free and endemic settings. Consequently, four main objectives have been identified, including (i) the improvement of the quality of existing FMD vaccines and diagnostics, (ii) the refinement and replacement of in vivo FMD vaccine quality tests, (iii) the development of new generation FMD vaccines and diagnostics by applying cutting edge technologies, (iv) the enhancement of our knowledge on FMDV spread and transmission following the use of high-potency monovalent or multivalent vaccines. The role of wildlife (buffalo, gazelles and wild boar) in FMDV maintenance and transmission will also be investigated. The project consists of seven different, yet interlinked, work packages (WP) each addressing one of the items listed in the Work Programme topic KBBE-2008-1-3-02, and led by renowned WP leaders with years of relevant experience in the field of FMD. As such, significant progress towards the objectives of the Community's Animal Health Strategy (2007-2013), the European Technology Platform for Global Animal Health, and the Global Roadmap for improving the Tools to Control FMD in Endemic Settings will be achieved.
Indian Immunologicals Limited
Lanzhou Veterinary Research Institute
Foundation for Interaction between Enterprises and Education
Agence Française de Sécurité Sanitaire des Aliments
Eidgenössisches Volkswirtschaftsdepartement
Kimron Veterinary Institute
University of Glasgow
Merial S.A.S.
Wageningen University & Research
Period: 01/04/2009 → 30/06/2012
Number of participants: 14
Acronym: FMD-DISCONVAC
Project ID: 22385
Project participant:
Paton, David (Ekstern)
Dekker, Aldo (Ekstern)
Brocchi, Emiliana (Ekstern)
Haas, Bernd (Ekstern)
Srinivasan, Viluppanoor (Ekstern)
Pan, Li (Ekstern)
Filgueira, Mariano Perez (Ekstern)
Zientara, Stephan (Ekstern)
Summerfield, Arthur (Ekstern)
Yadin, Hagai (Ekstern)
Haydon, Daniel (Ekstern)
Enøe, Claes (Intern)
Dubourget, Philippe (Ekstern)
Project Manager, organisational:
De Clercq, Kris (Ekstern)

Financing sources
Source: Forsk. EU - Rammeprogram
Name of research programme: Forsk. EU - Rammeprogram
Amount: 226,625.00 Danish Kroner

Improve tools and strategies for the prevention and control of classical swine fever
7th Framework programme

Research project aiming at the use of chimeric, live DIVA vaccines for practical use in wild boar and domestic pigs.

National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme
Centrum voor Onderzoek in Diergeneeskunde en Agrochemie
Agence Française de Sécurité Sanitaire des Aliments
CAO-DVMP
CVI Lelystad
Fort Dodge
Friedrich Loeffler Institute
Improve tools and strategies for the prevention and control of classical swine fever

Eradication of CSF in domestic pigs has been achieved in several areas within the EU. However, despite intensive efforts on national as well as on international level, the complete eradication of CSF in Europe has proved to be elusive. Additionally, the disease is still endemic in some new EU member states (Romania and Bulgaria) and sporadic outbreaks still occur in free areas. The latter is most likely due to the persistence of the virus in wild boar populations, which acts as a reservoir for the virus. Furthermore, population dynamics in back yard pigs is not fully understood, as this type of pig holdings is new to the European Community and hasn't been fully investigated. As a consequence, there is a strong need for improvement of knowledge and intervention strategies for back yard pigs. Currently a non-vaccination policy exists in the EU. However, due to the problems in wild boar and in domestic pigs in some member states derogations of this non-vaccination policy and some field trials are ongoing. In case of oral vaccinations in wild boar, the live C-strain vaccine is used, since only live vaccines can be used for oral vaccination. The disadvantage of this vaccine is that no differentiation between vaccinated and infected animals can be made. In Romania and Bulgaria some herds are vaccinated with the registered marker vaccine based on a baculovirus produced E2 subunit vaccine. As this use of the E2 marker vaccine is new, some very valuable information on the field use of this vaccine could be made available from these countries. Nevertheless, some experimental studies demonstrated that the licensed E2-subunit marker vaccines are not efficacious enough for use as emergency vaccines in domestic pigs, and in addition can not be used in bait vaccines for oral immunization of wild boar. Controlling CSFV outbreaks in domestic pigs as well as in wild boar and back yard herds would be significantly enhanced, if a safe and efficient live marker vaccine would be available with its accompanying DIVA assays.
Identifikation af virulens markører i marine VHS virus og brug i relation til diagnostik i akvakultur

National Veterinary Institute
Period: 01/02/2009 → 25/10/2012
Number of participants: 5
Phd Student:
Stegmann, Anders (Intern)
Supervisor:
Lorenzen, Niels (Intern)
Main Supervisor:
Einer-Jensen, Katja (Intern)
Examiner:
Evensen, Øystein (Ekstern)
Kurath, Gael (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Institut stipendie (DTU) Samf.
Project: PhD

Smitsom lungebetændelse hos mink

National Veterinary Institute
Period: 01/02/2009 → 06/02/2013
Number of participants: 7
Phd Student:
Salomonsen, Charlotte Mark (Intern)
Supervisor:
Heiby, Niels (Ekstern)
Molin, Søren (Intern)
Main Supervisor:
Boye, Mette (Intern)
Examiner:
Jensen, Tim Kåre (Intern)
Ciofu, Oana (Ekstern)
Segerstad, Carl Hård af (Ekstern)

Financing sources
Source: Internal funding (public)
Name of research programme: Institut stipendie (DTU) Samf.
Project: PhD

Betydning af tidlig kontakt for kalvens velfærd

Virology
Division of Veterinary Diagnostics and Research
National Veterinary Institute
Aarhus University
Period: 01/01/2009 → 31/12/2012
Number of participants: 2
Project ID: 22394
Project participant:
Larsen, Lars Erik (Intern)
Project Manager, organisational:
Jensen, Margit Bak (Ekstern)

Financing sources
Source: Forsk. Private danske - Fonde
Bisphenol A migration into foodstuffs and food simulants

Bisphenol A is a major industrial chemical used in the production of different food contact materials where the main applications are polycarbonate plastics and epoxy-phenolic resins. Polycarbonate is widely used in infant feeding bottles and in some tableware whereas epoxy resins are used as internal lining for food and beverages cans and other articles. Bisphenol A is an estrogenic endocrine-disrupting chemical. The actual specific migration limit is 0.6 mg/kg food based on a temporary TDI of 0.01 mg/kg bw. The aim of this project is to determine the level of bisphenol A migration into selected foods and food simulants to estimate the human exposure to bisphenol A in the Danish population. Development and validation of an analytical method with LC-MS/MS is a part of this project.

National Veterinary Institute
Division of Food Chemistry
National Food Institute
Period: 01/01/2009 → 31/12/2010
Number of participants: 1
Project Manager, organisational:
Pedersen, Gitte Alsing (Intern)

Danish Fish Immunology Research Network

Division of Poultry, Fish and Fur Animals
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Danish Institute for Fisheries and Marine Research
University of Southern Denmark
Aarhus University
Aquasearch farm ApS
Fishlab
Aquatic Diagnostics Ltd.
BioMar A/S
Norwegian School of Veterinary Science
University of Aberdeen
Marine Laboratory
Friedrich Loeffler Institute
Danish Aquaculture Association
Intervet/Schering-Plough Animal Health
Period: 01/01/2009 → 31/12/2013
Number of participants: 31
Acronym: DAFINET
Project ID: 22454
Contact person:
Skjødt, Karsten (Ekstern)
Henryon, Mark (Ekstern)
Nielsen, Torben (Ekstern)
Sørensen, Kirsten E. (Ekstern)
Adams, Alexandra (Ekstern)
Hjermitslev, Niels (Ekstern)
Evensen, Øystein (Ekstern)
Development of a Multi-Stage Vaccine against Paratuberculosis in Cattle

In this project we will identify antigens from different phases of Mycobacterium avium subsp. paratuberculosis (MAP) infection and formulate these into a vaccine with targeted activation of protective cell-mediated immune responses. The employment of antigens from both acute and latent stages of the infection is hypothesized to induce immune responses that are protective against new infections and prevent reactivation of chronic infections. Development of a multi-stage vaccine against paratuberculosis has the potential to significantly increase the health and welfare of infected cattle and reduce the environmental contamination with this potentially zoonotic bacterium.

Adaptive Immunology & Parasitology
Division of Veterinary Diagnostics and Research
National Veterinary Institute
Department of Systems Biology
Statens Serum Institut

Period: 01/01/2009 → 31/12/2012
Number of participants: 6
Project ID: 22340 X-1
Contact person:
Lund, Ole (Intern)

Project participant:
Riber, Ulla (Intern)
Aagaard, Claus (Ekstern)
Agger, Else Marie (Ekstern)

Project Manager, organisational:
Jungersen, Gregers (Intern)
**Financing sources**
Source: Forskningsrådene - Andre
Name of research programme: Forskningsrådene - Andre
Amount: 5,259,583.00 Danish Kroner

**Dyrevelfærd i husdyrbesætninger: Et samspil mellem husdyrbruger og myndigheder**

Section for Veterinary Epidemiology and public sector consultancy
Division of Veterinary Diagnostics and Research
National Veterinary Institute
FoodDTU
Aarhus University

University of Copenhagen
Period: 01/01/2009 → 31/12/2012
Number of participants: 13
Project ID: 22377
Project participant:
Vaarst, Mette (Ekstern)
Nielsen, Tine Rousing (Ekstern)
Bonde, Marianne (Ekstern)
Thomsen, Peter T. (Ekstern)
Ersbøll, Annette Kjær (Ekstern)
Christensen, Tove (Ekstern)
Jensen, Karsten Klint (Ekstern)
Mørkbak, Morten (Ekstern)
Vigre, Håkan (Intern)
Project Manager, organisational:
Sørensen, Jan Tind (Ekstern)
Houe, Hans (Ekstern)
Sandøe, Peter (Ekstern)
Enøe, Claes (Intern)

**Financing sources**
Source: Forskningsprojekter - Fødevareministeriet
Name of research programme: Forskningsprojekter - Fødevareministeriet
Amount: 1,051,000.00 Danish Kroner

**Food Survey of Fruits and Vegetables**
A food survey of fruits and vegetables on the Danish market are being performed in 2009 leading to a detailed sampling plan of fruits and vegetables for analysis of nutrients to the Danish food composition databank.

National Veterinary Institute
Division of Food Chemistry
National Food Institute
Period: 01/01/2009 → 31/12/2010
Number of participants: 2
Project participant:
Knuthsen, Pia (Intern)
Project Manager, organisational:
Saxholt, Erling (Intern)
Indsættelsesstrategi, lungebetændelse eller intensiv fodring som årsag til leverbylder

Virology
Division of Veterinary Diagnostics and Research
National Veterinary Institute
Aarhus University
AgroTech A/S
Period: 01/01/2009 → 12/07/2014
Number of participants: 3
Project ID: 22393
Project participant:
Larsen, Lars Erik (Intern)
Graumann, Anne Mette (Ekstern)
Project Manager, organisational:
Jungersen, Mogens Vestergaard (Intern)

Financing sources
Source: Forsk. Private danske - Fonde
Name of research programme: Forsk. Private danske - Fonde
Amount: 168,000.00 Danish Kroner

Nutrients in milk and dairy products
A food survey of milk and dairy products on the Danish market have been performed in 2004 leading to a detailed sampling plan of mainly Danish produced milk and dairy products. The analytical project have started. 180 samples are being sampled. Most samples are purchased in ordinary consumer stores and have been analysed for nitrogen, fat, fatty acids, dry matter, ash, sugars, starch, dietary fiber, retinol, vitamin D3, 25-OH-D3, tokoferol, thiamin, riboflavin, vitamin B6, folate, niacin, pantothenic acid, biotine, folate, vitamin B12, ascorbic acid, dehydrosacorbic acid, sodium, potassium, calcium, magnesium, iron, copper, zinc, manganese, phosphorus, chloride, nickle, chromium, cadmium, selenium, iodine and cholesterol.

National Veterinary Institute
Division of Food Chemistry
National Food Institute
Period: 01/01/2009 → 31/12/2011
Number of participants: 2
Project participant:
Saxholt, Erling (Intern)
Project Manager, organisational:
Knuthsen, Pia (Intern)

Velfærdsmæssige behov omkring kælvning og umiddelbart efter fødsel hos malkekvæg

Division of Veterinary Diagnostics and Research
National Veterinary Institute
Period: 01/01/2009 → 31/12/2012
Number of participants: 3
Project ID: 22441
Project Manager, organisational:
Larsen, Lars Erik (Intern)
Heegaard, Peter Mikael Helweg (Intern)
Jungersen, Gregers (Intern)

Financing sources
Source: Forskningsprojekter - Fødevareministeriet
Name of research programme: Forskningsprojekter - Fødevareministeriet
**Et symbiotisk foder til fravænningsgrise**

Microbial Ecology  
Division of Veterinary Diagnostics and Research  
National Veterinary Institute  
Aarhus University  
Dansk Svineproduktion  
Arla Foods  
Period: 15/12/2008 → 31/03/2013  
Number of participants: 7  
Project ID: 22365  
Contact person:  
Jensen, Bent Borg (Ekstern)  
Jørgensen, Lisbeth (Ekstern)  
Hvid, Claus (Ekstern)  
Project participant:  
Boye, Mette (Intern)  
Jensen, Tim Kåre (Intern)  
Fernández, José A. (Ekstern)  

**Financing sources**  
Source: Forskningsprojekter - Fødevareministeriet  
Name of research programme: Forskningsprojekter - Fødevareministeriet  
Amount: 2,018,000.00 Danish Kroner  

**Colostrum for gut protection and recovery**  
National Veterinary Institute  
Period: 01/12/2008 → 27/03/2013  
Number of participants: 6  
Phd Student:  
Støy, Ann Cathrine Findal (Intern)  
Supervisor:  
Sangild, Per (Ekstern)  
Main Supervisor:  
Heegaard, Peter Mikael Helweg (Intern)  
Examiner:  
Schou, Kirstine Klitgaard (Intern)  
Frøkiær, Hanne (Intern)  
Weström, Björn Ragnar (Ekstern)  

**Financing sources**  
Source: Internal funding (public)  
Name of research programme: Institut stipendie (DTU) Samf.  
Project: PhD

**Discriminating diagnostics for DIVA vaccines towards classical swine fever : Differentiating infected from Vaccinated Animals**  
Division of Virology  
National Veterinary Institute
University of Copenhagen  
Period: 01/12/2008 → 30/11/2011  
Number of participants: 3  
Project participant:  
Rasmussen, Thomas Bruun (Intern)  
Uttenhal, Åse (Intern)  
Project Manager, organisational:  
von Rosen, Tanya (Intern)  

Financing sources  
Source: Ph.d. Institut finansieret  
Name of research programme: Ph.d. Institut finansieret  
Amount: 0.00 Danish Kroner  

Origins of the metabolic syndrome  
National Veterinary Institute  
Period: 01/12/2008 → 06/02/2013  
Number of participants: 6  
Phd Student:  
Højbøge, Tina Rødgaard (Intern)  
Supervisor:  
Stagsted, Jan (Ekstern)  
Main Supervisor:  
Heegaard, Peter Mikael Helweg (Intern)  
Examiner:  
Jungersen, Gregers (Intern)  
Chavatte-Palmer, Pascale (Ekstern)  
Kristiansen, Karsten (Ekstern)  

Financing sources  
Source: Internal funding (public)  
Name of research programme: Institut stipendie (DTU) Samf.  
Project: PhD  

PCV2 award 2008 fra Boehringer Ingelheim  
Section for Veterinary Diagnostics  
Division of Veterinary Diagnostics and Research  
National Veterinary Institute  
Period: 01/12/2008 → 31/12/2015  
Number of participants: 2  
Project ID: 22335  
Project participant:  
Jensen, Tim Kåre (Intern)  
Project Manager, organisational:  
Larsen, Lars Erik (Intern)  

Financing sources  
Source: Gaver, Udenlandske offentlige og private  
Name of research programme: Gaver, Udenlandske offentlige og private  
Amount: 186,238.00 Danish Kroner  

The Microbiome and Functional foods for cloned lean/obese pigs  
National Veterinary Institute  
Period: 01/12/2008 → 06/02/2013  
Number of participants: 6
Nano Test, networking project
Engineered and designed nanoparticles (NPs) may pose a potential risk to human health and to the environment. The availability of results from relevant and systematic cross-disciplinary research is poor. Physico-chemical characterization and quantification should be incorporated among other parameters. It is mandatory to gain systematic knowledge before we are able to assess risk to humans and to the environment. The main purpose of this networking project is to establish a forum to gain and share such knowledge. The division for Toxicology and Risk Assessment (div. T) has a more than thirty years tradition for toxicological advice and risk assessment based on own interdisciplinary research and is a national and international leader in these areas. The division of Food Chemistry (div. K) has expert knowledge about chemical analyses in biological materials and testing of migration from food contact materials. Recently acquired knowledge includes studies of metal microparticulates and elemental speciation in food and biological matrices. Internally in the National Food Institute, div. T and K have established a thriving network that includes complimenting scientific skills useful in the cross-disciplinary area of nano research. Div. T and K are establishing national and international networks, presently including Danish governmental institutions and universities, and private companies. For the time being a.o. The Danish Food Agency, Danish Environmental Protection Agency, Aalborg University, University of Illinois, Risø National Laboratory, and DHI - Water and Environment are taking part. DFVF also is a member of two national nanotechnology networks: NaNet and iNANO. This thriving network has initiated initiatives for research including physico-chemical characterization and quantification and in vitro testing and has planned in vivo investigations. We can offer collaboration with other institutions in EU countries or elsewhere.

National Food Institute
National Veterinary Institute
UNEP Risoe Centre on Energy, Climate and Sustainable Development (URC)
Rise National Laboratory for Sustainable Energy
Aalborg University
DHI Denmark
Danish Agriculture and Food Agency
Environmental Protection Agency
Period: 01/08/2008 → 30/07/2010
Number of participants: 8
Project participant:
Madsen, Charlotte Bernhard (Intern)
Larsen, Erik Huusfeldt (Intern)
Pedersen, Gitte Alsing (Intern)
Jensen, Gunde Egeskov (Intern)
Sørensen, Ilona Kryspin (Intern)
Petersen, Jens Højslev (Intern)
Binderup, Mona-Lise (Intern)
Project Manager, organisational:
Hadrup, Niels (Intern)
Colostrum for gut protection and recovery

Colostrum, the first milk produced just after birth, has an unexplored therapeutic potential. Via growth-promoting, antimicrobial and immune effects, it may improve gut function in patients with inadequate digestive capacity, unstable microflora and impaired gut immunity. Two serious disorders with these characteristics are necrotizing enterocolitis (NEC) and short bowel syndrome (SBS). Colostrum remains however, poorly investigated beyond the well-known effect on neonatal survival of farm mammals. Development and validation of specific bovine colostral products could play a role in preventive nutrition approaches and in therapy for some vulnerable patient groups. In the project, we use a concerted action that include cell, animal and human investigations, to fully characterise the therapeutic effect of this unique biological fluid. Studies in human NEC and SBS patients will be paralleled by studies in novel pig models of NEC and SBS. Mechanisms underlying the clinical effects in vivo are described using several gut cell lines in vitro. The studies include separate investigations of hyper-immune colostrum with specific immunity against a key group of gut pathogens (Clostridia) and also studies on a colostral immunomodulatory peptide, transforming growth factor -- (TGF--). The project increases the basic understanding of gut diseases, and their relation to diet. It forms the basis for commercial development of an effective and safe clinical treatment of specific diseases based on oral intake of bovine colostrum.

Innate Immunology

Division of Veterinary Diagnostics and Research
National Veterinary Institute
University of Copenhagen
Aarhus University
Odense University Hospital
Period: 01/07/2008 → 31/12/2011
Number of participants: 13
Project ID: 22327
Project participant:
Thymann, Thomas (Ekstern)
Bering, Stine (Ekstern)
Bendixen, Emøke (Ekstern)
Stagsted, Jan (Ekstern)
Boye, Mette (Intern)
Quist, Niels (Ekstern)
Project Manager, organisational:
Sangild, Per T. (Ekstern)
Purup, Stig (Ekstern)
Heegaard, Peter Mikael Helweg (Intern)
Husby, Steffen (Ekstern)
Jeppesen, Palle B (Ekstern)
Hansen, Axel Komerup (Ekstern)
Michaelsen, Kim Fl. (Ekstern)

Financing sources
Source: Forskningsprojekter - Andre ministerier og styrelser
Name of research programme: Forskningsprojekter - Andre ministerier og styrelser
Amount: 1,733,189.00 Danish Kroner
Project

Diagnostik og reduktion af diarresygdomme hos grise

Division of Veterinary Diagnostics and Research
National Veterinary Institute
University of Copenhagen
Dansk Svineproduktion
Period: 01/07/2008 → 30/06/2012
Number of participants: 4
Project ID: 22334
Contact person:
Flavobacterium psychropilum, epidemiologi og virulens faktorer

National Veterinary Institute
Period: 01/06/2008 → 28/02/2013
Number of participants: 3
PhD Student:
Andersen, Julie Hove (Intern)
Supervisor:
Molin, Søren (Intern)
Main Supervisor:
Dalsgaard, Inger (Intern)

Financing sources
Source: Internal funding (public)
Name of research programme: Institut stipendie (DTU) Samf.
Project: PhD

Improved vaccination strategies in marine aquaculture

Section of Fish Diseases
Division of Poultry, Fish and Fur Animals
National Veterinary Institute
National Institute of Aquatic Resources
University of Copenhagen
Danish Aquaculture Association
Aller Aqua A/S
Fishlab
Aquasearch Vet
Schering-Plough A/S
Period: 01/04/2008 → 30/09/2012
Number of participants: 15
Project ID: 22452
Project participant:
Rasmussen, Jesper Skou (Intern)
Lorenzen, Ellen (Intern)
Olesen, Niels Jørgen (Intern)
Buchmann, Kurt (Ekstern)
Madsen, Simon B. (Ekstern)
Melingen, Geir Olav (Ekstern)
Project Manager, organisational:
Lorenzen, Niels (Intern)
Dalsgaard, Inger (Intern)
Pedersen, Karl (Ekstern)
Hansen, Per Juel (Ekstern)
Henriksen, Niels Henrik (Ekstern)
Hørlyck, Viggo (Ekstern)
Sørensen, Kirsten Engell (Ekstern)
Nielsen, Torben (Ekstern)
Nylén, Jørgen (Ekstern)

**Financing sources**
Source: Forskningsprojekter - Andre ministerier og styrelser
Name of research programme: Forskningsprojekter - Andre ministerier og styrelser
Amount: 1,444,780.00 Danish Kroner

**Project**

**Styrkelse af det vidennæssige beredskab overfor svinepest**

Division of Virology
National Veterinary Institute
Period: 01/04/2008 → 31/03/2011
Number of participants: 7
husbandry animal diseases, Classical Swine Fever virus, Diagnostics, Immuno-pathogenesis
Project ID: 22001_2008
Contact person:
Mortensen, Sten (Intern)
Boklund, Anette (Intern)
Project participant:
Lohse, Louise (Intern)
Nielsen, Jens (Intern)
Rasmussen, Thomas Bruun (Intern)
Enøe, Claes (Intern)
Project Manager, organisational:
Uttenthal, Åse (Intern)

**Financing sources**
Source: Forskningsprojekter - Andre ministerier og styrelser
Name of research programme: Forskningsprojekter - Andre ministerier og styrelser
Amount: 3,496,000.00 Danish Kroner

**Project**

**Animal Virology, studies on the development of Carrier animals or airborne spread**

National Veterinary Institute
Period: 01/02/2008 → 21/09/2011
Number of participants: 5
Phd Student:
Stenfeldt, Anna Carolina (Intern)
Main Supervisor:
Belsham, Graham (Intern)
Examiner:
Jungersen, Gregers (Intern)
De Clercq, Kris (Ekstern)
Valarcher, Jean-Francois P. (Ekstern)

**Financing sources**
Source: Internal funding (public)
Name of research programme: Institut, samfinansiering
Project: PhD
Analysis of gene expression in infectious diseases - development of tools for tomorrows therapeutics

The major objective of this project is to provide basis for the development of effective therapies against microbial infections currently affecting human and animal health worldwide. This will be achieved by an analysis of the molecular processes in vivo in both host and pathogen during infection. The porcine lung disease pleuropneumonia caused by Actinobacillus pleuropneumoniae (Ap) is used as a model for bacterial infection in a mammalian host. Based on in vivo infections of pigs by pathogen strains of low and high virulence, the link between bacterial virulence, genotype and gene expression will be determined and a correlation to the host expression “phenotype” and other host factors (e.g. genetic background, immunological status, physiological status) will be established. This will enable development of new tools for control of infectious diseases in mammals. The specific objectives of this project are 1. Characterise two serotypes of Actinobacillus pleuropneumoniae (Ap) by full genome sequencing and annotation. 2. Design and produce full genome microarrays targeting Ap strains of both high and low virulence. 3. Analyse the span of genetic variation between Ap strains of different serotypes by comparative genome hybridisation and sequence analysis of variable regions. 4. Conduct in vitro infections of porcine lung epithelial cells with two serotypes of Ap and study the complex interplay between pig and Ap cells during infection and transcriptional variation between the two serotypes. 5. Conduct in vivo experimental infection of pigs with two serotypes of Ap and study the molecular processes occurring simultaneously in both pig tissues and Ap by microarray expression profiling and real time quantitative PCR. 6. Combine the results and describe the fundamental molecular processes occurring in both host and pathogen during infections and thereby provide a scaffold for the development of effective therapies against microbial infections in mammals.

Microbial Ecology
Division of Veterinary Diagnostics and Research
National Veterinary Institute
Aarhus University
Period: 01/01/2008 → 30/06/2011
Number of participants: 5
Project ID: 22028
Project participant:
Angen, Øystein (Intern)
Hedegaard, Jakob (Ekstern)
Bendixen, Christian (Ekstern)
Panitz, Frank (Ekstern)
Project Manager, organisational:
Boye, Mette (Intern)

Financing sources
Source: Forskningsprojekter - Andre ministerier og styrelser
Name of research programme: Forskningsprojekter - Andre ministerier og styrelser
Amount: 3,076,450.00 Danish Kroner
Project

ASFV diagnostics
Background: After the occurrence of Blue Tongue in Germany, France, Belgium and the Netherlands following a long time of freedom the contingency planning for ASFV must be intensified. In 2007 ASFV has spread in Georgia, Armenia and some Russian counties, therefore it is necessary to maintain the basic research on this disease. We have analysed field sera from Uganda, but without detection of antibodies of ASFV in these herds. At Lindholm we base our diagnostic on a PriProET which has been validated on a variety of strains both based on sequence analysis and on practical testing of virus strains. The intention is to validate the PriProET to be used as the main diagnostic method. Our experience with ASFV allows us to take part in several project applications, the most recent one is an application for DANIDA on smallholder pig production in Mozambique where we have been invited to take over the ASFV part from the laboratory in Ondersteport, South Africa. The isolation of virus on cell cultures is very difficult as not all batches of macrophages are susceptible. The laboratory in Lindholm is one of the few national reference laboratories able to perform this virus isolation; therefore we were chosen to participate in an internal comparison. Experimental plan To perform research to assure the safe diagnostics of ASFV including validation of methods used in case of suspicions. The experience is obtained through the analysis of materials from experimentally infected pigs and participation in the annual ringtrial for ASFV. Real time PCR, virus isolation in cell cultures and methods to detect specific ASFV antibodies (primarily IPT) is used.

Division of Virology
National Veterinary Institute
Period: 01/01/2008 → 31/12/2011
Number of participants: 3
pig, virus, Vector transmission
BVD diagnostics and epidemiology

BVD is an exotic disease in Denmark and the present surveillance do detect occasional relapses of BVDV. In cooperation with the Danish Dairy Board we are optimising the diagnostic tools to have a very high sensitivity and therefore the general uses of BVD PCR for analysis of suspicions have now been incorporated in the Danish BVDV directive. Through the campaign we now have some very good tools for detection of PI animals in infected herds. When there are relapses of BVDV in cattle herds the sample will be analysed in a high throughput system using the new MagnaPure robot, this will be a good model for CSFV high throughput analysis. Bulk milk analysis is based on herd sizes up to 100 lactating cows, we now experience an increase in the herd size and therefore we need to reconsider the use of bulk milk or the sensitivity of this method.

Division of Virology
National Veterinary Institute
Period: 01/01/2008 → 31/12/2011
Number of participants: 3

Financing sources
Source: [Ordinær drift UK 10]
Name of research programme: [Ordinær drift UK 10]
Amount: 500,000.00 Danish Kroner

Chemoselective coupling of bacterial lipopolysaccharides for multiplex flow cytometry

Division of Veterinary Diagnostics and Research
National Veterinary Institute
Period: 01/01/2008 → 30/09/2011
Number of participants: 4

Financing sources
Source: Forskningsprojekter - Andre ministerier og styrelser
Name of research programme: Forskningsprojekter - Andre ministerier og styrelser
Amount: 2,768,380.00 Danish Kroner
Mapping of the immune response in poultry during parasite infections and development of a mucosal recombinant antigen vaccine

Parasite infections in poultry are common in deep-litter systems and in flocks with access to outdoor areas. These infections cause clinical disease, distress and welfare problems to the hens. Furthermore, zoonotic infections might establish better in parasite infected hens. Generally, flocks with access to outdoor areas have a higher mortality (15-25%) compared to caged hens (8-9%). In EU, a ban on hens kept in ordinary cages will take place in 2012 and will lead to more flocks in alternative production systems. Especially infections with Ascaridia galli, Heterakis gallinarum and Capillaria caudinflata are found with flock prevalences up to 100% in non-cage systems. Also new enriched cages will pose a threat via the sand bath etc. Parasite infections may cause reduced growth, increased feed consumption and higher mortality. Mortality might be up to 20-30%. Classic infections such as salmonella, erysipelas, pasteurellosis, E.coli and others are frequent in flocks with free access to outdoor areas. An additive effect is seen with concurrent infections of parasites an bacteria or vira leading to a more severe pathology of the bacterial or viral infections. The infections cause a 20% or more economic loss besides the distress for the hens. The aim of this project is to map the immune response in poultry with common parasitic infections, i.e. A. galli. Subsequently, the project will isolate antigens from A. galli and, on this basis, develop a vaccine against A. galli infections in poultry both for the benefit of the hens and production economy.

Adaptive Immunology & Parasitology
Division of Veterinary Diagnostics and Research
National Veterinary Institute
DHI Denmark
Aarhus University
Bioneer A/S
Period: 01/01/2008 → 31/12/2011
Number of participants: 7
Parasite infections in poultry, ascaridia galli, immune response, mucosal vaccine
Project ID: 22290
Project participant:
Norup, Liselotte R. (Ekstern)
Dal, Lene R. (Ekstern)
Svenstrup, Hanne (Ekstern)
Project Manager, organisational:
Permin, Anders (Ekstern)
Juul-Madsen, Helle R. (Ekstern)
Madsen, Søren (Ekstern)
Jungersen, Gregers (Intern)

Financing sources
Source: Forskningsprojekter - Andre ministerier og styrelser
Name of research programme: Forskningsprojekter - Andre ministerier og styrelser
Amount: 3,510,064.00 Danish Kroner
Microarray for detecting avian influenza (Aiv) suitable for Lab-on-a-Chip applications

National Veterinary Institute
Period: 01/01/2008 → 13/04/2011
Number of participants: 6
Phd Student:
Dhumpa, Raghuram (Intern)
Supervisor:
Wolff, Anders (Intern)
Main Supervisor:
Bang, Dang Duong (Intern)
Examiner:
Emnéus, Jenny (Intern)
Joos, Thomas O. (Ekstern)
Nielsen, Lars Peter (Intern)

Financing sources
Source: Internal funding (public)
Name of research programme: Globaliseringsmidler
Project: PhD

Opbygning af et Dansk veterinært beredskab for Bluetongue
Section for Veterinary Epidemiology and public sector consultancy
Division of Veterinary Diagnostics and Research
National Veterinary Institute
Aarhus University
Roskilde University
University of Copenhagen
Period: 01/01/2008 → 31/07/2011
Number of participants: 4
Project ID: 23331
Project participant:
Jensen, Karl-Martin Vagn (Ekstern)
Nielsen, Søren Achim (Ekstern)
Balstrøm, Thomas (Ekstern)
Project Manager, organisational: Bødker, Rene (Intern)

Financing sources
Source: Forskningsprojekter - Fødevareministeriet
Name of research programme: Forskningsprojekter - Fødevareministeriet
Amount: 678,000.00 Danish Kroner
Project

Opbygning af et Dansk veterinært beredskab for Bluetongue
Section for Veterinary Epidemiology and public sector consultancy
Division of Veterinary Diagnostics and Research
National Veterinary Institute
Aarhus University
Roskilde University
University of Copenhagen
Optimizing the control of foot-and-mouth disease in Denmark by simulation

Section for Veterinary Epidemiology and public sector consultancy

Division of Veterinary Diagnostics and Research

National Veterinary Institute

DTU Data Analysis

Department of Informatics and Mathematical Modeling

University of Copenhagen

University of California at Davis

Danish Veterinary and Food Administration

United States Department of Agriculture

Danish Meat Association

Danish Cattle Federation

Period: 01/01/2008 → 31/12/2011
Number of participants: 12
Project ID: 22314
Contact person:
Christiansen, Lasse Engbo (Intern)
Lund, Mogens (Ekstern)
Willeberg, Preben (Ekstern)
Mortensen, Sten (Ekstern)
Forde-Folle, Kimberly N. (Ekstern)
Boklund, Anette (Ekstern)
Nielsen, Jørgen (Ekstern)
Project participant:
Stockmarr, Anders (Intern)
Hansen, Henning Otte (Ekstern)
Carpenter, Tim (Ekstern)
Miller, Ryan (Ekstern)
Project Manager, organisational:
Enøe, Claes (Intern)

Financing sources
Source: Forskningsprojekter - Fødevareministeriet
Name of research programme: Forskningsprojekter - Fødevareministeriet
Amount: 4,822,468.00 Danish Kroner
Phthalates in plastics and their migration into foodstuffs and food simulants

Phthalates are high volume chemicals used in many technical applications, including certain food contact materials. With a few exceptions, phthalates have today been substituted with other plasticizers in such materials. However, processing equipment used in the food industry, such as plasticized tubing, gaskets and gloves, is a potential source of food contamination. More diffuse sources to contamination are atmospheric deposition of phthalates on crops and their release from vinyl floorings in industry and private homes. The aims of the project are to use newly developed analytical GC-MS-based methods capable of determining selected phthalates reliably, even at low concentrations in plastics, in food simulants and in selected foodstuffs. The methods are currently used in the enforcement of the rather new more restrictive EU regulation (into force from June 2008). Further analysis of selected foodstuffs will possibly take place in 2010 with the purpose of improving current estimates of human exposure to phthalates.

National Veterinary Institute
Division of Food Chemistry

Period: 01/01/2008 → 31/12/2010
Number of participants: 1
Project Manager, organisational:
Petersen, Jens Højslev (Intern)

Source account for Campylobacter infections in Denmark

The aim of this project is to develop the first source account for Campylobacter jejuni infections in Denmark based on results from Multi Locus Sequence Typing (MLST) and antibiotic resistance analyses of various Campylobacter jejuni isolates collected from relevant reservoirs (food, animals and environment) and from patients. Initially, the project will collect C. jejuni isolates from patients, production animals (pigs, cattle, lambs and broilers), Danish produced and imported meat (from broilers, turkeys, ducks and lambs) and environmental reservoirs. The isolates will primarily be collected through national surveillance programmes, but additional isolates from sources not included in the surveillance will also be sampled. Approximately 1,500 C. jejuni isolates will be collected in 2007-2008. The isolates will be sub-typed using MLST and analysed for resistance to selected antibiotics. The obtained data will, together with existing knowledge about occurrence, be used to develop a mathematical model describing the attribution of different sources to human infection with C. jejuni. For this purpose we will look into the existing source account models developed for food-borne bacterial pathogens. The approach will be to compare different subtypes from animal reservoirs, raw meat (domestic produced and imported) and humans, to determine the importance of different sources on human infections.

Division of Microbiology and Risk Assessment
Division of Poultry, Fish and Fur Animals
National Food Institute
National Veterinary Institute
Statens Serum Institut

Period: 01/01/2008 → 30/11/2010
Number of participants: 1
Acronym: CAMSA
Project Manager, organisational:
Nielsen, Eva Møller (Ekstern)

Bovin coccidiose - validering af undersøgelse for oocystudskillelse under praksisforhold

Adaptive Immunology & Parasitology
Division of Veterinary Diagnostics and Research
National Veterinary Institute

Period: 31/12/2007 → 31/12/2011
Number of participants: 1
Project ID: 22020
Project Manager, organisational:
Enemark, Heidi (Intern)
Targeted Design of DIVA Vaccines Using Reverse Genetics

This project involves research to provide the tools needed for the establishment of genetically modified pestiviruses engineered specifically for the requirements of the Differentiate Infected from Vaccinated Animals (DIVA) principle. New innovative strategies are needed to facilitate construction of stable infectious pestivirus clones in order to obtain genetically modified pestiviruses from a wider range of pestiviral strains. The novel full-genome amplification strategy for pestiviruses, that our group has developed recently opens new ways for targeted design of chimeric pestiviruses specifically tailored for use as DIVA vaccines against classical swine fever (CSF). In this project, this novel generic strategy for amplification of pestiviruses will be combined with the innovative BAC (bacterial artificial chromosome) technology. This allows construction of stable infectious clones of large RNA viruses and facilitates specific genetic manipulation hence a new set of molecular tools can be established, which will give increased flexibility in design of new modified pestiviruses for the future generation of DIVA vaccines. Using this strategy, for targeted design of genetically modified pestiviruses, the work can be expedited and focused in principal on any pestiviral strain and hence is not limited to the availability of an existing infectious clone. The long RT-PCR strategy will significantly simplify and streamline the workflow and pave the way for in vitro characterisation and in vivo testing of new and improved DIVA vaccine candidates.

Sektion for Eksotiske Virusygdemme

Division of Virology

National Veterinary Institute

Period: 01/12/2007 → 01/12/2010
Number of participants: 6
Project ID: 22107
Contact person:
Beer, Martin (Ekstern)
Reimann, Ilona (Ekstern)
Depner, Klaus (Ekstern)
Project participant:
Uttenthal, Åse (Intern)
Nielsen, Jens (Intern)

Project Manager, organisational:
Rasmussen, Thomas Bruun (Intern)

Financing sources
Source: Forskningsrådene - Andre
Name of research programme: Forskningsrådene - Andre
Amount: 2,200,000.00 Danish Kroner
Project

Nye produkter til passiv immunisering af spæd- og småkalve

Adaptive Immunology & Parasitology

Division of Veterinary Diagnostics and Research

National Veterinary Institute

Multimerics ApS

Period: 01/10/2007 → 30/06/2011
Number of participants: 2
Project ID: 22326
Contact person:
Bisgaard-Frantzen, Kirsten (Ekstern)
Project Manager, organisational:
Heegaard, Peter Mikael Helweg (Intern)

Financing sources
Source: Forskningsprojekter - Fødevareministeriet
Name of research programme: Forskningsprojekter - Fødevareministeriet
CSFV diagnostics and pathogenesis

Background (shortly). This project is a central project in the coordination of several CSFV projects, it is conducted in close collaboration with the project “Early immunopathogenesis of classical swine fever infections” and the materials obtained from the experimental infections are shared among these two projects. We have data from several experimental infections which are in the process of publication. The project provides co-funding for external projects and furthermore a considerable amount of hours has been used for writing applications for different purposes. In 2007 an FTP post doc position for Thomas Bruun Rasmussen on chimeric vaccines towards CSFV was funded. Another application written in cooperation with “Early Immuno-pathogenesis..” on “Styrkelse af det videnmassige beredskab for klassisk svinepest” was funded. Both these projects are active in 2008 and therefore the budget of the present project is reduced accordingly and some of the milestones intended for this project may be fulfilled in other projects.

Purpose and relevance

Classical swine fever is a devastating disease, which will ruin the Danish pig production if the disease spread in Denmark. The fast, sensitive and specific diagnosis of this disease is crucial for the ability to assure that CSFV will not be introduced through imported animals and in case the unhappy event should happen the laboratory procedures must be implemented, validated and able to be scaled up to thousands of samples. By performing experimental infections we gain experience in the clinical signs of CSFV, we teach the practitioners employed by the veterinary authorities in the diagnosis, sample submission and the easy understanding of the laboratory procedures during a suspicion. The work is aiming at improved ability to detect CSFV and we collaborate with the EU and OIE authorities to improve the directives in a way that is optimal for the typical Danish situation. As an example the use of vaccination has now become an option in EU, generally Denmark has a strict non-vaccination policy but as vaccination may end up as a requirement, not an option we now focus on DIVA vaccines which will allow the animals to be used for consumption even though they are vaccinated. Our aim is to assure that the safety and efficacy aspects of these vaccines will reach a level that 3rd world countries may accept to import animal products from vaccinated pigs.

Division of Virology

National Veterinary Institute
Period: 01/01/2007 → 31/12/2012
Number of participants: 6

classical swine fever, DIVA diagnostics, Pig, Real-time PCR, Pestivirus, virus
Project ID: 22125_150559
Project participant:
Rasmussen, Thomas Bruun (Intern)
Nielsen, Jens (Intern)
von Rosen, Tanya (Intern)
Lohse, Louise (Intern)
Gaoming, Lou (Intern)

Project Manager, organisational:
Utenthal, Åse (Intern)

Financing sources
Source: [Ordinær drift UK 10]
Name of research programme: [Ordinær drift UK 10]
Amount: 1,500,000.00 Danish Kroner

Early Immunopathogenesis of classical swine fever infections

Division of Virology

National Veterinary Institute
Period: 01/01/2007 → 31/12/2009
Number of participants: 4

Project participant:
Lohse, Louise (Intern)
Utenthal, Åse (Intern)
Rasmussen, Thomas Bruun (Intern)

Project Manager, organisational:
Nielsen, Jens (Intern)

Financing sources
Source: [Ordinær drift UK 10]
Nutriomics - functional foods for cloned, lean/obese pigs

Division of Veterinary Diagnostics and Research
National Veterinary Institute
Aarhus University
Chr. Hansen A/S
Period: 01/01/2007 → 31/03/2011
Number of participants: 13
Project participant:
Hedegaard, J. (Ekstern)
Bendixen, E. (Ekstern)
Knudsen, K. E. B. (Ekstern)
Bendixen, Christian (Ekstern)
Berg, Peer (Ekstern)
Vajta, Gabor (Ekstern)
Purup, Stig (Ekstern)
Bertram, Hanne (Ekstern)
Skovgaard, Kerstin (Intern)
Flambard, Benedicte (Ekstern)
Project Manager, organisational:
Stagsted, Jan (Ekstern)
Boye, Mette (Intern)
Heegaard, Peter Mikael Helweg (Intern)

Financing sources
Source: Forskningsprojekter - Andre ministerier og styrelser
Name of research programme: Forskningsprojekter - Andre ministerier og styrelser
Amount: 960,000.00 Danish Kroner
Project

Risk-based detection of cattle herds contaminated with Salmonella Dublin
Salmonella Dublin infections in cattle herds cause profit loss and despite a lowering in the number of contaminated herds in recent years, the numbers are still high in some regions. Therefore, Danish Dairy Board and Danish Veterinary and Food Administration together with research institutions have initiated an intervention campaign aiming to eradicate S. Dublin in cattle before 2014. To achieve this goal it is necessary to develop new methods for more efficient surveillance of S. Dublin spreading in and between herds in order to control the contamination. Then, info about trade patterns, specific risk factors associated with herds etc. will be used to build up a risk-based detection scheme. In addition, possible improvement of diagnostic tools will be assessed for better detection of contaminated herds.

Division of Microbiology and Risk Assessment
National Food Institute
National Veterinary Institute
University of Copenhagen
Aarhus University
Animal Health Service
Danish Veterinary and Food Administration
Danish Dairy Board
Period: 01/01/2007 → 31/12/2011
Number of participants: 1
Project participant:
Baggesen, Dorte Lau (Intern)

Relations

Publications:
Use of real-time PCR on faecal samples for detection of sub-clinical Salmonella infection in cattle did not improve the detection sensitivity compared to conventional bacteriology

Project

Strategies to improve health and welfare in rainbow trout farming (38193)
The main aim of the project is the developing of sustainable strategies for improving the health, welfare and quality of cultured rainbow trout by implementing three interrelated approaches: management, immune prophylactics, and selective breeding. The management approach determines how increased water current at given rearing densities and water temperatures can reduce the stress of trout. The immune prophylactic approach determines the relationship between immune response profiles and induction of protective immunity at different water temperatures and hereby establishing efficient strategies for use of vaccination and feed stimulants in prevention of diseases. The selective breeding approach determines how physiological and immunological traits can improve the genetically basis for resistance of trout to stress and disease.

The project is coordinated by DTU Aqua.
National Veterinary Institute
National Institute of Aquatic Resources
Section for Aquaculture
University of Copenhagen
Aarhus University
Period: 01/01/2007 → 31/12/2010
Number of participants: 5
Research area: Aquaculture
Project participant:
Höglund, Erik (Intern)
Larsen, Bodil Katrine (Intern)
Skov, Peter Vilhelm (Intern)
McKenzie, David D. (Ekstern)

Project Manager, organisational:
Jokumsen, Alfred (Intern)

Communication between the microbiota and host during intestinal disease in neonatal pigs.
The aim of this project is to understand the first bacterial colonization of the gastrointestinal tract and to identify specific bacterial species that positively or negatively influence infections in neonates.

National Veterinary Institute
Period: 01/07/2006 → 30/06/2009
Number of participants: 1
Project Manager, organisational:
Mølbak, Lars (Intern)

Financing sources
Source: Udenfor rammen
Name of research programme: Ukendt
Amount: 2,300,000.00 Danish Kroner

Development of improved tools for detection of paratuberculosis in livestock, M. paratuberculosis in food and for the assessment of the risk of human exposure : WP6: The optimisation of blood based tests for the early diagnosis of Johnes disease in cattle and goats
The main objective for the current WP (WP6) in ParaTBTools will be to optimise the antigen specific interferon-gamma whole blood test for paratuberculosis infection by potentiating it with cytokines (e.g. IL-12/IL-18) and assessing it on naturally infected cattle and experimentally infected cattle and goats.
Adaptive Immunology & Parasitology

Division of Veterinary Diagnostics and Research

National Veterinary Institute
Period: 01/06/2006 → 31/05/2010
Number of participants: 1
Acronym: ParaTBTools
Project ID: 22070 X-1
Project Manager, organisational:
Jungersen, Gregers (Intern)

Financing sources
Source: Forsk. EU - Rammeprogram
Name of research programme: Forsk. EU - Rammeprogram
Amount: 2,424,207.00 Danish Kroner

EPIZONE WP 4.1 : PCR diagnostics
PCR diagnostics is an important part of routine diagnostics as well as for research purposes

Virology

Division of Veterinary Diagnostics and Research

National Veterinary Institute
Period: 01/06/2006 → 01/06/2011
Number of participants: 2
classical swine fever, PCR, pig, diagnostics
Project ID: 22081_130597
Project participant:
Rasmussen, Thomas Bruun (Intern)
Uttenthal, Åse (Intern)

Financing sources
Source: Forsk. EU - Rammeprogram
Name of research programme: Forsk. EU - Rammeprogram
Amount: 200,000.00 Danish Kroner

EPIZONE WP 4.3 : DIVA diagnostics
For husbandry animals the ability to Differentiate Infected from Vaccinated Animals (DIVA) has a high priority as it allows for prophylactic vaccination to be applied. This workpackage focus on the different diagnostic methods that could be used on classical swine fever, Foot and mouth disease, Avian Influenza, Blue tongue and other animal diseases.

Division of Virology

National Veterinary Institute
Period: 01/06/2006 → 01/06/2011
Number of participants: 3
Differentiating infected from vaccinated animals (DIVA), diagnostics, vaccine
Project ID: 22081_130597
Project participant:
von Rosen, Tanya (Intern)
Rasmussen, Thomas Bruun (Intern)
Project Manager, organisational:
Uttenthal, Åse (Intern)

Financing sources
Source: Program. Andre statslige danske - Andre prog.midler
Name of research programme: Program. Andre statslige danske - Andre prog.midler
Amount: 1,000,000.00 Danish Kroner
EPIZONE WP 5.1 : Vaccine technologies

Division of Virology
National Veterinary Institute
Period: 01/06/2006 → 01/06/2011
Number of participants: 1
classical swine fever, Vaccine, DIVA vaccine, pestivirus
Project ID: 220323_130598
Project participant:
Utenthal, Åse (Intern)

Financing sources
Source: Forsk. EU - Rammeprogram
Name of research programme: Forsk. EU - Rammeprogram
Amount: 70,000.00 Danish Kroner

EPIZONE WP 7.3 : Clinical Support systems for Classical swine fever
To analyse the clinical scoring system which is the base for the clinical suspicion for classical swine fever (CSFV). Using computer based comparison and weighed data sampling for both CSFV as other febrile diseases an international disease detection system is produced. The server based system is running in Wageningen University, The Netherlands.

Sektion for Eksotiske Virussygdomme

Division of Virology
National Veterinary Institute
Period: 01/06/2006 → 01/06/2011
Number of participants: 3
classical swine fever, clinical support system, diagnosis
Acronym: CSS-CSFV
Project ID: 22088_130607
Project participant:
Nielsen, Jens (Intern)
Lohse, Louise (Intern)
Project Manager, organisational: 
Utenthal, Åse (Intern)

Financing sources
Source: Forsk. EU - Rammeprogram
Name of research programme: Forsk. EU - Rammeprogram
Amount: 300,000.00 Danish Kroner

Quality and Integrity of Organic Eggs, Chicken Meat and Pork (QEMP)
Organic piglets are born outdoor and stays with the sow longer than in conventional pig production, expected to provide better animal welfare. Nevertheless, organic pigs may still be challenged with weaning diarrhoea and exposure to parasites and pathogens. Our focus is how alternative feed types rich in fructan affect the intestinal microflora composition in weaning and slaughter pigs. In particular, if fructan-rich feed (prebiotic) promote growth of beneficial bacteria and possibly reduce the campylobacter excretion level. The later has implications for the food safety of pork. The overall objective of the collaborative project are to make a proposal for new and better production strategies for organic pork, chicken meat and eggs. These strategies should comply with the organic idea of integrated production and ensure organic products of high quality.

Division of Veterinary Diagnostics and Research
National Veterinary Institute
National Food Institute
Division of Food Microbiology
University of Copenhagen
Danish Meat Research Institute
Aarhus University  
**Period:** 01/03/2006 → 31/07/2010  
**Number of participants:** 3  
**Project participant:**  
Baggesen, Dorte Lau (Intern)  
Jensen, Annette Nygaard (Intern)  
**Project Manager, organisational:**  
Kongsted, Anne Grete (Ekstern)  

**Relations**  
**Activities:**  
21st International ICFMH Symposium  
Effects of feeding prebiotic to pigs for just or 2 weeks before slaughter  
**Project**

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**Genus Brachyspira in birds**  
National Veterinary Institute  
**Section for Bacteriology, Pathology and Parasitology**  
**Period:** 01/01/2006 → 13/03/2009  
**Number of participants:** 1  
**Examiner:**  
Jensen, Tim Kåre (Intern)  
**Documents:**  
Jansson SLU  
**Project**

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**Fiber and flora to the compromised newborn : - Early dietary prevention of later disease in infants and piglets**  
Division of Veterinary Diagnostics and Research  
National Veterinary Institute  
Royal Veterinary and Agricultural University  
Aarhus University  
State University Hospital  
Statens Serum Institut  
Technical University of Denmark  
Chr. Hansen A/S  
University of Hong Kong  
Danisco AS  
Numico Research  
**Period:** 01/01/2006 → 31/03/2011  
**Number of participants:** 21  
**Project ID:** 22015  
**Project participant:**  
Thymann, Thomas (Ekstern)  
Nielsen, Susanne (Ekstern)  
Michaelesen, Kim Fleisher (Ekstern)  
Jakobsen, Mogens (Ekstern)  
Jespersen, Lene (Ekstern)  
Hansen, Axel Kornerup (Ekstern)  
Boye, Mette (Intern)  
Heegaard, Peter Mikael Helweg (Intern)  
Jensen, Bent Borg (Ekstern)
Organic Aquaculture - the linkage between sustainable production and superior products

This project will contribute to the successful establishment of organic trout farming in Denmark. It will develop and optimise new recipes for organic fish feeds with high levels of organic vegetable protein of Danish origin. These will be fed to trout to investigate feed quality as digestibility, effects on the environment, feed conversion, and growth. Effects of the feeds upon general health and welfare, and immunocompetence (vaccination efficacy), will be assessed. Objective sensory and biochemical analyses will provide an overall picture of the eating quality of trout raised with the new organic feeds at an organic farm. Consumer preference for trout with pale coloured meat will be explored, plus other market issues for organic trout (supply chain, traceability, export). Results will be disseminated to industry, consumers and regulatory authorities with open workshops. Guidelines will be prepared for optimal rearing and marketing of organic trout.

National Veterinary Institute
National Food Institute
Division of Seafood Research
Division of Industrial Food Research
Danish Institute for Fisheries and Marine Research
Royal Veterinary and Agricultural University
Danish Technological Institute
Dansk Akvakultur
Period: 01/01/2006 → 31/12/2010
Number of participants: 11
Acronym: ORAQUA
Project ID: 22451
Project participant:
Jokumsen, Alfred (Ekstern)
Pedersen, Lars-Flemming (Ekstern)
Dalsgaard, Inger (Intern)
Nielsen, Henrik Hauch (Intern)
Jacobsen, Charlotte Munch (Ekstern)
Jessen, Flemming (Intern)
Larsen, Erling P. (Ekstern)
Nielsen, Michael Engelbrecht (Ekstern)
Kold, John (Ekstern)
Larsen, Villy J. (Ekstern)
Project Manager, organisational:
McKenzie, David J. (Ekstern)
Organotin compounds in food contact materials
Organotin compounds (mono-, di- and tri-substituted compounds) in food contact materials have several uses, such as heat stabilizers for PVC and as catalysts in polyurethanes and in silicones. Another possible use could be as biocide agents in both plastics and wood. During processing and storage, they can decompose into other known and unknown Sn containing substances. As they are loosely bound to the food contact material, they are at high risk of migrating upon contact with foods. Organotin compounds are generally very toxic and act as endocrine disruptors and exert immunotoxic effects. Recently (2005), the European Food Safety Agency (EFSA) issued a toxicological evaluation of organotin compounds and suggested a tolerable daily intake (TDI) as low as 0.25 µg/kg bodyweight for the sum of four organotin compounds (TBT, DBT, TPT and DOT), corresponding to a specific migration limit (SML) of 6 µg/kg. Research at DFVF focus on developing the first organotin multimethod capable of meeting the new limits in plastics (PVC and aliphatic polyurethanes) and in silicone, which is performed by GC-ICPMS. The project includes a screening and identification of reaction and degradation products that have not formerly been reported. The data from enforcement surveys are used to assess human exposure via food contact materials and are compared with present recommendations for tolerable intake.

National Veterinary Institute
Division of Food Chemistry

Vaccine development with the aim of preventing lameness in swine caused by Mycoplasma hyosynoviae
Most Danish pig herds are infected with Mycoplasma hyosynoviae, a bacterium that causes acute arthritis in pigs older than approx. 10 weeks of age. No effective prophylaxis is available. Therefore the aim of this project is to develop a vaccine with the potential to protect against arthritis caused by M. hyosynoviae. This is done through screening of the immunogenic effect of different antigen preparations in combination with different adjuvants. Immunogenic effects of vaccine candidates are evaluated by their ability to induce both serological and cell-mediated immune response. The two most promising antigen/adjuvant combinations obtained in the screening are tested as vaccine candidates in infection studies in pigs. Finally - if the protective effect of a vaccine candidate turns out to be satisfying - it will be tested in a controlled field study. An effective vaccine administered to pigs at risk would reduce the acute disease problems in herds with severe outbreaks of M. hyosynoviae arthritis. Also, a vaccine could be applied to young breeding animals, which often
suffer from this disease in relation to trading and moving.

Adaptive Immunology & Parasitology
Division of Veterinary Diagnostics and Research
National Veterinary Institute
Videncenter for Svineproduktion, Landbrug & Fødevarer
Period: 01/10/2005 → 31/12/2009
Number of participants: 6
Project participant:
Lauritsen, Klara Tølbøl (Intern)
Hansen, Mette Sif (Intern)
Riber, Ulla (Intern)
Nielsen, Elisabeth Okholm (Ekstern)
Bækbo, Poul (Ekstern)
Project Manager, organisational:
Jungersen, Gregers (Intern)

Financing sources
Source: Forskningsprojekter - Fødevareministeriet
Name of research programme: Forskningsprojekter - Fødevareministeriet
Amount: 5,500,000.00 Danish Kroner

Mass produced optical diagnostic labcards based on micro and nano SU8 layers
OptoLabCard is the acronym chosen to designate the project named “Mass produced optical diagnostic labcards based on micro and nano SU8 layers” (contract number 016727 for specific targeted research or innovation project - Sixth framework programme / 2nd Joint call IST-NMP).

The project, co-ordinated by Ikerlan, a member of the IK4 research alliance and CIC microGUNE, aims the development of a quick, portable and low-cost pathogen detection device (Lab on a Card) that integrates optoelectronic, microfluidic and microbiological advances. The device consists of a hand held base unit and a disposable cartridge (labcard) made of a negative thick photoresist (SU8). This instrument will carry out a Real Time Polymerase Chain Reaction (PCR) automatically from sample preparation to an optical detection in 15 minutes.

National Veterinary Institute
Department of Micro- and Nanotechnology
BioLabChip

Microsystems
Period: 01/05/2005 → 31/08/2008
Number of participants: 2
Lab-on-a-chip system
Acronym: OPTOLABCARD
Project participant:
Bang, Dang Duong (Intern)
Wolff, Anders (Intern)

Financing sources
Source: EU research programme (public)
Name of research programme: Sixth framwork programme/2nd join call IST-NMP
Amount: 2,975,501.00 Euro
Year of approval: 2005

Risk perception and cost benefit analysis of interventions to control Campylobacter
The objective of the project was to identify optimal reduction strategies for the control of Campylobacter in the Danish broiler production and thereby to reduce the number of human food-borne illnesses. For the first time, options to control a food-borne pathogen (Campylobacter) in a chain perspective (from rearing of broilers to consumption of chicken meat) were given in consideration of technical feasibility, costs, public perception of Campylobacter risk, the public acceptance of suggested reduction methods, the consumer's willingness to pay for low-risk products and the saved socio-economic costs due to the expected lower number of human infections.
Nutrients in biscuits and cakes
A survey of industrial produced biscuits and cakes serve as the basis for the food sampling of 211 samples representing 25 general food types of biscuits and cakes. All samples were purchased in ordinary consumerstores and have been analysed for nitrogen, fat, fatty acids, dry matter, ash, sugars, starch, dietary fiber, thiamin, riboflavin, vitamin B6, folate, niacin, pantothenic acid, sodium, potassium, calcium, magnesium, iron, copper, zinc, manganese, phosphorus, chloride, nickle, chromium, cadmium, selenium and iodine.

Nutrients in fish
After a food survey on the Danish market of fish and fish products in 2004, the analytical project have started. 125 samples representing 23 general food types of fish and fish products have been sampled. All samples were purchased in ordinary consumer stores and have been analysed for nitrogen, fat, fatty acids, dry matter, ash, sugars, starch, dietary fiber, retinol, vitamin D3, 25-OH-D3, tokoferol, thiamin, riboflavin, vitamin B6, folate, niacin, pantothenic acid, biotine, folate, vitamin B12, ascorbic acid, dehydrosacorbic acid, sodium, potassium, calcium, magnesium, iron, copper, zinc, manganese, phosphorus, chloride, nickle, chromium, cadmium, selenium, iodine and cholesterol.

RESTOCK (38566) (38400 pre-project)
The aim of the pre-project was to explore the potential for restocking the cod stock in the eastern Baltic. A theoretical study was conducted to explore the potential for restocking bringing together scientists from the aquaculture sector, fisheries managers, ecological scientists and scientists with a background in stock enhancement. The ecology, biology and fisheries biology of the eastern Baltic was reviewed and provided the basis for the study. The results indicated a good potential for restocking with first-feeding cod larvae (Stettrup et al. 2008). This was the first example of a study to examine the potential for large-scale restocking prior to the release of fish. A 2- 3-month delay in the spawning period compared to 20-30 years ago has altered feeding conditions and predation susceptibility in a way that may have exacerbated the decline in recruitment. Producing and releasing cod larvae during spring would mimic the spawning period recorded in previous times and would coincide with the spring peak in copepod production. An evaluation of 3 different release scenarios showed that a release of 474 million first-feeding larvae over 5 months (covering the historic and present day spawning period) would enhance the average population of 2 year old by 10% and be biologically and economically the
most feasible scenario.

Three years of a six year follow up project (RESTOCK) to verify the theoretical findings was funded, but due to political changes, funding for the final three years was not possible and the project was unable to empirically ascertain the potential for restocking. During the three years, 3 cod broodstocks were established with different photoperiods and subsequent spawning periods, together with the development of a technique to determine fish gender non-invasively (McEvoy et al., 2009). Egg and larval incubation techniques were developed and several investigations on temperature, salinity and food impacts on first feeding cod larvae to define the “window of opportunity” for release (i.e. time when the larvae were ready to start feeding to when they began to be too poor in condition to feed) (Støttrup et al., 2008; Overton et al. 2010; Meyer et al 2011a). A release strategy was developed and the first successful release of first-feeding fish larvae at 23 m depth was conducted, but needed further adjustments (Støttrup et al., 2008). An extensive disease monitoring program was established (Støttrup et al., 2008) and the presence of a protistan endoparasite generated a further study (Skovgård et al., 2010). Studies were also conducted to determine explore marking techniques for identification of released fish (Meyer et al., 2011b) and explore growth characteristics in cod larvae (Meyer et al., 2011a).

The project was coordinated by DTU Aqua.

National Institute of Aquatic Resources
Section for Ecosystem based Marine Management
National Veterinary Institute
Danish Fishermen's Association
University of Copenhagen
University of Hamburg
University of Caen
Period: 01/01/2005 → 31/12/2007
Number of participants: 9
Research area: Coastal Ecology
Project participant:
Sørensen, Sune Riis (Intern)
Røjbek, Maria (Intern)
Pedersen, Per Bovbjerg (Intern)
Tomkiewicz, Jonna (Intern)
Møllmann, Christian (Ekstern)
Sichlau, Morten (Ekstern)
Project Manager, academic:
Støttrup, Josianne Gatt (Intern)
Paulsen, Helge (Intern)
Dalsgaard, Inger (Intern)

Studies of the pathogenesis of porcine proliferative enteropathy caused by Lawsonia intracellularis

National Veterinary Institute
Section for Bacteriology, Pathology and Parasitology
Period: 01/06/2004 → 19/02/2009
Number of participants: 1
Supervisor:
Jensen, Tim Kåre (Intern)
Documents:
Torsten

Influence of Food Environment on the infective potential of Listeria

National Food Institute
Division of Veterinary Diagnostics and Research
National Veterinary Institute  
Period: 01/01/2004 → 31/12/2006  
Number of participants: 4  
Project participant:  
Andersen, Jens Bo (Intern)  
Christensen, Bjarke Bak (Intern)  
Boye, Mette (Intern)  
Project Manager, organisational:  
Licht, Tine Rask (Intern)  

Financing sources  
Source: Forskningsrådene - Andre  
Name of research programme: Forskningsrådene - Andre  
Amount: 2,100,000.00 Danish Kroner  

Nutrients in fastfood  
Fastfood from restaurants have been investigated and described in a food survey. 250 samples of 45 different fastfood dishes have been sampled and analysed for nitrogen, fat, fatty acids, dry matter, ash, dietary fiber, thiamin, riboflavin, sodium, potassium, calcium, magnesium, iron, copper, zinc, manganese, phosphorus and chloride. All samples are taken from street- and to-go-restaurants in metropols, major cities, villages, kiosks and highway service stations to represent demographic distributions. Samples for registration og ingredients are treated separately from analytical samples. Analytical samples are taken directly to sample pretreatment in the lab.

National Veterinary Institute  
Division of Food Chemistry  
National Food Institute  
Period: 01/01/2004 → 31/12/2008  
Number of participants: 2  
Project participant:  
Knuthsen, Pia (Intern)  
Project Manager, organisational:  
Saxholt, Erling (Intern)  

Prevention of intestinal disease caused by Lawsonia intracellularis  
The project is concentrated on the porcine disease proliferative enteropathy caused by Lawsonia intracellularis. The project is focused on vaccine development and development of a phylogenetic microarray targeting 16S rRNA to characterize the normal intestinal microbiota in relation to feeding, infection etc.

National Veterinary Institute  
Ministry of Food, Agriculture and Fisheries  
Period: 01/01/2004 → 31/12/2008  
Number of participants: 2  
Project participant:  
Mølbak, Lars (Intern)  
Project Manager, organisational:  
Jensen, Tim Kåre (Intern)  

Financing sources  
Source: Forskningsprojekter - Fødevareministeriet  
Name of research programme: Forskningsprojekter - Fødevareministeriet  
Amount: 11,200,000.00 Danish Kroner  

Minerals and trace elements in drinking Water  
Regarding drinking water as an important component of diet the aim of this project is to measure the content of minerals and trace elements in drinking water in Denmark. 150 samples of tap water from 50 different places, representative for the geographically different areas of Denmark were collected 2 times within one year. The samples were stored at -18°C and analysed for sodium, potassium, magnesium, calcium, chromium, iron, copper, zinc, cadmium, lead, mercury and iodine.
**Influence of probiotics and feed on organic rainbow trout health**

The aim of OPTIFISH is to optimize growth and survival for organic cultured rainbow trout, the dominant fish species produced in Denmark. A minor part of the rainbow trout is produced as organic fish. Currently, there is no production of organic fry, as the classification organic only can be given to fish that have been treated with antibiotics no more than twice in a lifetime. This is hard to achieve as recurrent disease outbreaks, especially with the bacterium Flavobacterium psychrophilum, are seen during the fry stage. A further challenge known from salmon culture is that diets with high plant contents cause enteritis and injury to the intestine, which will affect the absorption of nutrients, affecting the overall health status and welfare of the fish. The result is a higher risk of disease following exposure to pathogenic microorganisms.

OPTIFISH will investigate how organic diet types with varying amounts of fish and plant sources as well as with or without probiotics (lactic acid bacteria) will affect the intestine, the intestinal microbial flora and survival rates of rainbow trout following exposure to pathogens. The use of probiotics for fry are assumed to result in a higher health level. The overall result will be a sustainable production with an optimal utilization of the available organic resources as well as the scope for the industry that they by using the optimal diet type will achieve a robust and healthy fish, something that can be achieved not only in organic but also in traditional farming. A robust and disease-free fry is the most important factor for a higher production in organic aquaculture in the future.
Organochlorine compounds in Danish human milk
Humans are exposed to persistent organic environmental contaminants mainly through the intake of food. The compounds are distributed throughout the human body in the various fatty tissues. Human milk has for many years been used for monitoring purposes, as the samples are relatively easy to get and, if proper standardised, the chemical data can be compared between countries and used for time trends studies. The Danish surveys have been performed on milk samples collected from mothers aged 25-29 and giving birth for the first time. In 1986 and 1993-94 the collecting of samples was coordinated with the WHO human milk studies.
Project participant:
Jørgensen, P.E.V. (Ekstern)
Project Manager, organisational:
Olesen, Niels Jørgen (Intern)

Financing sources
Source: Udenfor rammen
Name of research programme: Ukendt

Activities:

Spread and control of livestock associated methicillin resistant Staphylococcus aureus (LA-MRSA) in Danish pig herds
Period: 1 Jun 2018
Carsten Thure Kirkeby (Internal examiner)
Sten Mortensen (External examiner)
Jaap Wagenaar (External examiner)
Section for Public sector service and commercial diagnostics
National Veterinary Institute
Epidemiology
Degree of recognition: International
Links:
Activity: Examinations and supervision › Internal examination

Thirteenth Workshop of National Reference Laboratories for Parasites
Period: 24 May 2018 → 25 May 2018
Heidi Huus Petersen (Participant)
National Veterinary Institute
Bacteriology & Parasitology
Degree of recognition: International

Related event

Thirteenth Workshop of National Reference Laboratories for Parasites
24/05/2018 → 25/05/2018
Rome, Italy
Activity: Attending an event › Participating in or organising a conference

Can we detect outbreaks at herd-level earlier when combining multiple data sources?
Period: 16 May 2018 → 18 May 2018
Ana Carolina Lopes Antunes (Guest lecturer)
National Veterinary Institute
Epidemiology
Degree of recognition: International

Related event

InnovSurv 2018
16/05/2018 → 18/05/2018
Montpellier, France
Activity: Talks and presentations › Conference presentations

CPH MINK
Period: 9 Apr 2018
Nanett Kvist Nikolaisen (Guest lecturer)
National Food Institute
Bacteriology & Parasitology
Degree of recognition: International

Related external organisation
Københavns Universitet
Thorvaldsensvej 40, 1871, Frederiksberg C, Denmark
Activity: Talks and presentations › Conference presentations

Joint Spring Symposium 2018: Danish Society for Parasitology and Danish Society
Period: 6 Apr 2018
Heidi Huus Petersen (Participant)
National Veterinary Institute
Bacteriology & Parasitology
Section for Public sector service and commercial diagnostics
Degree of recognition: National

Related event
Joint Spring Symposium 2018: Danish Society for Parasitology and Danish Society
06/04/2018 → 06/04/2018
Frederiksberg, Denmark
Activity: Attending an event › Participating in or organising a conference

Interactive, web-based health data visualisation with RStudio Shiny
Period: 26 Mar 2018 → 28 Mar 2018
Ana Carolina Lopes Antunes (Participant)
National Veterinary Institute
Epidemiology
Degree of recognition: International

Related event
Interactive, web-based health data visualisation with RStudio Shiny
26/03/2018 → 28/03/2018
Uppsala, Sweden
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

What to look for when monitoring endemic disease? Translating large volumes of data into valuable data for disease surveillance
Period: 5 Mar 2018
Ana Carolina Lopes Antunes (Invited speaker)
National Veterinary Institute
Epidemiology

Related event
High quality pork 2018
05/03/2018 → 06/03/2018
Da Nang, Viet Nam
Activity: Talks and presentations › Conference presentations

DTU mink seminar 2018
Period: 2 Mar 2018
Nanett Kvist Nikolaisen (Speaker)
National Veterinary Institute
Bacteriology & Parasitology
Degree of recognition: National

Related organisation

DTU mink seminar 2018
Nikolaisen, N. K. (Speaker)
2 Mar 2018
Activity: Talks and presentations › Conference presentations

First International Conference on the Quantification, Benchmarking and Stewardship of Veterinary Antimicrobial Usage
Period: 27 Feb 2018 → 28 Feb 2018
Nanett Kvist Nikolaisen (Participant)
National Veterinary Institute
Bacteriology & Parasitology
Degree of recognition: International
Documents:
AACTING_ItlConf_abstract_NK_Nikolaisen

Related event

First International Conference on the Quantification, Benchmarking and Stewardship of Veterinary Antimicrobial Usage
27/03/2018 → 28/03/2018
Ghent, Belgium
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

NJF Fur Animal Veterinary Meeting 2018
Period: 17 Jan 2018 → 19 Jan 2018
Nanett Kvist Nikolaisen (Speaker)
National Veterinary Institute
Bacteriology & Parasitology
Degree of recognition: International

Related external organisation

Nordic association for agricultural science
NJF General Secretariat c/o RISE Research Institutes of Sweden AB, Ultunallén 4, P.O. Box 7033, SE-750 07, Uppsala, Sweden
Activity: Talks and presentations › Conference presentations

Simulating control of paratuberculosis in Danish dairy herds
Period: 15 Nov 2017
Carsten Thure Kirkeby (Guest lecturer)
National Veterinary Institute
Epidemiology

Description
Presentation for CPH Cattle
Documents:
Abstract CKIR CPH Cattle

Related event

Copenhagen Cattle 2017
15/11/2017 → 15/11/2017
Copenhagen, Denmark
World Association for the Advancement of Veterinary Parasitology (External organisation)
Period: 6 Oct 2017
Heidi Huus Petersen (Member)
National Veterinary Institute
Bacteriology & Parasitology
Degree of recognition: International

Related external organisation

World Association for the Advancement of Veterinary Parasitology
Activity: Membership › Membership of research networks or expert groups

Risk factors associated with spatio-temporal clusters of high mortality in Danish swine herds
Period: 4 Oct 2017
Ana Carolina Lopes Antunes (Guest lecturer)
National Veterinary Institute
Epidemiology

Description
Presented at the ECVPH AGM & Annual Scientific Conference 2017
Degree of recognition: International
Documents:
Proceedings -ECVPH-2017-v06

Related event

ECVPH AGM & Annual Scientific Conference 2017
02/10/2017 → 04/10/2017
Liege, Belgium
Activity: Talks and presentations › Conference presentations

Gæsteforelæser på kurset Parasitic zoonoses
Period: 3 Oct 2017
Heidi Huus Petersen (Guest lecturer)
National Veterinary Institute
Bacteriology & Parasitology

Related external organisation

University of Copenhagen
Thorvaldsensvej 40, DK-1871 Frederiksberg C, Copenhagen, Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

How can we improve public health, food hygiene, and animal welfare in developing country slaughterhouses?
Period: 3 Oct 2017
Ana Carolina Lopes Antunes (Organizer)
National Veterinary Institute
Epidemiology
Degree of recognition: International

Related event

How can we improve public health, food hygiene, and animal welfare in developing country slaughterhouses?
03/10/2017 → …
Liege, Belgium
ECVPH AGM & Annual Scientific Conference 2017
Period: 2 Oct 2017 → 4 Oct 2017
Ana Carolina Lopes Antunes (Organizer)
National Veterinary Institute
Epidemiology

Related event
ECVPH AGM & Annual Scientific Conference 2017
02/10/2017 → 04/10/2017
Liege, Belgium
Activity: Attending an event › Participating in or organising a conference

Dynamics of intra-mammary infections causing pathogens: A herd-, cow- and strain-specific model.
Period: 21 Sep 2017
Carsten Thure Kirkeby (Guest lecturer)
National Veterinary Institute
Epidemiology

Description
Presentation at the EMRW meeting 2017
Degree of recognition: International
Links:
http://cphcattle.ku.dk/seminarer/emrw/

Related external organisation
University of Copenhagen
Thorvaldsensvej 40, DK-1871 Frederiksberg C, Copenhagen, Denmark
Activity: Talks and presentations › Conference presentations

Maul- und Klauenseuche – verschiedene Bekämpfungsmethoden und ihre Auswirkungen
Period: 6 Sep 2017 → 8 Sep 2017
Carola Sauter-Louis (Other)
Christoph Staubach (Other)
Thomas Selhorst (Other)
Tariq Hisham Beshara Halasa (Guest lecturer)
Christine Pottgieße (Other)
Jorn Gethmann (Other)
Carolina Probst (Other)
Brend Haas (Other)
Franz J. Conraths (Other)
National Veterinary Institute
Epidemiology

Description
Poster presentation in the DVG-Epidemiologie Conference, DACH-Epi 2017, 6th -8th September 2017, Hall in Tirol, Austria
Degree of recognition: International

Related event
the DVG-Epidemiologie Conference,
06/09/2017 → 08/09/2017
Activity: Talks and presentations › Conference presentations
26th International Conference of World Association for the Advancement of Veterinary Parasitology (WAAVP)
Period: 4 Sep 2017 → 8 Sep 2017
Heidi Huus Petersen (Organizer)
National Veterinary Institute
Bacteriology & Parasitology
Degree of recognition: International

Related event

26th International Conference of World Association for the Advancement of Veterinary Parasitology (WAAVP): Combating Zoonoses: Strength in East-West Partnership
04/09/2017 → 08/09/2017
Kuala Lumpur, Malaysia
Activity: Attending an event › Participating in or organising a conference

The effect of dietary fatty acid content on rainbow trout fry robustness towards Flavobacterium psychrophilum
Period: 4 Sep 2017
Nikolaj Reducha Andersen (Guest lecturer)
Ivar Lund (Guest lecturer)
Alfred Jokumsen (Guest lecturer)
Lone Madsen (Guest lecturer)
National Veterinary Institute
Fish Diseases
National Institute of Aquatic Resources
Section for Aquaculture
Degree of recognition: International

Related event

18th International Conference on Diseases of Fish and Shellfish: 18th International Conference on Diseases of Fish and Shellfish
04/09/2017 → 08/09/2017
Belfast, United Kingdom
Activity: Talks and presentations › Conference presentations

Frontiers in Veterinary Science (Journal)
Period: Aug 2017
Tim Kåre Jensen (Reviewer)
National Veterinary Institute
Pathology
Description
Review of manuscript for Frontiers in Veterinary Science
Degree of recognition: International

Related journal

Frontiers in Veterinary Science
2297-1769
BFI (2018): BFI-level 1, Scopus rating (2017): CiteScore 1.94
Indexed in DOAJ
Central database
Activity: Research › Peer review of manuscripts
Retinoic acid signalling is required for the pathogenicity of effector CD4+ T cells during the development of intestinal inflammation.

Period: 19 Jul 2017
Aymeric Marie Christian Rivollier (Guest lecturer)
National Veterinary Institute
Mucosal Immunology

Description
18th International Congress of Mucosal Immunology (ICMI 2017), Washington DC, USA - July 2017
Degree of recognition: International

Related event
18th International Congress of Mucosal Immunology
19/07/2017 → 22/07/2017
Washington DC, United States
Activity: Talks and presentations › Conference presentations

Modelling of disease spread
Period: 5 Jun 2017 → 23 Jun 2017
Ana Carolina Lopes Antunes (Participant)
National Veterinary Institute
Epidemiology

Related event
Modelling of disease spread
05/06/2017 → 23/06/2017
Lyngby, Denmark
Activity: Other

EUROLAB
Period: 29 May 2017
Heidi Huus Petersen (Organizer)
National Veterinary Institute
Bacteriology & Parasitology
Degree of recognition: Local

Related event
EUROLAB: Netværksmøde
29/05/2017 → 29/05/2017
Kgs. Lyngby, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

ETALEE 2017
Period: 23 May 2017 → 24 May 2017
Carsten Thure Kirkeby (Participant)
National Veterinary Institute
Epidemiology

Description
The aim of the conference is to shine the spot light on forms of teaching and learning that motivate, activate and engage students. The conference aims to provide a meeting place where you can interact and exchange experiences with colleagues from other engineering education institutions. Thus, you are encouraged to bring good examples from your
teaching practice on the use of active learning (article in danish - english) in engineering education.
The conference will be a mixture of active keynotes, practical Hands-on sessions, Explore sessions, an active Poster session and social arrangements.
Degree of recognition: International
Links:
http://www.etalee.dk

Related event

ETALEE 2017: Exploring Teaching for Active Learning in Engineering Education 2017
23/05/2017 → 24/05/2017
Odense, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Animal Parasitology
Period: 22 May 2017
Heidi Huus Petersen (Guest lecturer)
National Veterinary Institute

Related external organisation

University of Copenhagen
Thorvaldsensvej 40, DK-1871 Frederiksberg C, Copenhagen, Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

Twelfth Workshop of National Reference Laboratories for Parasites
Period: 18 May 2017 → 19 May 2017
Heidi Huus Petersen (Speaker)
National Veterinary Institute
Bacteriology & Parasitology
Degree of recognition: International

Related event

Twelfth Workshop of National Reference Laboratories for Parasites
18/05/2017 → 19/05/2017
Rom, Italy
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

One Health International Summer Course 2017
Period: 8 May 2017 → 18 Aug 2017
Tine Hald (Organizer)
Maria Vang Johansen (Organizer)
Liza Rosenbaum Nielsen (Panel member)
Lars Erik Larsen (Organizer)
Anders Dalsgaard (Organizer)
National Food Institute
Research Group for Genomic Epidemiology
National Veterinary Institute
Virology

Description
One Health International Summer Course 2017
5-week elearning part + 1-week on campus paert, a total of 5 ECTS
Degree of recognition: International

Related event

One Health International Summer Course 2017
08/05/2017 → 18/08/2017
Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

International Conference in Animal Health Surveillance 3
Period: 1 May 2017 → 4 May 2017
Ana Carolina Lopes Antunes (Speaker)
National Veterinary Institute
Epidemiology
Degree of recognition: International

Related event

International Conference in Animal Health Surveillance 3
01/05/2017 → 04/05/2017
Rotorua, New Zealand
Activity: Talks and presentations › Conference presentations

What tools are useful for monitoring endemic diseases? A simulation study based on different time-series components.
Period: 1 May 2017 → 4 May 2017
Ana Carolina Lopes Antunes (Speaker)
National Veterinary Institute
Epidemiology
Degree of recognition: International

Related event

International Conference in Animal Health Surveillance 3
01/05/2017 → 04/05/2017
Rotorua, New Zealand
Activity: Talks and presentations › Conference presentations

Digital dermatitis hos storfe – Identifikation og karakterisering av Treponema spp og andre mikrobiota
Period: 20 Apr 2017
Tim Kåre Jensen (Speaker)
National Veterinary Institute
Pathology

Description
Invited lecture.
Documents:
Digital dermatitis hos storfe – Identifikation og karakterisering

Related external organisation

Norwegian University of Life Sciences
Norway
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

Joint Spring Symposium 2017: Danish Society for Parasitology and Danish Society for Tropical Medicine and International Health
Period: 31 Mar 2017
Heidi Huus Petersen (Participant)
EVALUATION OF ADAPTIVE TEST STRATEGIES FOR CONTROL AND ERADICATION OF PARATUBERCULOSIS WITHIN DAIRY CATTLE HERDS
Period: 29 Mar 2017 → 31 Mar 2017
Carsten Thure Kirkeby (Invited speaker)
National Veterinary Institute
Epidemiology
Links:

Related event
2017 Annual Meeting of SVEPM 2017, 29-31 March, Inverness, Scotland
29/03/2017 → 31/03/2017
Scotland, United Kingdom
Activity: Talks and presentations › Conference presentations

Animal health surveillance in Denmark
Period: 23 Mar 2017
Tim Kåre Jensen (Speaker)
National Veterinary Institute
Pathology
Description
Invited guest lecture
Degree of recognition: National
Documents:
Animal health surveillance in Denmark

Related external organisation
Universidade Federal de Minas Gerais
Brazil
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

Bovine endometritis and abortions revisited
Period: 23 Mar 2017
Tim Kåre Jensen (Speaker)
National Veterinary Institute
Pathology

Description
Invited guest lecture
Degree of recognition: National

Related external organisation

Universidade Federal de Minas Gerais
Brazil
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

Bovine neurological diseases and BSE in Denmark
Period: 23 Mar 2017
Tim Kåre Jensen (Speaker)
National Veterinary Institute

Pathology

Description
Invited guest lecture
Degree of recognition: National
Documents:
National Veterinary Institute, Technical University of Denmark

Related external organisation

Universidade Federal de Minas Gerais
Brazil
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

Bovine digital dermatitis, the pathology and the association with Treponema species
Period: 22 Mar 2017
Tim Kåre Jensen (Speaker)
National Veterinary Institute

Pathology

Description
Invited guest lecture
Degree of recognition: National
Documents:
Bovine digital dermatitis, the pathology and the

Related external organisation

Universidade Federal de Minas Gerais
Brazil
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

Diagnostic application of FISH for Identification of bacterial pathogens
Period: 22 Mar 2017
Tim Kåre Jensen (Speaker)
National Veterinary Institute

Pathology

Description
Invited guest lecture
Degree of recognition: National
Documents:
Diagnostic application of FISH for Identification of

**Related external organisation**

**Universidade Federal de Minas Gerais**  
Brazil  
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

**Identification of bacterial pathogens using Fluorescent In Situ Hybridisation**  
Period: 21 Mar 2017  
Tim Kåre Jensen (Speaker)  
National Veterinary Institute  
Pathology  

**Description**  
Invited guest lecture  
Documents:  
Identification of bacteria by FISH

**Related external organisation**

**Universidade Federal de Minas Gerais**  
Brazil  
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

**National Veterinary Research Institute**  
Period: 20 Mar 2017 → 14 Apr 2017  
Ann Sofie Olesen (Visiting researcher)  
National Veterinary Institute  
Virology  
Activity: Visiting an external institution › Visiting another research institution

**Levedygtige økologiske kalve**  
Period: 15 Mar 2017  
Heidi Huus Petersen (Participant)  
National Veterinary Institute

**Related event**

**Levedygtige økologiske kalve**  
15/03/2017 → 15/03/2017  
Tjele, Denmark  
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

**Danish OIKOS Annual Meeting**  
Period: 10 Mar 2017 → 11 Mar 2017  
Najmul Haider (Speaker)  
National Veterinary Institute  
Epidemiology  

**Description**  
Oral Presentation in The Danish OIKOS Annual Meeting 2017  
Title: Vector-borne diseases transmission and microclimate  
Authors: Najmul Haider, Carsten Kirkeby, Birgit Kristensen, Lene Jung Kjær, Jens Havskov Sørensen, Rene Bedker  
Degree of recognition: Regional
Related event

Danish OIKOS Annual Meeting
10/03/2017 → 11/03/2017
Frederiksberg, Denmark
Activity: Talks and presentations › Conference presentations

Zoonosestormøde
Period: 7 Mar 2017
Julia Christensen (Organizer)
National Food Institute
Division of Risk Assessment and Nutrition
Division of Food Microbiology
Division of Food Production Engineering
Section for Diagnostics and Scientific Advice
Degree of recognition: National

Related event

Zoonosestormøde
07/03/2017 → 07/03/2017
København
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Personlig power for AC'er og leder
Period: 28 Feb 2017 → 28 Apr 2017
Heidi Huus Petersen (Participant)
National Veterinary Institute
Office for HR

Related event

Personlig power for AC'er og leder
28/02/2017 → 26/04/2017
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Changes in antimicrobial group treatment procedures of Danish finishers
Period: 1 Feb 2017
Mette Ely Fertner (Guest lecturer)
National Veterinary Institute
Bacteriology & Parasitology

Related event

Up to Date with Pig Research
01/02/2017 → 01/02/2017
Frederiksborg, Denmark
Activity: Talks and presentations › Conference presentations

Sørensen, AIV, Boklund, A, Toft, N, Espinosa-Gongora, C, Larsen, J & Halasa, T: Modelling within-herd spread of MRSA
Period: 1 Feb 2017
Anna Irene Vedel Sørensen (Speaker)
National Veterinary Institute

Epidemiology

**Description**
Oral presentation

**Links:**
http://cphpig.ku.dk/english/seminarer/up-to-date/

**Related event**

**4th CPH Pig seminar**
01/02/2017 → 01/02/2017
Frederiksberg, Denmark
Activity: Talks and presentations › Conference presentations

**Colombiansk delegation**
Start date: 23 Jan 2017 → 27 Jan 2017
Heidi Huus Petersen (Host)
National Veterinary Institute
Bacteriology & Parasitology
Degree of recognition: International
Activity: Hosting a guest lecturer

**Zoonosestor møde**
Period: 16 Dec 2016
Julia Christensen (Organizer)
Division of Food Microbiology
Division of Food Production Engineering
Section for Diagnostics and Scientific Advice
National Food Institute
Division of Risk Assessment and Nutrition
Degree of recognition: National

**Related event**

**Zoonosestor møde**
16/12/2016 → 16/12/2016
København
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

**2nd international symposium on alternatives to antibioticas (ATA)**
Period: 12 Dec 2016 → 15 Dec 2016
Chris Juul Hedegaard (Speaker)
National Veterinary Institute
Section for Immunology and Vaccinology

**Description**
Oral presentation: "Swine plasma immunoglobulins for treatment of post-weaning diarrhoea"

**Related event**

**2nd international symposium on alternatives to antibioticas (ATA)**
12/12/2016 → 15/12/2016
Paris, France
Activity: Talks and presentations › Conference presentations
Usage of antibiotics in veal calves - potentials and limitations of register based data
Period: 14 Nov 2016
Mette Ely Fertner (Guest lecturer)
National Veterinary Institute
Bacteriology & Parasitology

Related event
Up to Date with Cattle Research
14/11/2016 → 14/11/2016
Frederiksberg, Denmark
Activity: Talks and presentations › Conference presentations

Findings from the surveillance of avian influenza in wild birds and poultry in Denmark
Period: 8 Nov 2016
Charlotte Kristiane Hjulsager (Invited speaker)
National Veterinary Institute

Description
Nordic Poultry Conference, Billund, Denmark, 7th-9th November 2016.

Nordic Poultry Conference, Billund, Denmark, 7th-9th November 2016.
Documents:
Abstract for Nordic Poultry Conference_ findings from AI surveillance_ckhj

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Subtyping of swine influenza viruses using a high-throughput real time PCR platform
Period: 6 Nov 2016 → 9 Nov 2016
Nicole Bakkegård Goecke (Guest lecturer)
National Veterinary Institute
Virology
Degree of recognition: International

Related event
The 4th Congress of the European Association of Veterinary Laboratory Diagnosticians
06/11/2016 → 09/11/2016
Prag, Czech Republic
Activity: Talks and presentations › Conference presentations

Obduktionsfund og patogenese ved luftvejslidelser hos pattegrise og smågrise: v/Dyrlæge Svend Haugegaard, VSP Laboratorium, Kjellerup og Seniorforsker Mette Sif Hansen, DTU-Veterinærinstituttet
Period: 3 Nov 2016
Mette Sif Hansen (Invited speaker)
National Veterinary Institute
Section for Bacteriology, Pathology and Parasitology

Description
Sygdomme i luftvejene hos pattegrise og smågrise er ofte det vigtigste kliniske fund i sygdomsudbrud, hvor der ses både dødsfald og/eller utrivelighed. Sygdomme i luftvejene kan også bane vejen for andre infeksioner på grund af immunsvækkelse. Når vi får grise ind til obduktion på Laboratorium for Svinesygdomme, er den diagnostiske udfordring, at få symptomerne i besætningen, de patologiske fund og de påviste agens til at gå op i en højere enhed. Når vi påviser et eller flere patogener i luftvejene, er det en vigtig overvejelse, hvilken betydning de hver især skal tillægges. Nogle gange finder vi et kendt patogen, der stemmer overens med de patologiske forandringer, andre gange et agens med usikker
patogen betydning, der måske kræver tilstedeværelse af andre uheldige omstændigheder for at lave de fundne patologiske forandringer. Hvornår kan vi være sikre på at vi har fundet alle betydelige agens? Hvilken agens er det mest betydelig? I den diagnostiske proces opstår der ofte flere spørgsmål end svar og både afsender og modtager af et laboritoriesvar må kombinere faglige viden, erfaring, kendskab til besætningen og i yderste konsekvens sin intuition for at drage den rette konklusion.

Forhold der er af betydning for luftvejslidelser patogenese, dvs. mekanismerne bag sygdommens opståen er interaktionen mellem individet (fx alder, immunitetsstatus), miljøfaktorer (fx agens påvirkning, støv) og management. Respirationssystemets forsvarende mekanismer mod infektion i de forskellige luftvejsafsnit er vigtige for dyrets sundhed/sygdomsfridighed og spændende bag den generelle (fx det mucocilliære apparat) til de mere specialiserede mekanismer som det medfødte- (fx pulmonære alveolære makrofager) og erhvervede immunforsvar (fx immunoglobuliner). Hos især grise er mange luftvejsinfektioner multifaktorielle med flere agens og kan skyldes infektion med virus (fx Porcin cytomegalovirus, PCV2) og bakterier (fx Pasteurella multocida, Mycoplasma hyorrhinis, M. hyopneumoniae), samt miljøpåvirkninger/management faktorer.

v/Dyrlæge Svend Haugegaard, VSP Laboratorium, Kjellerup og Seniorforsker Mette Sif Hansen, DTU-Veterinærinstituttet

Related event

Dansk Veterinær Hyologisk Selskab
03/11/2016 → 04/11/2016
Kolding, Denmark
Activity: Talks and presentations › Conference presentations

IRF8-dependent DCs play a key role in the regulation of CD8 T cell responses to epithelial-derived antigen in the steady state but not in inflammation
Period: 21 Oct 2016
Thorsten Joeris (Speaker)
National Veterinary Institute
Section for Immunology and Vaccinology

Description
15 min oral presentation in the session "Immune disorders"
Documents:
EMIG_Joeris_2016

Related event

10th European Mucosal Immunology Group meeting
19/10/2016 → 21/10/2016
Copenhagen, Denmark
Activity: Talks and presentations › Conference presentations

10th INTERCOL International Wetlands Conference
Period: 19 Sep 2016 → 24 Sep 2016
Ana Carolina Cuellar (Participant)
National Veterinary Institute
Epidemiology

Description
Spatiotemporal flooding fluctuation analysis: wetland management Bañado La Estrella, Chaco region, Argentina

We propose an integrated approach, based on satellite imagery analysis (Landsat TM), The NDWI index (Normalized Difference Water) and decision trees, to analyze and characterize seasonal variations (1992-2012) and to map seasonal flooding in Bañado La Estrella wetlands.

Degree of recognition: International
Documents:
Abstract Book-china conference

Related event

10th INTERCOL International Wetlands Conference
19/09/2016 → 24/09/2016
Changshu, China
Activity: Attending an event › Participating in or organising a conference

**Bedre behandling og forebyggelse af orm i fårebesætninger**
Period: 16 Sep 2016
Heidi Huus Petersen (Participant)
National Veterinary Institute

Related event

**Bedre behandling og forebyggelse af orm i fårebesætninger**
16/09/2016 → …
Odense, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

**Zoonosestormøde**
Period: 6 Sep 2016
Julia Christensen (Organizer)
Division of Food Microbiology
Division of Food Production Engineering
Section for Diagnostics and Scientific Advice
National Food Institute
Division of Risk Assessment and Nutrition
Degree of recognition: National

Related event

**Zoonosestormøde**
06/09/2016 → 06/09/2016
København
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

**17th International Symposium on Staphylococci and Staphylococcal Infections**
Period: 30 Aug 2016 → 2 Sep 2016
Carmen Espinosa-Gongora (Participant)
National Veterinary Institute
Section for Bacteriology, Pathology and Parasitology

Description
Poster presentation

Documents:
Islam et al ISSSI 2016 poster

Links:

Related event

**17th International Symposium on Staphylococci and Staphylococcal Infections: ISSSI2016**
30/08/2016 → 02/09/2016
Seoul, Korea, Republic of
Activity: Attending an event › Participating in or organising a conference

**11th International Scientific Congress in Fur Animal Production**
Ronja Mathiesen (Participant)
Section for Immunology and Vaccinology
National Veterinary Institute

Description
Poster Presentation

Related event
11th International Scientific Congress in Fur Animal Production
23/08/2016 → 23/08/2016
Helsinki, Finland
Activity: Attending an event › Participating in or organising a conference

11th International Veterinary Immunology Symposium
Chris Juul Hedegaard (Speaker)
National Veterinary Institute
Section for Immunology and Vaccinology

Description
Oral presentation: Swine plasma immunoglobulins for prevention and treatment of post-weaning diarrhoea: Safety -and preclinical results

Related event
11th International Veterinary Immunology Symposium: IVIS
16/08/2016 → 19/08/2016
Gold Coast, Australia
Activity: Talks and presentations › Conference presentations

PhD boot camp - scientific writing
Ana Carolina Lopes Antunes (Participant)
National Veterinary Institute
Section for Epidemiology

Description
PhD boot camp - scientific writing

Related event
PhD boot camp - scientific writing
16/08/2016 → 18/08/2016
Ringsted, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Microbial Biofilm Techniques
Bettina Nonnemann (Participant)
Section for Bacteriology, Pathology and Parasitology
National Veterinary Institute
Section for Immunology and Vaccinology
Department of Systems Biology

Description
PhD course 27820 Microbial Biofilm Techniques
Related event

**Microbial Biofilm Techniques: PhD course 27820**
12/08/2016 → 19/08/2016
Lyngby, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

**24th International Pig Veterinary Society (IPVS) Congress**
Period: 7 Jun 2016 → 10 Jun 2016
Ana Carolina Lopes Antunes (Participant)
National Veterinary Institute
Section for Epidemiology

**Description**
24th International Pig Veterinary Society (IPVS) Congress, Dublin, Ireland.

Related event

**24th International Pig Veterinary Society (IPVS) Congress**
07/06/2016 → 10/06/2016
Dublin, Ireland
Activity: Attending an event › Participating in or organising a conference

**Zoonosestormøde**
Period: 7 Jun 2016
Julia Christensen (Organizer)
Division of Food Microbiology
Division of Food Production Engineering
Section for Diagnostics and Scientific Advice
National Food Institute
Division of Risk Assessment and Nutrition
Degree of recognition: National

Related event

**Zoonosestormøde**
06/09/2016 → 06/09/2016
København
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

**ESCMID Study Group of Veterinary Microbiology (ESGVM) EC member (External organisation)**
Period: 1 Jun 2016
Carmen Espinosa-Gongora (Participant)
National Veterinary Institute
Section for Bacteriology, Pathology and Parasitology

**Description**
European Society of Clinical Microbiology and Infectious Diseases (ESCMID) Study Group of Veterinary Microbiology (ESGVM)
Member of the Executive Committee
Degree of recognition: International
Links:
https://www.escmid.org/index.php?id=1755

Related external organisation
ESCMID Study Group of Veterinary Microbiology (ESGVM) EC member
Activity: Membership › Board duties in companies, associations, or public organisations

SPATIAL DISTRIBUTION AND ABUNDANCE OF CULICOIDES IMICOLA AND OBSOLETUS GROUP IN EUROPE
Period: 25 May 2016
Ana Carolina Cuellar (Speaker)
National Veterinary Institute
Section for Epidemiology

Description
20 minutes oral presentation
Documents:
Cuellar_Abstract_Zaragoza

Related event
3rd Conference on Neglected Vectors and Vector-Borne Diseases
24/05/2016 → 26/05/2016
Zaragoza, Spain
Activity: Talks and presentations › Conference presentations

Eleventh Workshop of National Reference Laboratories for Parasites
Period: 23 May 2016 → 24 May 2016
Heidi Huus Petersen (Participant)
National Veterinary Institute

Related event
Eleventh Workshop of National Reference Laboratories for Parasites
23/05/2016 → 24/05/2016
Rom, Italy
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

One Health International Summer Course 2016
Period: 9 May 2016 → 23 Aug 2016
Tine Hald (Organizer)
Maria Vang Johansen (Organizer)
Liza Rosenbaum Nielsen (Organizer)
Lars Erik Larsen (Organizer)
Anders Dalsgaard (Organizer)
National Food Institute
Research Group for Genomic Epidemiology
National Veterinary Institute
Virology

Description
One Health International Summer Course 2016
5-week elearning part + 1-week on campus part, a total of 5 ECTS
Degree of recognition: International

Related event
One Health International Summer Course 2016
09/05/2016 → 23/08/2016
Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.
Positive-Strand RNA Viruses (N1)
Period: 1 May 2016 → 5 May 2016
Camille Melissa Johnston (Participant)
National Veterinary Institute
Section for Virology

Related event
Positive-Strand RNA Viruses (N1)
01/05/2016 → 05/05/2016
Austin, Texas, United States
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

PhD Social committee (External organisation)
Period: Apr 2016 → …
Camille Melissa Johnston (Participant)
National Veterinary Institute
Section for Virology
Description
Social committee for PhD students at DTU Vet

Related external organisation
PhD Social committee
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

University of Southern Denmark
Ana Carolina Lopes Antunes (Visiting researcher)
National Veterinary Institute
Epidemiology
Activity: Visiting an external institution › Visiting another research institution

Joint Spring Symposium 2016: Danish Society for Parasitology and Danish Society for Tropical Medicine and International Health
Period: 1 Apr 2016
Heidi Huus Petersen (Participant)
National Veterinary Institute
Bacteriology & Parasitology

Related event
Joint Spring Symposium 2016: Danish Society for Parasitology and Danish Society for Tropical Medicine and International Health: Surprising discoveries by cross-disciplinary approaches
01/04/2016 → 01/04/2016
Frederiksberg, Denmark
Activity: Attending an event › Participating in or organising a conference

Kompetenceudvikling i forskningsbaseret myndighedsbetjening
Period: Mar 2016 → May 2016
Heidi Huus Petersen (Participant)
National Veterinary Institute
Dynamic generalized linear models for monitoring endemic diseases: moving beyond univariate process monitoring control algorithms.
Period: 17 Mar 2016
Ana Carolina Lopes Antunes (Speaker)
National Veterinary Institute
Section for Epidemiology

SPATIAL PATTERNS OF ANTIMICROBIAL RESISTANCE GENES IN DANISH PIG FARMS
Period: 17 Mar 2016
Anna Camilla Birkegård (Speaker)
National Veterinary Institute
Section for Epidemiology

Annual Conference of The Society for Veterinary Epidemiology and Preventive Medicine 2016
Ana Carolina Lopes Antunes (Participant)
National Veterinary Institute
Section for Epidemiology

SVEPM
Period: 16 Mar 2016
Carsten Thure Kirkeby (Organizer)
National Veterinary Institute
Section for Epidemiology

Description
Invited conference workshop organiser sponsored by the Carlsberg Foundation

Invited conference workshop organiser sponsored by the Carlsberg Foundation: "Introduction to modeling vectorborne diseases".
Related event

SVEPM: Annual Meeting 2016
16/03/2016 → 18/03/2016
Elsinore, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

SVEPM
Cecilie Grønlund Clausen (Participant)
National Veterinary Institute
Section for Epidemiology
Documents:
Communicating spatial risk of tick-borne infections: Creating a ScandTick Innovation website based on surveillance data

Related event

SVEPM: Annual Meeting 2016
16/03/2016 → 18/03/2016
Elsinore, Denmark
Activity: Attending an event › Participating in or organising a conference

SVEPM
Jana Schulz (Participant)
National Veterinary Institute
Section for Epidemiology

Description
Participation

Related event

SVEPM: Annual Meeting 2016
16/03/2016 → 18/03/2016
Elsinore, Denmark
Activity: Attending an event › Participating in or organising a conference

SVEPM 2016 Poster Prize
Ana Carolina Lopes Antunes (Other)
Section for Epidemiology
National Veterinary Institute

Description
Annual Conference of The Society for Veterinary Epidemiology and Preventive Medicine 2016
Ph.D. Student

Related event

SVEPM: Annual Meeting 2016
16/03/2016 → 18/03/2016
Elsinore, Denmark
Activity: Talks and presentations › Conference presentations

Trace back and trace forward in foodborne outbreak investigation
Period: 16 Mar 2016
Ana Carolina Lopes Antunes (Participant)
Related event

**Trace back and trace forward in foodborne outbreak investigation**
16/03/2016 → …
Elsinore, Denmark

Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

1**st International Workshop on Advanced MALDI Methods**
Period: 9 Mar 2016
Betina Nonnemann (Organizer)
National Veterinary Institute
Section for Bacteriology, Pathology and Parasitology
Section for Immunology and Vaccinology

**Description**
Member of organizing committee (Ulrike Lyhs, Peter Heegaard & Bettina Nonnemann)

Documents:
1st International Advanced MALDI Methods Workshop

Related event

1**st International Workshop on Advanced MALDI Methods**
09/03/2016 → 09/03/2016
Copenhagen, Denmark

Activity: Attending an event › Participating in or organising a conference

**Neonatal Porcine Diarrhoea (External organisation)**
Period: 5 Mar 2016
Tim Kåre Jensen (Participant)
National Veterinary Institute
Section for Bacteriology, Pathology and Parasitology

**Description**
PhD defence, Jenny Larsson, Swedish University of Agricultural Sciences, Uppasal

Official opponent
Degree of recognition: International

Related external organisation

**Neonatal Porcine Diarrhoea**
Activity: Membership › Membership in review committee

**Influenza A (H10N7) outbreak in harbor seals (Phoca vitulina) in Denmark 2014**
Period: 4 Mar 2016
Mette Sif Hansen (Speaker)
National Veterinary Institute
Section for Bacteriology, Pathology and Parasitology

Related event

13**th Danish Marine Mammal Symposium**
04/03/2016 → 05/03/2016
Kastrup, Denmark
**Laboratory Animal Science – Function ABD**
Bettina Nonnemann (Participant)
Section for Bacteriology, Pathology and Parasitology
National Veterinary Institute

**Description**
PhD course

**Related event**

**Laboratory Animal Science – Function ABD**
29/02/2016 → 18/03/2016
Copenhagen, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

**Aarhus University (External organisation)**
Period: 12 Feb 2016
Gregers Jungersen (Participant)
National Veterinary Institute
Section for Immunology and Vaccinology

**Description**
Thesis title: Functional Study of Protective Immunity following DNA Vaccination against Viral Haemorrhagic Septicaemia in Rainbow Trout

**Related external organisation**
Aarhus University
Inge Lehmanns Gade 10, 8000, Aarhus C, Denmark
Activity: Membership › Membership in review committee

**Monitoring PRRS using laboratory data**
Period: 3 Feb 2016
Ana Carolina Lopes Antunes (Speaker)
National Veterinary Institute
Section for Epidemiology

**Related event**

**Up to date with Pig Research**
03/02/2016 → ...
Copenhagen, Denmark
Activity: Talks and presentations › Conference presentations

**Up to date with Pig Research**
Period: 3 Feb 2016
Ana Carolina Lopes Antunes (Speaker)
National Veterinary Institute
Section for Epidemiology

**Description**
Monitoring PRRS using laboratory data

Up to date with Pig Research
Predicting spatial distribution of pathogens transmitted by ticks in Northern Europe

Period: 2 Feb 2016

Ana Carolina Cuellar (Speaker)
National Veterinary Institute
Section for Epidemiology

Description
The aim is to predict the spatial variation of tick borne pathogens in northern Europe using prevalence data from 13 sites in five different countries (England, France, Netherlands, Denmark and Sweden) and environmental variables obtained from remote sensing imagery as predictors. For two species out of seven, the model was significant. Remote sensing imagery is a powerful tool to model the prevalence of tick borne pathogens in northern Europe.

Related event
NordTick 2016
02/02/2016 → 04/02/2016
Örenäs, Sweden
Activity: Talks and presentations › Conference presentations

Mass Spectrometry Coupled to Separation Techniques in Bioanalytical Chemistry

Period: 22 Jan 2016 → 26 Jan 2016

Bettina Nonnemann (Participant)
National Veterinary Institute
Section for Bacteriology, Pathology and Parasitology

Related event
Mass Spectrometry Coupled to Separation Techniques in Bioanalytical Chemistry
22/02/2016 → 26/02/2016
Copenhagen, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

NJF seminar
Period: 20 Jan 2016 → 23 Jan 2016

Ronja Mathiesen (Participant)
National Veterinary Institute
Section for Immunology and Vaccinology

Description
NJF Seminar

Related event
NJF seminar '16: Fur animal research
20/01/2016 → 23/01/2016
Oslo, Norway
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Jagten på dødsårsager
Period: 2015

Mette Sif Hansen (Participant)
Section for Bacteriology, Pathology and Parasitology
National Veterinary Institute

**Description**
Interviewed af Pia Rindom til DVT (dansk veterinær tidsskrift)

Documents:
DVT 3.2015_Jagten på dødsårsager side 16-19
Activity: Other

**Zoonosestormøde**
Period: 9 Dec 2015
Julia Christensen (Participant)
Division of Food Microbiology
Division of Food Production Engineering
Division for Diagnostics & Scientific Advice
National Food Institute
Division of Risk Assessment and Nutrition

**Related event**

**Zoonosestormøde**
09/12/2015 → 09/12/2015
København
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

**Kan medicinforbruget sænkes hos slagtekalve? Hvad skal der til? Erfaringer fra praksis**
Period: Nov 2015
Mette Ely Fertner (Speaker)
National Veterinary Institute
Section for Epidemiology
Links:
http://www.dlbr.dk/Produkter/DLBRSpecialraadgivning/DLBRSlagtekalve/EfteraarsmoederForSlagtekalveproducenter2015.htm

**Related event**

**Kan medicinforbruget sænkes hos slagtekalve? Hvad skal der til? Erfaringer fra praksis**
10/11/2015 → 12/11/2015
Holstebro, Skejby, Sorø og Vojens, Denmark
Activity: Talks and presentations › Conference presentations

**Virus Y-PRV2 A new piscine orthoreovirus in rainbow trout: establishment of challenge model and long term pathogenetic study**
Period: 30 Nov 2015
Niccolò Vendramin (Speaker)
National Veterinary Institute
Section for Virology
Documents:
Virus Y final

**Related event**

**DAFINET and ProFish Workshop**
17/11/2015 → 18/11/2015
**International Association for Food and Waterborne Parasitology (IAFWP) (External organisation)**

**Period:** 19 Nov 2015

Heidi Huus Petersen (Participant)

National Veterinary Institute

**Description**

Body type: Forskningsnetværk

Degree of recognition: International

**Related external organisation**

International Association for Food and Waterborne Parasitology (IAFWP)

**Activity:** Membership › Membership of research networks or expert groups

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**Biostatistik for sygeplejersker**

**Period:** 18 Nov 2015 → 25 Nov 2015

Anette Boklund (Lecturer)

Section for Epidemiology

National Veterinary Institute

**Related external organisation**

Aarhus University

Inge Lehmanns Gade 10, 8000, Aarhus C, Denmark

**Activity:** Talks and presentations › Guest lectures, external teaching and course activities at other universities

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**DAFINET and ProFish Workshop**

**Period:** 17 Nov 2015 → 18 Nov 2015

Tine Moesgaard Iburg (Participant)

National Veterinary Institute

Section for Virology

**Related event**

**DAFINET and ProFish Workshop**

17/11/2015 → 18/11/2015

København, Denmark

**Activity:** Attending an event › Participating in or organising workshops, courses, seminars etc.

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**Applied Toxicology**

**Period:** 9 Nov 2015 → 26 Nov 2015

Ronja Mathiesen (Participant)

National Veterinary Institute

Section for Immunology and Vaccinology

**Description**

Applied Toxicology course, ECTS 7.5

**Related event**

**Applied Toxicology**

09/11/2015 → 26/11/2015

Copenhagen, Denmark

**Activity:** Attending an event › Participating in or organising workshops, courses, seminars etc.
Somatic Cell Count in Milk from Dairy Cattle: The Dilution Effect Matters
Period: 7 Nov 2015
Kaare Græsbøll (Speaker)
Department of Applied Mathematics and Computer Science
National Veterinary Institute
Section for Epidemiology
Documents:
Abstract

Related event
14th Conference of the International Society for Veterinary Epidemiology and Economics
03/11/2015 → 07/11/2015
Mérida, Yucatan, Mexico
Activity: Talks and presentations › Conference presentations

Predicting the Future Average Production of a Dairy Cow
Period: 6 Nov 2015
Kaare Græsbøll (Speaker)
Department of Applied Mathematics and Computer Science
National Veterinary Institute
Section for Epidemiology
Documents:
ISVEE FAP

Related event
14th Conference of the International Society for Veterinary Epidemiology and Economics
03/11/2015 → 07/11/2015
Mérida, Yucatan, Mexico
Activity: Talks and presentations › Conference presentations

14th international symposium on veterinary epidemiology and economics
Period: 3 Nov 2015
Carsten Thure Kirkeby (Speaker)
National Veterinary Institute
Section for Epidemiology

Description
Bio-economic simulation modeling: How to control Paratuberculosis on dairy farms?
Presentation of the iCull model and some of the results.
Documents:
ISVEEabstract_CKIR

Related event
14th Conference of the International Society for Veterinary Epidemiology and Economics
03/11/2015 → 07/11/2015
Mérida, Yucatan, Mexico
Activity: Talks and presentations › Conference presentations

Aquaexcel 2020: Kick off meeting 2015
Period: 1 Nov 2015 → 3 Nov 2015
Tine Moesgaard Ibarg (Participant)
Related event

**Aquaexcel 2020: Kick off meeting 2015**
01/11/2015 → 03/11/2015
Montpellier, France
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

**Food and Agriculture Organization of the United Nations (FAO) Participatory Epidemiology Forum**
Period: Oct 2015 → …
Ana Carolina Lopes Antunes (Participant)

National Veterinary Institute
Epidemiology
Degree of recognition: International
Links:
Activity: Other

**Molecular methodology in veterinary infectious disease biology**
Period: 29 Oct 2015 → 1 Apr 2016
Bettina Nonnemann (Participant)

National Veterinary Institute
Section for Bacteriology, Pathology and Parasitology

Related event

**Molecular methodology in veterinary infectious disease biology**
29/10/2015 → 01/04/2016
Copenhagen, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

**Expert group for swine fever (External organisation)**
Period: 19 Oct 2015 → …
Anette Boklund (Participant)
National Veterinary Institute
Section for Epidemiology

Description
National expert group for swine fever (CSF & ASF)

Related external organisation

**Expert group for swine fever**
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

**EURL-Fish training course**
Period: 12 Oct 2015
Tine Moesgaard Iburg (Organizer)
National Veterinary Institute
Section for Virology

Related event
EURL-Fish training course: Introduction to histopathology in fish diseases
12/10/2015 → 15/10/2015
Copenhagen, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

International trade of animal source foods from low income countries
Period: 8 Oct 2015
Ana Carolina Lopes Antunes (Participant)
National Veterinary Institute
Section for Epidemiology

Related event
International trade of animal source foods from low income countries: The good, the bad and the ugly
08/10/2015 → …
Belgrade, Serbia
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Annual General Meeting of the European College of Veterinary Public Health 2015
Ana Carolina Lopes Antunes (Participant)
National Veterinary Institute
Section for Epidemiology

Related event
Annual General Meeting of the European College of Veterinary Public Health 2015
07/10/2015 → 09/10/2015
Belgrade, Serbia
Activity: Attending an event › Participating in or organising a conference

Application of qPCR assays for diagnosing causes of viral mink diarrhea. Preliminary results.
Period: 1 Oct 2015
Christina Marie Lazov (Lecturer)
National Veterinary Institute

Description
Mundtligt oplæg under seminar programmets veterinære session

Related event
NJF Seminar 485: Autumn Meeting in Fur Animal Research
29/09/2015 → 01/10/2015
Turku, Finland
Activity: Talks and presentations › Conference presentations

Simulation modelling of paratuberculosis within herds
Period: 30 Sep 2015
Carsten Thure Kirkeby (Invited speaker)
National Veterinary Institute
Section for Epidemiology
Documents:
iCull_Seminar_Sydney

Related event
Seminar on Simulation modelling of paratuberculosis within herds
30/09/2015 → …
Sydney, Australia
Activity: Talks and presentations › Conference presentations

**NJF Seminar 485**
Period: 29 Sep 2015 → 1 Oct 2015
Christina Marie Lazov (Participant)
National Veterinary Institute

Related event

**NJF Seminar 485: Autumn Meeting in Fur Animal Research**
29/09/2015 → 01/10/2015
Turku, Finland
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

**Applied Immunology**
Period: 28 Sep 2015 → 9 Oct 2015
Bettina Nonnemann (Participant)
National Veterinary Institute
Section for Bacteriology, Pathology and Parasitology

Related event

**Applied Immunology**
28/09/2015 → 09/10/2015
Copenhagen, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

**Spørgeskema som redskab og metode til udvikling og udforskning af sygepleje**
Period: 17 Sep 2015 → 22 Oct 2015
Anette Boklund (Lecturer)
Section for Epidemiology
National Veterinary Institute

Related external organisation

**Aarhus University**
Inge Lehmanns Gade 10, 8000, Aarhus C, Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

**17th International Conference on Diseases of Fish and Shellfish**
Period: 7 Sep 2015 → 11 Sep 2015
Niccolò Vendramin (Organizer)
National Veterinary Institute
Section for Virology

Description
Organization of a specific WS on "Fish health in Mediterranean Aquaculture, past mistakes and future challenges" within the 17th EAFP conference
Documents:
Fish health in Mediterranean Aquaculture leaflet

Related event

**17th International Conference on Diseases of Fish and Shellfish**
07/09/2015 → 11/09/2015
Las Palmas, Spain
Activity: Attending an event › Participating in or organising a conference
17th International Conference on Diseases of Fish and Shellfish
Period: 7 Sep 2015 → 11 Sep 2015
Tine Moesgaard Iburg (Participant)
National Veterinary Institute
Section for Virology

Related event

17th International Conference on Diseases of Fish and Shellfish
07/09/2015 → 11/09/2015
Las Palmas, Spain
Activity: Attending an event › Participating in or organising a conference

17th International Conference on Diseases of Fish And Shellfish
Period: 7 Sep 2015 → 11 Sep 2015
Susie Sommer Mikkelsen (Speaker)
National Veterinary Institute
Section for Virology

Related event

17th International Conference on Diseases of Fish and Shellfish
07/09/2015 → 11/09/2015
Las Palmas, Spain
Activity: Talks and presentations › Conference presentations

NEAT
Period: 6 Sep 2015 → 8 Sep 2015
Carsten Thure Kirkeby (Participant)
National Veterinary Institute
Section for Epidemiology

Description
NEAT Economics of Animal Health workshop, Cesenatico, Italy, 2015
Links:
http://www.neat-network.eu/ (NEAT website)

Related event

NEAT: Economics of Animal Health
07/09/2015 → 08/09/2015
Cesenatico, Italy
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

SLA class I typing and expression analysis using Next Generation Sequencing
Period: 4 Sep 2015
Maria Rathmann Sørensen (Speaker)
National Veterinary Institute
Section for Immunology and Vaccinology

Description
Oral presentation in the Molecular Immunology workshop

Related event

5th European Veterinary Immunology Workshop
The pig as a model for therapeutic human anti-cancer vaccine development
Period: 4 Sep 2015
Nana Haahr Overgaard (Speaker)
National Veterinary Institute
Section for Immunology and Vaccinology
Description
Oral presentation
Documents:
EVIW 2015 abstract Overgaard et al

Related event
5th European Veterinary Immunology Workshop
Period: 2 Sep 2015 → 4 Sep 2015
Chris Juul Hedegaard (Participant)
National Veterinary Institute
Section for Immunology and Vaccinology
Documents:
POSTER_ EVIW_2015_CJHE

Related event
5th European Veterinary Immunology Workshop
Period: 02/09/2015 → 04/09/2015
Vienna, Austria
Activity: Talks and presentations › Conference presentations

Training School on Big Data and Data Warehousing
Period: 27 Aug 2015
Ana Carolina Lopes Antunes (Participant)
Department of Applied Mathematics and Computer Science
National Veterinary Institute

Related event
Training School on Big Data and Data Warehousing
Period: 26/08/2015 → 28/08/2015
Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Battling Bluetongue and Schmallenberg virus: Local scale behavior of transmitting vectors
Period: 10 Aug 2015
Anders Stockmarr (Invited speaker)
Department of Applied Mathematics and Computer Science
Statistics and Data Analysis
Abstract: The intestinal immune system has the complex task of generating tolerance towards harmless antigens derived from our diet, commensal microflora or tissue, while maintaining the ability to mount protective immune responses to mucosal pathogens. Much of our understanding regarding the regulation of mucosal T cell responses stems from studies on CD4+ T cells. However, the intestinal mucosa is a major entry site for intracellular pathogens, whose control requires cross-presentation of cell-associated antigens for the induction of protective CD8+ T cell responses. To assess the regulation of mucosal CD8+ T cell priming and differentiation in the steady state and inflammatory setting, we utilized IFABP-tOva mice, in which Ovalbumin (Ova) is expressed as an epithelial-derived antigen in the small intestine. In this model Ova-specific CD8+ T cells were found to differentiate into two distinct subsets, CD107a/b+ cytotoxic T cells (CTLs) and FoxP3+ CD8+ T cells with regulatory potential. Interestingly, neither IRF8 nor IRF4 expression by intestinal dendritic cells (DCs) was crucial for the expansion of CTLs. In contrast, presence of IRF8- but not IRF4-dependent DCs was critical for the development of FoxP3+ CD8+ T cells in the steady state. However in the inflammatory setting, expansion of the FoxP3+ subset was not affected by the absence of IRF8-dependent DCs, suggesting that other subsets of intestinal antigen presenting cells (APCs) can compensate their function in an inflammatory milieu. Collectively these findings further our understanding of the mechanisms regulating CD8+ T cell responses in the intestinal mucosa and have potential implications for mucosal vaccine design.
Carsten Thure Kirkeby (Participant)
National Veterinary Institute
Section for Epidemiology

**Description**
DAILY EVOLUTION OF THE INSECT BIOMASS SPECTRUM IN AN AGRICULTURAL LANDSCAPE ACCESSED WITH LIDAR

**Related event**
**International Laser Radar Conference**
03/07/2015 → 05/07/2015
New York, United States
Activity: Attending an event › Participating in or organising a conference

**RONAFA (Reduction of Need for Antimicrobials in Food-producing Animals) EFSA/EMA ad hoc working group (External organisation)**
Period: 3 Jul 2015 → 31 Dec 2016
Gregers Jungersen (Participant)
National Veterinary Institute
Section for Immunology and Vaccinology

**Description**
The European Commission has submitted to EFSA and to the European Medicines Agency (EMA) a request for a joint scientific opinion on “measures to reduce the need to use antimicrobial agents in animal husbandry in the European Union, and the resulting impacts on food safety”.

Scientific Expert

Body type: EFSA/EMA ad hoc working group
Degree of recognition: International

**Related external organisation**
**RONAFA (Reduction of Need for Antimicrobials in Food-producing Animals) EFSA/EMA ad hoc working group**
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

**Introduction to Bayesian Disease Mapping**
Period: 29 Jun 2015 → 3 Jul 2015
Ana Carolina Lopes Antunes (Participant)
National Veterinary Institute
Section for Epidemiology

**Related event**
**Introduction to Bayesian Disease Mapping**
29/06/2015 → 03/07/2015
Edinburgh, United Kingdom
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

**CBioVikings Virus Symposium**
Period: 25 Jun 2015
Kerstin Skovgaard (Invited speaker)
National Veterinary Institute
Section for Immunology and Vaccinology

**Description**
The pig as a large animal model for influenza

**Oral presentation**

**Related event**

**CBioVikings Virus Symposium**
25/06/2015 → …
Copenhagen, Denmark
Activity: Talks and presentations › Conference presentations

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**CoVetLab**
Period: 24 Jun 2015
Anette Boklund (Speaker)
Section for Epidemiology
National Veterinary Institute

**Description**
Workshop for France and Belgium in CoVetLab regi

Workshop of DTU-DADS preparation of data

**Related event**

**CoVetLab: Preparation of data for modelling**
24/06/2015 → 25/12/2015
Copenhagen, Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

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**Course in technical biomedicine**
Period: 17 Jun 2015
Carsten Thure Kirkeby (Invited speaker)
National Veterinary Institute
Section for Epidemiology
Section for Bacteriology, Pathology and Parasitology

**Description**
Lecture about epidemiology at DTU VET

Technical Biomedicine course at DTU VET.

**Related event**

**Course in technical biomedicine: TBM**
15/06/2015 → 28/06/2015
Lyngby, Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

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**In situ production of prebiotics**
Period: 10 Jun 2015
Mikael Lenz Strube (Invited speaker)
National Veterinary Institute
Section for Bacteriology, Pathology and Parasitology

**Related event**
Workshop of the African and Classical Swine Fever National Reference Laboratories  
Period: 9 Jun 2015 → 10 Jun 2015  
Thomas Bruun Rasmussen (Speaker)  
National Veterinary Institute  
Section for Virology  
Description  
Next Generation Sequencing of Classical Swine Fever Virus  
Related event  
Workshop of the African and Classical Swine Fever National Reference Laboratories  
09/06/2015 → 10/06/2015  
Madrid, Spain  
Activity: Talks and presentations › Conference presentations

Flow cytometry  
Period: 4 Jun 2015  
Maria Rathmann Sørensen (Lecturer)  
National Veterinary Institute  
Section for Immunology and Vaccinology  
Related event  
Assay Technology  
04/06/2015 → 22/09/2015  
Frederiksberg, Denmark  
Activity: Talks and presentations › Conference presentations

19th Annual Meeting of the National Reference Laboratories for Fish Diseases  
Susie Sommer Mikkelsen (Speaker)  
National Veterinary Institute  
Section for Virology  
Related event  
19th Annual Meeting of the National Reference Laboratories for Fish Diseases  
27/05/2015 → 28/05/2015  
København, Denmark  
Activity: Talks and presentations › Conference presentations

19th Annual Workshop for national reference laboratories for fish diseases  
Nicolò Vendramin (Participant)  
National Veterinary Institute  
Section for Virology  
Description  
4 Scientific talks and 1 coauthorship at the Annual workshop for national reference laboratories for fish diseases  
Documents:  
3-Update Med disease 2014 Niven
3- Parafish Control Niven
1-Proficiency test 2015
2-Training courses 2015
1- Overview of the disease situation and surveillance in Europe in 2014

Related event

19th Annual Workshop for national reference laboratories for fish diseases
27/05/2015 → 28/05/2015
Copenhagen, Denmark
Activity: Attending an event › Participating in or organising a conference

Tine Moesgaard Iburg (Participant)
National Veterinary Institute
Section for Virology

Related event

19th Annual Workshop for national reference laboratories for fish diseases
27/05/2015 → 28/05/2015
Copenhagen, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Syndromic surveillance using free tools
Period: 19 May 2015 → 22 May 2015
Ana Carolina Lopes Antunes (Participant)
National Veterinary Institute
Section for Epidemiology

Related event

Syndromic surveillance using free tools
19/05/2015 → 22/05/2015
Uppsala, Sweden
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Identification of novel T cell epitopes in breast cancer
Period: 13 May 2015
Sofie Ramskov (Speaker)
National Veterinary Institute
Section for Immunology and Vaccinology

Description
Short talk presentation

Related event

13th Annual meeting in the Association for Cancer Immunotherapy
11/05/2015 → 13/05/2015
Mainz, Germany
Activity: Talks and presentations › Conference presentations

The 2nd Management Committee and the 1st Working Groups meetings of the NEREUS COST Action ES1403
Rustam Aminov (Participant)
National Veterinary Institute
Section for Bacteriology, Pathology and Parasitology

**Description**
Management Committee member for Denmark

**Links:**
https://www.linkedin.com/pulse/nereus-cost-action-news-despo-fatta-kassinos (On 7th and 8th of May 2015, the 2nd Management Committee and the 1st Working Groups meetings of the NEREUS COST Action ES1403 took place in Barcelona. The Autonomous University of Barcelona hosted the event in which 84 members of the COST Action participated.)

**Related event**
The 2nd Management Committee and the 1st Working Groups meetings of the NEREUS COST Action ES1403
07/05/2015 → 08/05/2015
Barcelona, Spain
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

**International Conference in pig welfare**
Period: 29 Apr 2015 → 30 Apr 2015
Ana Carolina Lopes Antunes (Participant)
National Veterinary Institute
Section for Epidemiology

**Related event**
International Conference in pig welfare: Improving pig welfare - what are the ways forward?
29/04/2015 → 30/04/2015
Copenhagen, Denmark
Activity: Attending an event › Participating in or organising a conference

**Better Training for Safer Food Initiative: Monte Carlo Simulation Modeling**
Period: 23 Apr 2015
Anette Boklund (Lecturer)
Section for Epidemiology
National Veterinary Institute

**Related external organisation**
EU-fundet
Berlin, Germany
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

**One Health International Summer Course 2015**
Period: 13 Apr 2015 → 21 Aug 2015
Tine Hald (Organizer)
Maria Vang Johansen (Organizer)
Liza Rosenbaum Nielsen (Organizer)
Lars Erik Larsen (Organizer)
Anders Dalsgaard (Organizer)
National Food Institute
Research Group for Genomic Epidemiology
National Veterinary Institute
Virology
Description
One Health International Summer Course 2015

6-week elearning part + 2 week on campus part, a total of 5 ECTS
Degree of recognition: International

Related event
One Health International Summer Course 2015
13/04/2015 → 21/08/2015
Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Annual Conference of The Society for Veterinary Epidemiology and Preventive Medicine
Ana Carolina Lopes Antunes (Participant)
National Veterinary Institute
Section for Epidemiology

Related event
Annual Conference of The Society for Veterinary Epidemiology and Preventive Medicine
25/03/2015 → 27/03/2015
Ghent, Belgium
Activity: Attending an event › Participating in or organising a conference

Introduction to the Interactive visualisation of surveillance data with Google maps and Charts
Period: 25 Mar 2015
Ana Carolina Lopes Antunes (Participant)
National Veterinary Institute
Section for Epidemiology

Related event
Introduction to the Interactive visualisation of surveillance data with Google maps and Charts
25/03/2015 → …
Ghent, Belgium
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

SVEPM Annual Meeting 2015
Carsten Thure Kirkeby (Participant)
National Veterinary Institute
Section for Epidemiology

Description
Poster
Documents:
SVEPM_2015_CKIR_final_version

Related event
SVEPM Annual Meeting 2015
25/03/2015 → 27/03/2015
Ghent, Belgium
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.
**Symposium: Animal Health Surveillance 2.0 RISKSUR**  
Period: 24 Mar 2015  
Ana Carolina Lopes Antunes (Participant)  
National Veterinary Institute  
Section for Epidemiology

**Related event**

**Symposium: Animal Health Surveillance 2.0 RISKSUR**  
24/03/2015 → …  
Ghent, Belgium  
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

**PhD defense of Truc Thi Kim Thanh Hoang (External organisation)**  
Period: 6 Mar 2015  
Gregers Jungersen (Participant)  
National Veterinary Institute  
Section for Immunology and Vaccinology

**Description**  
Assessment of PhD Thesis “Pre- and Post-Exposure Vaccination against Mycobacterium Tuberculosis” submitted to the Faculty of Health and Medical Sciences, University of Copenhagen by Truc Thi Kim Thanh Hoang.  
Degree of recognition: International

**Related external organisation**

**PhD defense of Truc Thi Kim Thanh Hoang**  
Activity: Membership › Membership in review committee

**National Veterinary Institute Sweden**  
Period: Feb 2015 → Mar 2015  
Ana Carolina Lopes Antunes (Visiting researcher)  
National Veterinary Institute  
Epidemiology  
Activity: Visiting an external institution › Visiting another research institution

**Workshop: Molecular tracing of viral diseases in aquaculture**  
Period: 26 Jan 2015 → 30 Jan 2015  
Susie Sommer Mikkelsen (Speaker)  
National Veterinary Institute  
Section for Virology

**Description**  
Workshop: Molecular tracing of viral diseases in aquaculture  
Documents:  
Program of MOLTRAQ workshop in Montpellier Jan 2015 16.12.14

**Related event**

**Workshop: Molecular tracing of viral diseases in aquaculture**  
26/01/2015 → 30/01/2015  
Montpellier, France  
Activity: Talks and presentations › Conference presentations

**Immunity to Veterinary Pathogens**  
Period: 22 Jan 2015  
Heidi Mikkelsen Melvang (Speaker)
National Veterinary Institute
Section for Immunology and Vaccinology

Description
Documents:
Abstract_Keystone_Mikkelsen_290914
Abstract_Keystone_Mikkelsen_290914

Related event
Immunity to Veterinary Pathogens 2015: Informing Vaccine Development
20/01/2015 → 25/01/2015
Keystone, United States
Activity: Talks and presentations › Conference presentations

Session moderator: Mucosal Immune Responses to Infection
Period: 22 Jan 2015
Gregers Jungersen (Panel member)
National Veterinary Institute
Section for Immunology and Vaccinology

Related event
Immunity to Veterinary Pathogens 2015: Informing Vaccine Development
20/01/2015 → 25/01/2015
Keystone, United States
Activity: Talks and presentations › Conference presentations

Epidemiological analysis of clustered data – with emphasis on veterinary applications
Period: 15 Jan 2015 → 4 Feb 2015
Ana Carolina Lopes Antunes (Participant)
National Veterinary Institute
Section for Epidemiology

Related event
Epidemiological analysis of clustered data – with emphasis on veterinary applications
12/01/2015 → 04/02/2015
Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

ASF i drægtige søer: Eksperimentelt infektionsforsøg på Lindholm
Period: 14 Jan 2015
Louise Lohse (Speaker)
National Veterinary Institute

Description
Oral presentation of animal experimental study of african swine fever i pigs, presented at Dialogmøde FVST/VET

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Carp Edema Virus Workshop
Period: 12 Jan 2015 → 13 Jan 2015
Description
A total of 20 participants from 11 countries attended the meeting over the two days period. The workshop combined different single oral presentations and sessions with general discussions. The workshop was organized and held due to the increasing amount of diagnostic cases where CEV was detected in diseased cyprinids (both Koi and common carp). The primary aim of the workshop was to share knowledge, diagnostic protocols and material among participants and evaluate different strategies on how to tackle this issue.

Carp Edema Virus Workshop

Related event

Carp Edema Virus Workshop
12/01/2015 → 13/01/2015
København, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

CEV Meeting
Period: 12 Jan 2015 → 13 Jan 2015
Niccolò Vendramin (Organizer)
National Veterinary Institute
Section for Virology

Description
Organization of international 2 days workshop on Carp Edema Virus CEV
Documents:
Booklet final

Related event

CEV Meeting: Carp Edema Virus - CEV Workshop
12/01/2015 → 13/01/2015
Copenhagen, Denmark
Activity: Attending an event › Participating in or organising a conference

Making models usefull in contingency planning
Period: 12 Jan 2015
Anette Boklund (Lecturer)
Section for Epidemiology
National Veterinary Institute

Description
EUFMD Webinar

Internet
Links:
https://eufmd.rvc.ac.uk/course/view.php?id=47

Related event

EuFMD e-Learning
12/01/2015 → 12/01/2015
Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities
Introduction to experimental biomedicine
Period: 1 Jan 2015 → 31 Jan 2015
Carsten Thure Kirkeby (Participant)
National Veterinary Institute
Section for Epidemiology

Related event

Introduction to experimental biomedicine: DTU course
01/01/2015 → 31/01/2015
Copenhagen, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

European Pathosurveillance Network (External organisation)
Period: 2014
Tim Kåre Jensen (Participant)
National Veterinary Institute
Section for Bacteriology, Pathology and Parasitology

Description
Network of veterinary pathologists at European National Veterinary Institutes
Board member
Degree of recognition: International

Related external organisation

European Pathosurveillance Network
Activity: Membership › Membership of research networks or expert groups

Journal of General Virology (Journal)
Period: 2014 → 2017
Graham Belsham (Editor)
National Veterinary Institute
Section for Virology

Description
as per title

Related journal

Journal of General Virology
0022-1317
BFI (2018): BFI-level 1, Scopus rating (2017): CiteScore 2.68 SJR 1.325 SNIP 0.877, ISI indexed (2013): ISI indexed yes,
Web of Science (2018): Indexed yes
Central database
Activity: Research › Journal editor

Medical Research Council (UK) Tackling AMR – A Cross Council Initiative (External organisation)
Period: 2014 → 2015
Anders Folkesson (Participant)
National Veterinary Institute
Section for Bacteriology, Pathology and Parasitology

Description
Theme 1: Understanding resistant bacteria
Expert Panel Member
Degree of recognition: International
Related external organisation

Medical Research Council (UK) Tackling AMR – A Cross Council Initiative
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

Statens Serum Institut (External organisation)
Period: 2014
Gregers Jungersen (Participant)
National Veterinary Institute
Section for Immunology and Vaccinology

Description
Evaluation for Senior Scientist Dennis Christensen

Related external organisation

Statens Serum Institut
Denmark
Activity: Membership › Membership in review committee

Sharing Advances on Large Animal Models
Period: 15 Dec 2014 → 17 Dec 2014
Kerstin Skovgaard (Invited speaker)
National Veterinary Institute
Section for Immunology and Vaccinology

Description
High-throughput gene expression analysis in pigs as model for respiratory infections
Degree of recognition: International

Related event

Sharing Advances on Large Animal Models
15/12/2014 → 17/12/2014
Munich, Germany
Activity: Talks and presentations › Conference presentations

Journal of General Virology (Journal)
Graham Belsham (Editor)
National Veterinary Institute
Section for Virology

Description
Guest Editor

Related journal

Journal of General Virology
0022-1317
BFI (2018): BFI-level 1, Scopus rating (2017): CiteScore 2.68 SJR 1.325 SNIP 0.877, ISI indexed (2013): ISI indexed yes,
Web of Science (2018): Indexed yes
Central database
Activity: Research › Peer review of manuscripts
Fødevarestyrelsen (External organisation)
Period: 30 Nov 2014 → …
Anette Boklund (Chairman)
National Veterinary Institute
Section for Epidemiology

Description
Ekspertgruppe for Mund- og klovesyge
Ekspertgruppe nedsat af FVST

Related external organisation
Fødevarestyrelsen
Glostrup, Denmark

Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

Spatial and Temporal Statistical Modelling for Population Health Sciences Course
Period: 24 Nov 2014 → 28 Nov 2014
Ana Carolina Lopes Antunes (Participant)
Section for Epidemiology
National Veterinary Institute

Related event
Spatial and Temporal Statistical Modelling for Population Health Sciences Course
24/11/2014 → 28/11/2014
Liverpool, United Kingdom
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

University of Southern Denmark (External organisation)
Period: 20 Nov 2014
Gregers Jungersen (Participant)
National Veterinary Institute
Section for Immunology and Vaccinology

Description
PhD evaluation committee for Kristoffer Jarlov Jensen

Related external organisation
University of Southern Denmark
Odense, Denmark

Activity: Membership › Membership in review committee

New Concepts on the Mechanisms of Inflammation, Autoimmunity and Tumorigenesis
Period: 13 Nov 2014 → 14 Nov 2014
Rustam Aminov (Chairman)
National Veterinary Institute

Description
The role of microbiota in inflammation

Related event
New Concepts on the Mechanisms of Inflammation, Autoimmunity and Tumorigenesis
13/11/2014 → 14/11/2014
Denmark
Activity: Attending an event › Participating in or organising a conference
Brachyspira - the Pathology
Period: 12 Nov 2014
Tim Kåre Jensen (Invited speaker)
National Veterinary Institute
Section for Bacteriology, Pathology and Parasitology
Documents:
Fellströms kalas Uppsala 2014 DTU bibliotek
Fellströms kalas Uppsala 2014 DTU bibliotek

Related event
Brachyspira - the past, the present and the future
12/11/2014 → …
Uppsala, Sweden
Activity: Talks and presentations › Conference presentations

Dafinet 2014
Period: 11 Nov 2014 → 13 Nov 2014
Morten Sichlau Bruun (Participant)
National Veterinary Institute
Section for Virology

Related event
Dafinet 2014: Fish models in Research
Frederiksberg, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Porcin Epidemisk Diarre Virus
Period: 7 Nov 2014
Anette Bøtner (Invited speaker)
National Veterinary Institute

Related event
Dansk Veterinær Hyologisk Selskab: Efterårsmøde 2014
06/11/2014 → 07/11/2014
Kolding, Denmark
Activity: Talks and presentations › Conference presentations

Application of fluorescent in situ hybridisation for identification of Chlamydiaceae in formalin-fixed, paraffin-embedded tissue.
Period: 6 Nov 2014
Tim Kåre Jensen (Invited speaker)
National Veterinary Institute
Section for Bacteriology, Pathology and Parasitology
Documents:
DVHS klamydia 2014 DTU publikation tije

Related event
Dansk Veterinær Hyologisk Selskab: Efterårsmøde 2014
06/11/2014 → 07/11/2014
Kolding, Denmark
Activity: Talks and presentations › Conference presentations
Vidensformer og forskningsmetode: Biostatistik
Anette Boklund (Lecturer)
Section for Epidemiology
National Veterinary Institute

Related external organisation
Aarhus University
Inge Lehmanns Gade 10, 8000, Aarhus C, Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

MALDI Advanced Operator Training
Period: 29 Oct 2014
Bettina Nonnemann (Participant)
National Veterinary Institute

Description
Statistisk databehandling af MALDI-Imaging resultater

Related event
MALDI Advanced Operator Training: MALDI Imaging – Statistical evaluation
29/10/2014 → …
Bremen, Germany
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Antibiotics and Antibiotic Resistance in Aquaculture
Period: 27 Oct 2014
Morten Sichlau Bruun (Lecturer)
National Veterinary Institute
Section for Virology

Related event
24201 Diseases and Veterinary Aspects Related to Aquaculture
01/09/2014 → 01/12/2014
Frederiksberg, Denmark
Activity: Talks and presentations › Conference presentations

MALDI Essential Training – MALDI Imaging
Bettina Nonnemann (Participant)
National Veterinary Institute

Related event
MALDI Essential Training – MALDI Imaging
27/10/2014 → 28/10/2014
Bremen, Germany
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Annual Meeting of the United States Animal Health Association
Period: 19 Oct 2014
Gregers Jungersen (Invited speaker)
National Veterinary Institute
Section for Immunology and Vaccinology

**Description**
Vaccination as a tool for accelerated eradication of Mycobacterial diseases in ruminants in a context of other control programs

**Related event**
Annual Meeting of the United States Animal Health Association
16/10/2014 → 22/10/2014
Kansas City, United States
Activity: Talks and presentations › Conference presentations

**Development of a recombinant multi-stage DIVA vaccine against Johne's disease**
Period: 18 Oct 2014
Gregers Jungersen (Invited speaker)
National Veterinary Institute
Section for Immunology and Vaccinology

**Related event**
The Mycobacterial Diseases of Animals (MDA) multi-state initiative
18/12/2014 → …
Kansas City, United States
Activity: Talks and presentations › Conference presentations

**EU Working Group**
Anette Boklund (Invited speaker)
National Veterinary Institute
Section for Epidemiology

**Description**
European Commision, Working Group on animal Health contingency planning and emergency preparedness

**Related event**
16/10/2014 → 17/10/2014
Grange, Ireland
Activity: Talks and presentations › Conference presentations

**Molecular tracing of aquatic viruses - MOLTRAQ**
Period: 14 Oct 2014
Susie Sommer Mikkelsen (Lecturer)
National Veterinary Institute
Section for Virology

**Related event**
9th International Symposium on Viruses of Lower Vertebrates
01/10/2014 → 04/10/2014
Malaga, Spain
Activity: Talks and presentations › Conference presentations
EU-FMD
Period: 3 Oct 2014
Anette Boklund (Invited speaker)
National Veterinary Institute
Section for Epidemiology

Related event
EU-FMD: To vaccinate or not to vaccinate: using modelling to evaluate FMD control
29/09/2014 → 03/10/2014
Franscati, Italy
Activity: Talks and presentations › Conference presentations

9th International Symposium on Viruses of Lower Vertebrates
Susie Sommer Mikkelsen (Speaker)
National Veterinary Institute
Section for Virology

Description
Foredrag: MOLTRAQ - Tracing of VHSV in Denmark
Documents:
9th islvv abstract book

Related event
9th International Symposium on Viruses of Lower Vertebrates
01/10/2014 → 04/10/2014
Malaga, Spain
Activity: Talks and presentations › Conference presentations

8th Annual Meeting of Epizone
Period: 24 Sep 2014
Carsten Thure Kirkeby (Organizer)
Section for Epidemiology
National Veterinary Institute

Description
Epizone 2014 Conference, Copenhagen. Chairman for Epidemiology session 1.
Links:
http://www.epizone-eu.net/en/Home/Annual-meeting.htm (8th annual meeting Epizone)

Related event
8th Annual Meeting of Epizone: Primed for tomorrow
Copenhagen, Denmark
Activity: Attending an event › Participating in or organising a conference

8th Annual Meeting of Epizone
Period: 24 Sep 2014
Anette Boklund (Organizer)
National Veterinary Institute
Section for Epidemiology

Related event
8th Annual Meeting of Epizone: Primed for tomorrow
**8th Annual Meeting of Epizone**

**Period:** 23 Sep 2014 → 25 Sep 2014

Ana Carolina Lopes Antunes (Participant)

National Veterinary Institute

Section for Epidemiology

**Description**

Porcine Reproductive and Respiratory Syndrome (PRRS) epidemic in Denmark using laboratory submission data

**Related event**

**8th Annual Meeting of Epizone: Primed for tomorrow**


Copenhagen, Denmark

Activity: Attending an event › Participating in or organising a conference

**8th Annual Meeting of Epizone**

**Period:** 23 Sep 2014 → 25 Sep 2014

Per Kantsø Nielsen (Participant)

Section for Epidemiology

National Veterinary Institute

**Related event**

**Workshop on Communication**

**Period:** 23 Sep 2014

Ana Carolina Lopes Antunes (Participant)

National Veterinary Institute

Section for Epidemiology

**Related event**

**Workshop on Communication: YOUNG EPIZONE**

23/09/2014 → …

Coepnhagen, Denmark

Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

**Workshop on Communication**

**Period:** 23 Sep 2014

Per Kantsø Nielsen (Participant)

National Veterinary Institute

Section for Epidemiology

**Related event**

**Workshop on Communication: YOUNG EPIZONE**

23/09/2014 → …

Coepnhagen, Denmark
Assessment of zoonotic potential of four European swine influenza viruses in the ferret model
Period: 17 Sep 2014 → 19 Sep 2014
Kristina Fobian (Lecturer)
National Veterinary Institute
Section for Virology
Section for Bacteriology, Pathology and Parasitology

Description
The reverse zoonotic events that introduced the 2009 pandemic influenza virus into swine herds have drastically increased the diversity of reassortants throughout Europe. The pandemic potential of these novel reassortments is unknown, hence necessitating enhanced surveillance of European swine herds and enhanced focus on risk assessment of these new viruses. In this study, four European swine influenza viruses were assessed for their zoonotic potential. Of the four viruses, two were enzootic viruses of subtype H1N2 (with avian-like H1) and H3N2 and two were new reassortants, one with avian-like H1 and human-like N2 and one with pandemic H1 and swine-like N2. All viruses replicated to high viral titers in nasal wash- and nasal turbinate samples from inoculated ferrets and transmitted efficiently by direct contact. Only the H3N2 virus transmitted to naïve ferrets via respiratory droplets. Growth kinetics using human bronchial cells showed that all four viruses were able to replicate to high titers. Further, the viruses revealed preferential binding to the α2,6-sialylated glycans and investigation of the antiviral susceptibility of the viruses revealed that they were all sensitive to neuraminidase inhibitors. These findings suggest that the investigated viruses have the potential to infect humans and further underline the need for continued surveillance as well as pandemic and zoonotic assessment of new influenza reassortants.

Related event
Influenza2014: One Influenza, One World, One Health: Bringing together veterinary and human influenza
09/09/2014 → 11/09/2014
Oxford, United Kingdom
Activity: Talks and presentations › Conference presentations

Real-time PCR for diagnostics and surveillance of Fish Diseases
Period: 15 Sep 2014 → 17 Sep 2014
Susie Sommer Mikkelsen (Organizer)
National Veterinary Institute
Section for Virology

Description
Afholdelse af og undervisning i Real-time PCR for diagnostics and surveillance of Fish Diseases for internationale deltagere fra 12 lande.
Documents:
Training course Report

Related event
Real-time PCR for diagnostics and surveillance of Fish Diseases
15/09/2014 → 17/09/2014
Frederiksberg C, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Spørgeskema som redskab og metode til udvikling og udforskning af sygepleje
Period: 9 Sep 2014 → 14 Oct 2014
Anette Boklund (Lecturer)
Section for Epidemiology
National Veterinary Institute

Description
Kursus for sygeplejersker på kandidat-uddannelsen
Related external organisation

Aarhus University
Inge Lehmanns Gade 10, 8000, Aarhus C, Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

EURL training course 2014
Period: 8 Sep 2014 → 12 Sep 2014
Morten Sichlau Bruun (Organizer)
National Veterinary Institute
Section for Virology

Related event

EURL training course 2014
08/09/2014 → 17/09/2014
Kgs. Lyngby, Denmark
Activity: Attending an event › Participating in or organising a conference

Immunology and Infectious Diseases
Period: 4 Sep 2014
Kerstin Skovgaard (Invited speaker)
National Veterinary Institute
Section for Immunology and Vaccinology

Description
The pig as a large animal model for characterization of host-pathogen interactions

Related event

Immunology and Infectious Diseases
03/09/2014 → 05/09/2014
Sandbjerg, Denmark
Activity: Talks and presentations › Conference presentations

7th International Symposium on Aquatic Animal Health (ISAAH)
Period: 31 Aug 2014 → 4 Sep 2014
Lone Madsen (Participant)
National Veterinary Institute
Section for Bacteriology, Pathology and Parasitology

Description
Rainbow trout fed diets with varying content of marine and plant origin; how does that influence the outcome of experimental infections of the fry with Flavobacterium psychrophilum and Yersinia ruckeri?

Foredrag
Documents:
Abstract32e_ISAAH2014

Related event

7th International Symposium on Aquatic Animal Health (ISAAH)
31/08/2014 → 04/09/2014
Portland, OR, United States
Activity: Attending an event › Participating in or organising a conference

1st Dairy Care Conference
Ana Carolina Lopes Antunes (Participant)
National Veterinary Institute
Section for Epidemiology

Related event
1st Dairy Care Conference
22/08/2014 → 23/08/2014
Copenhagen, Denmark
Activity: Attending an event › Participating in or organising a conference

One Health Summer School 2014
Period: 13 Aug 2014
Carsten Thure Kirkeby (Lecturer)
National Veterinary Institute
Section for Epidemiology

Description
Carsten Kirkeby presented theory of vectorborne zoonotic disease modeling. The students did hands-on exercises with R0 simulation modeling.

Links:
http://healthsciences.ku.dk/education/summerschools/one-health/

Related event
One Health Summer School
11/08/2014 → 24/08/2014
Frederiksberg, Denmark
Activity: Talks and presentations › Conference presentations

iCULL – A herd-specific tool for financial evaluation of the impact of paratuberculosis
Period: 24 Jun 2014
Carsten Thure Kirkeby (Lecturer)
National Veterinary Institute
Section for Epidemiology

Description
iCull (intelligent Culling) is a newly started Danish project. The objective is to develop an economic, herd-specific model, which should be implemented in a smartphone app / computer software and serve as a tool for individual farmers to aid decision making on individual cows. The main focus will be on infections with Mycobacterium avium subsp. paratuberculosis (MAP), which can have a significant impact on the farmer’s economy. The iCull model can be used to evaluate the effect of control scenarios, such as breaking transmission routes by removing calves from their dam after birth or through pasteurization of colostrum, as well as for financial optimization of the culling approach in their herd. The iCull model estimates the retention pay-off (RPO) of each individual cow, while existing models address management decisions on herd-level. The iCull model can be used to assess actions deemed to lower the MAP infection pressure for a specific herd, and will aid the farmer’s decision making in ad hoc decisions about culling animals. For example, it can be used to test the optimal age for culling cows taking into account the milk yield and MAP infection status of the specific cow based on diagnostic test results. The model can also be used to evaluate if it is financially worthwhile to try to eradicate MAP from a farm or if it will be more beneficial to control the infection, or do nothing. Lastly, the iCull model can be useful for evaluating the financial impact of keeping cows with consistently low ELISA results in spite of a single positive value and culling cows with repeated positive results. It might be more ideal to use different test interpretations in different herds, e.g. adjusting the test cut-off or using more than just the latest ELISA test.

Links:
http://www.paratuberculosis.info/images/proc12/12icp.pdf (PROCEEDINGS of the 12th ICP)

Related event
12th International Colloquium on Paratuberculosis
22/06/2014 → 26/06/2014
Parma, Italy
12th International Colloquium on Paratuberculosis
Period: 22 Jun 2014 → 26 Jun 2014
Gregers Jungersen (Speaker)
National Veterinary Institute
Section for Immunology and Vaccinology

Related event

12th International Colloquium on Paratuberculosis
22/06/2014 → 26/06/2014
Parma, Italy
Activity: Talks and presentations › Conference presentations

Introduction to infectious disease modelling and its applications
Period: 16 Jun 2014 → 27 Jun 2017
Per Kantse Nielsen (Participant)
National Veterinary Institute
Section for Epidemiology

Related event

Introduction to infectious disease modelling and its applications
16/06/2014 → 27/06/2014
London, United Kingdom
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Comparative analysis of sequences from PT 2013
Period: 4 Jun 2014
Susie Sommer Mikkelsen (Lecturer)
National Veterinary Institute
Section for Virology

Related event

18th Annual Workshop of the National Reference Laboratories for Fish Diseases
03/06/2014 → 04/06/2014
Frederiksberg C, Denmark
Activity: Talks and presentations › Conference presentations

Molecular tracing of aquatic viruses: Tracing of VHSV in Denmark
Period: 4 Jun 2014
Susie Sommer Mikkelsen (Lecturer)
National Veterinary Institute
Section for Virology

Related event

18th Annual Workshop of the National Reference Laboratories for Fish Diseases
03/06/2014 → 04/06/2014
Frederiksberg C, Denmark
Activity: Talks and presentations › Conference presentations

18th Annual Workshop of the National Reference Laboratories for Fish Diseases
Period: 3 Jun 2014 → 4 Jun 2014
Morten Sichlau Bruun (Participant)
National Veterinary Institute
Section for Virology

**Related event**

18th Annual Workshop of the National Reference Laboratories for Fish Diseases
Period: 3 Jun 2014 → 4 Jun 2014
Frederiksberg C, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Niccolò Vendramin (Participant)
National Veterinary Institute
Section for Virology

**Description**
Scientific talk at Annual Workshop for national reference lab for fish diseases
Documents:
3- update on Med. Niven Abstract
3 - Training courses 2014
4- PT 2013

**Related event**

18th Annual Workshop of the National Reference Laboratories for Fish Diseases
Period: 3 Jun 2014
Copenhagen, Denmark
Activity: Attending an event › Participating in or organising a conference

PMCV and PRV occurrence in wild and farmed fish in Denmark
Period: 3 Jun 2014
Susie Sommer Mikkelsen (Lecturer)
National Veterinary Institute
Section for Virology

**Related event**

18th Annual Workshop of the National Reference Laboratories for Fish Diseases
Period: 3 Jun 2014 → 4 Jun 2014
Frederiksberg C, Denmark
Activity: Talks and presentations › Conference presentations
UPDATE ON FISH DISEASE SITUATION IN THE MEDITERRANEAN BASIN
Period: 3 Jun 2014
Niccolò Vendramin (Speaker)
National Veterinary Institute
Section for Virology
Documents:
3- update on Med. Niven Abstract

Related event
18th Annual Workshop of the National Reference Laboratories for Fish Diseases
03/06/2014 → 04/06/2014
Copenhagen, Denmark
Activity: Talks and presentations › Conference presentations

Vektorbårne infektioner
Period: 3 Jun 2014
Rene Bødker (Invited speaker)
National Veterinary Institute
Section for Epidemiology
Description
Kortlægning af risiko for vektorbårne infektioner
Documents:
Akademisk dag

Related event
Vektorbårne infektioner
03/06/2014 → …
Odense, Denmark
Activity: Talks and presentations › Conference presentations

PhD Cup 2014
Period: 24 May 2014
Carsten Thure Kirkeby (Other)
Section for Epidemiology
National Veterinary Institute
Description
The PhD Cup is a national competition about presenting the PhDs project to a broad audience. Eight persons from all Universities in Denmark are selected to present their project in 3 minutes in the award show. The show was broadcast on the national TV channel DR2.

Carsten Kirkeby won the third prize in the presentation contest.
Links:
http://www.vet.dtu.dk/Nyheder/2014/06/phdcup
http://www.dr.dk/Nyheder/Viden/phdcup/2014/05/09115247.htm

Related event
PhD Cup 2014
24/05/2014 → 24/05/2014
Activity: Talks and presentations › Conference presentations

MOLTRAQ Workshop
Period: 19 May 2014 → 23 May 2014
Susie Sommer Mikkelsen (Organizer)
National Veterinary Institute
Section for Virology

**Description**
Workshop for interne partnere m.h.p. at præsentere projekter og teknikker for samarbejdspartnere, efterfulgt af et progress meeeting.

**Related event**

**MOLTRAQ Workshop**
19/03/2014 → 23/03/2014
Berlin, Germany
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Molar Traq Workshop
Period: 19 May 2014 → 23 May 2014
Morten Sichlau Bruun (Participant)
National Veterinary Institute
Section for Virology

**Related event**

**MOLTRAQ Workshop**
19/03/2014 → 23/03/2014
Berlin, Germany
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Treponema species and the association with Bovine digital dermatitis
Period: 15 May 2014
Tim Kåre Jensen (Lecturer)
National Veterinary Institute
Section for Bacteriology, Pathology and Parasitology

**Description**
Invited speaker.
Documents:
BDD Uppsala May 2014 DTU Vet tije
BDD Uppsala May 2014 DTU Vet tije

**Related event**

**Treponemafestival: International Symposium on Treponema Infection**
15/05/2014 → …
Uppsala, Sweden
Activity: Talks and presentations › Conference presentations

2nd International Conference on Animal Health and Surveillance
Period: 7 May 2014 → 9 May 2014
Ana Carolina Lopes Antunes (Participant)
National Veterinary Institute
Section for Epidemiology

**Related event**

**2nd International Conference on Animal Health and Surveillance**
07/05/2014 → 09/05/2014
Havana, Cuba
**Data mining and knowledge discovery – an introductory course with focus on veterinary epidemiology applications**  
Period: 4 May 2014 → 6 May 2014  
Ana Carolina Lopes Antunes (Participant)  
National Veterinary Institute  
Section for Epidemiology  

**Related event**  
**Data mining and knowledge discovery – an introductory course with focus on veterinary epidemiology applications**  
04/05/2014 → 06/05/2014  
Havana, Cuba  
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

**Developing a recombinant vaccine against Mycobacterium paratuberculosis**  
Period: 2 May 2014 → 3 May 2014  
Gregers Jungersen (Invited speaker)  
National Veterinary Institute  
Section for Immunology and Vaccinology  

**Related event**  
**Veterinary Immunology Workgroup (VIA) of the German Society for Immunology (DGfI)**  
02/05/2014 → 03/05/2014  
Jena, Germany  
Activity: Talks and presentations › Conference presentations

**Bayesian Statistics, Simulation and software - With a view to Application Examples**  
Period: 29 Apr 2014 → 4 Jun 2014  
Per Kantsø Nielsen (Participant)  
National Veterinary Institute  
Section for Epidemiology  

**Related event**  
**Bayesian Statistics, Simulation and software - With a view to Application Examples**  
29/04/2014 → 04/06/2014  
Aalborg, Denmark  
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

**University of Copenhagen (External organisation)**  
Period: 28 Apr 2014  
Gregers Jungersen (Participant)  
National Veterinary Institute  
Section for Immunology and Vaccinology  

**Description**  
PhD evaluation committee for Anne Deen Christensen  

**Related external organisation**  
**University of Copenhagen**  
Thorvaldsensvej 40, DK-1871 Frederiksberg C, Copenhagen, Denmark  
Activity: Membership › Membership in review committee
Related event

**VI Congresso da Sociedade Portuquesa de Ciências Veterinárias**
*Period: 3 Apr 2014 → 5 Apr 2014*

Ana Carolina Lopes Antunes (Participant)

National Veterinary Institute

Section for Epidemiology

How to estimate the risk of exotic disease incursion
*Period: 26 Mar 2014*

Ana Carolina Lopes Antunes (Participant)

National Veterinary Institute

Section for Epidemiology

Related event

**SVEPM Annual Meeting 2014**
*Period: 26 Mar 2014 → 28 Mar 2014*

Ana Carolina Lopes Antunes (Participant)

National Veterinary Institute

Section for Epidemiology

Related event

**SVEPM Annual Meeting 2014**
*Period: 26 Mar 2014 → 28 Mar 2014*

Per Kantsø Nielsen (Participant)

National Veterinary Institute

Section for Epidemiology

Related event

**SVEPM Annual Meeting 2014**
*Period: 26 Mar 2014 → 28 Mar 2014*

Dublin, Ireland

Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.
Section for Immunology and Vaccinology

**Description**
PhD evaluation committee for Per Skallerup

**Related external organisation**

**University of Copenhagen**
Thorvaldsensvej 40, DK-1871 Frederiksberg C, Copenhagen, Denmark
Activity: Membership › Membership in review committee

**Vectorborne Threats in northern Europe**
Period: 13 Mar 2014
Carsten Thure Kirkeby (Participant)
National Veterinary Institute
Section for Epidemiology

**Description**
Workshop on preparedness tool for vectorborne diseases

**Related event**

**Vectorborne Threats in northern Europe**
13/03/2014 → 14/03/2014
Amsterdam, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

**Euraxess Career Roadshow**
Period: 11 Mar 2014
Ana Carolina Lopes Antunes (Participant)
National Veterinary Institute
Section for Epidemiology

**Related event**

**Euraxess Career Roadshow**
11/03/2014 → …
Copenhagen, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

**Workgroup for Sampling and Diagnostic Procedures for the Surveillance and Confirmation of KHV Disease**
Period: 25 Feb 2014 → 26 Feb 2014
Susie Sommer Mikkelsen (Participant)
National Veterinary Institute
Section for Virology

**Related event**

**Workgroup for Sampling and Diagnostic Procedures for the Surveillance and Confirmation of KHV Disease**
25/02/2014 → 26/02/2014
Frederiksberg C, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

**Up to date with pig research**
Period: 29 Jan 2014
Ana Carolina Lopes Antunes (Participant)
National Veterinary Institute
Section for Epidemiology

Related event

Up to date with pig research
29/01/2014 → …
Copenhagen, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

National Veterinary Institute: Gastro-intestinal research
Period: 15 Jan 2014
Tim Kåre Jensen (Lecturer)
National Veterinary Institute
Section for Bacteriology, Pathology and Parasitology

Description
Invited speaker
Documents:
Gastric Ulcers in Pigs 2014 DTU VET
Gastric Ulcers in Pigs 2014 DTU VET

Related event

International Seminar on Gastric Ulcers in Pigs
15/01/2014 → …
Copenhagen, Denmark
Activity: Talks and presentations › Conference presentations

P L o S One (Journal)
Period: 1 Jan 2014 → …
Carsten Thure Kirkeby (Reviewer)
National Veterinary Institute
Section for Epidemiology
Links:
http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0150341&utm_source=plos&utm_medium=email&utm_campaign=one-1602-revty#sec001 (Reviewer list 2015)

Related journal

P L o S One
1932-6203
Indexed in DOAJ
Central database
Activity: Research › Peer review of manuscripts

Koordineringsudvalget for kvæg, SEGES (External organisation)
Period: 2013 → 2015
Tim Kåre Jensen (Participant)
National Veterinary Institute
Section for Bacteriology, Pathology and Parasitology

Description
DTU repræsentant i koordinationsudvalget for kvæg, SEGES

Related external organisation
Koordineringsudvalget for kvæg, SEGES
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

10th Workshop in Protein.DTU
Period: 27 Nov 2013
Chris Juul Hedegaard (Participant)
National Veterinary Institute
Section for Immunology and Vaccinology
Documents:
Poster

Related event
10th Workshop in Protein.DTU
27/11/2013 → 27/11/2013
Kgs. Lyngby, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Danish Fish Immunology Research Network (DAFINET) workshop
Period: 12 Nov 2013 → 14 Nov 2013
Morten Sichlau Bruun (Participant)
National Veterinary Institute
Section for Virology
National Institute of Aquatic Resources
Description
DAFINET Workshop, Fish Immunology: From Egg to Adult Fish

Related event
Danish Fish Immunology Research Network (DAFINET) workshop: Fish Immunology: From Egg to Adult Fish
12/11/2013 → 14/11/2013
Frederiksberg, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Dr Philos in Veterinary Sciences, 1. opponent (External organisation)
Period: 6 Nov 2013 → 7 Nov 2013
Åse Uttenthal (External examiner)
Section for Virology
National Veterinary Institute
Description
Dr Thesis Gelagay Ayelet Melasse: "Epidemiological investigation and molecular characterisation of major viral diseases of livestock: Implication for disease control in Ethiopia"

1. opponent in Dr Philos Commitee. Veterinary University of Oslo

Body type: Evaluation comittee
Degree of recognition: International
Activity: Examinations and supervision › External examination

Antibiotics and antibiotic resistance: evolutionary and ecological implications
Rustam Aminov (Speaker)
National Veterinary Institute
**Description**
International Scientific Committee, Organizer, Plenary Lecture, Chair
Degree of recognition: International

**Documents:**
Conference Armenia

**Related event**

**Perspectives for development of molecular and cellular biology - 4**
21/10/2013 → 22/10/2013
Yerevan, Armenia
Activity: Talks and presentations › Conference presentations

**Aqua Excel**
Period: 16 Oct 2013 → 18 Oct 2013
Susie Sommer Mikkelsen (Participant)
National Veterinary Institute
Section for Virology

**Description**
Main elements of the course:
The genome – introduction, sequencing, construction, annotation and comparative genome mapping.
How genomic information can help to refine phenotyping.
Identification and exploration of genomic regions associated with variation of aquaculture-related traits.
Practical training.

**Related event**

**Aqua Excel: Contribution of genomic approaches to the development of a sustainable aquaculture for temperate and Mediterranean fish**
16/10/2013 → 18/12/2013
Rennes, France
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

**EPIZONE Annual Meeting (External organisation)**
Period: 2 Oct 2013 → 5 Oct 2013
Åse Uttenthal (Member)
National Veterinary Institute

**Description**
Member of Scientific Commitee, responsible for "Diagnostics"

Body type: Network of Excellence
Degree of recognition: International
Links:
http://www.epizone-eu.net/

**Related external organisation**

**EPIZONE Annual Meeting**
Activity: Membership › Membership in review committee

**Spørgeskema som redskab og metode til udvikling og udforskning af sygepleje**
Period: 1 Oct 2013 → 15 Nov 2013
Anette Boklund (Lecturer)
National Veterinary Institute
Description
Kursus for sygeplejersker på kandidat-uddannelsen

Related external organisation

Aarhus University
Inge Lehmanns Gade 10, 8000, Aarhus C, Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

Mucosal Vaccines, Adjuvants & Delivery
Period: 25 Sep 2013 → 27 Sep 2013
Chris Juul Hedegaard (Participant)
National Veterinary Institute
Section for Immunology and Vaccinology
Documents:
Poster

Related event

Mucosal Vaccines, Adjuvants & Delivery
25/09/2013 → 27/09/2013
Copenhagen, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Dyreforsøgstilsynets mini-seminar
Period: 24 Sep 2013
Morten Sichlau Bruun (Participant)
National Veterinary Institute
Section for Virology
National Institute of Aquatic Resources

Related event

Dyreforsøgstilsynets mini-seminar: Vurdering af belastning af forsøgsdyr
24/09/2013 → 24/09/2013
Bagsværd, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

53rd Interscience Conference on Antimicrobial Agents and Chemotherapy
Period: 12 Sep 2013
Anders Folkesson (Speaker)
National Veterinary Institute
Section for Bacteriology, Pathology and Parasitology

Description
Presentation:
C1-1440a Antibiotic Combination Therapy Leads to Broad Range Multi-Antibiotic Resistance in Pseudomonas aeruginos
Links:
http://www.icaac.org/

Related event

53rd Interscience Conference on Antimicrobial Agents and Chemotherapy
10/09/2013 → 13/09/2013
Denver, CO, United States
Activity: Talks and presentations › Conference presentations
Whole inactivated virus vaccine prototype protects against viral encephalopathy and retinopathy in European sea bass (D. labrax)
Period: 2 Sep 2013 → 6 Sep 2013
Niccolò Vendramin (Speaker)
National Veterinary Institute
Section for Virology

Description
Oral presentation at EAFP Conference semptember 2013 Tampere.
Documents:
C:\Users\Niven\Desktop\0101_001

Related event
16th International Conference on Diseases of Fish and Shellfish
02/09/2013 → 06/09/2013
Tampere, Finland
Activity: Talks and presentations › Conference presentations

Informations Medieskole
Period: 1 Sep 2013 → 14 Dec 2013
Carsten Thure Kirkeby (Participant)
National Veterinary Institute
Section for Epidemiology
Links:
http://phdcup.dk/skribenter/carsten-kirkeby/

Related event
Informations Medieskole
01/09/2013 → 14/12/2013
Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Comparing control strategies against foot-and-mouth disease: will vaccination be cost-effective in Denmark?
Period: 30 Aug 2013
Anette Boklund (Lecturer)
National Veterinary Institute
Section for Epidemiology

Related event
Disease Control and Dynamics – In a One Health Setting
26/08/2013 → 30/08/2013
Frederiksberg, Denmark
Activity: Talks and presentations › Conference presentations

10th International Veterinary Immunology Symposium
Period: 28 Aug 2013 → 1 Sep 2013
Chris Juul Hedegaard (Participant)
National Veterinary Institute
Section for Immunology and Vaccinology
Documents:
Poster

Related event
10th International Veterinary Immunology Symposium
28/08/2013 → 01/09/2013
Milano, Italy
Activity: Attending an event › Participating in or organising a conference
10th International Veterinary Immunology Symposium  
Period: 28 Aug 2013 → 1 Sep 2013  
Ann Cathrine Findal Støy (Participant)  
National Veterinary Institute  
Section for Immunology and Vaccinology  
Documents:  
poster

Related event

10th International Veterinary Immunology Symposium  
28/08/2013 → 01/09/2013  
Milano, Italy  
Activity: Attending an event › Participating in or organising a conference

Disease Control and Dynamics – In a One Health Setting  
Period: 26 Aug 2013 → 30 Aug 2013  
Anette Boklund (Lecturer)  
Section for Epidemiology  
National Veterinary Institute  
Description  
Masterkursus  
Related external organisation

University of Copenhagen  
Thorvaldsensvej 40, DK-1871 Frederiksberg C, Copenhagen, Denmark  
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

Bayesian spatial modelling of disease vector data on Danish farmland  
Period: 22 Aug 2013  
Carsten Thure Kirkeby (Lecturer)  
National Veterinary Institute  
Section for Epidemiology  
Description  
Spatially distributed ecological count data, such as abundance of disease vectors, typically cannot be modelled statistically using the Gaussian framework but require a more elaborate approach such as the generalised linear geostatistical model (GLGM).

We applied the GLGM to a dataset with counts of Culicoides disease vectors around farms in Denmark. The GLGM assumes a Poisson distribution for the dependent variable whose intensity is governed by explanatory factors such as distance to farms, and by a spatially correlated stochastic signal. We calibrated the model on counts of traps catching disease vector in 25 locations in a grassland area over 25 consecutive nights. Separate models were fitted for all nights, resulting models compared and differences interpreted and related to temporal meteorological conditions (e.g. wind speed, temperature, rainfall and moisture). All statistical analyses were conducted using the geoRglm package in R.

Results show that one of the most important spatial explanatory factors for the abundance of Culicoides vectors is the distance to host animals. Comparisons of fitted models under different meteorological conditions indicated that the weather had a marked effect on the model parameters and spatial distribution of the disease vectors.

The GLGM used in this study provided a sound representation of the data and indicated that distance to host animals and meteorological conditions are important controlling factors. Further improvements are foreseen by incorporating both temporal and spatial factors in an integrated spatio-temporal GLGM.

Related event
15th International Conference on Production Diseases in Farm Animals
Period: 24 Jun 2013 → 28 Jun 2013
Chris Juul Hedegaard (Participant)
National Veterinary Institute
Section for Immunology and Vaccinology

16th International Symposium of the World Association for Veterinary Laboratory Diagnosticians
Period: 7 Jun 2013
Åse Uttenthal (Chairman)
National Veterinary Institute
Section for Virology

Comparing control strategies against foot-and-mouth disease: will vaccination be cost-effective in Denmark?
Period: 18 Jun 2013
Anette Boklund (Lecturer)
National Veterinary Institute
Section for Epidemiology

Concentrating antibodies towards BVDV from milk
Period: 6 Jun 2013
Åse Uttenthal (Lecturer)
National Veterinary Institute
Section for Virology

Aktualitetsdag
18/06/2013 → …
Herning, Denmark
Activity: Talks and presentations › Conference presentations

15th International Conference on Production Diseases in Farm Animals
24/06/2013 → 28/06/2013
Uppsala, Sweden
Activity: Attending an event › Participating in or organising a conference
Dyreforsøgstilsynets mini-seminar om fisk som forsøgsdyr
Period: 4 Jun 2013
Morten Sichlau Bruun (Participant)
National Veterinary Institute
Section for Virology
National Institute of Aquatic Resources

Related event
Dyreforsøgstilsynets mini-seminar om fisk som forsøgsdyr
04/06/2013 → 04/06/2013
Kastrup, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

EURL Training courses. Report and topics for future courses.
Period: 30 May 2013
Susie Sommer Mikkelsen (Lecturer)
National Veterinary Institute
Section for Virology
Documents:
17th Annual Meeting of the National Reference Laboratories for Fish Diseases

Related event
17th Annual Workshop of the National Reference Laboratories for Fish Diseases
29/05/2013 → 30/05/2013
Copenhagen, Denmark
Activity: Talks and presentations › Conference presentations

MOLTRAQ - molecular epidemiology for fish diseases
Period: 30 May 2013
Susie Sommer Mikkelsen (Lecturer)
National Veterinary Institute
Section for Virology

Description
Oral presentation.
Documents:
17th Annual Meeting of the National Reference Laboratories for Fish Diseases

Related event
17th Annual Workshop of the National Reference laboratories for Fish Diseases
29/05/2013 → 30/05/2013
Frederiksberg, Denmark
Activity: Talks and presentations › Conference presentations

17th Annual Workshop of the National Reference Laboratories for Fish Diseases
Period: 29 May 2013 → 30 May 2013
Morten Sichlau Bruun (Participant)
National Veterinary Institute
Section for Virology
National Institute of Aquatic Resources

Description
17th Annual Workshop of the National Reference Laboratories for Fish Diseases.

Related event

17th Annual Workshop of the National Reference Laboratories for Fish Diseases
29/05/2013 → 30/05/2013
Copenhagen, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

17th Annual Workshop of the National Reference Laboratories for Fish Diseases
Period: 29 May 2013 → 30 May 2013
Susie Sommer Mikkelsen (Speaker)
National Veterinary Institute
Section for Virology

Description
Oral presentation: MOLTRAQ - molecular epidemiology for fish diseases Oral presentation: EURL training courses. Report
and topics for future courses

17th Annual Workshop of the National Reference Laboratories for Fish Diseases.
Documents:
17th Annual Meeting of the

Related event

17th Annual Workshop of the National Reference Laboratories for Fish Diseases
29/05/2013 → 30/05/2013
Copenhagen, Denmark
Activity: Talks and presentations › Conference presentations

17th Annual Workshop of the National Reference Laboratories for Fish Diseases
Period: 29 May 2013 → 30 May 2013
Torsten Snogdal Boutrup (Speaker)
National Veterinary Institute
Section for Virology

Description
Årligt møde for de Europæiske referencelaboratorier for fiskesygdomme, med opdatering på diagnostik, forskning og
sygdomssituation i Europa.

17th annual Workshop of the National Reference Laboratories for Fish Diseases. Copenhagen, Denmark, May 29-30, 2013.

Related event

17th Annual Workshop of the National Reference Laboratories for Fish Diseases
29/05/2013 → 30/05/2013
Copenhagen, Denmark
Activity: Talks and presentations › Conference presentations

Overlevelse af virus i miljøet
Period: 29 May 2013
Åse Uttenthal (Lecturer)
National Veterinary Institute
Section for Virology

**Description**
Lecturing veterinarians in the Veterinary Administration

Fødevarestyrelsens aktualitetskursus, Vejle, Danmark

**Related external organisation**

**Unknown external organisation**
Activity: Talks and presentations › Conference presentations

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**Det er en virus! Hvorfor bliver man syg?**
**Period:** 3 May 2013
**Åse Uttenthal (Lecturer)**
National Veterinary Institute
Section for Virology

**Description**
Vilvorde laborantskole, dyrepasser klasse

**Related event**

**Bestil en forsker: Forskningens døgn**
02/05/2013 → 04/05/2013
Denmark
Activity: Talks and presentations › Conference presentations

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**Det er en virus! Hvorfor bliver man syg?**
**Period:** 2 May 2013
**Åse Uttenthal (Lecturer)**
National Veterinary Institute
Section for Virology

**Description**
Ørestadens Gymnasium, København S

**Related event**

**Bestil en forsker: Forskningens døgn**
02/05/2013 → 04/05/2013
Denmark
Activity: Talks and presentations › Conference presentations

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**Is the intestinal microbiota in rainbow trout (oncorhynchus mykiss) influenced by diet type and challenge by yersinia ruckeri?**
**Period:** 10 Apr 2013
**Hans-Christian Ingerslev (Lecturer)**
National Veterinary Institute
Section for Bacteriology, Pathology and Parasitology

**Description**
Dafinet (Danish Fish Immunology Research Center & Network) workshop (www.dafinet.dk).
Documents:
Dafinet_abstract
**EDENext Annual Meeting**
Period: 22 Mar 2013
Carsten Thure Kirkeby (Speaker)
National Veterinary Institute
Section for Epidemiology
Links:
http://www.edenext.eu/the-project/news/annual-meeting-prize-winners (EDENext Barcelona 2013)

**Related event**

**EDENext Annual Meeting**
19/03/2013 → 22/03/2013
Barcelona, Spain
Activity: Talks and presentations › Conference presentations

**5th Meeting on Global Microbial Identifier**
Period: 27 Feb 2013 → 28 Feb 2013
Susie Sommer Mikkelsen (Participant)
National Food Institute
National Veterinary Institute
Section for Virology

**Description**
GMI focuses on the use of genome sequencing techniques in a global system for microbiological identification and epidemiological surveillance
Links:
http://www.food.dtu.dk/english/News/2012/12/Invitation_5th_Meeting_on_Global_Microbial_Identifier (Link to invitation)

**Related event**

**5th Meeting on Global Microbial Identifier**
27/02/2013 → 28/02/2013
København, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

**Dissemination on CSFV_goDIVA**
Period: 30 Jan 2013 → 31 Jan 2013
Åse Uttenthal (Organizer)
National Veterinary Institute
Section for Virology

**Description**
Dissemination meeting for stake holders, CODA-CERVA Ukkels, Brussels, Belgium

CSFV_goDIVA dissemination meeting
Links:
http://www.csfvaccine.org/ (CSFV_goDIVA project)

**Related event**

**Dissemination on CSFV_goDIVA: Improve tools and strategies for the prevention and control of classical swine fever.**
31/01/2013 → …
Brussels, Belgium
Svinepest i en globaliseret verden  
Period: 29 Jan 2013  
Åse Uttenthal (Invited speaker)  
National Veterinary Institute  
Section for Virology  

Description  
Talk on swine fevers for a group of pig farmers  

Related event  
Ø-Vet årsmøde  
29/01/2013 → …  
Ringsted, Denmark  
Activity: Talks and presentations › Conference presentations  

EUURL training course 2013  
Period: 28 Jan 2013 → 31 Jan 2013  
Susie Sommer Mikkelsen (Organizer)  
National Veterinary Institute  
Section for Virology  

Description  
Course responsible and teacher  
Documents:  
Training Course Report 2013  

Related event  
EUURL training course 2013: Advanced Bio-Molecular techniques and bio-informatics  
28/01/2013 → 31/07/2013  
Aarhus, Denmark  
Activity: Attending an event › Participating in or organising a conference  

NOSOVE  
Period: 14 Jan 2013 → 17 Jan 2013  
Anette Boklund (Participant)  
National Veterinary Institute  
Section for Epidemiology  

Related event  
NOSOVE  
14/01/2013 → 17/01/2013  
Copenhagen, Denmark  
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.  

Parasites & Vectors (Journal)  
Period: 1 Jan 2013 → …  
Carsten Thure Kirkeby (Reviewer)  
National Veterinary Institute  
Section for Epidemiology  

Related journal
European Association of Veterinary Laboratory Diagnosticians, EAVLD (External organisation)
Period: 2012 → 2016
Lars Ole Andresen (Participant)
National Veterinary Institute

Description
EAVLD is a non-profit, independent association with the mission of improving veterinary and public Health by providing a platform for communication among veterinary laboratory diagnosticians and to promote the highest standards in European veterinary laboratories.

Board member and editor of the EAVLD Newsletter

Body type: Governing board
Degree of recognition: International
Links:
http://www.eavld.org/

Related external organisation
European Association of Veterinary Laboratory Diagnosticians, EAVLD
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

Expert groups in Denmark with special reference to Classical and African swine fever
Period: 3 Dec 2012
Åse Uttenthal (Invited speaker)
National Veterinary Institute
Section for Virology

Related event
Nordic-Baltic Veterinary Contingency Group: Expert group Ad hoc meeting
03/12/2012 → 04/12/2012
Copenhagen, Denmark
Activity: Talks and presentations › Conference presentations

CoVetLab
Period: 27 Nov 2012 → 28 Nov 2012
Susie Sommer Mikkelsen (Participant)
National Veterinary Institute
Section for Virology

Description
The aim of the workshop will be for CoVetLab members to share information (previous experiences/ current best practice, etc) about the use of microarrays and next generation sequencing for detection and characterization of diseases of unknown aetiology

Related event
CoVetLab: Emerging Approaches to Novel Pathogen Discovery
27/11/2012 → 28/11/2012
Weybridge, United Kingdom
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.
The need to measure and predict vector abundance and biting rate
Period: 1 Nov 2012
Rene Bødker (Speaker)
National Veterinary Institute
Section for Epidemiology

Description
Presentation at half-day seminar about arthropods as vectors of diseases at the Swedish National Veterinary Institute (SVA).
Links:
http://www.sva.se/en/

Related event
Arthropods as vectors of diseases
01/11/2012 → …
Uppsala, Sweden
Activity: Talks and presentations › Conference presentations

Risk based surveillance for vector borne diseases
Period: 30 Oct 2012
Rene Bødker (Keynote speaker)
National Veterinary Institute
Section for Epidemiology

Related event
NJF seminar 457 : Sustainable Agriculture in The Baltic Sea Region with focus on climate change
30/10/2012 → 31/10/2012
Uppsala, Sweden
Activity: Talks and presentations › Conference presentations

Workshop on ASFV
Åse Uttenthal (Participant)
National Veterinary Institute
Section for Virology

Description
ASFV laboratory expert
ASFV workshop in Latvia

Related event
Workshop on ASFV: EU - Russian collaboration
29/10/2012 → 31/10/2012
Sigunda, Latvia
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Svinepest - faglig dag for svinedyrlæger på Lindholm: Vesikulaere sygdomme hos gris
Period: 28 Sep 2012
Louise Lohse (Speaker)
National Veterinary Institute
Section for Virology
**The Effect of Antimicrobial Peptides on Microbial Biofilms**

**Period:** 23 Sep 2012 → 26 Sep 2012  
**Anders Folkesson (Invited speaker)**  
**Department of Systems Biology**  
**Center for Systems Microbiology**  
**National Veterinary Institute**  
**Section for Bacteriology, Pathology and Parasitology**

**Description**  
10:30-12:00 Session 8: Biofilm  
IL17 Anders Folkesson (Denmark)  
The Effect of Antimicrobial Peptides on Microbial Biofilms  
Links:  
http://www.hmd-cms.hr/cesar2012/

**Related event**

**Central European Symposium on Antimicrobials and Antimicrobial Resistance**  
23/09/2012 → 26/09/2012  
**Primosten, Croatia**  
**Activity:** Talks and presentations › Conference presentations

**9th International Congress of Veterinary Virology**  
**Period:** 6 Sep 2012  
**Åse Uttenthal (Speaker)**  
**National Veterinary Institute**  
**Section for Virology**

**Related event**

**9th International Congress of Veterinary Virology**  
04/09/2012 → 07/09/2012  
**Madrid, Spain**  
**Activity:** Talks and presentations › Conference presentations

**Schmallenberg virus - et nyt virus hos drøvtyggere: Forekomst, spredning, klinik og diagnostik**  
**Period:** 5 Sep 2012  
**Louise Lohse (Lecturer)**  
**National Veterinary Institute**  
**Division of Virology**  
**Sektion for Eksotiske Virussygdomme**

**Description**  
Indlæg på Kvægkonference 2012  
Documents:

Schmallenberg_virus_Kv_gkonference_05092012.docx
Related event

**Kvægkonference 2012: Sikring af sunde og sygdomsfri dyr i kvægbruget**

04/09/2012 → ...

Bredsten, Denmark

Activity: Talks and presentations › Conference presentations

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**Brachyspirainfektioner hos svin og in situ identifikation**

Period: 30 Aug 2012

Tim Kåre Jensen (Lecturer)

National Veterinary Institute

Division of Veterinary Diagnostics and Research

Bacteriology & Pathology

Description

Foredrag for dyrlæger ansat i Landbrugets Veterinære Konsulenttjeneste, d. 30/8 2012 i Hobro.

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**2012 Gordon Research Conference Drug Resistance**


Anders Folkesson (Participant)

National Veterinary Institute

Section for Bacteriology, Pathology and Parasitology

Description

Poster Presentation

Links:


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**Hvad er vigtigt for et stærkt beredskab - set fra en laboratoriedyrlæges indfaldsvinkel?**

Period: 26 Jul 2012

Jens Nielsen (Speaker)

National Veterinary Institute

Section for Virology

Description

Mundtlig præsentation ved "Åben høring om det danske veterinære beredskab" arrangeret af Folketingets Udvalg for Fødevarer, Landbrug og Fiskeri. Høringen fandt sted i Landstingssalen på Christiansborg.

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**Studies of Classical Swine Fever in pigs based on experimental infections**

Period: 24 Jul 2012

Åse Uttenthal (Lecturer)
**Description**
Lecture at Sichuan University, Chengdu, China

**Related external organisation**
Unknown external organisation
Activity: Talks and presentations › Conference presentations

**Studies of Classical Swine Fever in pigs based on experimental infections**
Period: 24 Jul 2012
Åse Uttenthal (Lecturer)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Description**
Lecture at Sichuan University, Chengdu, China

**Related external organisation**
Unknown external organisation
Activity: Talks and presentations › Conference presentations

**Epizone Satellite Symposium: Schmallenberg virus**
Period: 15 Jun 2012
Carsten Thure Kirkeby (Participant)
National Veterinary Institute
Section for Epidemiology

**Related event**
Epizone Satellite Symposium: Schmallenberg virus: 6th Epizone Conference
15/06/2012 → …
Brighton, United Kingdom
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

**6th Annual Meeting EPIZONE**
Period: 13 Jun 2012
Åse Uttenthal (Participant)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme
Description
EPIZONE, 6th annual meeting "Viruses on the move"

Chairman of the session "Epidemiology and emerging diseases"

Links:
http://www.epizone-eu.net/ (EU Network of Excellence)

Related event

6th Annual Meeting EPIZONE
13/06/2012 → 14/06/2012
Brighton, United Kingdom
Activity: Attending an event › Participating in or organising a conference

National reference laboratories swine fevers
Period: 6 Jun 2012
Åse Uttenthal (Speaker)
National Veterinary Institute
Section for Virology

Description
The efficacy of CP7_E2alf: an animal study involving piglets from C-strain vaccinated sows. Rangelova, Nielsen, Strandbygaard, Blome, Uttenthal.

Workshop for ASFV and CSFV laboratories

Related event

National reference laboratories swine fevers
05/06/2012 → 08/12/2012
Hannover, Germany
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

Serological analysis of CP7_E2alf efficacy in face of maternal immunity
Period: 5 Jun 2012
Desislava Yordanova Rangelova (Speaker)
National Veterinary Institute

Related organisation

Serological analysis of CP7_E2alf efficacy in face of maternal immunity
Rangelova, D. Y. (Speaker)
5 Jun 2012
Activity: Talks and presentations › Conference presentations

DFSTM Annual Meeting
Period: 30 May 2012 → 31 May 2012
Tina Rødgaard Højbøge (Participant)
National Veterinary Institute
Section for Immunology and Vaccinology

Description
The Danish Society of Pharmacology, Toxicology and Medicinal Chemistry's annual meeting with the title "Frontiers in Obesity Research".
Documents:
Poster_DSFTM

Related event

DFSTM Annual Meeting: Frontiers in Obesity Research
Virus og vaccination, hvorfor bliver man syg?
Period: 19 Apr 2012
Åse Uttenthal (Lecturer)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
"Bestil en forsker", populærvidenskabelig formidling. Foredrag for 270 elever fra 7-9 klasse, Lille Næstved skole, april 2012
Links:
http://forsk.dk/

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Nano Update 2012
Sofie Bruun Hartmann (Participant)
National Veterinary Institute
Section for Immunology and Vaccinology

Related event
Nano Update 2012
29/03/2012 → 30/03/2012
Helsingborg, Sweden
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Mitternes verden - epidemiologiske studier
Period: 22 Mar 2012
Carsten Thure Kirkeby (Lecturer)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Section for Veterinary Epidemiology and public sector consultancy

Description
De fleste danskere er blevet bidt af en mitte på et eller andet tidspunkt, oftest uden at vide det. Mitter er dem vi kender fra Sverige som "knott", der optræder i uhyrlige antal om sommeren. Men vi har faktisk omkring 40 arter af mitter i Danmark, og de findes overalt i landet. De bider både dyr og mennesker, og kan opleves i enorme mængder om aftenen når de går på vingerne. For eksempel er der fanget ca. 20.000 mitter på én nat, i en enkelt fælde som stod tæt ved en kostald i Nordsjælland.


Jeg vil i dette foredrag fortælle om egne og andres forskning omkring mitter og bluetongue. I forbindelse med mit ph.d.-studie, har jeg de sidste fire somre arbejdet med mitter i flesten i Danmark og vil demonstrere fangstmetoder, eksperimentelle opstillinger, analytiske overvejelser og metoder der bruges til at analysere de indsamlede data.

Foredrag i Dansk Naturhistorisk Forening.
7th World Immune Regulation Meeting
Tina Rødgaard Højbege (Participant)
National Veterinary Institute
Section for Immunology and Vaccinology
Documents:
Poster_WIRM

Related event
7th World Immune Regulation Meeting: Innate and Adaptive Immune Response and Role of Tissues in Immune Regulation
18/03/2012 → 21/03/2012
Davos, Switzerland
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Medicines Research Academy Symposium
Period: 1 Mar 2012
Sofie Bruun Hartmann (Participant)
National Veterinary Institute
Section for Immunology and Vaccinology

Related event
Medicines Research Academy Symposium
01/03/2012 → 01/03/2012
Lund, Sweden
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Mathematical Models for Infectious Disease Dynamics
Period: 13 Feb 2012 → 24 Feb 2012
Carsten Thure Kirkeby (Participant)
National Veterinary Institute
Section for Epidemiology
Links:
http://www.nature.com/natureevents/science/events/13305-Mathematical_Models_for_Infectious_Disease_Dynamics

Related event
Mathematical Models for Infectious Disease Dynamics
13/02/2012 → 24/02/2012
Hinxton, Cambridge, United Kingdom
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Conference and Science dating on Nanotechnology for Medical use
Period: 11 Jan 2012
Sofie Bruun Hartmann (Participant)
National Veterinary Institute
Section for Immunology and Vaccinology

Related event
Case Reports in Rheumatology (Journal)
Period: 2011
Rustam Aminov (Editor)
National Veterinary Institute

Description
Case Reports in Rheumatology is a peer-reviewed, open access journal that publishes case reports in all areas of rheumatology.

Editorial Board

Related journal

Geostatistics course for PhD students
Period: 13 Dec 2011 → 16 Dec 2011
Carsten Thure Kirkeby (Participant)
National Veterinary Institute
Section for Epidemiology
Links:
http://geostat-course.org/node/772 (Description)

Related event

Controlling CSFV without vaccination: CSFV control from an EU perspective
Period: 18 Dec 2011
Åse Uttenthal (Lecturer)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Lecture at Shaoguan University, Guangdong, China

Unknown external organisation
Activity: Talks and presentations › Conference presentations

CSFV_goDIVA project meeting: Characterization of a recent CSFV strain
Period: 29 Nov 2011
Åse Uttenthal (Speaker)
National Veterinary Institute
Division of Virology

Description
Place: Barcelona, Spain

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

**CSFV_goDIVA project meeting: Characterization of a recent CSFV strain**
Period: 29 Nov 2011
Lou Gaoming (Participant)
National Veterinary Institute

Related event

**CSFV_goDIVA project meeting: Characterization of a recent CSFV strain**
Barcelona, Spain
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

**Efficacy of CP7_E2alf in piglets from sows vaccinated with C-strain live attenuated vaccine**
Period: 29 Nov 2011
Desislava Yordanova Rangelova (Speaker)
National Veterinary Institute

Description
Place: Barcelona

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

**African Swine Fever experiments within NADIR**
Period: 6 Nov 2011
Mette Sif Hansen (Speaker)
National Veterinary Institute

Related event

**African Swine Fever experiments within NADIR: Interest, prospects, contributions and practical feasibilities at DTU Vet, Denmark**
06/11/2011 → 06/11/2011
Centro de Investigación en Sanidad Animal (CISA), Valdeolmos, Madrid, Spain
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

**African Swine Fever experiments within NADIR (Event)**
Period: 6 Nov 2011
Jens Nielsen (Reviewer)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Related event
African Swine Fever experiments within NADIR: Interest, prospects, contributions and practical feasibilities at DTU Vet, Denmark
06/11/2011 → 06/11/2011
Centro de Investigación en Sanidad Animal (CISA), Valdeolmos, Madrid, Spain
Activity: Research › Peer review of manuscripts

Efficacy study on a new marker vaccine -CP7_E2alf in piglets with maternal derived antibodies (CSFVgo_DIVA)
Period: 4 Nov 2011
Desislava Yordanova Rangelova (Speaker)
National Veterinary Institute

Workshop on Immunopathology of Classical swine fever
Period: 27 Sep 2011
Åse Uttenthal (Chairman)
National Veterinary Institute

Description
Workshop on immunopathology of Classical Swine Fever: "Is the immune system a double-edge sword in CSFV-infections?" Chair: Åse Uttenthal, DTU Vet, Lindholm, Denmark " Introduction Jens Nielsen, DTU Vet, Lindholm, Denmark
Followed by a debate Initially addressing the question "Is the immune system a double-edge sword in CSFV-infections?, the workshop will create an informal forum to discuss the challenges of recent and future research on immunopathological aspects of classical swine fever. All interested delegates are invited to participate in the debate.

Related event

Workshop on Immunopathology of Classical swine fever
27/09/2011 → …
Hannover, Germany
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.
Division of Virology

Description
Workshop on immunopathology of Classical Swine Fever: "Is the immune system a double-edge sword in CSFV-infections?" Chair: Åse Uttenthal, DTU Vet, Lindholm, Denmark " Introduction Jens Nielsen, DTU Vet, Lindholm, Denmark Following by a debate Initially addressing the question "Is the immune system a double-edge sword in CSFV-infections?, the workshop will create an informal forum to discuss the challenges of recent and future research on immunopathological aspects of classical swine fever. All interested delegates are invited to participate in the debate.

Related event
Workshop on Immunopathology of Classical swine fever
27/09/2011 → …
Hannover, Germany
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

The role of antibiotics and antibiotic resistance in nature
Period: 28 Jun 2011
Rustam Aminov (Keynote speaker)
National Veterinary Institute

Related event
4th Symposium on Antimicrobial Resistance in Animals and the Environment
27/06/2011 → 29/06/2011
Tours, France
Activity: Talks and presentations › Conference presentations

Dialogmøde med Fødevarestyrelsen: Svinepest virus i gødning, undersøgt med henblik på transportbiler
Period: 8 Jun 2011
Åse Uttenthal (Speaker)
National Veterinary Institute
Division of Virology

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations
Efficacy study of CP7_E2alf in piglets obtained from sows vaccinated with C-strain (in progress) (CSFVgo_DIVA)
Period: 25 May 2011
Desislava Yordanova Rangelova (Speaker)
National Veterinary Institute

Description
Place: Veterinary Institute

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Persistent classical swine fever virus infection in pigs; 5: NoE EPIZONE annual meeting
Period: 12 Apr 2011
Åse Uttenthal (Speaker)
National Veterinary Institute
Division of Virology

Description
Place: Papendal, The Netherlands

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Efficacy study on a new marker vaccine -CP7_E2alf in piglets with maternal derived antibodies, CSFVgo_DIVA (CSFV_goDIVA)
Period: 10 Apr 2011
Desislava Yordanova Rangelova (Speaker)
National Veterinary Institute

Related event
Efficacy study on a new marker vaccine -CP7_E2alf in piglets with maternal derived antibodies, CSFVgo_DIVA (CSFV_goDIVA)
10/04/2011 → 10/04/2011
Annual Virology Seminar, Comwell Klarskovgaard -Denmark
Activity: Talks and presentations › Conference presentations

Swine fevers and pestivirus: Virology at 4. semester, Students of Vet Science
Period: 17 Feb 2011
Åse Uttenthal (Guest lecturer)
National Veterinary Institute
Division of Virology

Related external organisation
University of Copenhagen
Thorvaldensesvej 40, DK-1871 Frederiksberg C, Copenhagen, Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

Time Series Analysis (TSA); 02417
Period: 3 Feb 2011 → 5 May 2011
Anders Stockmarr (Lecturer)
Section for Veterinary Epidemiology and public sector consultancy
Department of Applied Mathematics and Computer Science

Related event

time series analysis

03/02/2011 → 05/05/2011
Kgs. Lyngby, Denmark
Activity: Other

National Veterinary Institute Sweden
Period: 24 Jan 2011 → 11 Feb 2011
Tanya von Rosen (Visiting researcher)
National Veterinary Institute

Description
EPIZONE Short term mission
The main focus of the visit to SVA was a thorough introduction to the use and application of the Luminex/BioPlex microsphere (bead) assay based technology. As described earlier in the “Plan of activities” the principle of the assay is similar to a capture sandwich immunoassay, but instead of coating the well in a plate, beads are being coated, which allows for the simultaneous analysis of multiple proteins, peptides, and nucleic acids in a single well of a 96-well microtiter plate. As the expectations to the end output of the short term mission is “a novel serological multiplex assay for detection and differentiation of antibodies against CSFV” the introductory training was based on an already developed microsphere-based immunoassay for the detection of BVDV antibodies that was recently developed by a group of researchers from SVA/SLU (Xia et al., 2010), including Sandor Belak, Hongyan Xia and Liu Lihong. The laboratory training was supervised by Hongyan Xia and Liu Lihong. More specific did the introductory training include intensive training in each of the various steps integrated in building up the BVDV microsphere-based immunoassay: -coupling of capture molecules to magnetic beads, different beads and capture molecules was used -optimization and confirmation of the effectiveness of the coupling, it was here additionally investigated whether it makes a difference for the optimal coating concentration whether magnetic/non-magnetic beads are used -running of the established BVDV microsphere-based immunoassay with beads I had coupled with capture molecules, known positive and negative clinical samples were used for verification -optimization of an assay – what parameters to adjust: samples (diluted/undiluted), secondary Ab (what concentration), incubation time, volumes etc. -how to get the most optimal performance and reproducible results (the minimum bead count needed for statistically significant analyses and optimal bead regions to use in a multiplexed assay) -validation of results – how to determine whether irregular assay results are due to hardware, software, or assay artifacts
The most important achievements from the short-term research stay at SVA have been: -that I have gained routine in coupling magnetic beads with capture molecules -that I have gained routine in optimization and confirmation of the effectiveness of the coupling -that I have become familiar in using the Luminex machine system as well as building up assays, which on my own hand would have taken months -that I have got protocols to bring home which I can easily modify for own purposes -that I have got a network of scientists that I know I can always contact in case I need help solving problems regarding the Luminex/Bioplex system.
Activity: Visiting an external institution › Visiting another research institution

Applied and Environmental Microbiology (Journal)
Period: 2010 → 2013
Rustam Aminov (Editor)
National Veterinary Institute

Description
Applied and Environmental Microbiology (AEM) publishes papers that make significant contributions to (a) applied microbiology, including biotechnology, protein engineering, bioremediation, and food microbiology, (b) microbial ecology, including environmental, organismic, and genomic microbiology, and (c) interdisciplinary microbiology, including invertebrate microbiology, plant microbiology, aquatic microbiology, and geomicrobiology.

Editorial Board

Related journal

Applied and Environmental Microbiology
Local database
Frontiers in Microbiology (Journal)
Period: 2010
Rustam Aminov (Editor)
National Veterinary Institute

Description
Frontiers in Microbiology

Frontiers in Microbiology publishes articles on the most outstanding discoveries across a wide research spectrum of Microbiology. The mission of the journal is to bring all relevant Microbiology areas together on a single platform. The specialty sections of Frontiers in Microbiology welcome submission of the following tier 1 articles: Book Review, Editorial, General Commentary, Hypothesis & Theory, Methods, Mini Review, Opinion, Original Research, Perspective, Review, Specialty Grand Challenge and Technology Report. When submitting a manuscript to Frontiers in Microbiology, authors must submit the material directly to one of the specialty sections. Manuscripts are peer reviewed by the associate and review editors of the respective specialty section. Articles published in the specialty sections above will be subject to the Frontiers evaluation system after online publication. Authors of published original research with the highest impact, as judged democratically by the readers, will be invited by the Chief Editor to write a prestigious Frontiers Focused Review - a tier 2 article. This is referred to as "democratic tiering". The author selection is based on article impact analytics of original research published in the Frontiers specialty journals and sections. Focused Reviews are centered on the original discovery, place it into a broader context, and aim to address the wider community across all of Microbiology.

Specialty Chief Editor, section Antimicrobials, Resistance and Chemotherapy

Related journal
Frontiers in Microbiology
1664-302X
Indexed in DOAJ
Central database
Activity: Research › Journal editor

MODERN VETERINARY VACCINES & ADJUVANTS 2010 ( MVVA 2010)
Period: 17 Nov 2010 → 19 Nov 2010
Gregers Jungersen (Speaker)
National Veterinary Institute
Division of Veterinary Diagnostics and Research

Description
Place: Budapest, Hungary

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Presentation on requirements for registration of GMO biological products
Period: 17 Nov 2010
Desislava Yordanova Rangelova (Speaker)
National Veterinary Institute

Description
Place: Paris

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations
**CSFV DIVA diagnostic using the yeast Pichia pastoris for production of recombinant CSFV proteins**
Period: 3 Nov 2010 → 5 Nov 2010
Tanya von Rosen (Speaker)
National Veterinary Institute

**Description**
Place: Theme 5 Meeting EPIZONE 2010, Copenhagen, Denmark

**Related external organisation**
Unknown external organisation
Activity: Talks and presentations › Conference presentations

**Young EPIZONE: Theme 5 meeting**
Period: 3 Nov 2010 → 5 Nov 2010
Åse Uttenthal (Speaker)
National Veterinary Institute
Division of Virology

**Description**
Classical swine fever: How to reach a diagnosis based on clinic and laboratory work
Place: Copenhagen, DTU-Vet

**Related external organisation**
Unknown external organisation
Activity: Talks and presentations › Conference presentations

**NOSOVE Course: Economics of animal health and surveillance**
Period: 1 Nov 2010 → 3 Nov 2010
Carsten Thure Kirkeby (Participant)
National Veterinary Institute
Section for Epidemiology

**Related event**
NOSOVE Course: Economics of animal health and surveillance
01/11/2010 → 03/11/2010
Oslo, Norway
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

**Virology Seminar**
Period: 6 Oct 2010
Louise Lohse (Speaker)
National Veterinary Institute
Division of Virology

**Description**
Presentation of results achieved in animal experimental studies including classical swine fever virus in a current national research project. Title: CSFV - persistent infection in piglets
Note: The National Veterinary Institute, DTU, Hjalet
Place: Vordingborg, Denmark

**Related external organisation**
Unknown external organisation
Activity: Talks and presentations › Conference presentations
Presentation of a new PhD project on CSF- CSFV_goDIVA project (CSFV_goDIVA)
Period: 4 Oct 2010
Desislava Yordanova Rangelova (Speaker)
National Veterinary Institute

Related event
Annual Virology Seminar
04/10/2010 → ...
Denmark
Activity: Talks and presentations › Conference presentations

Presentation of PhD project to the Danish Medicine Agency
Period: 20 Sep 2010
Desislava Yordanova Rangelova (Speaker)
National Veterinary Institute

Description
Place: Lindholm, Denmark

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Time Series Analysis (TSA); 02417
Period: 3 Sep 2010 → 3 Dec 2010
Anders Stockmarr (Lecturer)
Section for Epidemiology
Department of Applied Mathematics and Computer Science

Description
Place: DTU Informatics

Related event
Time Series Analysis
03/09/2010 → 03/12/2010
Kgs. Lyngby, Denmark
Activity: Other

Animal virology (24003)
Åse Uttenthal (Organizer)
National Veterinary Institute
Division of Virology

Description
Course including 6 full day theoretical lessons and 1 week intensive Lab course.

Related event
Animal virology (24003): Phd Course
15/08/2010 → 13/10/2010
Lindholm, Bülowsvej, Århus, Flakkebjerg, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.
Presentation of PhD project: Improved tools and strategies for prevention and control of CSF_goDIVA
Period: 11 Aug 2010
Desislava Yordanova Rangelova (Speaker)
National Veterinary Institute

Description
Place: Copenhagen, Denmark

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

2010 Gordon Research Conference on Microbial Stress Response
Period: 18 Jul 2010 → 23 Jul 2010
Anders Folkesson (Participant)
National Veterinary Institute
Section for Bacteriology, Pathology and Parasitology

Description
Poster presentation

Related event

2010 Gordon Research Conference on Microbial Stress Response
18/07/2010 → 23/07/2010
South Hadley, MA, United States
Activity: Attending an event › Participating in or organising a conference

4th Annual Meeting EPIZONE
Period: 7 Jun 2010 → 10 Jun 2014
Carsten Thure Kirkeby (Participant)
National Veterinary Institute
Section for Epidemiology

Related event

4th Annual Meeting EPIZONE
07/06/2010 → 10/06/2010
Saint Malo, France
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Improve tools and strategies for the prevention and control of classical swine fever (CSFV_goDIVA)
Period: 7 Jun 2010 → 10 Jun 2010
Åse Uttenthal (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
During a “project fair” the CSFVgo_DIVA project was presented by an oral presentation. The project coordinator Frank Koenen was unable to participate in the meeting so as the deputy coordinator I gave the presentation of this EU Strep FP7 project.
Place: EPIZONE 4. annual meeting. Saint Malo, France

Related external organisation
**Unknown external organisation**  
Activity: Talks and presentations › Conference presentations

**Task A-Work Package -3: Vaccination of pigs with C-strain(Riemser)-(pilot study)preliminary results**  
**Period:** 25 May 2010 → 27 May 2010  
Desislava Yordanova Rangelova (Speaker)  
National Veterinary Institute

**Description**  
Place: Leipzig Germany

**Related external organisation**

**Unknown external organisation**  
Activity: Talks and presentations › Conference presentations

**Annual meeting of the National Reference Laboratories for Swine fever**  
**Period:** 19 May 2010 → 20 May 2010  
Jens Nielsen (Participant)  
National Veterinary Institute  
Division of Virology

**Description**  
Joined experiences from experimental infections with CSFV Lithuania

Place: Annual meeting of the National Reference Laboratories for Swine fever, Pulawy, Poland

**Related event**

**Annual meeting of the National Reference Laboratories for Swine fever**  
19/05/2010 → 20/05/2010  
Pulawy, Poland  
Activity: Attending an event › Participating in or organising a conference

**Annual meeting of the National Reference Laboratories for Swine fever**  
**Period:** 19 May 2010 → 20 May 2010  
Thomas Bruun Rasmussen (Participant)  
National Veterinary Institute  
Division of Virology

**Description**  
Joined experiences from experimental infections with CSFV Lithuania

Place: Annual meeting of the National Reference Laboratories for Swine fever, Pulawy, Poland

**Related event**

**Annual meeting of the National Reference Laboratories for Swine fever**  
19/05/2010 → 20/05/2010  
Pulawy, Poland  
Activity: Attending an event › Participating in or organising a conference

**Annual meeting of the National Reference Laboratories for Swine fever**  
**Period:** 19 May 2010 → 20 May 2010  
Louise Lohse (Participant)  
National Veterinary Institute  
Division of Virology

**Description**  
Joined experiences from experimental infections with CSFV Lithuania

Place: Annual meeting of the National Reference Laboratories for Swine fever, Pulawy, Poland

**Related event**

**Annual meeting of the National Reference Laboratories for Swine fever**  
19/05/2010 → 20/05/2010  
Pulawy, Poland  
Activity: Attending an event › Participating in or organising a conference
Description
Joined experiences from experimental infections with CSFV Lithuania

Related event

Annual meeting of the National Reference Laboratories for Swine fever
19/05/2010 → 20/05/2010
Pulawy, Poland
Activity: Attending an event › Participating in or organising a conference

Annual meeting of the National Reference Laboratories for Swine fever
Period: 19 May 2010 → 20 May 2010
Bertel Strandbygaard (Participant)
National Veterinary Institute
Division of Virology

Description
Joined experiences from experimental infections with CSFV Lithuania

Place: Annual meeting of the National Reference Laboratories for Swine fever, Pulawy, Poland

Related event

Comparison of clinical and paraclinical parameters as tools for early diagnosis of classical swine fever
Period: 19 May 2010 → 20 May 2010
Louise Lohse (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Presentation of results achieved in animal experimental studies including CSFV in a current national research project.
Place: CSF annual meeting, Poland

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

Joined experiences from experimental infections with CSFV Lithuania
Period: 19 May 2010 → 20 May 2010
Åse Uttenthal (Speaker)
National Veterinary Institute
Division of Virology

Description
Place: Annual meeting of the National Reference Laboratories for Swine fever, Pulawy, Poland

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations
Presentation of a new PhD project on CSFV: go_DIVA project (CSFVgo_DIVA)
Period: 16 Apr 2010
Desislava Yordanova Rangelova (Speaker)
National Veterinary Institute

Related event

Presentation of a new PhD project on CSFV: go_DIVA project (CSFVgo_DIVA)
16/04/2010 → 16/04/2010
Veterinary Institute, Lindholm
Activity: Other

Klassisk svinepest (CSF) i Verden
Period: 15 Apr 2010 → 15 Feb 2011
Åse Uttenthal (Speaker)
National Veterinary Institute
Division of Virology

Description
Place: Workshop vedr svinepestovervågning, Frederecia, Danmark

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

Workshop omkring tidlig diagnose og overvågning af svinepest i Danmark
Period: 15 Apr 2010
Louise Lohse (Speaker)
National Veterinary Institute

Related event

Workshop omkring tidlig diagnose og overvågning af svinepest i Danmark
15/04/2010 → 15/04/2010
Fredericia, Danmark
Activity: Talks and presentations › Conference presentations

Workshop on Laboratory Contingency Planning and laboratory exercises; 1
Period: 11 Mar 2010 → 12 Mar 2010
Åse Uttenthal (Organizer)
National Veterinary Institute
Division of Virology

Description
A workshop was conducted funded by NoE EPIZONE on the improvement of Laboratory contingency planning and Laboratory Exercises. These written SOPs on the work performed to diagnose exotic viral infections is needed in any accredited laboratory.
Note: The final version will be uploaded when finalised

Related event

Workshop on Laboratory Contingency Planning and laboratory exercises; 1: LCP workshop
11/03/2010 → 12/03/2010
Padova, Italy
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.
Use of cell-mediated immune responses in control of bovine paratuberculosis
Period: 1 Jan 2010
Gregers Jungersen (Speaker)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Adaptive Immunology & Parasitology
Description
Place: Tokyo, Japan

MedReoNet 3rd Annual Meeting Lisbon
Period: 2 Dec 2009 → 4 Dec 2009
Carsten Thure Kirkeby (Participant)
National Veterinary Institute
Section for Epidemiology
Links:

FVST workshop, mistankehåndtering for dyrlæger i beredskabssektionen
Period: 1 Oct 2009
Louise Lohse (Speaker)
National Veterinary Institute
Division of Virology
Description
Place: FVST region nord, Herning, Danmark

MedReoNet 3rd Annual Meeting Lisbon
02/12/2009 → 04/12/2009
Lisbon, Portugal
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.
Brucella ovis and Brucella melitensis serology in sheep and goat

**Period:** 24 Sep 2009 → 25 Sep 2009

Anna-Bodil Christoffersen (Speaker)

National Veterinary Institute
Division of Veterinary Diagnostics and Research
Section for Veterinary Diagnostics

**Description**

Place: The 3rd Workshoo of the EU Brucellosis NRL in Portugal

Documents:
Brucella ovis and Brucella melitensis Lissabon 2009 serology in sheep - rev.ppt

**Related external organisation**

**Unknown external organisation**

Activity: Talks and presentations › Conference presentations

Antibiotic tolerance and microbial biofilms

**Period:** 23 Sep 2009 → 26 Sep 2009

Anders Folkesson (Invited speaker)

Department of Systems Biology
Center for Systems Microbiology
National Veterinary Institute
Section for Bacteriology, Pathology and Parasitology

**Description**

Saturday, September 26, 2009
Session 7 Biofilm
9:00-9:30
IL13 Antibiotic tolerance and microbial biofilms
Anders Folkesson (Denmark)

Links:
http://www.hmd-cms.hr/cesar2009/

**Related event**

Central European Symposium on Antimicrobial Resistance: Antibiotic tolerance and microbial biofilms
Zadar, Croatia

Activity: Talks and presentations › Conference presentations

Time Series Analysis (TSA); 02417

**Period:** 4 Sep 2009 → 4 Dec 2009

Anders Stockmarr (Lecturer)

Division of Veterinary Diagnostics and Research
Section for Veterinary Epidemiology and public sector consultancy
National Veterinary Institute

**Description**

Lectured by Anders Stockmarr

**Related event**

Time Series Analysis
04/09/2009 → 04/12/2009
Pathology of enteritis in pigs
Tim Kåre Jensen (Speaker)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Section for Veterinary Diagnostics

Description
Place: First European College of Porcine Health Management, Copenhagen, Denmark

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Evaluation of the influence of lyophilisation on ASF diagnostic tests – studies in Denmark
Period: 17 Jun 2009
Thomas Bruun Rasmussen (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Related event
Annual Meeting of the National African Swine Fever Laboratories
17/06/2009 → 17/06/2009
Madrid, Spain
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

Comparison of early pathogenesis of CSFV-Glentorf and CSFV-Romania in Danish pigs
Louise Lohse (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Presentation of results achieved in a animal experimental study including CSFV in a current 3-year National research project.
Place: CSF annual meeting, Spain

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Bovine digital dermatitis: A spirochetal skin disease of polytreponemal aetiology
Period: 8 Jun 2009 → 10 Jun 2009
Tim Kåre Jensen (Speaker)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Section for Veterinary Diagnostics

**Description**
Place: Fifth International conference on Colonic Spirochaetal Infections in Animals and Humans in Leon, Spain

**Related external organisation**

**Unknown external organisation**
Activity: Talks and presentations › Conference presentations

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**Genetic stability of pestivirus genomes cloned into BACs (EPIZONE): 3rd EPIZONE Annual Meeting "Crossing Borders"**
Period: 13 May 2009
Thomas Bruun Rasmussen (Speaker)
Division of Virology
Sektion for Eksotiske Virussygdomme
National Veterinary Institute

**Description**
Genetic stability of pestivirus genomes cloned into BACs Thomas Bruun Rasmussen, DTU Vet Ilona Reimann, FLI Åse Uttenthal, DTU Vet Martin Beer, FLI Infectious cDNA clones are a prerequisite for directed genetic manipulations of pestivirus genomes to obtain attenuated pestiviruses designed as new modified live DIVA vaccine candidates against classical swine fever. However, the construction of new infectious pestivirus cDNA clones has been hampered due to the large size of the pestivirus genome and due to genetic instability of the cloned cDNA, which in combination with plasmid vectors tend to be unstable and deleterious in the bacterial host. Therefore, new strategies are needed to facilitate construction of stable infectious cDNA clones of pestivirus strains. In a collaborative research project, between DTU Vet and FLI, on the establishment of genetically modified pestiviruses engineered specifically for the DIVA principle, we cloned a series of complete pestivirus genomes, obtained by full-length RT-PCR, directly into the bacterial artificial chromosome (BAC) vector "pBeloBAC11". This BAC vector provides a markedly higher stability of cloned sequences in E. coli compared to plasmids that form the basis for the existing pestivirus cDNA clones. In this study, two of the newly constructed BAC clones were analysed for genetic stability of the cloned pestivirus genomes to demonstrate the suitability of the BAC vector for harbouring pestivirus genomes. Two BAC clones, comprising the complete genomes of BDV Gifhorn (pBeloGif3) and CSFV Paderborn (pBeloPader10) were passaged 15 times in E.coli representing at least 360 bacteria generations. From 15th passage of the BAC clones, the entire 5' and 3' ends of the cloned genomes and parts of the open reading frame were sequenced and compared to the sequences of the parent BAC clones. The sequenced areas represent approximately 20 % of the cloned genome. No mutations were observed after the extensive passaging of the cDNA clones in the bacterial host, indicating a highly stable system for cloning and maintenance of complete pestivirus genomes. This work was supported by the by the Danish Research Council for Technology and Production Sciences (DRCTPS grant 274-07-0198) and the EU Network of Excellence, EPIZONE (Contract No FOOD-CT-2006-016236).

Place: Antalya, Turkey
Degree of recognition: International

**Related event**

**3rd Annual Meeting of EPIZONE**
12/05/2009 → 15/05/2009
Antalya, Turkey
Activity: Talks and presentations › Conference presentations

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**Hepatitis E Virus - en ny zoonose?**
Period: 8 May 2009 → 9 May 2009
Solvej Østergaard Breum (Speaker)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Virology

**Description**
Place: Dansk Veterinær Hyologisk Selskab

**Related external organisation**
**Unknown external organisation**  
Activity: Talks and presentations › Conference presentations

**Asfaviridae and arbovirus**  
Period: 24 Mar 2009  
Åse Uttenthal (Lecturer)  
National Veterinary Institute  
Division of Virology  

Description  
Note: vector borne diseases

**Related external organisation**

**University of Copenhagen**  
Thorvaldsensvej 40, DK-1871 Frederiksberg C, Copenhagen, Denmark  
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

**Toga and Flaviviridae**  
Period: 24 Mar 2009  
Åse Uttenthal (Lecturer)  
National Veterinary Institute  
Division of Virology

**Related external organisation**

**University of Copenhagen**  
Thorvaldsensvej 40, DK-1871 Frederiksberg C, Copenhagen, Denmark  
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

**MedReoNet Taxonomy Meeting Strasbourg 2009**  
Period: 16 Mar 2009 → 20 Mar 2009  
Carsten Thure Kirkeby (Participant)  
National Veterinary Institute  
Section for Epidemiology  
Links:  

**Related event**

**MedReoNet Taxonomy Meeting Strasbourg 2009**  
16/03/2009 → 20/03/2009  
Strasbourg, France  
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

**Classical Swine Fever: Surveillance and contingency**  
Period: 2 Mar 2009  
Åse Uttenthal (Speaker)  
National Veterinary Institute  
Division of Virology

**Related external organisation**

**Thiempu, Bhutan**  
Activity: Talks and presentations › Conference presentations
Biomedicin
Period: 16 Feb 2009
Tanya von Rosen (Lecturer)
Division of Virology
Sektion for Eksotiske Virussygdomme
National Veterinary Institute

Description
Modul 2a: DIVA Diagnostic

Related external organisation

University of Copenhagen
Thorvaldsensvej 40, DK-1871 Frederiksberg C, Copenhagen, Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

Patobiologisk basiskursus - Virologi: RT-PCR påvisning af hundesygevirus nukleinsyre
Period: 9 Feb 2009 → 20 Feb 2009
Tanya von Rosen (Lecturer)
Division of Virology
Sektion for Eksotiske Virussygdomme
National Veterinary Institute

Related external organisation

University of Copenhagen
Thorvaldsensvej 40, DK-1871 Frederiksberg C, Copenhagen, Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

Time Series Analysis (TSA); 2417
Period: 5 Feb 2009 → 7 May 2009
Anders Stockmarr (Lecturer)
Division of Veterinary Diagnostics and Research
Section for Veterinary Epidemiology and public sector consultancy
National Veterinary Institute

Description
Place: DTU Informatics

Related event

Time Series Analysis
05/02/2009 → 07/05/2009
Kgs. Lyngby, Denmark
Activity: Other

*Discriminating diagnostics for DIVA vaccines towards classical swine fever*
Period: 1 Jan 2009 → …
Tanya von Rosen (Speaker)
National Veterinary Institute
Division of Virology

Description
Place: Friedrich Loeffler Institute (FLI), Insel Riems, Germany

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Undervisning af Ph.d. studerende ved årlige kurser i immunologi, der blev arrangeret af Danmarks Veterinærinstitut
Period: 1 Jan 2009 → …
Vibeke Sørensen (Lecturer)
Division of Veterinary Diagnostics and Research
Secretariat
National Veterinary Institute

Related event

Undervisning af Ph.d. studerende ved årlige kurser i immunologi, der blev arrangeret af Danmarks Veterinærinstitut
01/01/2009 → …
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

Undervisning ved kurser på Danmarks Veterinærinstitut for to hold af kolleger, som har gennemført uddannelsen som svinefagdyrlæge
Period: 1 Jan 2009 → …
Vibeke Sørensen (Lecturer)
Division of Veterinary Diagnostics and Research
Secretariat
National Veterinary Institute

Related external organisation
Danmarks Veterinærinstitut
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

Organisation of rabies control and rabies prevention in Denmark: CRL Rabies Workshop
Period: 16 Dec 2008
Thomas Bruun Rasmussen (Speaker)
Division of Virology
Sektion for Eksotiske Virussygdomme
National Veterinary Institute

Description
Place: Nancy, France

Related event

CRL Rabies Workshop
01/01/2008 → …
Nancy, France
Activity: Talks and presentations › Conference presentations

MedReoNet 2nd Annual Meeting Giulianova
Carsten Thure Kirkeby (Participant)
National Veterinary Institute
Section for Epidemiology
Links:

Related event
MedReoNet 2nd Annual Meeting Giulianova
09/12/2008 → 11/12/2008
Giulianova, Teramo, Italy
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

**Medreonet; 2: Surveillance network of Reoviruses, Bluetongue and African Horse Sickness, in the Mediterranean basin and Europe (Event)**
Lasse Dam Rasmussen (Participant)
National Veterinary Institute
Division of Virology

**Description**
Medreonet; 2: Surveillance network of Reoviruses, Bluetongue and African Horse Sickness, in the Mediterranean basin and Europe

**Related event**
**Medreonet; 2: Surveillance network of Reoviruses, Bluetongue and African Horse Sickness, in the Mediterranean basin and Europe**
09/12/2008 → 11/12/2008
Activity: Membership › Membership of research networks or expert groups

**5th International Interdisciplinary Meeting on Bioanalysis**
Period: 24 Nov 2008 → 25 Nov 2008
Bill Vestergaard (Participant)
National Veterinary Institute

**Description**
Talk about "Combining Microfluidics and Small Angle X-ray Scattering for Structural Analysis of Proteins: Small Chip - Large Detector - Perfect Marriage" Presented at CECE 2008 - 5th International Interdisciplinary Meeting on Bioanalysis.

Place: Brno, Czech
Degree of recognition: International

**Related event**
**5th International Interdisciplinary Meeting on Bioanalysis**
24/11/2008 → 25/11/2008
Brno, Czech Republic
Activity: Attending an event › Participating in or organising a conference

**Scientific Panel on Animal Health and Welfare (AHAW), EFSA (External organisation)**
Period: Oct 2008 → …
Anette Bøtner (Participant)
National Veterinary Institute

**Description**
Body type: European Food and Safety Authority
Degree of recognition: International

**Related external organisation**
**Scientific Panel on Animal Health and Welfare (AHAW), EFSA**
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

**Hepatitis E Virus is prevalent in the Danish pig population**
Period: 31 Oct 2008
Solvej Østergaard Breum (Speaker)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Virology

**Description**
Place: Statens Serum Institut - Dansk Virologisk Selskab

**Related external organisation**
Unknown external organisation
Activity: Talks and presentations › Conference presentations

**DIVA diagnostics.: Different approaches towards the same goal**
Åse Uttenthal (Keynote speaker)

National Veterinary Institute

**Description**
Talk at the Young EPIZONE meeting on how to obtain DIVA diagnostics for virus vaccines
Place: El Escorial, Madrid, Spain

**Related external organisation**
Unknown external organisation
Activity: Talks and presentations › Conference presentations

**12th International Conference on Miniaturized Systems for Chemistry and Life Sciences**
Bill Vestergaard (Participant)

National Veterinary Institute

**Description**
Talk about "Automated High-Throughput Structural Protein Analysis Using Small Angle X-ray Scattering Combined with a Microfluidic Approach" presented at MicroTAS 2008
Place: San Diego, USA
Degree of recognition: International

**Related event**
12th International Conference on Miniaturized Systems for Chemistry and Life Sciences
12/10/2008 → 16/10/2008
San Diego, United States
Activity: Attending an event › Participating in or organising a conference

**1st COST 929 SYMPOSIUM**
Anne Ahlmann Nielsen (Participant)

National Veterinary Institute
Division of Poultry, Fish and Fur Animals
Section of Poultry Diseases

**Related event**
1st COST 929 SYMPOSIUM: CURRENT DEVELOPMENTS IN FOOD AND ENVIRONMENTAL VIROLOGY
09/10/2008 → 11/10/2008
Pisa, Italy
Activity: Attending an event › Participating in or organising a conference
Dyrlægernes dag (DDD): Vektorbårne sygdomme - hvilken vej blæser vinden
Period: 3 Oct 2008
Rene Bedker (Speaker)
Division of Veterinary Diagnostics and Research
Section for Veterinary Epidemiology and public sector consultancy
National Veterinary Institute

Description
Place: SAS Radison, Silkeborg
Degree of recognition: National

Related event
Dyrlægernes dag (DDD)
03/10/2008 → …
Silkeborg, Denmark
Activity: Talks and presentations › Conference presentations

Q-fever: Epidemiology, serological diagnostic and prevalence in Denmark
Period: 24 Sep 2008
Anna-Bodil Christoffersen (Speaker)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Section for Veterinary Diagnostics

Description
Place: Slagterierne Faglige Dag - Holstebro

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

7th ESVV Pestivirus Symposium: Generation of recombinant pestiviruses using a full genome amplification strategy.
Period: 16 Sep 2008 → 19 Sep 2008
Thomas Bruun Rasmussen (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

ESVV Pestivirus symposium; 7 (External organisation)
Period: 16 Sep 2008 → 19 Sep 2008
Åse Uttenthal (Chairman)
National Veterinary Institute
Division of Virology

Description
Place: Uppsala, Sweden
**Dyreforsøg på Lindholm 2008**
*Period: 10 Sep 2008*
Louise Lohse (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Description**
Place: Fødevarestyrelsens aktualitetskursus for det Veterinære Beredskab, Haderslev

**Related external organisation**

**Unknown external organisation**
Activity: Talks and presentations › Conference presentations

**Time Series Analysis (TSA); 2417**
*Period: 29 Aug 2008 → 12 Dec 2008*
Anders Stockmarr (Lecturer)
Division of Veterinary Diagnostics and Research
Section for Veterinary Epidemiology and public sector consultancy
National Veterinary Institute

**Description**
Place: DTU Informatics

**Related event**

**Time Series Analysis**
29/08/2008 → 12/12/2008
Kgs. Lyngby, Denmark
Activity: Other

**Diagnosis of PRRSV – a review**
*Period: 24 Jul 2008 → 25 Jul 2008*
Lars Erik Larsen (Speaker)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Virology

**Related event**

**Diagnosis of PRRSV – a review: EuroPRRSnet workshop**
24/07/2008 → 25/07/2008
Brussels
Activity: Talks and presentations › Conference presentations

**Building Bridges: Workshop on Swine Diseases**
*Period: 4 Jul 2008 → 11 Jul 2008*
Åse Uttenthal (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
CSF- The global situation. How to obtain information on the current CSFV situation globally and measures in Denmark to assure freedom from CSFV.
Place: Shanghai, China

Unknown external organisation
Activity: Talks and presentations › Conference presentations

Identification of a new porcine circovirus type 2 (PCV2) genotype in Danish archive pig-samples
Kitt Dupont (Speaker)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Microbial Ecology

Description
PCV2 is the major causative agent of postweaning multisystemic wasting syndrome (PMWS) in pigs. Two genotypes of PCV2 have been identified: genotype 1 and 2 (Olvera et al., 2007). PCV2 genotype 2 was involved in the first cases of PMWS in Canada (Hamel et al., 1998). PCV2 genotype 1 may be more pathogenic than PCV2 genotype 2, as a recent study from Grau-Roma et al. (2007) showed that genotype 2 primary was found in non-PMWS affected herds in Spain, while genotype 1 was found in PMWS affected herds.
Place: IPVS 2008, Durban, South Africa

Related external organisation
Activity: Talks and presentations › Conference presentations

Using free-cost spatial technology as a tool for assessment of antimicrobial consumption data and spatial distribution of pig herds
Hans Houe (Speaker)
National Veterinary Institute

Description
Place: Copenhagen, Denmark

Related external organisation
Activity: Talks and presentations › Conference presentations

EU-BTNET Workshop 2008
Period: 10 Jun 2008 → 11 Jun 2008
Carsten Thure Kirkeby (Participant)
National Veterinary Institute
Section for Epidemiology
Links:

Related event
EU-BTNET Workshop 2008
Animal Brucellosis in Denmark
Period: 29 May 2008 → 30 May 2008
Anna-Bodil Christoffersen (Speaker)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Section for Veterinary Diagnostics
Description
Serological surveillance and control and FPSR.
Related event
Animal Brucellosis in Denmark
29/05/2008 → 30/05/2008
Workshop in Brucellosis - Paris
Activity: Talks and presentations › Conference presentations

Hepatitis E Virus (HEV) - en ny zoonose?
Period: 27 May 2008
Solvej Østergaard Breum (Speaker)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Virology
Description
Place: FOOD DTU - Aftagerkonference
Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Early detection of Salmonella Dublin herds at risk for changing test status in the Danish surveillance program
Period: 22 May 2008
Anders Stockmarr (Speaker)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Section for Veterinary Epidemiology and public sector consultancy
Description
Place: D4, Nordre Sti, KU LIFE
Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations
Seroconversion and Maternal Immunity as risk factors for pigs acquiring PMWS
Period: 20 May 2008
Anders Stockmarr (Speaker)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Section for Veterinary Epidemiology and public sector consultancy
Description
Place: 8th PCVD Meeting, Budapest, Hungary
Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

4th annual Advances in Microarray Technology (AMT) conference
Period: 7 May 2008 → 8 May 2008
Dang Duong Bang (Participant)
Division of Poultry, Fish and Fur Animals
National Veterinary Institute
Description
Talk about "An Inexpensive and Simple Method for Covalent Immobilization of DNA to unmodified Glass surfaces for the use in Thermal Cycling reactions. Presented at "Advances in Microarray Technology"
Place: Barcelona, Spain
Degree of recognition: International
Related event
4th annual Advances in Microarray Technology (AMT) conference
07/05/2008 → 08/05/2008
Barcelona, Spain
Activity: Attending an event › Participating in or organising a conference

Serokonvertering og maternal immunitet som risikofaktorer for udvikling af PMWS
Period: 29 Apr 2008
Anders Stockmarr (Speaker)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Description
Place: Danish Meat Association, Axelborg, Copenhagen
Related external organisation
Unknown external organisation
22nd International Symposium on MicroScale Bioseparations
Bill Vestergaard (Participant)
National Veterinary Institute

Description

Place: Berlin, Germany
Degree of recognition: International

Related event
22nd International Symposium on MicroScale Bioseparations
09/03/2008 → 13/03/2008
Berlin, Germany
Activity: Attending an event › Participating in or organising a conference

Real time PCR / Rotorgene: af kursus i brug af Rotorgene real-time PCR maskine for laboranter. Teori og øvelser.
Period: 6 Mar 2008
Charlotte Kristiane Hjulsager (Lecturer)
Division of Veterinary Diagnostics and Research
Section for Veterinary Diagnostics
National Veterinary Institute

Description
Place: DTU, Veterinæristituttet, Bülowvej 27, 1790 KBH V
Lectured by Charlotte Kristiane Hjulsager

Related organisation
Real time PCR / Rotorgene: af kursus i brug af Rotorgene real-time PCR maskine for laboranter. Teori og øvelser.
Hjulsager, C. K. (Lecturer)
6 Mar 2008
Activity: Other

Bluetongue
Period: 1 Mar 2008
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Foredrag om Bluetongue for veterinærstuderende på kurset Biomedicin

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Virus diagnostik – med fokus på influenzavirus, real-time PCR, PCR pakker: Teori og laboratorium-demonstration for Veterinærstuderende, Produktionsdyrlinien, svin.
Period: 1 Mar 2008 → 1 Apr 2008
Charlotte Kristiane Hjulsager (Lecturer)
Division of Veterinary Diagnostics and Research
Section for Veterinary Diagnostics
National Veterinary Institute

**Description**
Place: Veterinærinstituttet DTU, Bülowsvej 27

**Related event**

**Virus diagnostik – med fokus på influenzavirus, real-time PCR, PCR pakker**
01/03/2008 → 01/04/2008
København, Denmark
Activity: Other

Biomedicin 2a. Virus diagnostik, PCR.: Teori og øvelseskursus
Period: 1 Feb 2008
Charlotte Kristiane Hjulsager (Lecturer)
Division of Veterinary Diagnostics and Research
Section for Veterinary Diagnostics
National Veterinary Institute

**Description**
Place: Veterinærinstituttet, DTU, Bülowsvej 27
Course lecturer

**Related organisation**

Biomedicin 2a. Virus diagnostik, PCR.: Teori og øvelseskursus
Hjulsager, C. K. (Lecturer)
1 Feb 2008
Activity: Other

Aftagerkonference: FoodDTU - konference 27. maj 2008
Period: 9 Jan 2008 → 27 May 2008
Rene Bødker (Speaker)
National Veterinary Institute

**Description**
Place: Lyngby

**Related external organisation**

Unknown external organisation
Activity: Talks and presentations › Conference presentations

Bluetongue i Europa med fokus på introduktion af bluetongue virus serotype 8 i nordvest Europa
Period: 1 Jan 2008
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virusyndromme

**Description**
Place: Regionalforening for dyrlæger i Nordjylland, Ålborg

**Related external organisation**
**unknown**

**Activity:** Talks and presentations › Conference presentations

**Period:** 1 Jan 2008 → …

Bill Vestergaard (Participant)

National Veterinary Institute

**Description**

Talk about "Design and Fabrication Issues of Microfluidic Devices for Protein Analysis" Presented at Microfluidics for X-ray Nanoanalytics

**Place:** Graz, Austria

**Related event**

**unknown**

01/01/2008 → …

Graz, Austria

**Activity:** Attending an event › Participating in or organising a conference

**Bluetongue situationen**

**Period:** 1 Nov 2007

Anette Bøtner (Speaker)

National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virusygdømme

**Description**

Note: Dialogmøde imellem Veterinærinstituttet og Fødevarestyrelsen. Veterinærinstituttet

**Related external organisation**

**National Veterinary Institute**

Denmark

**Activity:** Other

**Bluetongue: The virus, clinical signs, transmission and diagnosis, Dansk Selskab for Veterinær Patologi og Hygiejne**

**Period:** 1 Oct 2007

Anette Bøtner (Speaker)

National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virusygdømme

**Description**

Note: KU-Life

**Activity:** Other

**European Association of Fish Pathologists (EAFP) (External organisation)**

**Period:** 1 Sep 2007 → 1 Sep 2015

Lone Madsen (Secretary)

National Veterinary Institute
Section for Bacteriology, Pathology and Parasitology
Section for Virology
Description
General secretary of the EAFP council (the council having 6 members: president, vice-president, treasurer, general secretary, publications officer, meetings secretary)

Body type: Council of the association
Degree of recognition: International

Related external organisation
European Association of Fish Pathologists (EAFP)
Activity: Membership › Board duties in companies, associations, or public organisations

IPC for CSFV real-time assay
Period: 1 Sep 2007
Thomas Bruun Rasmussen (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Note: Real-time PCR Workshop" EPIZONE WP4.1
Place: Insel Riems, Germany

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

IPC for CSFV real-time assay
Period: 1 Sep 2007
Åse Uttenthal (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Note: Real-time PCR Workshop" EPIZONE WP4.1
Place: Insel Riems, Germany

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Cattle Consultancy Days
Anette Bøtner (Participant)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Bluetongue in Europe with focus on the recent introduction of bluetongue virus in north-western Europe

Note: Cattle Consultancy Days

Related event
Cattle Consultancy Days
29/08/2007 → 30/08/2007
Nyborg, Denmark
Activity: Attending an event › Participating in or organising a conference

20th NKVet symposium on perinatal death in domestic animals; 20
Period: 1 Apr 2007
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related event
20th NKVet symposium on perinatal death in domestic animals; 20
01/04/2007 → 01/04/2007
Iceland
Activity: Attending an event › Participating in or organising a conference

Forelæsning ved Biomedicin 2a kursus på KVL: Virus diagnostics – focus on influenza virus
Period: 14 Feb 2007
Charlotte Kristiane Hjulsager (Guest lecturer)
Division of Veterinary Diagnostics and Research
Section for Veterinary Diagnostics
National Veterinary Institute

Related external organisation
University of Copenhagen
Thorvaldsensvej 40, DK-1871 Frederiksberg C, Copenhagen, Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

Internal positive control for CSFV real-time assay: novel approach to control reverse transcription.
Period: 1 Jan 2007 → …
Thomas Bruun Rasmussen (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Note: Annual Meeting of National Classical Swine Fever Laboratories
Place: Hannover, Germany

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Internal positive control for CSFV real-time assay: novel approach to control reverse transcription.
Period: 1 Jan 2007 → …
Åse Uttenthal (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme
Description
Note: Annual Meeting of National Classical Swine Fever Laboratories
Place: Hannover, Germany

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

Marker properties of the chimeric pestivirus CP7_E2gif.
Period: 1 Jan 2007 → …
Thomas Bruun Rasmussen (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Note: Oral presentation at the EPIZONE WP4.3 DIVA meeting
Place: Copenhagen, Denmark

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

Marker properties of the chimeric pestivirus CP7_E2gif.
Period: 1 Jan 2007 → …
Åse Uttenthal (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Note: Oral presentation at the EPIZONE WP4.3 DIVA meeting
Place: Copenhagen, Denmark

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

Medvejleder for Ph.d. studerende Hanne Bak (External organisation)
Period: 1 Jan 2007 → …
Vibeke Sørensen (Supervisor)
Division of Veterinary Diagnostics and Research
Secretariat
National Veterinary Institute
Activity: Examinations and supervision › Supervisor activities

Medvejleder for Ph.d. studerende Thomas Bjarregaard Jensen (External organisation)
Period: 1 Jan 2007 → …
Vibeke Sørensen (Supervisor)
Division of Veterinary Diagnostics and Research
Secretariat
Multicenter comparison of nucleic acid extraction robots using quantitative RT-PCR.: Stratagene Regional QPCR Meeting
Period: 1 Jan 2007 → …
Thomas Bruun Rasmussen (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Place: Symbion Science Park, January 2007

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Multicenter comparison of nucleic acid extraction robots using quantitative RT-PCR.: Stratagene Regional QPCR Meeting
Period: 1 Jan 2007 → …
Åse Uttenthal (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Place: Symbion Science Park, January 2007

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Dialogmøde imellem Danmarks Fødevareforskning og Fødevarestyrelsen
Period: 1 Nov 2006
Anette Bøtner (Participant)
Division of Virology
Sektion for Eksotiske Virussygdomme
National Veterinary Institute

Description
Bluetongue

Note: Dialogmøde imellem Danmarks Fødevareforskning og Fødevarestyrelsen

Related event
Dialogmøde imellem Danmarks Fødevareforskning og Fødevarestyrelsen
Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

19th International Pig Veterinary Society Congress
Period: 1 Jul 2006
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related event

19th International Pig Veterinary Society Congress
16/07/2006 → 19/07/2006
Copenhagen, Denmark
Activity: Attending an event › Participating in or organising a conference

PMWS in Denmark: Epidemiology, Diagnosis and Control
Period: 1 Jul 2006
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
PCV2- Symposium, Merial, 19th IPVS

Related event

2006 Gordon Research Conference Bacterial Cell Surface
Anders Folkesson (Participant)
National Veterinary Institute
Section for Bacteriology, Pathology and Parasitology

Description
Poster presentation
Links:
Related event

2006 Gordon Research Conference Bacterial Cell Surface
25/06/2006 → 30/06/2006
New London, NH, United States
Activity: Attending an event › Participating in or organising a conference

Biosafety forhold på Lindholm herunder bygning af nye mund- og klovesyge faciliteter
Period: 1 Jun 2006
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Related event

Biosafety forhold på Lindholm herunder bygning af nye mund- og klovesyge faciliteter
01/06/2006 → 01/06/2006
Activity: Talks and presentations › Conference presentations

Evaluation of factors affecting the analytical sensitivity of bacteriological methods for investigation of S. Dublin in bovine faecal samples
Period: 10 May 2006 → 12 May 2006
Rene Bødker (Speaker)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Section for Veterinary Epidemiology and public sector consultancy

Description
Place: The I3S International Symposium Salmonella and Salmonellosis, Saint-Malo, France

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

Antimicrobial use in pig herds with and without Post-weaning Multisystemic Wasting Syndrome
Period: 1 Jan 2006 → …
Claes Enøe (Speaker)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Section for Veterinary Epidemiology and public sector consultancy

Description
Place: Copenhagen

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

Dimensions of socioeconomic status related to body mass index among Danish women and men
Period: 1 Jan 2006 → …
Anders Stockmarr (Speaker)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Section for Veterinary Epidemiology and public sector consultancy

**Description**

**Related external organisation**

**Unknown external organisation**
Activity: Talks and presentations › Conference presentations

**DIVA vaccines to pigs based on genetically modified pestiviruses: Oral presentation at Virology meeting**
Period: 1 Jan 2006 → …
Thomas Bruun Rasmussen (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Description**
Place: Hjalet

**Related external organisation**

**Unknown external organisation**
Activity: Talks and presentations › Conference presentations

**Establishment and characterisation of chimeric pestivirus: Oral presentation at Virusdag 2006**
Period: 1 Jan 2006 → …
Thomas Bruun Rasmussen (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Description**
Place: Danish Society for Virology, Denmark.

**Related external organisation**

**Unknown external organisation**
Activity: Talks and presentations › Conference presentations
Establishment and characterisation of chimeric pestivirus: Oral presentation at Virusdag 2006
Period: 1 Jan 2006 → …
Åse Uttenthal (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Place: Danish Society for Virology, Denmark.

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Current Trends in Microbiology (Journal)
Period: 2005
Rustam Aminov (Editor)
National Veterinary Institute

Description
Current Trends in Microbiology is an international journal devoted to the publication of review articles and original research papers on all aspects of microbiology research.

Editorial Advisory Board

Related journal
Current Trends in Microbiology
0972-7736
Local database
Activity: Research › Journal editor

The Danish Society for Parasitology (External organisation)
Period: 2005 → …
Heidi Huus Petersen (Participant)
National Veterinary Institute

Related external organisation
The Danish Society for Parasitology
Activity: Membership › Membership of research networks or expert groups

Minisymposium om svineinfluenza
Period: 30 Nov 2005
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related event
Minisymposium om svineinfluenza
30/11/2005 → 30/11/2005
Kolding, Danmark
Activity: Attending an event › Participating in or organising a conference
Dansk Veterinær Hyologisk Selskabs halvårsmøde 2005
Period: 1 Nov 2005
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related event

Dansk Veterinær Hyologisk Selskabs halvårsmøde 2005
01/11/2005 → 01/11/2005
Activity: Attending an event › Participating in or organising a conference

DFVF’s rolle i det veterinarian beredskab og service
Period: 1 Nov 2005
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Note: Forelæsning i Retsmedicin

Related event

Forelæsning i Retsmedicin
01/11/2005 → 01/11/2005
Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

NKVet symposium on prevention of boar taint
Period: 1 Nov 2005
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related event

NKVet symposium on prevention of boar taint
01/11/2005 → 01/11/2005
Gardemoen, Norway
Activity: Attending an event › Participating in or organising a conference

6th International Pestivirus Symposium of the European Society of Veterinary Virology
Period: 13 Sep 2005 → 16 Sep 2005
Thomas Bruun Rasmussen (Participant)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
ESVV Pestivirus Symposium; 6
Uniform extraction of RNA and DNA for quantitative multiplex PCR detection of classical and African swine fevers in blood or meat juice.
Place: Thun, Switzerland

**Related event**

**6th International Pestivirus Symposium of the European Society of Veterinary Virology**
Thun, Switzerland
Activity: Attending an event › Participating in or organising a conference

**ESVV Pestivirus Symposium; 6**
Period: 13 Sep 2005 → 16 Sep 2005
Åse Uttenthal (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Description**
Uniform extraction of RNA and DNA for quantitative multiplex PCR detection of classical and African swine fevers in blood or meat juice.
Place: Thun, Switzerland

**Related external organisation**

**Unknown external organisation**
Activity: Talks and presentations › Conference presentations

**Annual Newcastle disease/Avian influenza meeting/symposium for EU national reference laboratories**
Period: 1 Sep 2005
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

**Related event**

**Annual Newcastle disease/Avian influenza meeting/symposium for EU national reference laboratories**
01/09/2005 → 01/09/2005
Brussels, Belgium
Activity: Attending an event › Participating in or organising a conference

**Den Danske Dyrlægeforenings årsmøde september, 2005**
Period: 31 Aug 2005
Vibeke Sørensen (Participant)
Division of Veterinary Diagnostics and Research
Secretariat
National Veterinary Institute

**Related event**

**Den Danske Dyrlægeforenings årsmøde september, 2005**
31/08/2005 → 31/08/2005
Activity: Attending an event › Participating in or organising a conference

**APP symposium 2005**
Period: 1 Jun 2005
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related event

**APP symposium 2005**
01/06/2005 → 01/06/2005
Madrid, Spain
Activity: Attending an event › Participating in or organising a conference

Certifikatkursus for dyrlæger i kødkontrollen med begrænset autorisation
Period: 1 Jun 2005
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Note: MKS og SP

Related external organisation

Tåstrup
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

Club 5 extended directors meeting, May 2005 (External organisation)
Period: 1 May 2005
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Description
Place: Uppsala, Sweden

Related external organisation

Club 5 extended directors meeting, May 2005
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

Mund- klovesyge
Period: 1 May 2005
Anette Bøtner (Guest lecturer)
Division of Virology
Sektion for Eksotiske Virussygdomme
National Veterinary Institute

Description
Note: Beredskabskursus for dyrlæger i fødevareafdelingerne samt kødkontrollen

Related external organisation

Vejle
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities
Epidemiologiske undersøgelser og prøveudtagelse. MKS, SP, ND, Aj.
Period: 1 Apr 2005
Anette Bøtner (Lecturer)
Division of Virology
Sektion for Eksotiske Virussygdomme
National Veterinary Institute
Activity: Other

NKVet board meeting, april 2005 (External organisation)
Period: 1 Apr 2005
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Description
Place: Oslo, Norway

Related external organisation
NKVet board meeting, april 2005
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

Censor ved Veterinært Speciale for Karin Rosendal Hansen
Period: 1 Jan 2005
Vibeke Sørensen (Internal examiner)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Activity: Examinations and supervision › Internal examination

The standardisation, quality control and validation of molecular diagnostic tests (OIE/WAVLD); 7: Seminar on Application of Biotechnology to Zoonotic Disease Diagnosis
Period: 1 Jan 2005 → …
Åse Uttenthal (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Place: Montevideo, Uruguay

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

The standardisation, quality control and validation of molecular diagnostic tests (OIE/WAVLD); 7: Seminar on Application of Biotechnology to Zoonotic Disease Diagnosis
Period: 1 Jan 2005 → …
Thomas Bruun Rasmussen (Speaker)
Mund- kløvesyge
Period: 1 Nov 2004
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Note: Beredskabskursus for dyrlæger i fødevareafdelingerne samt kødkontrollen

Related event
Beredskabskursus for dyrlæger i fødevareafdelingerne samt kødkontrollen
01/11/2004 → 01/11/2004
Vejle, Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

Serumbehandling af PMWS. Resultater af afprøvning af serum mod PMWS
Period: 1 Nov 2004
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Note: DVHS efterårsmøde
Activity: Other

Mund- kløvesyge
Period: 1 Oct 2004
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Note: Beredskabskursus for regionsdyrlæger

Related event
Beredskabskursus for regionsdyrlæger
01/10/2004 → 01/10/2004
Aarhus, Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities
NKVet symposium on Emerging Zoonoses
Period: 1 Oct 2004
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related event

NKVet symposium on Emerging Zoonoses
01/10/2004 → 01/10/2004
Uppsala, Sweden
Activity: Attending an event › Participating in or organising a conference

Annual Newcastle disease/Avian influenza meeting/symposium for EU national reference laboratories
Period: 1 Sep 2004
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related event

Annual Newcastle disease/Avian influenza meeting/symposium for EU national reference laboratories
01/09/2004 → 01/09/2004
Weybridge, England
Activity: Attending an event › Participating in or organising a conference

Swinebrucellosis, COST 845 meeting
Period: 1 May 2004
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Description
Swinebrucellosis, COST 845 meeting

Related event

Swinebrucellosis, COST 845 meeting
01/05/2004 → …
Lisbon, Portugal
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

DVHS Forårsmøde: PCV2 enteritis som differentialdiagnose til Lawsonia intracellularis
Period: 29 Apr 2004 → 30 Apr 2004
Tim Kåre Jensen (Speaker)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Section for Veterinary Diagnostics
Activity: Other
Clinical significance, diagnosis and control of ileitis & colitis - Danish experiences 1995-2004
Period: 22 Apr 2004 → 23 Apr 2004
Tim Kåre Jensen (Speaker)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Section for Veterinary Diagnostics

Related event

NAH European Swine Ileitis/Colitis workshop
22/04/2004 → 23/04/2004
Alpbach, Austria
Activity: Talks and presentations › Conference presentations

Club 5 annual meeting on surveillance systems
Period: 1 Apr 2004
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related event

Club 5 annual meeting on surveillance systems
01/04/2004 → 01/04/2004
Lelystad, The Netherlands
Activity: Attending an event › Participating in or organising a conference

Mund- klovesyge
Period: 1 Feb 2004
Anette Bøtner (Guest lecturer)
Division of Virology
Sektion for Eksotiske Virussygdomme
National Veterinary Institute

Related external organisation

Vejle
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

PRRS, PMWS/PDNS, Svineinfluenza
Period: 1 Feb 2004
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Related external organisation

Århus
Activity: Other
Annual Meeting Nordic Society for Veterinary Pathology (NSVP): Application of immunohistochemistry and fluorescent in situ hybridization for the detection of Lawsonia intracellularis, Porcine Circo Virus type 2, Brachyspira hyodysenteriae, Brachyspira pilosicoli, Brachyspira innocens and Brachyspira intermedia in pigs
Period: 1 Jan 2004
Tim Kåre Jensen (Speaker)
Division of Veterinary Diagnostics and Research
Section for Veterinary Diagnostics
National Veterinary Institute

Related event
Annual Meeting Nordic Society for Veterinary Pathology
01/01/2004 → 01/01/2004
Copenhagen, Denmark
Activity: Talks and presentations › Conference presentations

Intestinal bacterial community analysis, Lawsonia intracellularis a case study: AFAC workshop: Alternatives to Feed Antibiotics and Anticoccidials in Pig and Poultry Meat Production.
Period: 1 Jan 2004
Lars Melbak (Speaker)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Microbial Ecology

Description
Place: Aarhus, Denmark

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Mund- klovesyge
Period: 1 Jan 2004
Anette Bøtner (Guest lecturer)
Division of Virology
Sektion for Eksotiske Virussygdomme
National Veterinary Institute

Description
Note: Beredskabskursus for regionsdyrlæger

Related external organisation
Århus
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

Annual Newcastle disease/Avian influenza meeting/symposium for national reference laboratories
Period: 1 Dec 2003
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related event
Annual Newcastle disease/Avian influenza meeting/symposium for national reference laboratories  
01/12/2003 → 01/12/2003  
Bruxelles, Belgium  
Activity: Attending an event › Participating in or organising a conference

Experiences with eradication of PRRS in Danish swine herds  
Period: 1 Dec 2003  
Anette Bøtner (Speaker)  
National Veterinary Institute  
Division of Virology  
Sektion for Eksotiske Virussygdomme

Related event

Association Francaise de Medicine Veterinaire Porcine (AFMVP) Congress  
01/12/2003 → …  
Paris, France  
Activity: Talks and presentations › Conference presentations

NKVet symposium on Animal transports – disease risks and welfare aspects  
Period: 1 Nov 2003  
Vibeke Sørensen (Participant)  
National Veterinary Institute  
Division of Veterinary Diagnostics and Research  
Secretariat

Related event

NKVet symposium on Animal transports – disease risks and welfare aspects  
01/11/2003 → 01/11/2003  
Finland  
Activity: Attending an event › Participating in or organising a conference

Nordisk Veterinærmøde om beredskab  
Period: 1 Oct 2003  
Vibeke Sørensen (Participant)  
National Veterinary Institute  
Division of Veterinary Diagnostics and Research  
Secretariat

Related event

Nordisk Veterinærmøde om beredskab  
01/10/2003 → 01/10/2003  
Stockholm, Sweden  
Activity: Attending an event › Participating in or organising a conference

PMWS – Status over viden og forskning  
Period: 1 Oct 2003  
Anette Bøtner (Speaker)  
National Veterinary Institute  
Division of Virology  
Sektion for Eksotiske Virussygdomme
Related event

PMWS – Status over viden og forskning
01/10/2003 → 01/10/2003
Herning
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

SAFEPORK 5th International Symposium on the Epidemiology and Control of Foodborne Pathogens in Pork
Erik Jacobsen (Participant)
Division of Veterinary Diagnostics and Research
Section for Veterinary Epidemiology and public sector consultancy
National Veterinary Institute

Description
Vetstat-The Danish Nation-wide monitoring of veterinary medicine use on herd level

Place: Heraklion, Crete-Greece
Degree of recognition: International

Related event

SAFEPORK 5th International Symposium on the Epidemiology and Control of Foodborne Pathogens in Pork
01/10/2003 → 04/10/2003
Crete, Greece
Activity: Attending an event › Participating in or organising a conference

Den Danske Dyrlægeforenings årsmøde 2003
Period: 1 Sep 2003
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related event

Den Danske Dyrlægeforenings årsmøde 2003
01/09/2003 → 01/09/2003
Nyborg Strand, Danmark
Activity: Attending an event › Participating in or organising a conference

PMWS og PRRS – Opdatering og aktuelt nyt
Period: 1 Sep 2003
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Note: Årsmøde i DDD
Activity: Other

Lawsonia intracellularis: patologi, påvisning og differential diagnostik: Dyrlægemøder
Period: 20 Jun 2003
Tim Kåre Jensen (Speaker)
Lawsonia intracellularis: patologi, påvisning og differential diagnostik: Dyrlægemøder
Period: 19 Jun 2003
Tim Kåre Jensen (Speaker)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Section for Veterinary Diagnostics
Related external organisation
Kolding
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

Club 5 annual meeting on orphan zoonoses
Period: 1 May 2003
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat
Related event
Club 5 annual meeting on orphan zoonoses
01/05/2003 → 01/05/2003
Copenhagen, Denmark
Activity: Attending an event › Participating in or organising a conference

NKVet bestyrelsesmøde, april 2003 (External organisation)
Period: 1 Apr 2003
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat
Description
Place: Helsinki, Finland
Related external organisation
NKVet bestyrelsesmøde, april 2003
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

PMWS og circo virus hos grise
Period: 1 Mar 2003
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Description**
Gæsteforelæsning ved KVL ved uddeling af Intervets legat for unge veterinærvidenskabelige forskere

**Related external organisation**
Royal Veterinary and Agricultural University
Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

PMWS – status: Grundforskning og langsigtede løsninger – diagnostik, x-virus, serumudvikling og vaccineudvikling
Period: 1 Mar 2003
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Description**
Note: Møde med formænd og ledende konsulenter. Landsudvalget

**Related external organisation**
Kolding Fjord Hotel, Kolding
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

In situ visualization of plasmid transfer from Pseudomonas putida to the indigenous bacterial population of Alfalfa sprouts
Period: 1 Jan 2003 → …
Lars Mølbak (Speaker)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Microbial Ecology

**Description**
Place: FEMS Congress of European Microbiologists. Ljubljana, Slovenia

**Related external organisation**
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Meeting of the EU national reference laboratories for brucellosis
Period: 1 Jan 2003
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

**Related event**
Meeting of the EU national reference laboratories for brucellosis
01/01/2003 → 01/01/2003
Bruxelles, Belgium
Activity: Attending an event › Participating in or organising a conference
National expert ved EU kommissionens mission til Washington DC og Californien vedrørende udbrud af Newcastle Disease i USA (External organisation)
Period: 1 Jan 2003
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related external organisation

National expert ved EU kommissionens mission til Washington DC og Californien vedrørende udbrud af Newcastle Disease i USA
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

Transfer of Broad Host Range Plasmids to the bacterial Rhizosphere Population: The Microbial Diversity and Molecular Ecology Workshop
Period: 1 Jan 2003 → …
Lars Mølbak (Speaker)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Microbial Ecology

Description
Place: Höör; Sweden

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

F E M S Microbiology Letters (Journal)
Period: 2002
Rustam Aminov (Editor)
National Veterinary Institute

Description
FEMS Microbiology Letters

As one of the five FEMS Microbiology, free to publish, print and online journals, FEMS Microbiology Letters offers rapid review and publication of outstanding research in all aspects of Microbiology, except virology (other than Bacteriophages).

The Editors of FEMS Microbiology Letters give priority to concise papers that merit urgent publication by virtue of their originality, general interest and their contribution to new developments in microbiology. All aspects of microbiology, except virology (other than bacteriophages), are covered.

Editor in Genetics and Molecular Biology

Related journal

F E M S Microbiology Letters
0378-1097
BFI (2018): BFI-level 1, Scopus rating (2017): CiteScore 1.8 SJR 0.79 SNIP 0.58, ISI indexed (2013): ISI indexed yes, Web of Science (2018): Indexed yes
Central database
Activity: Research › Journal editor
**Governing Board of the International Association for Paratuberculosis (External organisation)**

*Period: 2002 → …*

Gregers Jungersen (Member)

Section for Immunology and Vaccinology

National Veterinary Institute

**Description**

The Association is a non-profit organization devoted to the advancement of knowledge and scientific achievement toward the eradication of paratuberculosis in domestic livestock and other species affected by Mycobacterium paratuberculosis. Countries with 5 or more IAP members can select a national representative to the governing board.

IAP Governing Board Danish representative selected by Danish members of the association

Degree of recognition: International

Links:

http://www.paratuberculosis.net

**Related external organisation**

**Governing Board of the International Association for Paratuberculosis**

Activity: Membership › Membership of commitees, commissions, boards, councils, associations, organisations, or similar

**Beyond antimicrobial growth promotors in food animal production: Effects of the termination of AGP use on outbreaks of Lawsonia intracellularis in pigs: Danish experiences with porcine proliferative enteropathy 1995-2002**

*Period: 6 Nov 2002 → 7 Nov 2002*

Tim Kåre Jensen (Speaker)

National Veterinary Institute

Division of Veterinary Diagnostics and Research

Section for Veterinary Diagnostics

**Description**

Place: Foulum, Tjele

**Related external organisation**

**Unknown external organisation**

Activity: Talks and presentations › Conference presentations

**NKVet bestyrelsesmøde, oktober 2002 (External organisation)**

*Period: 1 Oct 2002*

Vibeke Sørensen (Participant)

National Veterinary Institute

Division of Veterinary Diagnostics and Research

Secretariat

**Description**

Place: Oslo, Norge

**Related external organisation**

**NKVet bestyrelsesmøde, oktober 2002**

Activity: Membership › Membership of commitees, commissions, boards, councils, associations, organisations, or similar

**NKVet symposium on Xenotransplantation**

*Period: 1 Oct 2002*

Vibeke Sørensen (Participant)

National Veterinary Institute
Division of Veterinary Diagnostics and Research

Secretariat

Related event

NKVet symposium on Xenotransplantation  
01/10/2002 → 01/10/2002  
Oslo, Norway  
Activity: Attending an event › Participating in or organising a conference

PMWS status I Danmark  
Period: 1 Sep 2002  
Anette Bøtner (Speaker)  
National Veterinary Institute  
Division of Virology  
Sektion for Eksotiske Virussygdomme

Description  
Note: DDD's årsmøde

Related event

DDD's årsmøde  
01/09/2002 → ...  
Denmark  
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

17th International Pig Veterinary Society Congress  
Period: 1 Jun 2002  
Vibeke Sørensen (Participant)  
National Veterinary Institute  
Division of Veterinary Diagnostics and Research  
Secretariat

Related event

17th International Pig Veterinary Society Congress  
02/06/2002 → 05/06/2002  
Ames, Iowa, United States  
Activity: Attending an event › Participating in or organising a conference

Annual Newcastle disease/Avian influenza meeting/symposium for national reference laboratories  
Period: 1 Jun 2002  
Vibeke Sørensen (Participant)  
National Veterinary Institute  
Division of Veterinary Diagnostics and Research  
Secretariat

Related event

Annual Newcastle disease/Avian influenza meeting/symposium for national reference laboratories  
01/06/2002 → 01/06/2002  
Padova, Italy  
Activity: Attending an event › Participating in or organising a conference
Intervets Fjerkræsymposium 2002
Period: 4 Apr 2002
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related event
Intervets Fjerkræsymposium 2002
04/04/2002 → 04/04/2002
Vejle, Danmark
Activity: Attending an event › Participating in or organising a conference

Brucellosis in man and animals
Period: 1 Apr 2002
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related event
Brucellosis in man and animals: Meeting in EU Cost Action 845
01/04/2002 → 01/04/2002
Paris, France
Activity: Attending an event › Participating in or organising a conference

NKVet bestyrelsesmøde, april 2002 (External organisation)
Period: 1 Apr 2002
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Description
Place: Oslo, Norge

Related external organisation
NKVet bestyrelsesmøde, april 2002
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

Medlem af bedømmelsesudvalget for Annette Cleveland Nielsens Ph.d. afhandling (External organisation)
Period: 1 Jan 2002
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related external organisation
Medlem af bedømmelsesudvalget for Annette Cleveland Nielsens Ph.d. afhandling
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar
Medlem af bedømmelsesudvalget for Zhuang Qikuns Ph.d. afhandling (External organisation)
Period: 1 Jan 2002
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related external organisation

Medlem af Nordisk komite for veterinærvidenskabeligt samarbejde (NKVet), udpeget af Den Danske Dyrlæge forening (External organisation)
Period: 1 Jan 2002
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related external organisation

Medlem af Nordisk komite for veterinærvidenskabeligt samarbejde (NKVet), udpeget af Den Danske Dyrlæge forening (External organisation)

Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

Molecular typing of Salmonella used in the Danish collaborating network for tracing sources of human salmonellosis
Period: 1 Jan 2002 → …
Flemming Bager (Speaker)
National Veterinary Institute
Division of Poultry, Fish and Fur Animals
Administration and Service

Description
Place: Int Symp on Salmonella and Salmonellosis. Ploufragan, France

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

Den Danske Dyrlægeforenings årsmøde 2001
Period: 11 Sep 2001 → 14 Sep 2001
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related event

Den Danske Dyrlægeforenings årsmøde 2001
Nyborg Strand, Danmark
Activity: Attending an event › Participating in or organising a conference
Reproduction of PMWS in immunostimulated and non-immunostimulated conventional 3-week-old piglets experimentally infected with PCV2
Period: 1 Sep 2001
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Conference on ssDNA Viruses of Plants and Birds, Pigs and Primates, PMWS

Related event
Reproduction of PMWS in immunostimulated and non-immunostimulated conventional 3-week-old piglets experimentally infected with PCV2
01/09/2001 → 01/09/2001
St. Malo, France
Activity: Talks and presentations › Conference presentations

Annual Newcastle disease/Avian influenza meeting/symposium for national reference laboratories
Period: 1 Apr 2001
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related event
Annual Newcastle disease/Avian influenza meeting/symposium for national reference laboratories
01/04/2001 → 01/04/2001
Uppsala, Sweden
Activity: Attending an event › Participating in or organising a conference

Brucellosis in man and animals; 3
Period: 1 Mar 2001
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related event
Brucellosis in man and animals; 3: Cost Action 845 , 3 rd management committee meeting, WG 3 meeting
01/03/2001 → 01/03/2001
Nimes, France
Activity: Attending an event › Participating in or organising a conference

Post-weaning Multisystemic Wasting Syndrome (PMWS) og circovirus type 2
Period: 1 Feb 2001
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme
First annual meeting of EU national reference laboratories for brucellosis; 1
Period: 1 Dec 2000
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related event
First annual meeting of EU national reference laboratories for brucellosis; 1
01/12/2000 → 01/12/2000
Brussels, Belgium
Activity: Attending an event › Participating in or organising a conference

Circovirus og PMWS – hvor står vi
Period: 1 Nov 2000
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme
Activity: Other

Post-weaning Multisystemic Wasting Syndrome (PMWS) og circovirus type 2
Period: 1 Oct 2000
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Related external organisation
Hotel Kolding Fjord
Activity: Other

Brucellosis 2000, Incl. The 53rd brucellosis research conference; 53
Period: 1 Sep 2000
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related event
Brucellosis 2000, Incl. The 53rd brucellosis research conference; 53
01/09/2000 → 01/09/2000
Nimes, France
Activity: Attending an event › Participating in or organising a conference

**Brucellosis in man and animals**
Period: 1 Sep 2000
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

**Related event**
**Brucellosis in man and animals: EU meeting, Cost Action 845**
01/09/2000 → 01/09/2000
Nimes, France
Activity: Attending an event › Participating in or organising a conference

**Post-weaning Multisystemic Wasting Syndrome (PMWS) og circovirus type 2**
Period: 1 Sep 2000
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Description**
Note: DDD's årsmøde Hotel Nyborg Strand

**Related external organisation**
**Den Danske Dyrlægeforening**
Peter Bangs Vej 30, DK-2000, Frederiksberg, Denmark
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

**PRRS**
Period: 1 Jul 2000
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Description**
Place: Kina

**Related external organisation**
**Unknown external organisation**
Activity: Talks and presentations › Conference presentations

**PRRSV diversitet: Immunologisk problem eller epidemiologisk værktøj**
Period: 4 May 2000 → 5 May 2000
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme
Application of fluorescent in situ hybridization for the detection of porcine intestinal pathogens
Period: 1 Jan 2000
Tim Kåre Jensen (Lecturer)
Division of Veterinary Diagnostics and Research
Section for Veterinary Diagnostics
National Veterinary Institute

Related event
Application of fluorescent in situ hybridization for the detection of porcine intestinal pathogens: PhD course in infection microbiology
01/01/2000 → 01/01/2000
Department of Veterinary Microbiology, KVL
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

Field experiences with Porcine Reproductive and Respiratory Syndrome (PRRS) and with the use of a live PRRS-vaccine in Denmark
Period: 1 Jan 2000
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Related event
Field experiences with Porcine Reproductive and Respiratory Syndrome (PRRS) and with the use of a live PRRS-vaccine in Denmark
01/01/2000 → 01/01/2000
China
Activity: Talks and presentations › Conference presentations

Medlem af Management Committee of COST 845 "Brucellosis in Animals and Man", (External organisation)
Period: 1 Jan 2000 → 1 Jan 2006
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related external organisation
Medlem af Management Committee of COST 845 "Brucellosis in Animals and Man"
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

Nomineret expert fra DK for: Annual meetings of EU national reference laboratories for Brucellosis (External organisation)
Period: 1 Jan 2000 → 1 Jan 2003
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related external organisation

Nomineret expert fra DK for: Annual meetings of EU national reference laboratories for Brucellosis
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

Pig Veterinary Society, Autumn meeting 2000
Period: 1 Jan 2000
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related event

Pig Veterinary Society, Autumn meeting 2000
01/01/2000 → 01/01/2000
Market Bosworth, England
Activity: Attending an event › Participating in or organising a conference

Pre-harvest control of salmonella in broilers, layers and swine – results, public health effects and cost effectiveness
Period: 1 Jan 2000 → …
Flemming Bager (Speaker)
National Veterinary Institute
Division of Poultry, Fish and Fur Animals
Administration and Service

Description
Place: Int Conf Emerg Infect Dis, Atlanta, GA, USA

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

Research in Veterinary Science (Journal)
Period: 1 Jan 2000 → May 2005
Tim Kåre Jensen (Reviewer)
National Veterinary Institute
Section for Bacteriology, Pathology and Parasitology

Description
Research in Veterinary Science is an International journal publishing original articles, reviews and short communications of a high scientific and ethical standard in the veterinary sciences.

Completed assignments primo 2015: 10

Related journal

Research in Veterinary Science
0034-5288
The consequences of discontinued use of antimicrobial growth promoters (AGP’s) for food producing animals in Denmark
Period: 1 Jan 2000 → …
Flemming Bager (Speaker)
National Veterinary Institute
Division of Poultry, Fish and Fur Animals
Administration and Service

Description
Place: Int Conf Emerg Infect Dis, Atlanta, GA, USA

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Veterinary Microbiology (Journal)
Period: 1 Jan 2000 → 5 May 2015
Tim Kåre Jensen (Reviewer)
National Veterinary Institute
Section for Bacteriology, Pathology and Parasitology

Description
An International Journal.
Veterinary Microbiology is concerned with microbial (bacterial, fungal, viral) diseases of domesticated vertebrate animals (livestock, companion animals, fur-bearing animals, game, poultry, and fish).

Completed assignments by primo 2015: 14

Related journal
Veterinary Microbiology
0378-1135
BFI (2018): BFI-level 2, Scopus rating (2017): CiteScore 2.7 SJR 1.175 SNIP 1.241, ISI indexed (2013): ISI indexed yes,
Web of Science (2018): Indexed yes

Virussygdomme hos svin. PPV, svineinfluenza, PRRS samt porcint circovirus (PMWS)
Period: 25 Nov 1999
Anette Bøtner (Lecturer)
Division of Virology
Sektion for Eksotiske Virussygdomme
National Veterinary Institute

Description
Note: Fagdyrlægekursus vedrørende svin

Related event
Fagdyrlægekursus vedrørende svin
01/01/1999 → …
Slagelse
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities
Patologiske forandringer ved diarréer: Dyrlægemøder
Period: 23 Nov 1999
Tim Kåre Jensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Section for Veterinary Diagnostics

Description
Arrangeret af ScherringPlough
Activity: Other

Patologiske forandringer ved diarréer
Period: 17 Nov 1999
Tim Kåre Jensen (Speaker)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Section for Veterinary Diagnostics

Description
Arrangeret af ScherringPlough

Related external organisation
Odense
Activity: Other

Annual meeting of the National Newcastle Disease and Avian Influenza Laboratories
Period: 1 Nov 1999
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related event
Annual meeting of the National Newcastle Disease and Avian Influenza Laboratories
01/11/1999 → 01/11/1999
Brussels, Belgium
Activity: Attending an event › Participating in or organising a conference

PMWS – en ny svinesygdom
Period: 27 Oct 1999
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Conference

Related event
PMWS – en ny svinesygdom
27/10/1999 → 27/10/1999
Diagnosing vaccine induced PRRS. Distinction between infections with European and American/vaccine type PRRS virus after vaccination with a modified-live PRRS vaccine

Period: 22 Jun 1999
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
3rd International Symposium on PRRS

Related event
Diagnosing vaccine induced PRRS. Distinction between infections with European and American/vaccine type PRRS virus after vaccination with a modified-live PRRS vaccine
22/06/1999 → 22/06/1999
Ploufragan
Activity: Talks and presentations › Conference presentations

Status vedrørende circovirus infektioner i Danmark
Period: 7 May 1999
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Note: Forårsøende i Dansk Veterinær Hyologisk Selskab

Related event
DVHS forårsøende
07/05/1999 → …
Denmark
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

Nyt om tarmledelser hos svin: Dyrlægemøder
Period: 11 Mar 1999
Tim Kåre Jensen (Speaker)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Section for Veterinary Diagnostics

Description
Arrangeret af DLG, MSD AGVET og Løvens

Related external organisation
Odense
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

Nyt om tarmledelser hos svin: Dyrlægemøder
Period: 10 Mar 1999
Tim Kåre Jensen (Speaker)
Description
Arrangører af DLG, MSD AGVET og Løvens

Related external organisation
Viborg
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

Virussygdomme hos svin. PPV, PRRS, svineinfluenza og porcint circovirus
Period: 28 Jan 1999
Anette Bøtner (Lecturer)
Division of Virology
Sektion for Eksotiske Virussygdomme
National Veterinary Institute

Description
Note: Fagdyrlægekursus vedrørende svin

Related event
Fagdyrlægekursus vedrørende svin
01/01/1999 → …
Slagelse
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

Application of fluorescent in situ hybridization for the detection of porcine intestinal pathogens
Period: 1 Jan 1999
Tim Kåre Jensen (Participant)
Division of Veterinary Diagnostics and Research
National Veterinary Institute

Description

Related event
Application of fluorescent in situ hybridization for the detection of porcine intestinal pathogens: PhD course in infection microbiology
01/01/1999 → 01/01/1999
Department of Veterinary Microbiology, KVL
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

International symposium on PRRS
Period: 1 Jan 1999
Vibeke Sørensen (Participant)
Division of Veterinary Diagnostics and Research
National Veterinary Institute

Related event
International symposium on PRRS
01/01/1999 → 01/01/1999
Ploufragan, France
**Activity: Attending an event › Participating in or organising a conference**

**Medlem af bedømmelsesudvalget for Margit Andreasens Ph.d.afhandling (External organisation)**
*Period: 1 Jan 1999*

Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

**Related external organisation**

**Medlem af bedømmelsesudvalget for Margit Andreasens Ph.d.afhandling**
*Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar*

**Nominator Expert i arbejdskompetence under EU kommissionen vedrørende tuberkulose, brucellose og leukose hos kvæg (External organisation)**
*Period: 1 Jan 1999 → …*

Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

**Description**
Place: EU

**Related external organisation**

**Nominator Expert i arbejdskompetence under EU kommissionen vedrørende tuberkulose, brucellose og leukose hos kvæg**
*Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar*

**Porcin Reproduktions- og Respirationssygdom (PRRS) - fokuseret på situationen i Danmark, herunder erfaringer med anvendelsen af en levende PRRS-vaccine**
*Period: 1 Dec 1998*

Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Description**
*Note: Virologisk Selskab*

**Related external organisation**

**Unknown external organisation**
*Activity: Talks and presentations › Conference presentations*

**Field experiences with PRRS and with the use of a live vaccine in Denmark**
*Period: 12 Nov 1998*

Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Description**
Swine Disease Conference for Swine Practitioners, Iowa State University
Place: Iowa State University
Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

PCR til påvisning og tyning af PRRS-virus
Period: 6 Nov 1998
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Note: Efterårsmøde i Dansk Veterinær Hyologisk Selskab

Related event
DVHS efterårsmøde
06/11/1998 → …
Denmark
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

The EU commisions annual meeting for national reference laboratories on AI and ND
Period: 1 Nov 1998
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related event
The EU commisions annual meeting for national reference laboratories on AI and ND
Vienna, Austria
Activity: Attending an event › Participating in or organising a conference

Pato-anatomiske aspekter ved diarré - eksemplificeret ved spirochætose
Period: 28 Aug 1998
Tim Kåre Jensen (Speaker)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Section for Veterinary Diagnostics

Description
Foredrag ved Veterinærskolens 225 års jubilæum

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

PRRS - The Danish experience
Period: 6 Aug 1998
Anette Bøtner (Speaker)
National Veterinary Institute
Challenge of previously PRRS infected pigs with PRRS vaccine virus
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

PRRS - "der Dänische Fall" aus dänischer Sicht
Period: 24 Apr 1998
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Epidemiology and control of PRRS: The Danish experience with use of a live modified PRRS vaccine in a PRRS control programme
Period: 27 Mar 1998
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Epidemiology and control of PRRS - "der Dänische Fall" aus dänischer Sicht
Munich
Activity: Talks and presentations › Conference presentations

Epidemiology and control of PRRS: The Danish experience with use of a live modified PRRS vaccine in a PRRS control programme
Period: 27 Mar 1998
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

S.I.P.A.S. 1998 annual meeting "Epidemiology and control of PRRS"
Place: Parma, Italy
Fodringsseminar
Period: 19 Mar 1998
Tim Kåre Jensen (Speaker)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Section for Veterinary Diagnostics

Description
Danisco Ingredients

Related event
Fodringsseminar: Tarminfektioner hos ung- og slagtesvin
19/03/1998 → 19/03/1998
Brabrand
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

Kompleksitet ved tarminfektioner
Period: 25 Feb 1998
Tim Kåre Jensen (Lecturer)
Division of Veterinary Diagnostics and Research
Section for Veterinary Diagnostics
National Veterinary Institute

Related external organisation
Randers Amt og Østjysk Dyrlægeforening
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

Kompleksitet ved tarminfektioner
Period: 27 Jan 1998
Tim Kåre Jensen (Lecturer)
Division of Veterinary Diagnostics and Research
Section for Veterinary Diagnostics
National Veterinary Institute

Related external organisation
Viborg og Rinkøbing Amts Dyrlægeforeninger
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

15th International Pig Veterinary Society Congress
Period: 1 Jan 1998
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related event
15th International Pig Veterinary Society Congress
05/07/1998 → 09/07/1998
Birmingham, United Kingdom
Activity: Attending an event › Participating in or organising a conference

Nominator expert from DK for: Annual meetings of EU national reference laboratories for Avian Influenza and Newcastle Disease (External organisation)
Period: 1 Jan 1998 → 1 Jan 2005
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related external organisation
Nominator expert from DK for: Annual meetings of EU national reference laboratories for Avian Influenza and Newcastle Disease
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

Kompleksitet ved tarminfektioner
Period: 12 Nov 1997
Tim Kåre Jensen (Lecturer)
Division of Veterinary Diagnostics and Research
Section for Veterinary Diagnostics
National Veterinary Institute

Related external organisation
Ålborg og Vensyssel Amts Dyrlægeforeninger
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

Appearance of acute PRRS-like symptoms in sow herds after vaccination with modified-live PRRS vaccine
Period: 18 Sep 1997
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Related event
Appearance of acute PRRS-like symptoms in sow herds after vaccination with modified-live PRRS vaccine
18/09/1997 → 18/09/1997
Iowa State University
Activity: Talks and presentations › Conference presentations

International Society of Veterinary Epidemiology and Economics, VIIIth symposium; 8
Period: 1 Jul 1997
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related event
Eksperimentelle infektioner med Serpulina pilosicoli og Serpulina hyodysenteriae hos svin. Komparative studier:

**Dyrisgemøder**

**Period:** 26 May 1997 → 28 May 1997

Tim Kåre Jensen (Speaker)

National Veterinary Institute

Division of Veterinary Diagnostics and Research

Section for Veterinary Diagnostics

**Related external organisation**

**DLG a.m.b.a**

Denmark

Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

**DVHS’ forårsmøde: Eksperimentel Serpulina pilosicoli colitis hos svin**

**Period:** 1 May 1997 → 2 May 1997

Kristian Møller (Speaker)

National Veterinary Institute

Management

**Related event**

**DVHS’ Forårsmøde**

01/05/1997 → 02/05/1997

Denmark

Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

**DVHS’ forårsmøde: Påvisning af Lawsonia intracellularis i 3 endemisk inficerede besætninger**

**Period:** 1 May 1997 → 2 May 1997

Tim Kåre Jensen (Speaker)

National Veterinary Institute

Division of Veterinary Diagnostics and Research
Section for Veterinary Diagnostics

Related event

**DVHS' Forårsmede**
01/05/1997 → 02/05/1997
Denmark
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

**DVHS' forårsmede: Påvisning af Lawsonia intracellularis i 3 endemisk inficerede besætninger**
Period: 1 May 1997 → 2 May 1997
Kristian Møller (Speaker)
National Veterinary Institute
Management

**Related event**

**DVHS' Forårsmede**
01/05/1997 → 02/05/1997
Denmark
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

**Serologiske besætningsprofiler: PRRS, influenza: Kontrol af luftvejslidelser hos svin i fremtidens produktionssystemer**
Period: 13 Mar 1997
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Description**
Note: Pfizer symposium

**Related external organisation**

**Unknown external organisation**
Activity: Talks and presentations › Conference presentations

**Porcine salmonella infections as a human health risk**
Period: 1 Jan 1997 → …
Flemming Bager (Speaker)
National Veterinary Institute
Division of Poultry, Fish and Fur Animals
Administration and Service

**Description**
Place: Second International Symposium in Epidemiology and Control of Salmonella in Pork, Copenhagen, Denmark

**Related external organisation**

**Unknown external organisation**
Activity: Talks and presentations › Conference presentations

**Risk management: Intervention to control competing sources of infection in food borne salmonellosis**
Period: 1 Jan 1997 → …
Flemming Bager (Speaker)
National Veterinary Institute
Description
Place: World Congress Veterinary Food Hygiene, Haag, Holland

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Surveillance of antimicrobial resistance - requirements for monitoring programmes
Period: 1 Jan 1997 → …
Flemming Bager (Speaker)
National Veterinary Institute
Division of Poultry, Fish and Fur Animals
Administration and Service

Description
Place: Epidemiol Sante Anim (ISVEE)

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

The second international symposium on epidemiology and control of salmonella in pork; 2
Period: 1 Jan 1997
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related event
The second international symposium on epidemiology and control of salmonella in pork; 2
01/01/1997 → 01/01/1997
Copenhagen, Denmark
Activity: Attending an event › Participating in or organising a conference

PRRS-serologi
Period: 20 Nov 1996
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme
Activity: Other

Seriologi, epidemiologi og produktionsresultater i danske besætninger med PRRS
Period: 8 Nov 1996
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Place: Kolding

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

DVHS’ efterårsøde: Patologi ved tarmssygdomme hos ung- og slagtesvin
Period: 7 Nov 1996 → 8 Nov 1996
Tim Kåre Jensen (Speaker)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Section for Veterinary Diagnostics
Activity: Other

On the risk of transfer of PRRS-virus between herds and the Danish strategy of control
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Eight European A.I. Vets Meeting 7-9 October 1996

Related external organisation
Billund, Denmark
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

PRRS vaccination of boars
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Eight European A.I. Vets Meeting

Related external organisation
Billund, Denmark
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

Vertical integration of zoonosis control in Denmark
Period: 6 May 1996 → 8 May 1996
Flemming Bager (Speaker)
National Veterinary Institute
Division of Poultry, Fish and Fur Animals
Administration and Service

**Description**
Place: International Symposium on Food Associated Pathogens, Uppsala

**Related external organisation**

**Unknown external organisation**
Activity: Talks and presentations › Conference presentations

**PRRS - Sygdommen og vaccinen**
**Period:** 11 Apr 1996
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Description**
Place: Ringsted

**Related external organisation**

**Unknown external organisation**
Activity: Talks and presentations › Conference presentations

**PRRS - Sygdommen og vaccinen**
**Period:** 28 Mar 1996
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Description**
Place: Aalborg

**Related external organisation**

**Unknown external organisation**
Activity: Talks and presentations › Conference presentations

**PRRS - Sygdommen og vaccinen**
**Period:** 27 Mar 1996
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Description**
Note: Veterinaerfagligt debatmøde om PRRS

**Related external organisation**

**Kolding**
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations
PRRS, Porcin Reproduktions- og Respirationssygdom: "Ætiologi og klinik" samt "Vaccineafprøvning incl. serologiske undersøgelser for PRRS"
Period: 20 Mar 1996
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Note: Dansk Selskab for Veterinær patologi og hygiejne

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

PRRS: Sygdommen og vaccinen
Period: 19 Feb 1996
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
PRRS-møde for svineproducenter

Related external organisation

Åbenrå
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

PRRS: Sygdommen og vaccinen
Period: 13 Feb 1996
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
PRRS-møde for svineproducenter

Related external organisation

Ringsted
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

PRRS: Sygdommen og vaccinen
Period: 9 Feb 1996
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
PRRS-møde for svineproducenter
Related external organisation

Brædstrup
Activity: Talks and presentations › Conference presentations

PRRS: Sygdommen og vaccinen
Period: 8 Feb 1996
Anette Bøtner (Participant)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Note: PRRS-møder for svineproducenter

Related event

Sygdommen og vaccinen: PRRS-møde for svineproducenter
08/02/1996 → 08/02/1996
Aalborg, Denmark
Activity: Other

International Conference on the Haemophilus, Actinobacillus, Pasteurella Group of Organisms
Period: 1 Jan 1996
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related event

International Conference on the Haemophilus, Actinobacillus, Pasteurella Group of Organisms
13/10/1996 → 17/10/1996
Acapulco, Mexico
Activity: Attending an event › Participating in or organising a conference

Medlem af "SPF-VET" udvalget som repræsentant for Danmarks Veterinærinstitut (External organisation)
Period: 1 Jan 1996 → 1 Jan 2001
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related external organisation

Medlem af "SPF-VET" udvalget som repræsentant for Danmarks Veterinærinstitut
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

The mechanism behind the distribution of zoonotic agents in animal production
Period: 1 Jan 1996 → …
Flemming Bager (Speaker)
National Veterinary Institute
Division of Poultry, Fish and Fur Animals
Administration and Service
**Description**
Place: ECCEAMST Meeting, Roskilde, Denmark

**Related external organisation**

**Unknown external organisation**
Activity: Talks and presentations › Conference presentations

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**Diarré og colitis hos slagtesvin: Danske erfaringer**
Period: 8 Oct 1995
Tim Kåre Jensen (Speaker)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Section for Veterinary Diagnostics

**Description**
Place: Uppsala, Sverige

**Related external organisation**

**Unknown external organisation**
Activity: Talks and presentations › Conference presentations

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**Diagnosis of PRRS**
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Description**
2nd International Symposium on Porcine Reproductive and Respiratory Syndrome (PRRS)

**Related event**

**Diagnosis of PRRS: 2nd International Symposium on Porcine Reproductive and Respiratory Syndrome (PRRS)**
09/08/1995 → 10/08/1995
Copenhagen
Activity: Talks and presentations › Conference presentations

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**Foreløbige resultater fra PRRSV podningsforsøg på orner fremlagt for Landsudvalget for svin**
Period: 9 May 1995
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Description**
Bestyrelsesmøde

**Related external organisation**

**Axelborg**
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

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**Danske erfaringer med serologiske undersøgelser for PRRS og nyt vedr. PRRS vacciner**
Period: 1 Dec 1994
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Description**
Note: Dansk Veterinær Hyologisk Selskab's efterårsmøde

**Related event**

DVHS' efterårsmøde
01/12/1994 → …
Denmark
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

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**13th International Pig Veterinary Society Congress**
Vibeke Sørensen (Chairman)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

**Description**
13th International Pig Veterinary Society Congress

**Related event**

13th International Pig Veterinary Society Congress
26/06/1994 → 30/06/1994
Bangkok, Thailand
Activity: Attending an event › Participating in or organising a conference

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Virologiske risici ved anvendelse af husdyrgødning og affald
Period: 23 Jun 1994
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Related event**

Virologiske risici ved anvendelse af husdyrgødning og affald
23/06/1994 → 23/06/1994
Kolding
Activity: Talks and presentations › Conference presentations

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PRRS-virologi, diagnostik
Period: 21 Jun 1994
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Description**
Møde med svinerådgivere om PRRS
Related external organisation

Åbenrå
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

PPV, PRRS, Svineinfluenza
Period: 17 Jan 1994
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Afholdt for Svinefagdyrlæge-kursister

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

13th International Pig Veterinary Society Congress
Period: 1 Jan 1994
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related event

13th International Pig Veterinary Society Congress
26/06/1994 → 30/06/1994
Bangkok, Thailand
Activity: Attending an event › Participating in or organising a conference

3rd International Conference on the Haemophilus, Actinobacillus, Pasteurella Group of Organisms
Period: 1 Jan 1994
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related event

3rd International Conference on the Haemophilus, Actinobacillus, Pasteurella Group of Organisms
31/07/1994 → 04/08/1994
Edinburgh, United Kingdom
Activity: Attending an event › Participating in or organising a conference

Vilth International Symposium in World Association of Veterinary Laboratory Diagnosticians; 7
Period: 1 Jan 1994
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat
Related event

VIIth International Symposium in World Association of Veterinary Laboratory Diagnosticians; 7
01/01/1994 → 01/01/1994
Buenos Aires, Argentina
Activity: Attending an event › Participating in or organising a conference

Virusinfektioner som årsag til reproduktionsforstyrrelser hos svin – herunder serologiske aspekter
Period: 29 Oct 1993
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Related event

Virusinfektioner som årsag til reproduktionsforstyrrelser hos svin – herunder serologiske aspekter: Immunologi og Reproduktion
29/10/1993 → …
Vejle, Denmark
Activity: Talks and presentations › Conference presentations

Virusinfektioner som årsag til reproduktionsforstyrrelser hos svin – herunder serologiske aspekter
Period: 28 Oct 1993
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Related event

Virusinfektioner som årsag til reproduktionsforstyrrelser hos svin – herunder serologiske aspekter: Immunologi og Reproduktion
28/10/1993 → …
Ålborg, Denmark
Activity: Talks and presentations › Conference presentations

Virusinfektioner som årsag til reproduktionsforstyrrelser hos svin – herunder serologiske aspekter
Period: 12 Oct 1993
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Related event

Virusinfektioner som årsag til reproduktionsforstyrrelser hos svin – herunder serologiske aspekter: Immunologi og Reproduktion
12/10/1993 → …
Næstved, Denmark
Activity: Talks and presentations › Conference presentations

Status vedrørende porcin reproduktions- og respirationssygdom
Period: 27 Aug 1992
Anette Bøtner (Lecturer)
Description
Præstø amts dyrlægeforening på besøg på Lindholm

Related external organisation

Lindholm
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

12th International Pig Veterinary Society Congress
Vibeke Sørensen (Chairman)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Description
12th International Pig Veterinary Society Congress

Related event

12th International Pig Veterinary Society Congress
17/08/1992 → 20/08/1992
Hague, Netherlands
Activity: Attending an event › Participating in or organising a conference

Status vedrørende porcin reproduktions- og respirationssygdom
Period: 7 May 1992
Anette Bøtner (Speaker)
Division of Virology
Sektion for Eksotiske Virussygdomme
National Veterinary Institute

Description
Dansk Veterinær Hyologisk Selskab

Related external organisation

Dansk Veterinær Hyologisk Selskab, Kolding, Danmark
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

Virus og diagnostik af virusinfektioner
Period: 7 May 1992
Anette Bøtner (Lecturer)
Division of Virology
Sektion for Eksotiske Virussygdomme
National Veterinary Institute

Description
Dansk Veterinær Hyologisk Selskab

Related external organisation
Veterinary Medicines in Post-1992 Europe
Period: 1 Feb 1992
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related event
Veterinary Medicines in Post-1992 Europe
01/02/1992 → 01/02/1992
Brussels, Belgium
Activity: Attending an event › Participating in or organising a conference

12th International Pig Veterinary Society Congress
Period: 1 Jan 1992
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related event
12th International Pig Veterinary Society Congress
17/08/1992 → 20/08/1992
Hague, Netherlands
Activity: Attending an event › Participating in or organising a conference

VIth International Symposium in World Association of Veterinary Laboratory Diagnosticians; 6
Period: 1 Jan 1992
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related event
VIth International Symposium in World Association of Veterinary Laboratory Diagnosticians; 6
01/01/1992 → 01/01/1992
Lyon, France
Activity: Attending an event › Participating in or organising a conference

Mave-tarm-sygdomme hos svin "TGE, svinepest"
Period: 12 Dec 1991
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Kollokvium i svinesygdomme, SVS, “Svineinfluenza”

An epizootic of pseudorabies in Denmark: epizootiological investigations providing further evidence of long distance airborne transmission of virus

Evidence of spread of derivatives of attenuated vaccine strains of suid herpesvirus 1 (pseudorabies virus)
Svineinfluenza - Ny subtype i Danmark
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Foredrag holdt for Ringkøbing og Sønderjyllands amts dyrlægeforeninger

11th International Pig Veterinary Society Congress
Period: 30 Nov 1989
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

5th International Symposium in World Association of Veterinary Laboratory Diagnosticians; 5
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

International Conference on the Haemophilus, Actinobacillus, Pasteurella Group of Organisms
Vibeke Sørensen (Participant)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Secretariat

Related event

International Conference on the Haemophilus, Actinobacillus, Pasteurella Group of Organisms
21/06/1989 → 24/06/1989
Guelph, Canada
Activity: Attending an event › Participating in or organising a conference

Total immunoglobulin hos regnbueørred: Vurdering af IgM-koncentration i sera fra regnbueørreder fra forskellige miljøer
Period: 1 Jan 1985
Niels Jørgen Olesen (Participant)
Division of Poultry, Fish and Fur Animals
Section of Fish Diseases
National Veterinary Institute

Description
Head : Niels Jørgen Olesen

Related external organisation

SVS, Statens Veterinære Seruminstitut, Århus
Activity: Other

Fiskesygdomme på EDB
Period: 1 Jan 1984
Niels Jørgen Olesen (Participant)
Division of Poultry, Fish and Fur Animals
Section of Fish Diseases
National Veterinary Institute

Description
Head : Niels Jørgen Olesen

Related external organisation

Den Kongelige Veterinær og Landbohøjskole
Activity: Other

Prizes:

4th annual meeting EPIZONE, St. Malo, France, 2010: Poster prize
Tanya von Rosen (Recipient)
National Veterinary Institute

Details
Awarded date: 7 Jun 2010
Granting Organisations: St. Malo, France
Prize: Prizes, scholarships, distinctions

Best overseas poster
Tim Kåre Jensen (Recipient)
National Veterinary Institute, Pathology
Details
Awarded date: 9 Jul 1998
Degree of recognition: International
event: 15th International Pig Veterinary Society Congress
Prize: Prizes, scholarships, distinctions

IUIS VIC Keystone rejse legat
Simon Welner (Recipient)
National Veterinary Institute, Center for Biological Sequence Analysis, Section for Immunology and Vaccinology, Section for Virology

Description
Fondsmidler til at hjælpe PhD/DVM studerende med at deltage i Keystone symposiet ad 20.-25.01.2015: "Immunity to veterinary pathogens: Informing vaccine development"

Modtog et legat på 1000 USD. Dog skal jeg betale nogle af pengene tilbage, da jeg også modtog et andet legat udbudt af Keystone, så jeg i alt har modtaget flere penge end mine rejseomkostninger er budgetteret til.

Details
Awarded date: 20 Jan 2015
Granting Organisations: IUIS VIC: International Union of Immunological Societies - Veterinary Immunology Commitee
Prize: Prizes, scholarships, distinctions

Keystone symposia future of science fund scholarship
Simon Welner (Recipient)
National Veterinary Institute, Center for Biological Sequence Analysis, Section for Immunology and Vaccinology, Section for Virology

Description
Fik bevilget 1200 USD

Details
Awarded date: 20 Jan 2015
Prize: Prizes, scholarships, distinctions

Keystone Symposia scholarship
Heidi Mikkelsen Melvang (Recipient)
National Veterinary Institute, Section for Immunology and Vaccinology

Description

Details
Awarded date: 20 Jan 2015
Granting Organisations: Keystone Symposia
Prize: Prizes, scholarships, distinctions

MSD Animal Health names 2018 High Quality Pork Ph.D. award
Ana Carolina Lopes Antunes (Recipient)
National Veterinary Institute, Epidemiology

Details
Awarded date: 2018
Degree of recognition: International
Prize: Prizes, scholarships, distinctions

Poster Prize
Anna Irene Vedel Sørensen (Recipient)
National Veterinary Institute, Epidemiology

Description
Poster prize awarded for the poster: "Modelling spread of MRSA within a pig herd"
Roberto Chizzoline Memorial Poster Award 2017
Ana Carolina Lopes Antunes (Recipient)
National Veterinary Institute, Epidemiology

Description
Poster presented at the ECVPH AGM & Annual Scientific Conference 2017

YOUNG EPIZONE Poster Prize
Ana Carolina Lopes Antunes (Recipient)
National Veterinary Institute, Section for Epidemiology

Description
Poster Prize at EPIZONE 8th Annual meeting

Press clippings:

Uudforskede data giver ny viden om svins dødelighed
Ana Carolina Lopes Antunes
19/12/2017
National Veterinary Institute, Epidemiology

Media coverage (1)

Antibiotika: Forbrug, resistens, behandling
Nanett Kvist Nikolaisen
02/10/2017
National Veterinary Institute, Bacteriology & Parasitology

Media contribution (1)
**Computermodel skal overvåge kvægsygdom**
Carsten Thure Kirkeby
20/10/2016

**Description**
Short communication about iCull in Ingeniøren
National Veterinary Institute, Section for Epidemiology

**Media contribution (1)**

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**Afrikansk svinepest: Danmark kan let blive ramt**
Anette Bøtner
05/08/2016

**Subject**
Afrikansk svinepest
National Veterinary Institute, Section for Diagnostics and Scientific Advice

**Media contribution (1)**

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**Dansk laser-radar skal redde bier og andre små truede dyr**
Carsten Thure Kirkeby
03/04/2015

**Subject**
Insects, vectorborne diseases, laser
National Veterinary Institute, Section for Epidemiology

**Media contribution (1)**

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**Harddisken 2014: Om laserradar og malariamyg**
Carsten Thure Kirkeby
12/12/2014

**Subject**
Laserrader, LIDAR, insekter, malaria
National Veterinary Institute, Section for Epidemiology

**Media contribution (1)**
Harddisken 2014: Om laserradar og malariamyg
12/12/2014
DR P1, Radio
Søren Storm
12 min.
http://www.dr.dk/p1/harddisken/harddisken-158
Carsten Thure Kirkeby
National Veterinary Institute, Section for Epidemiology
Press / Media

Irriterende insekter er fascinerende: Insekter, sygdomsudbrud, forskning og teknologi
Carsten Thure Kirkeby
24/11/2014

Subject
Insekter
National Veterinary Institute, Section for Epidemiology

Media contribution (1)

Irriterende insekter er fascinerende: Insekter, sygdomsudbrud, forskning og teknologi
24/11/2014
Radio24syv, Radio
Claus Cancel
Ca. 7 minutter
http://www.radio24syv.dk/programmer/24syv-morgen/10619706/33:13/
Link to the program.
Carsten Thure Kirkeby
National Veterinary Institute, Section for Epidemiology
Press / Media

Carsten Thure Kirkeby
19/11/2014

Subject
Sygdomsspredning, insekter, LIDAR, entomologi
National Veterinary Institute, Section for Epidemiology

Media contribution (1)

19/11/2014
DR online, Web
Hanne Kokkegård
http://www.dr.dk/Nyheder/Viden/Miljoe/2014/11/19165348.htm
Link
Carsten Thure Kirkeby
National Veterinary Institute, Section for Epidemiology
Press / Media

Researcher discovered Siberian midge on Sweden trip
Carsten Thure Kirkeby
10/08/2014

Description
Popular article about the discovery of Culicoides gornostaevae in Norway, Sweden and Poland.

Subject
Culicoides, Disease spread, bluetongue, Schmallenberg
National Veterinary Institute, Section for Epidemiology
Media contribution (1)

Researcher discovered Siberian midge on Sweden trip
10/08/2014
DTU Avisen, Print
Mette Buck Jensen
http://emagstudio.win.dtu.dk/E-books/DTU-Avisen/DTU_Avisen_1408/#/18/
Link to the article.
Carsten Thure Kirkeby
National Veterinary Institute, Section for Epidemiology

Relations
Research outputs:
Culicoides (Avaritia) gornostaevae Mirzaeva, 1984 (Diptera: Ceratopogonidae) a possible vector species of the Obsoletus group new to the European fauna.
Projects:
Vector-borne threats in northern Europe
Press / Media

Hjemekassen på P1
Carsten Thure Kirkeby
16/06/2014

Subject
PhD Cup 2014 og PhD projekter.
National Veterinary Institute, Section for Epidemiology

Media contribution (1)

PhD Cup 2014
Carsten Thure Kirkeby
24/05/2014

Description
The PhD Cup is a national competition about presenting the PhD sproject to a broad audience. Eight persons from all Universities in Denmark are selected to present their project in 3 minutes in the award show. The show was broadcast on the national TV channel DR2.

Carsten Kirkeby won the third prize in the presentation contest.

Subject
Biting midges and spread of diseases.
National Veterinary Institute, Section for Epidemiology

Media contribution (1)

PhD Cup 2014
24/05/2014
DR2, Television
Peter Lund Madsen
3 minutter
http://www.vet.dtu.dk/Nyheder/2014/06/phdcup
Carsten Thure Kirkeby
National Veterinary Institute, Section for Epidemiology
Feltarbejde med mitter 2011: Spatielle adfærdsmønstre hos mitter, Stevns 2011
Carsten Thure Kirkeby
01/09/2011
National Veterinary Institute, Division of Veterinary Diagnostics and Research, Section for Veterinary Epidemiology and public sector consultancy

Mediapartnere (1)

Feltarbejde med mitter 2011: Spatielle adfærdsmønstre hos mitter, Stevns 2011
01/09/2011
Klippinge, Stevns & Vector Lab, Bülowsvæj, Television
http://www.tv2lorry.dk/artikel/74217
EXT-OA
Carsten Thure Kirkeby
National Veterinary Institute, Division of Veterinary Diagnostics and Research, Section for Veterinary Epidemiology and public sector consultancy
Press / Media

Har Klippinge fået besøg fra rummet?
Carsten Thure Kirkeby
24/08/2011
National Veterinary Institute, Division of Veterinary Diagnostics and Research, Section for Veterinary Epidemiology and public sector consultancy

Mediapartnere (1)

Har Klippinge fået besøg fra rummet?
24/08/2011
Klippinge, Stevns, Print
PUB-OA
Carsten Thure Kirkeby
National Veterinary Institute, Division of Veterinary Diagnostics and Research, Section for Veterinary Epidemiology and public sector consultancy
Press / Media

Beskidte lastbiler kan bringe svinepest til Danmark
Åse Uttenthal
17/09/2010
National Veterinary Institute, Division of Virology, Sektion for Eksotiske Virussygdomme

Mediapartnere (1)

Beskidte lastbiler kan bringe svinepest til Danmark
17/09/2010
Landbrugsavisen, Print
Åse Uttenthal
National Veterinary Institute, Division of Virology, Sektion for Eksotiske Virussygdomme
Press / Media

Svin smitter svin med influenza
Lars Erik Larsen
01/08/2009
National Veterinary Institute, Division of Veterinary Diagnostics and Research, Virology

Mediapartnere (1)

Svin smitter svin med influenza
01/08/2009
Print
http://www.dyrlaegemagasinet.dk
Valle mod Kalvediarré
Lars Erik Larsen
01/01/2008
National Veterinary Institute, Division of Veterinary Diagnostics and Research, Virology

Valle mod Kalvediarré
Valle mod Kalvediarré
01/01/2008
Print
Lars Erik Larsen
National Veterinary Institute, Division of Veterinary Diagnostics and Research, Virology

Valle mod Kalvediarré
Peter Mikael Helweg Heegaard
01/01/2008
National Veterinary Institute, Division of Veterinary Diagnostics and Research, Innate Immunology

Valle mod Kalvediarré
Valle mod Kalvediarré
01/01/2008
Print
Peter Mikael Helweg Heegaard
National Veterinary Institute, Division of Veterinary Diagnostics and Research, Innate Immunology

Valle-baseret immunglobulin-produkt mod kalvediarré
Peter Mikael Helweg Heegaard
01/01/2008
National Veterinary Institute, Division of Veterinary Diagnostics and Research, Innate Immunology

Valle-baseret immunglobulin-produkt mod kalvediarré
Valle-baseret immunglobulin-produkt mod kalvediarré
01/01/2008
Dansk Veterinærtidsskrift 2008 15. april nr. 8 - Årgang 91, Print
Peter Mikael Helweg Heegaard
National Veterinary Institute, Division of Veterinary Diagnostics and Research, Innate Immunology

Immunsystemet slår alarm
Peter Mikael Helweg Heegaard
01/01/2008
National Veterinary Institute, Division of Veterinary Diagnostics and Research, Innate Immunology

Immunsystemet slår alarm
Peter Mikael Helweg Heegaard
01/01/2008
DTU Avisen, Print
National Veterinary Institute, Division of Veterinary Diagnostics and Research, Innate Immunology