Animal Models for Influenza A Virus Infection Incorporating the Involvement of Innate Host Defenses: Enhanced Translational Value of the Porcine Model

Influenza is a viral respiratory disease having a major impact on public health. Influenza A virus (IAV) usually causes mild transitory disease in humans. However, in specific groups of individuals such as severely obese, the elderly, and individuals with underlying inflammatory conditions, IAV can cause severe illness or death. In this review, relevant small and large animal models for human IAV infection, including the pig, ferret, and mouse, are discussed. The focus is on the pig as a large animal model for human IAV infection as well as on the associated innate immune response. Pigs are natural hosts for the same IAV subtypes as humans, they develop clinical disease mirroring human symptoms, they have similar lung anatomy, and their respiratory physiology and immune responses to IAV infection are remarkably similar to what is observed in humans. The pig model shows high face and target validity for human IAV infection, making it suitable for modeling many aspects of influenza, including increased risk of severe disease and impaired vaccine response due to underlying pathologies such as low-grade inflammation. Comparative analysis of proteins involved in viral pattern recognition, interferon responses, and regulation of interferon-stimulated genes reveals a significantly higher degree of similarity between pig, ferret, and human compared with mice. It is concluded that the pig is a promising animal model displaying substantial human translational value with the ability to provide essential insights into IAV infection, pathogenesis, and immunity.

General information
State: Accepted/In press
Organisations: Translational Immunology, Department of Biotechnology and Biomedicine, Innate Immunology, Virology, National Veterinary Institute, Adaptive Immunology, Beltsville Human Nutrition Research Center
Number of pages: 15
Publication date: 2018
Peer-reviewed: Yes

Publication information
Journal: Ilar Journal
Article number: ilj009
ISSN (Print): 1930-6180
Ratings:
Web of Science (2018): Indexed yes
Scopus rating (2017): CiteScore 3.93
Scopus rating (2016): CiteScore 3.52
Scopus rating (2015): CiteScore 1.87
Scopus rating (2014): CiteScore 1.77
Scopus rating (2013): CiteScore 1.39
Scopus rating (2012): CiteScore 1.98
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 ApS, SEGES Pig Research Center, OE-Vet
Number of pages: 10
Publication date: 2018
Peer-reviewed: Yes

Publication information
Journal: Porcine Health Management
Volume: 4
Issue number: 2
ISSN (Print): 2055-5660
Original language: English
Keywords: Diagnostics, Finishers, Oral fluid, Pooling, Porcine circovirus type 2, Serum

Electronic versions:
10.1186_2Fs40813_018_0079_4.pdf
DOIs:
10.1186/s40813-018-0079-4

Bibliographical note
This article is distributed under the terms of the Creative Commons Attribution 4.0 International License (http://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons license, and indicate if changes were made. The Creative Commons Public Domain Dedication waiver http://creativecommons.org/publicdomain/zero/1.0/ applies to the data made available in this article, unless otherwise stated.

Source: FindIt
Source-ID: 2395290637
Research output: Research - peer-review › Journal article – Annual report year: 2018
Diarrhoea in neonatal piglets: a case control study on microbiological findings

Many factors can influence the occurrence of neonatal diarrhoea in piglets. Currently, well-known pathogens such as enterotoxigenic Escherichia coli and Clostridium perfringens type C appear to play a minor role in development of disease. Other infectious pathogens may be involved. In this study, we aimed to investigate the presence of selected infectious pathogens in neonatal piglets with clinical and pathological signs of enteric disease. The association between rotavirus A, Enterococcus hirae, Clostridium difficile and Clostridium perfringens type A/C and diarrhoea was investigated in a case control study on piglet level. The possible role of E. coli virulence factors was investigated in a multistep-procedure using herd-pools of E.coli isolates to screen for their presence. Rotavirus A was detected more often in cases (25%) than in controls (6%) (P

General information
State: Published
Organisations: National Veterinary Institute, Bacteriology & Parasitology, Virology, Diagnostic & Development, Aarhus University, SEGES Pig Research Center
Contributors: Kongsted, H., Pedersen, K., Hjulsager, C. K., Larsen, L. E., Pedersen, K. S., Jorsal, S. E., Bækbo, P.
Number of pages: 7
Publication date: 2018
Peer-reviewed: Yes

Publication information
Journal: Porcine Health Management
Volume: 4
Article number: 17
ISSN (Print): 2055-5660
Original language: English
Keywords: AIDA-1, Beta 2, C. difficile, C. perfringens type a, E. coli virulence factors, EAST1, Enterococcus hirae, Neonatal diarrhoea, Piglets, Rotavirus a
Electronic versions: s40813_018_0094_5.pdf

Bibliographical note
Open Access This article is distributed under the terms of the Creative Commons Attribution 4.0 International License (http://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons license, and indicate if changes were made. The Creative Commons Public Domain Dedication waiver (http://creativecommons.org/publicdomain/zero/1.0/) applies to the data made available in this article, unless otherwise stated
Source: FindIt
Source-ID: 2436471240
Research output: 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 air 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 PRRSV 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
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.

General information
State: Published
Organisations: National Veterinary Institute, Virology, Animal and Plant Health Agency, Wageningen Bioveterinary Research, National Veterinary Institute
Pages: 1-8
Publication date: 2018
Peer-reviewed: Yes

Publication information
Journal: Epidemiology and Infection
ISSN (Print): 0950-2688
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
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.
Højpatogen fugleinfluenza med subtypen H5N6 er forblevet i Danmark

General information
State: Published
Organisations: National Veterinary Institute, Virology
Contributors: Hjulsager, C. K., Larsen, L. E.
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.
Overvågning af aviær influenza i vilde fugle i Danmark 2017

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
Number of pages: 4
Publication date: 2018

Publication information

Publisher: SEGES Svineproduktion
Volume: 2018
Edition: 1807
Original language: Danish
Electronic versions:
Notat_1807_1_.pdf
URLs:
http://svineproduktion.dk/publikationer/kilder/notater/2018/1807
Source: FindIt
Source-ID: 2406500676
Research output: Research › Report – Annual report year: 2018

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.
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.
General information
State: Published
Organisations: Molecular Evolution, Department of Biotechnology and Biomedicine, Department of Bio and Health Informatics, Disease Intelligence and Molecular Evolution, National Veterinary Institute, Virology, Kopenhagen Fur
Pages: 1360-1371
Publication date: 2017
Peer-reviewed: Yes

Publication information
Journal: Journal of General Virology
Volume: 98
Issue number: 6
ISSN (Print): 0022-1317
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.68 SJR 1.325 SNIP 0.877
Web of Science (2017): Impact factor 2.514
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.93 SJR 1.544 SNIP 0.891
Web of Science (2016): Impact factor 2.838
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 3.26 SJR 1.738 SNIP 0.998
Web of Science (2015): Impact factor 3.192
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 3.25 SJR 1.69 SNIP 1.057
Web of Science (2014): Impact factor 3.183
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 3.64 SJR 1.764 SNIP 1.154
Web of Science (2013): Impact factor 3.529
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 3.28 SJR 1.525 SNIP 1.034
Web of Science (2012): Impact factor 3.127
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 3.6 SJR 1.684 SNIP 1.145
Web of Science (2011): Impact factor 3.363
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): Impact factor 3.568
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
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
Pages: 74-83
Publication date: 2017
Peer-reviewed: Yes

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): Impact factor 2.524
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): Impact factor 2.628
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.56 SJR 1.413 SNIP 1.21
Web of Science (2015): Impact factor 2.564
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.54 SJR 1.291 SNIP 1.256
Web of Science (2014): Impact factor 2.511
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Original language: English
Keywords: PRRSV, PRRSV-2, Type 2, Virulence, Pigs, Experimental infection
Electronic versions:
1_s2.0_S0378113517305096_main.pdf
DOIs:
10.1016/j.vetmic.2017.10.001

Bibliographical note
This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/BY-NC-ND/4.0/).
Research output: Research - peer-review › Journal article – Annual report year: 2017

Global gruppering af plasmacytosevirus isoleret fra mink (Neovison vison)

General information
Global phylogenetic analysis of contemporary aleutian mink disease viruses (AMDV)

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 significant 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.
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, Autonomous University of Barcelona, Centro de Investigación en Sanidad Animal
Contributors: Baratelli, M., Pedersen, L. E., Trebbien, R., Larsen, L. E., Jungersen, G., Blanco, E., Nielsen, J., Montoya, M.
Pages: 895-899
Publication date: 2017
Peer-reviewed: Yes

Publication information
Journal: Journal of General Virology
Volume: 98
Issue number: 5
ISSN (Print): 0022-1317
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.68 SJR 1.325 SNIP 0.877
Web of Science (2017): Impact factor 2.514
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.93 SJR 1.544 SNIP 0.891
Web of Science (2016): Impact factor 2.838
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 3.26 SJR 1.738 SNIP 0.998
Web of Science (2015): Impact factor 3.192
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 3.25 SJR 1.69 SNIP 1.057
Web of Science (2014): Impact factor 3.183
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 3.64 SJR 1.764 SNIP 1.154
Web of Science (2013): Impact factor 3.529
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 3.28 SJR 1.525 SNIP 1.034
Web of Science (2012): Impact factor 3.127
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 3.6 SJR 1.684 SNIP 1.145
Web of Science (2011): Impact factor 3.363
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): Impact factor 3.568
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
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.593 SNIP 1.131
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.709 SNIP 1.128
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.654 SNIP 1.137
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 1.55 SNIP 1.215
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 1.58 SNIP 1.145
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 1.369 SNIP 1.083
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
Pages: 1045-1062
Publication date: 2017
Peer-reviewed: Yes

Publication information
Journal: Hydrogeology Journal
Volume: 25
Issue number: 4
ISSN (Print): 1431-2174
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.03 SJR 0.886 SNIP 1.153
Web of Science (2017): Impact factor 2.071
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.13 SJR 1.134 SNIP 1.144
Web of Science (2016): Impact factor 2.109
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 1.96 SJR 0.977 SNIP 1.281
Web of Science (2015): Impact factor 2.028
Lungebetændelse hos mink med ansamlinger af mononukleære inflammationsceller

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

Bibliographical note
This article is distributed under the terms of the Creative Commons Attribution 4.0 International License.
Source: FindIt
Source-ID: 2351817171
Research output: Research - peer-review › Journal article – Annual report year: 2017
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 diagnosticus 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 influenzasyge personer, samt sikre at minkfoder indeholdende biprodukter fra slagtesvin er varmebehandlet eller inaktiveteret på anden vis.

General information
State: Published
Organisations: National Veterinary Institute, Virology, Bacteriology & Parasitology, Diagnostic & Development
Pages: 102-105
Publication date: 2017
Peer-reviewed: No

Publication information
Journal: Faglig Årsberetning
Volume: 2017
ISSN (Print): 2445-9437
Original language: English
Keywords: Influenza A virus, Mink, Zoonose
Electronic versions:
Mink_kan ogs have influenza.pdf
URLs:
Source: PublicationPreSubmission
Source-ID: 146104619
Research output: Research › Journal article – 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.
Nyt virus beskrevet hos svin – Porcint circovirus type 3 (PCV3)

General information
State: Published
Organisations: National Veterinary Institute, Virology, SEGES Pig Research Center
Contributors: Larsen, L. E., Sonne Kristensen, C.
Number of pages: 3
Publication date: 2017
Peer-reviewed: Unknown

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
URLs:
http://svineproduktion.dk/publikationer/kilder/notater/2017/1721
Source: PublicationPreSubmission
Source-ID: 140842806
Research output: Communication – Journal article – Annual report year: 2017

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 Paroviridae 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 unthriftness 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
Overvågning af aviar influenza i vilde fugle i Danmark 2016


**General information**

**State:** Published  
**Organisations:** National Veterinary Institute, Virology, University of Copenhagen  
**Contributors:** Hjulsager, C. K., Krogh, J. S., Madsen, J. J., Thorup, K., Larsen, L. E.  
**Number of pages:** 40  
**Publication date:** 2017

**Publication information**

**Place of publication:** Frederiksberg C  
**Publisher:** Veterinarinstituttet, Danmarks Tekniske Universitet  
**Original language:** English  
**Electronic versions:** Overvågning af avian influenza i vilde fugle i Danmark 2016 til orbit.pdf  
**Research output:** Research > Report – Annual report year: 2017

**Overvågning af influenza A virus i svin - Slutrapport 2016**

findes i Danmark. Introduktion af dette virus kan frygtes at få epizootisk karakter, da immunitten i populationen mod dette virus forventes at være 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 danske svinebesætninger. 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, Virology
Contributors: Krog, J. S., Hjulsager, C. K., Larsen, L. E.
Number of pages: 31
Publication date: 2017

**Publication information**

Place of publication: Frederiksborg C
Publisher: Veterinærinstituttet, Danmarks Tekniske Universitet
Original language: English
Electronic versions: Afrapportering_SIV_overv_gning_2016_offentlig.pdf
Research output: Research › Report – Annual report year: 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
Pages: 13-19
Publication date: 2017
Peer-reviewed: Yes

**Publication information**

Journal: Veterinary Microbiology
Volume: 209
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): Impact factor 2.524
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): Impact factor 2.628
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.56 SJR 1.413 SNIP 1.21
Web of Science (2015): Impact factor 2.564
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.
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.2 SJR 1.249 SNIP 0.716
Web of Science (2016): Impact factor 2.092
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.47 SJR 1.573 SNIP 0.813
Web of Science (2015): Impact factor 2.303
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.28 SJR 1.228 SNIP 0.823
Web of Science (2014): Impact factor 2.227
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.48 SJR 1.303 SNIP 0.771
Web of Science (2013): Impact factor 2.488
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.91 SJR 1.382 SNIP 0.943
Web of Science (2012): Impact factor 2.894
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.83 SJR 1.32 SNIP 0.885
Web of Science (2011): Impact factor 2.934
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.217 SNIP 0.848
Web of Science (2010): Impact factor 2.942
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.502 SNIP 0.843
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.408 SNIP 0.774
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.266 SNIP 0.742
Scopus rating (2006): SJR 1.232 SNIP 0.767
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.565 SNIP 0.82
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 1.535 SNIP 0.923
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 1.382 SNIP 0.713
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 1.357 SNIP 0.712
Scopus rating (2001): SJR 1.264 SNIP 0.639
Scopus rating (2000): SJR 1.206 SNIP 0.663
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 1.336 SNIP 0.902
Original language: English
Keywords: Cytotoxic T lymphocytes, NetMHCpan, PopCover, Positional scanning combinatorial peptide library (PSCPL), Swine leukocyte antigen, Vaccine
Background. Rotavirus A (RVA) is a well-known cause of diarrhoea 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 diarrhoea.

Material/Methods. Two commercial swine herds with neonatal diarrhoea 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 beginning and at the end of study. The outbreak day was defined as the day where >25% of the litter showed clinical diarrhoea, 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 analysed 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 diarrhoea 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 diarrhoea within 24 hours after a positive RVA diagnosis. The results confirmed that RVA has a significant impact on incidence of diarrhoea and weight gain also in E. coli negative litters.

General information
State: Published
Organisations: National Veterinary Institute, Virology, Technical University of Denmark, Aarhus University
Publication date: 2017
Peer-reviewed: Yes
Event: Abstract from 9th European Symposium of Porcine Health Management (ESPHM 2017), Prague, Czech Republic.
Source: PublicationPreSubmission
Source-ID: 140461466
Research output: Research - peer-review Conference abstract for conference – Annual report year: 2017
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-PCR (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
Contributors: Goecke, N. B., Krog, J. S., Hjulsager, C. K., Skovgaard, K., Harder, T., Larsen, L. E.
Publication date: 2017
Peer-reviewed: Yes
Event: Abstract from 9th European Symposium of Porcine Health Management (ESPHM 2017), Prague, Czech Republic.
Electronic versions:
ESPHM2017_Proceedings_SIV_Fluidigm_chip.pdf
Source: PublicationPreSubmission
Source-ID: 140461499
Research output: Research - peer-review » Conference abstract for conference – Annual report year: 2017

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.

General information
State: Published
Organisations: National Veterinary Institute, Virology, Merial Norden A/S
Number of pages: 6
Pages: 298-303
Publication date: 2017
Peer-reviewed: Yes

Publication information
Journal: Influenza and Other Respiratory Viruses
Volume: 11
Issue number: 3
ISSN (Print): 1750-2640
Ratings:
Web of Science (2018): Indexed yes
Scopus rating (2017): CiteScore 2.88 SJR 1.966 SNIP 1.073
Web of Science (2017): Impact factor 2.954
Web of Science (2017): Indexed yes
Scopus rating (2016): CiteScore 2.2 SJR 1.461 SNIP 0.981
Web of Science (2016): Impact factor 2.677
Web of Science (2016): Indexed yes
Scopus rating (2015): CiteScore 2.23 SJR 1.668 SNIP 0.857
Web of Science (2015): Impact factor 2.378
A fast and robust method for whole genome sequencing of the Aleutian Mink Disease Virus (AMDV) genome

Aleutian Mink Disease Virus (AMDV) is a frequently encountered pathogen associated with commercial mink breeding. AMDV infection leads to increased mortality and compromised animal health and welfare. Currently little is known about the molecular evolution of the virus, and the few existing studies have focused on limited regions of the viral genome. This paper describes a robust, reliable, and fast protocol for amplification of the full AMDV genome using long-range PCR. The method was used to generate next generation sequencing data for the non-virulent cell-culture adapted AMDV-G strain as well as for the virulent AMDV-Utah strain. Comparisons at nucleotide- and amino acid level showed that, in agreement with existing literature, the highest variability between the two virus strains was found in the left open reading frame, which encodes the non-structural (NS1–3) genes. This paper also reports a number of differences that potentially can be linked to virulence and host range. To the authors’ knowledge, this is the first study to apply next generation sequencing on the entire AMDV genome. The results from the study will facilitate the development of new diagnostic tools and can form the basis for more detailed molecular epidemiological analyses of the virus.

General information
State: Published
Organisations: Department of Systems Biology, Molecular Evolution, National Veterinary Institute, Section for Virology, Center for Biological Sequence Analysis, Kopenhagen Fur
Number of pages: 9
Pages: 43-51
Publication date: 2016
Peer-reviewed: Yes

Publication information
Journal: Journal of Virological Methods
Volume: 234
ISSN (Print): 0166-0934
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.82 SJR 0.858 SNIP 0.817
Web of Science (2017): Impact factor 1.756
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. Polyepitope 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.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Department of Systems Biology, Center for Biological Sequence Analysis, Department of Bio and Health Informatics, Section for Immunology and Vaccinology, Institute of Virology and Immunology
Number of pages: 1
Publication date: 2016
Peer-reviewed: Yes
Event: Abstract from 11th International Veterinary Immunology Symposium, Gold Coast, Australia.
Electronic versions:
Welner_et_al_IVIS_Abstract.pdf
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2016

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.

General information
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.
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
Peer-reviewed: Yes
Event: Poster session presented at 24th International Pig Veterinary Society (IPVS) Congress, Dublin, Ireland.
Electronic versions:
IPVS2016_340.pdf
Source: PublicationPreSubmission
Source-ID: 124140967
Research output: Research - peer-review › Poster – Annual report year: 2016

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
Pages: 335-335
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-PT2-278
Electronic versions:
Book of abstracts
Research output: Research - peer-review › Conference abstract in proceedings – Annual report year: 2016

International ring trials for adoption and validation of real-time RT-PCR protocols for sub-typing European swine influenza viruses
**Introduction of replacement gilts to PRRS-positive sow herds**

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, SEGES Pig Research Center
Contributors: Hoelstad, B. E., Larsen, L. E., Hjulsager, C. K., Kristensen, C.
Pages: 568-568
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-PW1-197
Electronic versions:
Book of abstracts
Research output: Research - peer-review › Conference abstract in proceedings – Annual report year: 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 udskilte 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 luftrom 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 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
Number of pages: 4
Publication date: 2016

Publication information
Publisher: Videncenter for Svineproduktion
Original language: English
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 GmbH
Contributors: Holmgren, S., Kvisgaard, L. K., Bak, H., Larsen, L. E.
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
Publisher: Royal Dublin Society
Article number: PO-PW1-087
Electronic versions: Book of abstracts
Research output: Research - peer-review » Conference abstract in proceedings – Annual report year: 2016

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
Electronic versions: IFASA2016_Vol.40_1_.pdf
Research output: Research - peer-review » 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
Pages: 91-94
Publication date: 2016

Host publication information
Title of host publication: Faglig årsberetning 2015 : Kopenhagen Fur
Overvågning af aviær influenza i vilde fugle i Danmark 2015

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, University of Copenhagen
Number of pages: 33
Publication date: 2016

Publication information
Place of publication: Frederiksberg C
Publisher: Veterinarinstituttet, Danmarks Tekniske Universitet
Original language: Danish
Electronic versions:
AI_overvaagning_vilde_fugle_2015_rapport.pdf
Source: FindIt
Source-ID: 2305680084
Research output: Research › Report – Annual report year: 2016

Overvågning af influenza A virus i svin - Slutrapport 2015

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Contributors: Krog, J. S., Hjulsager, C. K., Larsen, L. E.
Number of pages: 29
Publication date: 2016

Publication information
Place of publication: Frederiksberg C
Publisher: DTU Veterinarinstituttet
Original language: Danish
Electronic versions:
Afrapportering_SIV_overv_gning_2015_nn_.pdf
Source: PublicationPreSubmission
Source-ID: 127962091
Research output: Research › Report – Annual report year: 2016

Pooling of faecal samples for quantitative virus diagnostics by real-time PCR

General information
State: Published
Organisations: National Veterinary Institute, Virology, Section for Virology
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
Electronic versions:
IFASA2016_Vol.40_1_.pdf
URLs:
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.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Friedrich-Loeffler-Institute, Universite Paris-Est, Animal and Plant Health Agency, Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia
Number of pages: 14
Pages: 504-517
Publication date: 2016
Peer-reviewed: Yes

Publication information
Journal: Influenza and Other Respiratory Viruses
Volume: 10
Issue number: 6
ISSN (Print): 1750-2640
Ratings:
Web of Science (2018): Indexed yes
Scopus rating (2017): CiteScore 2.88 SJR 1.966 SNIP 1.073
Web of Science (2017): Impact factor 2.954
Web of Science (2017): Indexed yes
Scopus rating (2016): CiteScore 2.2 SJR 1.461 SNIP 0.981
Web of Science (2016): Impact factor 2.677
Web of Science (2016): Indexed yes
Scopus rating (2015): CiteScore 2.23 SJR 1.668 SNIP 0.857
Web of Science (2015): Impact factor 2.378
Scopus rating (2014): CiteScore 1.86 SJR 1.34 SNIP 0.745
Web of Science (2014): Impact factor 2.201
Scopus rating (2013): CiteScore 2.33 SJR 1.292 SNIP 0.935
Web of Science (2013): Impact factor 1.895
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
Scopus rating (2012): CiteScore 2.9 SJR 1.835 SNIP 1.019
Web of Science (2012): Impact factor 1.471
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
Contributors: Krog, J. S., Hjulsager, C. K., Haugegaard, S., Larsen, L. E.
Pages: 452-452
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-PF3-156
Electronic versions:
Book of abstracts
Research output: Research - peer-review » Conference abstract in proceedings – Annual report year: 2016

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, University of Warsaw
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
Electronic versions:
Book of abstracts
Research output: Research - peer-review » Conference abstract in proceedings – Annual report year: 2016

Subtypning af influenza på danske minkfarmer i 2014

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
The global antigenic diversity of swine influenza A viruses
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
Peer-reviewed: Yes

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): CiteScore 6.88 SJR 7.121 SNIP 1.572
Web of Science (2017): Impact factor 7.616
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): Impact factor 7.725
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 4.91 SJR 7.741 SNIP 1.654
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 4.85 SJR 7.888 SNIP 1.664
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 4.24 SJR 6.086 SNIP 1.562
Web of Science (2013): Impact factor 8.519
Original language: English
Keywords: epidemiology, global health, human, infectious disease, influenza, microbiology, pandemic, swine, virus
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.
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. Coronavirus and calicivirus 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.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Number of pages: 3
Publication date: 2015
Peer-reviewed: Yes
Event: Abstract from Nordic Association of Agricultural Scientists, Turku, Finland.
Electronic versions:
NJF_qPCR_assays_for_viral_mink_diarrhea_endelig_version.pdf
Source: PublicationPreSubmission
Source-ID: 116757331
Beskytter de eksisterende vacciner godt nok mod PCV2-mutant (PCV2d)?

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Contributors: Larsen, L. E., Krog, J. S., Hjulsager, C. K.
Pages: 48-48
Publication date: 2015
Peer-reviewed: Yes

Publication information
Journal: Dansk Veterinaertidsskrift
ISSN (Print): 0106-6854
Peer-reviewed: Yes

Bioinformatics prediction of swine MHC class I epitopes from Porcine Reproductive and Respiratory Syndrome Virus
Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) causes one of the most important diseases in all swine producing countries. The infection has a high impact on animal welfare, food safety and production economics. PRRSV possesses multiple immunoevasive strategies, from suppression of the host cell antiviral machinery, to the deceptive induction of a non-neutralizing antibody response through decoy antigen presentation. This, combined with a very high mutation rate, has hampered the development of safe and effective vaccines. With the overall aim to design a vaccine that induces an effective CTL response against PRRSV, we have taken a bioinformatics approach to identify common PRRSV epitopes predicted to react broadly with predominant swine MHC (SLA) alleles. First, the genomic integrity and sequencing method was examined for 334 available complete PRRSV type 2 genomes leaving 104 strains of high quality. For each strain, a library of all possible 9- and 10-mer peptides was generated considering the known ribosomal frame shift sites and sites for post translational cleavage. All peptides were in silico analyzed for binding affinity to either of five common SLA class I alleles. A quantitative rank score was generated for each peptide by combining two algorithms based on the NetMHCpan neural network and lab determined SLA binding affinity of each amino acid at any position in the peptide, respectively. Peptides with a rank score above a predefined threshold were further analyzed by the PopCover algorithm, providing a final list of 54 epitopes prioritized according to maximum coverage of PRRSV strains and SLA alleles. This bioinformatics approach provides a rational strategy for selecting peptides for a CTL-activating vaccine with broad coverage of both virus and swine diversity. The immunogenicity of the selected peptides is in the process of being verified in vivo.

General information
State: Published
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
Number of pages: 1
Publication date: 2015
Peer-reviewed: Yes
Event: Abstract from 7th International Symposium on Emerging and Re-emerging Pig Diseases, Kyoto, Japan.
Electronic versions: iserpd2015abstract_FINAL.pdf
Source: PublicationPreSubmission
Source-ID: 119057195
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2015

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
Contributors: Hjulsager, C. K., Krog, J. S., Larsen, L. E.
Pages: 47-47
Publication date: 2015
Peer-reviewed: Yes

Publication information
Journal: Dansk Veterinaertidsskrift
Issue number: 15
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
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
Contributors: Hjulsager, C. K., Hartby, C. M., Krog, J. S., Holm, E., Larsen, L. E.
Publication date: 2015
Peer-reviewed: Yes
Event: Abstract from 9th International Symposium on Avian Influenza, Athens, Georgia, United States.
Electronic versions:
AI_lomvier_til_ORBIT.pdf

Bibliographical note
Abstract for oral presentation by Christina Hartby at 9th International Symposium on Avian Influenza, Athens, Georgia, US. April 12-15, 2015.
Source: PublicationPreSubmission
Source-ID: 112051286
Research output: Research - peer-review › Conference abstract for conference – 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
Number of pages: 1
Publication date: 2015
Peer-reviewed: Yes
Event: Abstract from International Porcine Reproductive And Respiratory Syndrome Congress, Ghent, Belgium.
Electronic versions:
abstract1_priebe_final.pdf
Source: PublicationPreSubmission
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
Contributors: Kvisgaard, L. K., Hjulsager, C. K., Botti, S., Larsen, L. E.
Number of pages: 1
Publication date: 2015
Peer-reviewed: Yes
Event: Abstract from International Porcine Reproductive And Respiratory Syndrome Congress, Ghent, Belgium.
Electronic versions:
Development_of_a_real_time_RT_PCR_assay_final.pdf
Source: PublicationPreSubmission
Source-ID: 119055993
Research output: 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.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Ghent University
Number of pages: 17
Publication date: 2015
Peer-reviewed: Yes

Publication information
Journal: Veterinary Research
Volume: 46
Article number: 37
ISSN (Print): 0928-4249
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): SJR 1.266 SNIP 1.139
Web of Science (2017): Impact factor 2.903
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): SJR 1.44 SNIP 1.303
Web of Science (2016): Impact factor 2.798
Web of Science (2016): Indexed yes
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
Contributors: Skovgaard, K., Brogaard, L., Schou, K. K., Larsen, L. E., Mortensen, S., Dürrwald, R., Schengel, M., Heegaard, P. M. H.
Number of pages: 1
Publication date: 2015
Peer-reviewed: Yes
Event: Abstract from 7th international qPCR & NGS Event Symposium & Industrial Exhibition & Application Workshops, Germany.

Electronic versions:


Source: PublicationPreSubmission
Source-ID: 122152957
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2016

**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.

**General information**

State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Section for Virology, Anholt Gartneri & Naturpleje, Aalborg University
Number of pages: 4
Pages: 684-687
Publication date: 2015
Peer-reviewed: Yes

**Publication information**

Journal: Emerging Infectious Diseases
Volume: 21
Issue number: 4
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): Impact factor 7.422
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): Impact factor 8.222
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 4.23 SJR 3.101 SNIP 2.012
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 4.59 SJR 3.509 SNIP 2.406
Web of Science (2014): Impact factor 6.751
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
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.
**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 AI 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
Contributors: Larsen, L. E., Krog, J. S., Madsen, J. J., Thorup, K., Hjulsager, C. K.
Publication date: 2015
Peer-reviewed: Yes
Event: Abstract from 9th International Symposium on Avian Influenza, Athens, Georgia, United States.
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

**Research output: 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.

**INFORMATION**

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
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:
DOIs:
10.1128/JVI.00840-15
Research output: Research - peer-review › Journal article – Annual report year: 2015

Mutant stamme af PCV2: opdatering af tilgængelig viden

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Contributors: Larsen, L. E., Hjulsager, C. K.
Number of pages: 5
Publication date: 2015

Publication information
Publisher: DTU Veterinærinstituttet
Original language: Danish
Electronic versions:
mutant_PCV2_opdatering_150513.pdf
Source: PublicationPreSubmission
Source-ID: 110175471
Research output: Education › Compendium/lecture notes – Annual report year: 2015

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
Pages: 181-181
Publication date: 2015

Host publication information
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
Contributors: Fobian, K., P. Fabrizio, T., Yoon, S., Hansen, M. S., Webby, R. J., Larsen, L. E.
Pages: 1603-1612
Publication date: 2015
Peer-reviewed: Yes

**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): CiteScore 2.68 SJR 1.325 SNIP 0.877
Web of Science (2017): Impact factor 2.514
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.93 SJR 1.544 SNIP 0.891
Web of Science (2016): Impact factor 2.838
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 3.26 SJR 1.738 SNIP 0.998
Web of Science (2015): Impact factor 3.192
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 3.25 SJR 1.69 SNIP 1.057
Web of Science (2014): Impact factor 3.183
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 3.64 SJR 1.764 SNIP 1.154
Web of Science (2013): Impact factor 3.529
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Overvågning af aviær influenza i vilde fugle i Danmark 2014

Overvågning af avian influenza i vilde fugle i Danmark 2014 til ORBIT.pdf

Bibliographical note
Scientific report
Source: PublicationPreSubmission
Source-ID: 112051265
Overvågning af influenza afslører flere subtyper

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Contributors: Krog, J. S., Hjulsager, C. K., Larsen, L. E.
Pages: 34-38
Publication date: 2015
Peer-reviewed: No

Publication information
Journal: Dyrlægen
Issue number: 6
ISSN (Print): 1903-153X
Original language: Danish
Source: PublicationPreSubmission
Source-ID: 119053935
Research output: Research > Journal article – Annual report year: 2015

Overvågning af influenza A virus i svin i 2014

Der er i 2014 gennemført en systematisk, prospektiv passiv overvågning af cirkulerende influenzavirus subtyper i danske svin. Det overordnede formål med overvågningen var, at identificere hvilke influenzavirus subtyper og stammer, der cirkulerer blandt danske svin, og at kortlægge sygdomsårsager i svinepopulationen med henblik på at sikre det strategiske mål: at mindske antibiotikaforbruget i danske svinebesætninger. Overvågningen har bestået i: 1) Undersøgelse for influenzavirus vha. pan-influenza A virus real time RT-PCR på brugerbetalte diagnostiske indsendelser til influenzaavisejournalerne på DTU-VET 2) Test af influenzavirus positive prøver for pandemisk H1N1 (H1N1pdm09) ved real time RT-PCR der specifikt detekterer HA-genet i H1N1pdm09 virus 3) Isolering af virus i MDCK celler 4) Subtypning af positive virusisolater ved sekvensanalyse (HA og NA generer) 5) Komplet genom karakterisering af udvalgte virusisolater

Dette er vigtigt at understrege, at influenza virus på 1173 prøver forekom på 35 indsendelser fra 422 besætninger. I alt var 435 (37 %) af prøverne positive og 239 (44 %) af indsendelserne havde minimum en positiv prøve for mindst en af de fem forskellige besætninger. Der blev totalt i 2014 iverktagt indsendelser for influenza A virus på 1173 prøver fordelt på 53 indsendelser fra 422 besætninger. I alt var 435 (37 %) af prøverne positive og 239 (44 %) af indsendelserne havde minimum en positiv prøve for mindst en af de fem forskellige besætninger. Indsendelserne forklarede sig over hele landet og over hele året. Der var flest indsendelser til undersøgelse i de kolde måneder, men influenza virus blev påvist med større hyppighed hele året. I alt blev 80 influenza virus positive indsendelser opdyrket 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 H1N1pdm09. Prævalensen af det almindelige svineinfluenza virus “avian-like swine” var meget højt, og det formodes at der er stor grad af immunitet mod denne type. Dette er vigtigt for at sikre, at det ikke kommer til en mulig pandemi med denne type. Resultaterne af overvågningen i 2014 understøtter antagelsen om, at de nye virusisolater i de foregående år: H1N2hu, H1pdmN2hu og H1pdmN2sw, nu er fast etableret i de danske svin. Resultaterne af overvågningen i 2014 understøtter antagelsen om, at de nye virusisolater i de foregående år: H1N2hu, H1pdmN2hu og H1pdmN2sw, nu er fast etableret i de danske svin. Disse analyser viste, at de to mest almindelige subtyper i danske svin i 2014 var den danske variant af H1N2 og H1N1pdm09. Prævalensen af det almindelige svineinfluenza virus “avian-like swine” var meget højt, og det formodes at der er stor grad af immunitet mod denne type. Dette er vigtigt for at sikre, at det ikke kommer til en mulig pandemi med denne type. Dette er vigtigt for at sikre, at det ikke kommer til en mulig pandemi med denne type. Resultaterne af overvågningen i 2014 understøtter antagelsen om, at de nye virusisolater i de foregående år: H1N2hu, H1pdmN2hu og H1pdmN2sw, nu er fast etableret i de danske svin.

Overvågningen har endvidere påvist adskillige nye virus reassertions, hvor gener fra H1N1pdm09 indgår, bl.a. tyder det på at H1N2 virus med de interne gener fra H1N1pdm09 har etableret sig i de danske svinepopulation, hvor den cirkulerer uafhængigt af den humane influenza virus sæson. Overvågningen har endvidere påvist adskillige nye virus reassertions, hvor gener fra H1N1pdm09 indgår, bl.a. tyder det på at H1N2 virus med de interne gener fra H1N1pdm09 har etableret sig i de danske svinepopulation, hvor den cirkulerer uafhængigt af den humane influenza virus sæson.

Overvågningen har endvidere påvist adskillige nye virus reassertions, hvor gener fra H1N1pdm09 indgår, bl.a. tyder det på at H1N2 virus med de interne gener fra H1N1pdm09 har etableret sig i de danske svinepopulation, hvor den cirkulerer uafhængigt af den humane influenza virus sæson. Overvågningen har endvidere påvist adskillige nye virus reassertions, hvor gener fra H1N1pdm09 indgår, bl.a. tyder det på at H1N2 virus med de interne gener fra H1N1pdm09 har etableret sig i de danske svinepopulation, hvor den cirkulerer uafhængigt af den humane influenza virus sæson.

Overvågningen har endvidere påvist adskillige nye virus reassertions, hvor gener fra H1N1pdm09 indgår, bl.a. tyder det på at H1N2 virus med de interne gener fra H1N1pdm09 har etableret sig i de danske svinepopulation, hvor den cirkulerer uafhængigt af den humane influenza virus sæson.

Overvågningen har endvidere påvist adskillige nye virus reassertions, hvor gener fra H1N1pdm09 indgår, bl.a. tyder det på at H1N2 virus med de interne gener fra H1N1pdm09 har etableret sig i de danske svinepopulation, hvor den cirkulerer uafhængigt af den humane influenza virus sæson.

Overvågningen har endvidere påvist adskillige nye virus reassertions, hvor gener fra H1N1pdm09 indgår, bl.a. tyder det på at H1N2 virus med de interne gener fra H1N1pdm09 har etableret sig i de danske svinepopulation, hvor den cirkulerer uafhængigt af den humane influenza virus sæson.

Overvågningen har endvidere påvist adskillige nye virus reassertions, hvor gener fra H1N1pdm09 indgår, bl.a. tyder det på at H1N2 virus med de interne gener fra H1N1pdm09 har etableret sig i de danske svinepopulation, hvor den cirkulerer uafhængigt af den humane influenza virus sæson.
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 proaktiivt 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
Contributors: Krog, J. S., Hjulsager, C. K., Larsen, L. E.
Publication date: 2015

**Publication information**
Publisher: DTU Veterinærinstitut
Original language: English
Electronic versions:
Overvågning af influenza A virus i svin i 2014 ORBIT.pdf
Source: PublicationPreSubmission
Source-ID: 112090824
Research output: Research - peer-review ▶ Report – Annual report year: 2015

**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 GmbH, Svinevet Pig Practise
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
Source: PublicationPreSubmission
Source-ID: 119056467
Research output: Research - peer-review ▶ 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 GmbH, Technical University of Denmark, Boehringer Ingelheim Danmark A/S, Svinevet Pig Practise
Pages: 171-171
Publication date: 2015

**Host publication information**
Title of host publication: Proceedings of the 7th European symposium of porcine health management, a comparison analysis of air sampling vs blood sampling
Place of publication: Nantes, France
Electronic versions:
Priebe_2015_P86.pdf
Source: PublicationPreSubmission
Source-ID: 119056388
Research output: Research - peer-review ▶ Conference abstract in proceedings – 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
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.

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Section for Virology, Pig Research Centre
Contributors: Lopes Antunes, A. C., Hisham Beshara Halasa, T., Lauritsen, K. T., Kristensen, C. S., Larsen, L. E., Toft, N.
Number of pages: 11
Publication date: 2015
Peer-reviewed: Yes

Publication information
Journal: B M C Veterinary Research
Volume: 11
Issue number: 1
Article number: 303
ISSN (Print): 1746-6148
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.16 SJR 0.934 SNIP 1.108
Web of Science (2017): Impact factor 1.958
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): Impact factor 1.75
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 1.86 SJR 0.981 SNIP 1.009
Web of Science (2015): Impact factor 1.643
Web of Science (2015): Indexed yes
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
Number of pages: 1
Publication date: 2015
Peer-reviewed: Yes
Event: Abstract from International Porcine Reproductive And Respiratory Syndrome Congress, Ghent, Belgium.
Electronic versions:
Sonnes_abstract.pdf
Source: PublicationPreSubmission
Source-ID: 2289946454
Research output: Research - peer-review › Conference abstract for conference – 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
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
Publication date: 2015
Peer-reviewed: Yes
Event: Abstract from 5th European Veterinary Immunology Workshop, Vienna, Austria.
Electronic versions:
Abstract_EVIW_2015_CJHE.pdf
Research output: 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

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 ssp. 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 Enterobacteiracea 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.
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
Number of pages: 1
Publication date: 2015
Peer-reviewed: Yes
Event: Abstract from International Porcine Reproductive And Respiratory Syndrome Congress, Ghent, Belgium.
Electronic versions:
Ivan_Trus_abstract.pdf

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 LNA™ (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
Contributors: Skovgaard, K., Brogaard, L., Larsen, L. E., Mortensen, S., Dürwald, R., Schengel, M., Heegaard, P. M. H.
Number of pages: 1
Publication date: 2015
Peer-reviewed: Yes
Electronic versions:
1._THE_PIG_AS_A_LARGE_ANIMAL_MODEL_FOR_INFLUENZA_A_VIRUS_INFECTION.pdf

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
udformning af overvågningen, der dog har skiftet gennem årene i takt med indhøstede erfaringer.

I 2013 blev der udført passiv overvågning af døde wilde 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 indsamlerne.

General information
State: Published
Organisations: National Veterinary Institute, Section for Public sector service and commercial diagnostics, Section for Virology, Natural History Museum of Denmark
Publication date: 15 Mar 2014

Publication information
Place of publication: Frederiksberg
Publisher: Technical University of Denmark (DTU)
Original language: Danish
Research output: Commissioned › Report – Annual report year: 2014

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 produktionsystemer, karantænebrug 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 sørene), så grisene var PRRS-fri (grise uden PRRS-virus) ved 30 kg. I hver besætning blev der taget blodprøver af 10 hold grise ved 30 kg.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Dansk Svineproduktion
Contributors: Kristensen, C. S., Larsen, L. E., Hjulsager, C. K.
Number of pages: 7
Publication date: 2014

Publication information
Publisher: Videncenter for Svineproduktion
Volume: 1404
Original language: Danish
Electronic versions:
Erfaring_1404_3_PRRS_stabile_sohold_liverede_hver_10_hold_PRRS_fri_smaagrise.pdf
Source: PublicationPreSubmission
Source-ID: 103451204
Research output: Commissioned › Report – 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, Autonomous University of Barcelona, The Pirbright Institute, Centro de Investigacion en Alimentacion y Desarrollo  
**Contributors:** Martín-Valls, G. E., Kvisgaard, L. K., Tello, M., Danwich, L., Cortey, M., Burgara-Estrella, A. J., Hernández, J., Larsen, L. E., Mateu, E.  
**Pages:** 3170-3181  
**Publication date:** 2014  
**Peer-reviewed:** Yes

**Publication information**

**Journal:** Journal of Virology  
**Volume:** 88  
**Issue number:** 6  
**ISSN (Print):** 0022-538X  
**Ratings:**  
  - BFI (2018): BFI-level 2  
  - Web of Science (2018): Indexed yes  
  - BFI (2017): BFI-level 2  
  - Scopus rating (2017): CiteScore 4.24 SJR 2.853 SNIP 1.096  
  - Web of Science (2017): Impact factor 4.368  
  - 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): Impact factor 4.663  
  - Web of Science (2016): Indexed yes  
  - BFI (2015): BFI-level 2  
  - Scopus rating (2015): CiteScore 4.42 SJR 3.282 SNIP 1.132  
  - Web of Science (2015): Indexed yes  
  - BFI (2014): BFI-level 2  
  - Scopus rating (2014): CiteScore 4.4 SJR 3.187 SNIP 1.208  
  - Web of Science (2014): Indexed yes  
  - BFI (2013): BFI-level 2  
  - Scopus rating (2013): CiteScore 4.92 SJR 3.496 SNIP 1.251  
  - Web of Science (2013): Impact factor 4.648  
  - ISI indexed (2013): ISI indexed yes  
  - Web of Science (2013): Indexed yes  
  - BFI (2012): BFI-level 2  
  - Scopus rating (2012): CiteScore 5.2 SJR 3.19 SNIP 1.222  
  - Web of Science (2012): Impact factor 5.076  
  - ISI indexed (2012): ISI indexed yes  
  - Web of Science (2012): Indexed yes  
  - BFI (2011): BFI-level 2  
  - Scopus rating (2011): CiteScore 5.37 SJR 3.429 SNIP 1.282  
  - Web of Science (2011): Impact factor 5.402  
  - 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): Impact factor 5.189  
  - Web of Science (2010): Indexed yes
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 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.

General information

State: Published
Organisations: National Veterinary Institute, Section for Virology, Section for Bacteriology, Pathology and Parasitology, St. Jude Children’s Research Hospital, Korea Research Institute of Bioscience and Biotechnology
Contributors: Fobian, K., P. Fabrizio, T., Yoon, S., Hansen, M. S., Webby, R. J., Larsen, L. E.
Publication date: 2014
Peer-reviewed: Yes
Event: Abstract from Influenza 2014, Oxford, United Kingdom.
Source: PublicationPreSubmission
Source-ID: 103646129
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2014
Clinical characterization of a type 2 PRRSV causing significant clinical disease in the field in Denmark

**General information**
State: Published
Organisations: National Veterinary Institute, Section for Virology, Section for Immunology and Vaccinology, Section for Bacteriology, Pathology and Parasitology, Danvet K/S, Boehringer Ingelheim Danmark A/S, Technical University of Denmark
Contributors: Larsen, L. E., Kvisgaard, L. K., Hjulsager, C. K., Bøtner, A., Rathkjen, P. H., Heegaard, P. M. H., Bisgaard, N., Hansen, M. S., Nielsen, J.
Publication date: 2014

**Host publication information**
Title of host publication: Proceedings of the 23rd IPVS Congress
Electronic versions:
PRRSV_BI_abstract_IPVS2014.pdf
Source: PublicationPreSubmission
Source-ID: 103450993
Research output: Research - peer-review › Conference abstract in proceedings – Annual report year: 2014

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
Contributors: Jensen, M. B., Larsen, L. E.
Pages: 5035-5044
Publication date: 2014
Peer-reviewed: Yes

**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): CiteScore 2.84 SJR 1.35 SNIP 1.491
Web of Science (2017): Impact factor 2.749
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.66 SJR 1.331 SNIP 1.484
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 commercial mussels. Based on 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.
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 1,887 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

**Peer-reviewed**: Yes

**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)**: CiteScore 3.32 SJR 1.427 SNIP 1.136
- **Web of Science (2015)**: Indexed yes
- **BFI (2014)**: BFI-level 1
- **Scopus rating (2014)**: CiteScore 3.54 SJR 1.559 SNIP 1.148
- **Web of Science (2014)**: Indexed yes
- **BFI (2013)**: BFI-level 1
- **Scopus rating (2013)**: CiteScore 3.94 SJR 1.772 SNIP 1.153
- **ISI indexed (2013)**: ISI indexed yes
- **Web of Science (2013)**: Indexed yes
- **BFI (2012)**: BFI-level 1
- **Scopus rating (2012)**: CiteScore 4.15 SJR 1.982 SNIP 1.156
- **Web of Science (2012)**: Impact factor 3.73
- **ISI indexed (2012)**: ISI indexed yes
- **Web of Science (2012)**: Indexed yes
- **BFI (2011)**: BFI-level 1
- **Scopus rating (2011)**: CiteScore 4.58 SJR 2.425 SNIP 1.233
- **Web of Science (2011)**: Impact factor 4.092
- **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)**: Impact factor 4.411
- **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
Gastric ulcers in nursery pigs.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Section for Bacteriology, Pathology and Parasitology, Danish Agriculture and Food Council, Universidade Federal de Minas Gerais, National Veterinary Institute, University of Copenhagen
Publication date: 2014
Peer-reviewed: Yes
Event: Abstract from 6th European Symposium of Porcine Health Management (ESPHM 2014), Italy.
Source: PublicationPreSubmission
Source-ID: 103450889
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2014

Genetic and antigenic drift of Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) in a closed population evaluated by full genome sequencing
Porcine Reproductive and Respiratory Syndrome (PRRS) viruses are divided into two major genotypes (Type 1 and Type 2) based on their genetic diversity. Type 1 PRRSV is further divided into at least 3 subtypes, but until now only subtype 1 has been detected in Western Europe and North America. Both genotypes are circulating in Denmark and since gilt vaccinations are widely used it is essential to monitor the diversity of circulating PRRS viruses. Prior to the present study, however, the diversity of circulating viruses in Denmark was virtually unknown. The main objective was to assess the diversity of circulating PRRS viruses in Danish pigs and to investigate the genetic drift of the virus in a closed population with very limited introductions of new animals. The study included phylogenetic analysis of full genome sequences of eight Type 1 and nine Type 2 PRRS viruses, including the very first Danish isolated Type 1 virus and the very first Danish Type 2 PRRS virus isolated from a non-vaccinated pig herd. Furthermore, by sequencing ORF5 and ORF7 of 43 Type 1 and 57 Type 2 viruses isolated between 2003 and 2013, the level of genetic diversity was assessed. The results showed a very high genetic diversity among the Danish viruses throughout the genome within the same genotype. A global phylogenetic analysis showed that the Danish Type 1 PRRSV formed two major clusters, one vaccine (Porcilis)-like clade exclusively containing viruses isolated after the Porcilis vaccine was introduced and another distinct clade consisting mainly of viruses isolated in Denmark. Phylogenetic analysis in a global Type 2 PRRSV framework classified all Danish Type 2 viruses to a single cluster (sub-lineage 5.1) which comprised viruses closely related to the Type 2 prototype isolate VR2332. Both Type 1 and Type 2 harbored deletions in the region encoding nsp2 and some significant amino acid changes were also seen in antigenic sites. Acknowledgement: The study was supported by EU Grant n° 245141 (New tools and approaches to control Porcine Reproductive and Respiratory Syndrome in the EU and Asia (PoRRSCoN) coordinated by Prof. H. Nauwynck.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Contributors: Kvisgaard, L. K., Hjulsager, C. K., Larsen, L. E.
Publication date: 2014
Peer-reviewed: Yes
Event: Abstract from 13th International Nidovirus Symposium, Salamanca, Spain.
Electronic versions:
PRRSV_abstract_Lise_Kirstine_Kvisgaard_Nidovirus_2014.pdf

Bibliographical note
**High-throughput gene expression analysis in pigs as model for respiratory infections**

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.

**General information**

State: Published  
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Section for Bacteriology, Pathology and Parasitology, Section for Virology  
Contributors: Skovgaard, K., Brogaard, L., Schou, K. K., Larsen, L. E., Mortensen, S., Dürrwald, R., Schengel, M., Heegaard, P. M. H.  
Publication date: 2014  
Peer-reviewed: Yes  
Event: Abstract from Conferences and Workshops of COST Action BM1308, Munich, Germany.

**Identification of swine influenza virus epitopes and analysis of multiple specificities expressed by cytotoxic T cell subsets**

Background: Major histocompatibility complex (MHC) class I peptide binding and presentation are essential for antigen-specific activation of cytotoxic T lymphocytes (CTLs) and swine MHC class I molecules, also termed swine leukocyte antigens (SLA), thus play a crucial role in the process that leads to elimination of viruses such as swine influenza virus (SwIV). This study describes the identification of SLA-presented peptide epitopes that are targets for a swine CTL response, and further analyses multiple specificities expressed by SwIV activated CTL subsets. Findings: Four SwIV derived peptides were identified as T cell epitopes using fluorescent influenza: SLA tetramers. In addition, multiple CTL specificities were analyzed using peptide sequence substitutions in two of the four epitope candidates analyzed. Interestingly both conserved and substituted peptides were found to stain the CD4⁺CD8⁺ T cell subsets indicating multiple specificities. Conclusions: This study describes a timely and cost-effective approach for viral epitope identification in livestock animals. Analysis of T cell subsets showed multiple specificities suggesting SLA-bound epitope recognition of different conformations.

**General information**

State: Published  
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Section for Virology  
Number of pages: 5  
Publication date: 2014  
Peer-reviewed: Yes
Locally increased mortality of harbour seals (Phoca vitulina) in the Danish Limfjord

At the end of August 2014 an aerial seal counting was done by Aarhus University (Galatius, A) and increased mortality was observed on a small island Ejerslev Røn (56° 56'N 0° 8'57"Ø) and a sand bank Blinderøn about 4 km south-east of Ejerslev Røn. Both islands/sandbanks are protected nature reserves. The islands were inspected the following day by boat/walking. In total, 56 dead seals were found on Ejerslev Røn and Blinderøn. Four were shot due to severe respiratory symptoms and these four seals did not escape into the water when approached.

All 60 seals except one with fishing net around the neck were dead within few days. One of the seals had a tag showing it had been through rehabilitation in the Netherlands (Zeehondencreche Pieterburen) in 2010, where it was treated for a lungworm infection (information from Lenie’t Hart about the tagged seal). This indicates the long distances seals are travelling and that lungworm infections can be successfully treated.

A field necropsy was done on the four shot seals and all suffered from pneumonia. Three of the seals had empty stomachs and intestines but all 4 seals were in good nutritional condition with blubber thickness ranging from 1.2 cm to 2.0 cm suggesting a short duration of the pneumonia. Influenza virus was found in the lungs, subtyping is pending.

At inspection, 12 days later only 1 recently dead seal was found indicating the mortality had peaked within a short time and only within a small geographic area.
**Overvågning af influenza A virus i svin i 2013. Slutrapport 2013: Opsummering og konklusion**

Der er i 2013 gennemført en systematisk passiv overvågning af cirkulerende influenzavirus subtyper i danske svin. Det overordnede formål med overvågningen var at identificere hvilke influenzavirus subtyper og stammer, der cirkulerer blandt danske svin, og at kortlægge sygdomsårsager i svinepopulationen med henblik på at sikre det strategiske mål: at mindske antibiotikaforbruget i danske svinebesætninger.

**PRDC - Validation of a new diagnostic procedure for the diagnosis of PRDC in pigs**

**Real-time PCR diagnostic package for diagnosis of porcine respiratory disease.**
Real-time PCR diagnostic package for diagnosis of porcine respiratory disease.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Section for Virology
Contributors: Jorsal, S. E. L., Hjulsager, C. K., Kokotovic, B., Larsen, L. E.
Publication date: 2014
Peer-reviewed: Yes
Event: Poster session presented at 6th European Symposium of Porcine Health Management (ESPHM 2014), Italy.
Electronic versions:

Respiratory disease in finishers – comparisons of diagnostic tools

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Section for Virology, Technical University of Denmark, Danish Agriculture and Food Council
Contributors: Jakobsen, S., Hjulsager, C. K., Christensen, C., Lind, P., Bak, H., Larsen, L. E.
Publication date: 2014

Host publication information
Title of host publication: Proceedings of the 23rd IPVS Congress

Surveillance programs in Denmark has revealed the circulation of novel reassortant influenza A viruses in swine
Swine influenza is a respiratory disease caused by multiple subtypes of influenza A virus. Swine influenza virus (SIV) is enzootic in swine populations in Europe, Asia, North and South America. The influenza A virus genome consist of eight distinct gene segments and SIV subtypes are defined by the combination of the gene segments hemagglutinin (HA) and neuraminidase (NA). In most European countries, the avian-like (av)H1N1, the 2009 pandemic variant (H1N1pdm09), H1N2 and H3N2 subtypes have constituted the dominating SIV subtypes during recent years. In Denmark, the H1N2 subtype is a reassortant between avH1N1 and H3N2 which is different from the dominating European H1N2 subtype (1). The prevalence of the H1N1pdm09 virus in swine has increased since 2009 in some countries including Denmark. Here we present the results of the national passive surveillance program on influenza in swine performed from 2009-13.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Contributors: Larsen, L. E., Hjulsager, C. K., Trebbien, R., Krog, J. S., Breum, S. Ø.
Publication date: 2014

Host publication information
Title of host publication: Proceedings of the 23rd IPVS Congress

Svært at afgøre om grise smittes med PRRSV før eller efter fravænning
Til at afgøre om Porcin Reproduktions- og Respiratorisk Syndrom Virus (PRRSV) cirkulerer i farestalden eller kun i smågrisestalden kan næsesvaberprøver af alle grise ved fravænning være en hjælp. Resultatet fra et enkelt
Swine Influenza Viruses – Evolution and Zoonotic Potential

Influenza A virus (IAV) is an important respiratory pathogen with a broad host range. The natural reservoir for IAV is waterfowls, but both human and swine are considered natural hosts. During the past century IAV has caused severe pandemics as well as seasonal epidemics in the human population. In pigs, swine influenza virus (SIV) is endemic worldwide and is associated with economic losses for the farmer due to the impact on pig health causing lowered production. Swine has been shown to be susceptible to infection with IAVs of different host origin and has hence been considered as potential mixing vessels of new IAVs. Furthermore, transmission of IAVs from swine to human and vice versa has been documented on several occasions and further classifies this virus as a highly important zoonosis. This aspect enhances the possibility of the formation and establishment of new and potentially more virulent viruses with the capacity to cause severe pandemics. Therefore, it is important to gain a deeper understanding of the evolution of SIVs, their zoonotic potential as well as host-range characteristics and this PhD project aimed at elucidating parts of these important points.

The PhD thesis begins with a presentation of the aims and a brief introduction of the situation of SIV in Denmark. In the background section an extensive review on IAVs with emphasis on SIV is provided. The results obtained during the PhD are presented in two complete manuscripts and one work in progress, followed by a joint discussion of the main results. Manuscript I analyze the genetic and antigenic evolution of two of the most prevalent SIVs circulating in Denmark. In total, 78 sequences of the H1N1 and H1N2 subtypes, collected in the period 2003-2012, was analyzed. The genetic analysis was based on several computational methods for estimation of phylogeny, selection pressure, evolutionary rates and time of most recent common ancestor for the surface glycoproteins, HA and NA. The antigenic relationship of the Danish H1 SIVs was determined by antigenic cartography. High evolutionary rates of HA and NA compared with low evolution suggests that evolution is primarily controlled by purifying selection. Further, a high level of genetic relatedness and of low evolution was observed for the Danish H1 sequences, this observation was supported by both phylogeny and antigenic cartography. Antigenic cartography also revealed few antigenic outliers that potentially indicated drift away from current H1 viruses. The time of most recent common ancestor for H1 was estimated to be markedly earlier than previously suggested. Phylogenetic analysis of the Danish N2 gene revealed that two different lineages are circulating in Denmark. Manuscript II describes the biological characterization of four different Danish SIVs and includes an experimental pathogenesis study performed in ferrets, which are regarded as the most appropriate small animal model for human IAV infections. The viruses chosen for this study were two enzootic SIVs (H3N2 and H1N2) and two new SIV reassortants (H1avN2hu and H1pdmN2sw). The two reassortants were detected for the first time in 2011 and have since then become established and are now circulating in Danish pigs. Viral replication in nasal wash samples and viral load in respiratory organs were determined. Growth kinetics of the four SIVs were determined in vitro using respiratory swine and human cell lines. The affinity of HA of the four SIVs for a2,3- and a2,6-receptors were assessed as well as receptor kinetics and antiviral susceptibility of NA. This study showed that all four SIVs were able to infect and transmit efficiently and to high titers via direct contact and H3N2 was found also to transmit efficiently via the airborne route. H3N2 and H1pdmN2sw were found to induce the most severe lung lesions, consistent with these two viruses expressing the highest viral load in lung tissue samples. Growth kinetics demonstrated that all four SIVs were able to infect and replicate to high titers in both swine and human respiratory cell lines.

Receptor studies showed a high preference for binding to a2,6-receptors for the Danish SIVs. NA kinetics revealed a high enzyme activity for H1pdmN2sw compared to the remaining viruses, suggesting that NA activity alone is not sufficient for the observed airborne transmission of H3N2. Furthermore, it was revealed that the Danish SIVs were found to be sensitive to all of the neuraminidase inhibitors tested. Based on the findings in this study it was proposed that viruses with a human-like HA play a more significant role in transmission compared to viruses with only a human-like NA. Furthermore, this study also underlined the importance of continued surveillance of SIVs in order to detect new reassortants as well as the necessity of assessing their zoonotic potentials.

Manuscript III describes the establishment of a reverse genetics system based on a backbone from the Danish H1N2 SIV, which is one of the two most prevalent subtypes in Denmark. Recently, a variant of a North American swine H3N2 virus
containing a pandemic M gene was transmitted to humans in the US and on few occasions human-to-human transmission was observed. These events underline the need for a reverse genetics system to be used for an analysis of the behavior of a pandemic M gene in a Danish SIV.

**General information**

State: Published
Organisations: National Veterinary Institute, Section for Virology
Contributors: Fobian, K., Larsen, L. E., Breum, S. Ø.
Number of pages: 154
Publication date: 2014

**Publication information**

Publisher: National Veterinary Institute
Original language: English
Electronic versions: Thesis_til_tryk2..PDF
Research output: Research › Ph.D. thesis – Annual report year: 2014

**Wildlife Reservoirs of Canine Distemper Virus Resulted in a Major Outbreak in Danish Farmed Mink (Neovison vison)**

A major outbreak of canine distemper virus (CDV) in Danish farmed mink (Neovison vison) started in the late summer period of 2012. At the same time, a high number of diseased and dead wildlife species such as foxes, raccoon dogs, and ferrets were observed. To track the origin of the outbreak virus full-length sequencing of the receptor binding surface protein hemagglutinin (H) was performed on 26 CDV's collected from mink and 10 CDV's collected from wildlife species. Subsequent phylogenetic analyses showed that the virus circulating in the mink farms and wildlife were highly identical with an identity at the nucleotide level of 99.45% to 100%. The sequences could be grouped by single nucleotide polymorphisms according to geographical distribution of mink farms and wildlife. The signaling lymphocytic activation molecule (SLAM) receptor binding region in most viruses from both mink and wildlife contained G at position 530 and Y at position 549; however, three mink viruses had an Y549H substitution. The outbreak viruses clustered phylogenetically in the European lineage and were highly identical to wildlife viruses from Germany and Hungary (99.29% - 99.62%). The study furthermore revealed that fleas (Ceratophyllus sciurorum) contained CDV and that vertical transmission of CDV occurred in a wild ferret. The study provides evidence that wildlife species, such as foxes, play an important role in the transmission of CDV to farmed mink and that the virus may be maintained in the wild animal reservoir between outbreaks.

**General information**

State: Published
Organisations: National Veterinary Institute, Section for Virology, Section for Public sector service and commercial diagnostics, Copenhagen Diagnostics
Number of pages: 11
Publication date: 2014
Peer-reviewed: Yes

**Publication information**

Journal: PLOS ONE
Volume: 9
Issue number: 1
Article number: e85598
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): CiteScore 3.32 SJR 1.427 SNIP 1.136
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 3.54 SJR 1.559 SNIP 1.148
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 3.94 SJR 1.772 SNIP 1.153
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 4.15 SJR 1.982 SNIP 1.156
Web of Science (2012): Impact factor 3.73
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 4.58 SJR 2.425 SNIP 1.233
Web of Science (2011): Impact factor 4.092
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): Impact factor 4.411
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 (2006): Indexed yes
Original language: English
Electronic versions:
fetchObject.pdf
DOI:
10.1371/journal.pone.0085598

Bibliographical note
Copyright: 2014 Trebbien et al. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.
Source: FindIt
Source-ID: 259571410
Research output: Research - peer-review › Journal article – Annual report year: 2014

Overvågning af aviær influenza i vilde fugle 2012 i Danmark

General information
State: Published
Organisations: National Veterinary Institute, Section for Public sector service and commercial diagnostics, Section for Virology, Natural History Museum of Denmark
Number of pages: 33
Publication date: 15 Mar 2013

Publication information
Place of publication: Frederiksberg
Publisher: Technical University of Denmark (DTU)
Original language: Danish

Bibliographical note
scientific report
33 pages
A fast and robust method for full genome sequencing of Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) Type 1 and Type 2

PRRSV is a positive-sense RNA virus with a high degree of genetic variability among isolates. For diagnostic sensitivity and vaccine design it is essential to monitor PRRSV genetic diversity. However, to date only a few full genome sequences of PRRSV isolates have been made publicly available. In the present study, fast and robust methods for long range RT-PCR amplification and subsequent next generation sequencing (NGS) were developed and validated on nine Type 1 and nine Type 2 PRRSV viruses. The methods generated robust and reliable sequences both on primary material and cell culture adapted viruses and the protocols performed well on all three NGS platforms tested (Roche 454 FLX, Illumina HiSeq2000, and Ion Torrent PGM™ Sequencer). These methods will greatly facilitate the generation of more full genome PRRSV sequences globally.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Section for Public sector service and commercial diagnostics, Molecular Evolution, University of Edinburgh
Pages: 697-705
Publication date: 2013
Peer-reviewed: Yes

Publication information
Journal: Journal of Virological Methods
Volume: 193
Issue number: 2
ISSN (Print): 0166-0934
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.82 SJR 0.858 SNIP 0.817
Web of Science (2017): Impact factor 1.756
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.78 SJR 0.873 SNIP 0.729
Web of Science (2016): Impact factor 1.693
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Detection of Porcine Circovirus Type 2 and Viral Replication by In Situ Hybridization in Primary Lymphoid Organs From Naturally and Experimentally Infected Pigs

Porcine circovirus type 2 (PCV2) infection is the cause of postweaning multisystemic wasting syndrome (PMWS). It has been speculated whether cell types permissive of replication are found in the primary lymphoid organs and whether infection of these tissues has an important role in the pathogenesis of PMWS. The aim of this study was to determine if primary lymphoid organ cells support viral replication during PCV2 infection. This was done by histopathological examination of thymus and bone marrow from pigs experimentally inoculated with PCV2 (n = 24), mock-infected pigs (n = 12), pigs naturally affected by PMWS (n = 33), and age-matched healthy control animals (n = 29). In situ hybridization (ISH) techniques were used to detect PCV2 nucleic acid irrespective of replicative status (complementary probe, CP) or to detect only the replicative form of the virus (replicative form probe, RFP). PCV2 was not detected in the experimentally PCV2-inoculated pigs or the control animals. Among the PMWS-affected pigs, 19 of 20 (95%) thymuses were positive for PCV2 by CP ISH, and 7 of 19 (37%) of these also supported viral replication. By CP ISH, PCV2 was detected in 16 of 33 (48%) bone marrow samples, and 5 of 16 (31%) of these also supported replication. The 2 ISH probes labeled the same cell types, which were histiocytes in both organs and lymphocytes in thymus. The RFP labeled fewer cells than the CP. Thus, PCV2 nucleic acids and replication were found in bone marrow and thymus of PMWS-affected pigs, but there was no evidence that primary lymphoid organ cells are major supporters of PCV2 replication.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Section for Virology, Autonomous University of Barcelona, CReSA - Centre for Animal Health Research, University of Copenhagen
Pages: 20980-988
Publication date: 2013
Peer-reviewed: Yes

Publication information
Journal: Veterinary Pathology
Volume: 50
Issue number: 6
ISSN (Print): 0300-9858
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.16 SJR 1.078 SNIP 1.356
Web of Science (2017): Impact factor 1.795
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.68 SJR 0.938 SNIP 1.148
Web of Science (2016): Impact factor 1.996
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.05 SJR 1.09 SNIP 1.308
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 1.74 SJR 0.916 SNIP 1.155
Web of Science (2014): Impact factor 1.869
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2 SJR 1.12 SNIP 1.288
Web of Science (2013): Impact factor 2.038
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 1.64 SJR 0.812 SNIP 1.057
Web of Science (2012): Impact factor 1.929
ISI indexed (2012): ISI indexed yes
Diagnostic performance of fecal quantitative real-time polymerase chain reaction for detection of *Lawsonia intracellularis*–associated proliferative enteropathy in nursery pigs

Quantitative polymerase chain reaction (qPCR) tests for detection and quantification of *Lawsonia intracellularis* in feces from pigs have been developed. The objective of the current study was to evaluate the diagnostic performance of a fecal qPCR test for detection of nursery pigs with *L. intracellularis*–associated proliferative enteropathy (PE) under field conditions. Furthermore, the diagnostic performance for different subpopulations of pigs was investigated, including pigs infected or noninfected with Porcine circovirus-2, *Brachyspira pilosicoli*, and *Escherichia coli*. The diagnostic performance was evaluated in terms of diagnostic sensitivity and specificity. Data from pigs originating from 20 herds with antibiotic treatment requiring diarrhea outbreaks from a prior study were reused. Before treatment, pigs were randomly selected for histopathological and immunohistochemical examination of intestinal segments and fecal quantification of *L. intracellularis* by qPCR. A total of 313 pigs (157 without diarrhea, 156 with diarrhea) were included in the statistical analysis, and 37 pigs (11.8%) were classified as PE positives (defined as proliferative histological lesions in combination with *L. intracellularis* demonstration by immunohistochemistry). *Lawsonia intracellularis* was detected by qPCR in feces from 91 pigs (29.1%). A nonparametric receiver operating characteristic (ROC) analysis provided an area under the ROC curve (0.93) and an optimal cutoff value of 4.8 log10 *L. intracellularis* bacteria/g feces. This cutoff provided a diagnostic sensitivity of 0.84 and diagnostic specificity of 0.93. The diagnostic sensitivity and specificity were significantly different between herds (P < 0.0001). Numerically, diagnostic sensitivity and specificity were different between subpopulations of pigs, but no significant differences were demonstrated.

**General information**

State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Section for Public sector service and commercial diagnostics, Section for Virology, Universidade Federal de Minas Gerais, University of Copenhagen
Pages: 336-340
Experimental Airborne Transmission of Porcine Postweaning Multisystemic Wasting Syndrome

The objective of these studies was to investigate if porcine postweaning multisystemic wasting syndrome (PMWS) could be induced in healthy pigs following contact with air from pigs with clinical signs of PMWS. The pigs were housed in different units. Either 31 (study I) or 25 (study II) pigs with clinical symptoms of PMWS from a PMWS-affected herd and 25 healthy pigs from a PMWS-free, but PCV2-positive, herd were housed in unit A. Fifty pigs from a PMWS-free herd were housed in unit B, which were connected by pipes to unit A. In unit C, 30 pigs from a PMWS-free herd were housed as controls. In study II, the pigs in units A and B from the PMWS-free herd developed clinical signs of PMWS 2-3 weeks after arrival. PMWS was confirmed at necropsy and the diseased pigs had increased PCV2 load and increased antibody titers against PCV2 in serum that coincided with the development of clinical signs typical of PMWS. Sequence analysis revealed that the PCV2 isolate belonged to genotype 2b. In conclusion, the present study showed that PMWS can be induced in pigs from a PMWS-free herd by airborne contact with pigs from a PMWS-affected herd.

General information

State: Published
Organisations: National Veterinary Institute, Section for Public sector service and commercial diagnostics, Section for Epidemiology, Section for Virology, Danish Agriculture and Food Council
Number of pages: 7
Pages: 534342
Publication date: 2013
Peer-reviewed: Yes

Publication information

Journal: Journal of Pathogens
Volume: 2013
ISSN (Print): 2090-3065
Ratings:
Web of Science (2018): Indexed yes
Scopus rating (2017): CiteScore 3.26 SJR 1.034 SNIP 1.883
Web of Science (2017): Indexed yes
Scopus rating (2016): CiteScore 0 SJR 0.734 SNIP 1.774
Scopus rating (2015): SJR 0.241 SNIP 0.179
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
Original language: English
Electronic versions:
534342.pdf
DOIs:
10.1155/2013/534342

Bibliographical note
This is an open access article distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.
Experimental infection of pigs with two East European variants of Type 1 PRRSV

Porcine reproductive and respiratory syndrome viruses (PRRSV) have been divided into Type 1 (European) and Type 2 (North American) viruses. PRRSV are very diverse and Type 1 viruses have even been further divided into subtypes. While Type 1 viruses from Western Europe belong to subtype 1, viruses from Eastern Europe have been divided into at least 3 different subtypes based on the length of ORF7 and in addition, atypical Type 1 viruses do not readily group into the subtype groups. In experimental trials it has been shown that some of these viruses, e.g. strain Lena, are more virulent than the subtype 1 strains.

The aim of this project was to study the infection dynamics and clinical and pathological impact of two east European Type 1 strains. In an experimental trial, infection of pigs with the Russian subtype 2 strain "Ili6" and the Belarusian atypical isolate "Bor59" were compared to an early "Lelystad-like" Danish subtype 1 isolate "18794". Groups of seven pigs of unique high sanitary status were infected with one of the three PRRSV isolates, and a fourth group served as sham-inoculated controls. The pigs were monitored for 24 days, and nasal swabs and blood samples were taken at 0, 3, 7, 10, 14, 17, 21 and 24 days post infection (dpi).

The pigs infected with the "Bor59" virus developed higher body temperature and more severe clinical symptoms compared to the other three groups, although the clinical signs in general were mild. The acute phase response was measured in serum samples as an objective indicator of infection. Acute phase protein C-reactive protein (CRP) showed an increase in levels in pigs infected with the Eastern European viruses with an earlier rise for Bor59 than for Ili6, both peaking at 10 dpi. In contrast, the CRP level did not increase significantly in neither the subtype 1 virus inoculated pigs nor the sham-inoculated controls. Acute phase protein haptoglobin showed a very early increase in Bor59 infected pigs, peaking at 3 dpi, while no increase was observed in Ili6 infected pigs.

All of the virus inoculated pigs seroconverted, as measured by IPMA and ELISA, around 7 dpi, and virus was detected by real-time RT-PCR in serum in various quantities and times after infection; detailed PCR analyses are ongoing.

Taken together, these preliminary data suggested that the east European subtype 2 isolate Ili6 and the atypical Bor59 strain induced more severe infection compared to the type 1 “Lelystad-like” virus isolate. This correlates with results obtained from studies of other east European PRRSV strains.

General information
State: Published
Organisations: National Veterinary Institute, Section for Public sector service and commercial diagnostics, Section for Virology, Section for Immunology and Vaccinology, University of Warsaw
Contributors: Hjulsager, C. K., Larsen, L. E., Heegaard, P. M. H., Stadejek, T., Bøtner, A., Nielsen, J.
Number of pages: 1
Publication date: 2013
Peer-reviewed: Yes
Event: Abstract from International Porcine Reproductive and Respiratory Syndrome Symposium (PRRS 2013), Beijing, China.

Bibliographical note
Oral presentation.
Source: dtu
Source-ID: u:7603
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2013

Fast and robust methods for full genome sequencing of Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) Type 1 and Type 2

The high level of diversity among PRRS viruses makes it very important to monitor the overall genetic variations in relation to the sensitivity of diagnostic tests and vaccination efficacy, but only few full genome sequences of PRRSV strains isolated in Europe have been made public available. In the present study, fast and robust methods for long range RT-PCR amplification and subsequent next generation sequencing (NGS) of PRRSV Type 1 and Type 2 viruses were developed and validated on nine Type 1 and nine Type 2 PRRSV viruses. The methods were shown to generate robust and reliable sequences both on primary material and cell culture adapted viruses and the protocols were shown to perform well on all three NGS platforms tested (Roche 454 FLX, Illumina HiSeq 2000, and Ion Torrent PGM™ Sequencer). To complete the sequences at the 5’ end, 5’ Rapid Amplification of cDNA Ends (5’ RACE) was conducted followed by cycle sequencing of clones. The genome lengths were determined to be 14,876-15,098 and 15,342-15,408 nucleotides long for the Type 1 and Type 2 strains, respectively. These methods will greatly facilitate the generation of more complete genome PRRSV sequences globally which in turn may lead to identification of markers of virulence and improve our understanding of PRRSV evolution and pathogenesis.
Genetic and antigenic characterization of complete genomes of Type 1 Porcine Reproductive and Respiratory Syndrome viruses (PRRSV) isolated in Denmark over a period of 10 years

Porcine Reproductive and Respiratory Syndrome (PRRS) caused by the PRRS virus (PRRSV) is considered one of the most devastating swine diseases worldwide. PRRS viruses are divided into two major genotypes, Type 1 and Type 2, with pronounced diversity between and within the genotypes. In Denmark more than 50% of the herds are infected with Type 1 and/or Type 2 PRRSV. The main objective of this study was to examine the genetic diversity and drift of Type 1 viruses in a population with limited introduction of new animals and semen. A total of 43 ORF5 and 42 ORF7 nucleotide sequences were obtained from viruses collected from 2003 to February 2013. Phylogenetic analysis of ORF5 nucleotide sequences showed that the Danish isolates formed two major clusters within the subtype 1. The nucleotide identity to the subtype 1 protogenotype Lelystad virus (LV) spanned 84.9–98.8% for ORF5 and 90.7–100% for ORF7. Among the Danish viruses the pairwise nucleotide identities in ORF5 and ORF7 were 81.2–100% and 88.9–100%, respectively. Sequencing of the complete genomes, including the 5′- and 3′-end nucleotides, of 8 Danish PRRSV Type 1 showed that the genome lengths differed from 14,876 to 15,098 nucleotides and the pairwise nucleotide identity among the Danish viruses was 86.5–97.3% and the identity to LV was 88.7–97.9%. The study strongly indicated that there have been at least two independent introductions of Type 1 PRRSV in Denmark and analysis of the full genomes revealed a significant drift in several regions of the virus.
Genetic and antigenic characterization of influenza A virus circulating in Danish swine during the past decade

Influenza A virus has been endemic in Danish swine for the last 30 years, with H1N1 and H1N2 being the dominating subtypes. The purpose of this study was to investigate the genetic and antigenic evolution of the influenza viruses found in Danish swine during the last 10 years. A total of 78 samples were isolated in MDCK cells, RNA extracted and the hemagglutinin and neuraminidase genes full length sequenced. In addition, the isolates were tested in hemagglutination inhibition (HI) tests against a panel of known antisera raised against a range of European swine influenza virus isolates. Phylogenetic analysis of the HA and NA genes revealed continuous evolutionary drift as expected for RNA viruses with low mutational selection pressure. Estimated selection pressures indicated that more purifying and less diversifying selection controlled the H1 evolution. The mean rates of synonymous and non-synonymous substitutions for H1, N1 and N2 were found to be in agreement with previously observed values for Eurasian swine lineages. Calculation of possible...
glycosylation sites in the hemagglutinin gene revealed that the H1N2 and H1N1 subtypes had three well conserved glycosylation sites in common. The results of the HI tests were analysed by antigenic cartography to quantify the antigenic relationship between the virus isolates. The antigenic cartography map showed that most of the Danish viruses were antigenic very similar, with only a few outliers. In conclusion, this study provided an important contribution to the complex epidemiology of circulating swine influenza virus in Denmark and indicates that vaccine development targeted against Danish H1N1 and H1N2 need only to include few components for the induction of cross protection against the predominant strains.

The study was supported by grants from “European surveillance network for influenza in pigs (ESNIP) 3” (http://www.esnip3.eu) and The Danish Veterinary and Food Administration.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Department of Systems Biology, Integrative Systems Biology, Molecular Evolution, Section for Public sector service and commercial diagnostics, University of Cambridge
Number of pages: 1
Publication date: 2013
Peer-reviewed: Yes
Event: Abstract from Influenza2013, Oxford, United Kingdom.
Keywords: Swine influenza, Phylogeny, Antigenic cartography
Electronic versions: Oxford2013ver2_abstract.pdf

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Section for Immunology and Vaccinology, Section for Public sector service and commercial diagnostics, Statens Serum Institut, University of Copenhagen
Number of pages: 16
Publication date: 2013
Genetic characterization of canine distemper virus involved in outbreaks in farmed mink in Denmark 2012

Danish farmed mink herds experienced a large outbreak of canine distemper virus in 2012. Full-length sequence analysis (1824 nucleotides) of the variable hemagglutinin (H) gene were performed on 27 viruses collected from mink and on 7 viruses collected from wild foxes. Results of the study showed that the farmed mink and wild fox population were infected by identical viruses which strongly indicate an epidemiological link between these populations. Accordingly, diseased and dead foxes were observed in some of the mink herds in connection to the outbreak. The Danish virus strain clustered phylogenetically with other European canine distemper viruses and showed the highest level of similarity (99.3 - 99.6 %) to viruses isolated from wild foxes in Germany. The fox should therefore be considered as an important wild life reservoir of canine distemper virus and may also contribute to the transmission of the virus between mink farms during outbreaks.

Genetic dissection of complete genomes of Type 2 PRRS viruses isolated in Denmark over a period of 15 years

Type 2 Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) was first detected in Europe in 1996 co-incident with the introduction of a live attenuated vaccine. Since then, only limited ORF5 and ORF7 sequences of Type 2 PRRS viruses have been reported throughout Europe. In the present study, the genetic and antigenic diversity of 11 complete genomes and 49 ORF5 and 55 ORF7 nucleotide sequences obtained from 57 viruses in Denmark from 2003 to 2012 were examined. The genetic identity of the 11 complete genomes to the vaccine strain (Ingelvac PRRS MLV) ranged between 93.6 and 99.6% while the 49 ORF5 sequences examined were 94.0–99.8% identical to the vaccine strain. Among the Danish sequences, the pairwise nucleotide identity was 90.9–100% and 93.0–100.0% for ORF5 and ORF7, respectively. Analysis of the genetic region encoding NSP2 revealed high diversity among the Danish viruses with an 86.6–98.9% range in similarity. Furthermore, several of the sequenced viruses harbored deletions in the NSP2 coding region. Phylogenetic analysis in a global Type 2 PRRSV framework classified all Danish isolates to a single cluster (sub-lineage 5.1) which comprised strains closely-related to the Type 2 prototype isolate VR2332.
Hepatitis E virus Variant in Farmed Mink, Denmark

Hepatitis E virus (HEV) is a zoonotic virus for which pigs are the primary animal reservoir. To investigate whether HEV occurs in mink in Denmark, we screened feces and tissues from domestic and wild mink. Our finding of a novel HEV variant supports previous findings of HEV variants in a variety of species.

**General information**
State: Published
Organisations: National Veterinary Institute, Section for Virology, Aalborg University
Contributors: Krog, J. S., Breum, S. Ø., Jensen, T. H., Larsen, L. E.
Pages: 2028-2030
Publication date: 2013
Peer-reviewed: Yes

**Publication information**
Journal: Emerging Infectious Diseases (Print Edition)
Volume: 19
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): Impact factor 7.422
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): Impact factor 8.222
Web of Science (2016): Indexed yes

BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 4.23 SJR 3.101 SNIP 2.012
Web of Science (2015): Indexed yes

BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 4.59 SJR 3.509 SNIP 2.406
Web of Science (2014): Impact factor 6.751
Web of Science (2014): Indexed yes

BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 4.68 SJR 3.254 SNIP 2.266
Web of Science (2013): Impact factor 7.327
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes

BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 4.25 SJR 2.858 SNIP 2.131
Web of Science (2012): Impact factor 5.993
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes

BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 4.46 SJR 2.785 SNIP 2.19
Web of Science (2011): Impact factor 6.169
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): Impact factor 6.859
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
Influenza A Virus with a Human-Like N2 Gene Is Circulating in Pigs

A novel reassortant influenza A virus, H1avN2hu, has been found in Danish swine. The virus contains an H1 gene similar to the hemagglutinin (HA) gene of H1N1 avian-like swine viruses and an N2 gene most closely related to the neuraminidase (NA) gene of human H3N2 viruses from the mid-1990s.

Investigation of the association of growth rate in grower-finishing pigs with the quantification of Lawsonia intracellularis and porcine circovirus type 2

As a part of a prospective cohort study in four herds, a nested case control study was carried out. Five slow growing pigs (cases) and five fast growing pigs (controls) out of 60 pigs were selected for euthanasia and laboratory examination at the
end of the study in each herd. A total of 238 pigs, all approximately 12 weeks old, were included in the study during the first week in the grower-finisher barn. In each herd, approximately 60 pigs from four pens were individually ear tagged. The pigs were weighed at the beginning of the study and at the end of the 6–8 weeks observation period. Clinical data, blood and faecal samples were serially collected from the 60 selected piglets every second week in the observation period. In the killed pigs serum was examined for antibodies against Lawsonia intracellularis (LI) and procine circovirus type 2 (PCV2) and in addition PCV2 viral DNA content was quantified. In faeces the quantity of LI cells/g faeces and number of PCV2 copies/g faeces was measured by qPCR. The objective of the study was to examine if growth rate in grower-finishing pig is associated with the detection of LI and PCV2 infection or clinical data. This study has shown that diarrhoea is a significant risk factor for low growth rate and that one log10 unit increase in LI load increases the odds ratio for a pig to have a low growth rate by 2.0 times. Gross lesions in the small intestine and LI load > log10 6/g were significant risk factors for low growth. No association between PCV2 virus and low growth was found.

General information
State: Published
Organisations: National Veterinary Institute, Division of Veterinary Diagnostics and Research, Section for Veterinary Diagnostics, Bacteriology & Pathology, Adaptive Immunology & Parasitology, Virology, Danish Agriculture and Food Council
Pages: 63-72
Publication date: 2013
Peer-reviewed: Yes

Publication information
Journal: Preventive Veterinary Medicine
Volume: 108
Issue number: 1
ISSN (Print): 0167-5877
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 2.26 SJR 1.144 SNIP 1.31
Web of Science (2017): Impact factor 1.924
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): Impact factor 1.987
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.1 SJR 1.282 SNIP 1.177
Web of Science (2015): Impact factor 2.182
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.37 SJR 1.27 SNIP 1.407
Web of Science (2014): Impact factor 2.167
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 2.49 SJR 1.264 SNIP 1.529
Web of Science (2013): Impact factor 2.506
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 2.45 SJR 1.265 SNIP 1.436
Web of Science (2012): Impact factor 2.389
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 2.24 SJR 1.194 SNIP 1.295
Microbiological, pathological and histological findings in four Danish pig herds affected by a new neonatal diarrhoea syndrome

BACKGROUND: Neonatal diarrhoea is a frequent clinical condition in commercial swine herds, previously regarded to be uncomplicated to treat. However, since 2008 it seems that a new neonatal diarrhoeic syndrome unresponsive to antibiotics and common management practices has emerged. Routine laboratory examinations have not detected any pathogen related to this syndrome. The primary purpose of this study was to evaluate if well-known enteric pathogens could be associated with outbreaks of neonatal diarrhoea, thus question the hypotheses of a new syndrome. Furthermore, we wanted to evaluate macroscopic and microscopic findings associated with these outbreaks and if possible propose a preliminary piglet-level case-definition on syndrome New Neonatal Porcine Diarrhoea syndrome (NNPDS).

RESULTS: Four well-managed herds experiencing neonatal diarrhoea with no previously established laboratory conclusion and suspected to suffer from New Neonatal Porcine Diarrhoea Syndrome, were selected. Within these herds, 51 diarrhoeic and 50 non-diarrhoeic piglets at the age of three to seven days were necropsied and subjected to histological and microbiological examination. Faeces were non-haemorrhagic. Neither enterotoxigenic E. coli, Clostridium perfringens type A or C, Clostridium difficile, rotavirus, coronavirus, Cryptosporidium spp, Giardia spp, Cystoisospora suis nor Strongyloides ransomi were associated with diarrhoea in the investigated outbreaks. Macroscopically, the diarrhoeic piglets were characterized by filled stomachs and flaccid intestines without mucosal changes. The predominant histological lesions were villous atrophy in jejunum and ileum. Epithelial lesions in colon were seen in one third of the case piglets.

CONCLUSIONS: The results of the study supported the hypothesis that a new neonatal porcine diarrhoea was present in the investigated herds, since no known pathogen(s) or management factors could explain the diarrhoeal outbreaks. Based
on the findings in the four herds the following case-definition of NNPDS was suggested: Non-haemorrhagic diarrhoea during the first week of life, without detection of known infectious pathogens, characterized by milk-filled stomachs and flaccid intestines at necropsy.

**General information**

State: Published

Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Section for Public sector service and commercial diagnostics, Section for Virology, Danish Agriculture and Food Council, University of Copenhagen


Number of pages: 9
Publication date: 2013
Peer-reviewed: Yes

**Publication information**

Journal: B M C Veterinary Research

Volume: 9
Issue number: 1
Article number: 206
ISSN (Print): 1746-6148

Ratings:

BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes

BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 2.16 SJR 0.934 SNIP 1.108
Web of Science (2017): Impact factor 1.958
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): Impact factor 1.75
Web of Science (2016): Indexed yes

BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 1.86 SJR 0.981 SNIP 1.009
Web of Science (2015): Impact factor 1.643
Web of Science (2015): Indexed yes

BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 1.81 SJR 0.943 SNIP 1.018
Web of Science (2014): Impact factor 1.777
Web of Science (2014): Indexed yes

BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 1.85 SJR 0.861 SNIP 0.853
Web of Science (2013): Impact factor 1.743
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes

BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 1.94 SJR 0.779 SNIP 1.023
Web of Science (2012): Impact factor 1.861
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes

BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.66 SJR 1.165 SNIP 1.447
Web of Science (2011): Impact factor 2
ISI indexed (2011): ISI indexed no

BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.076 SNIP 1.396
Web of Science (2010): Impact factor 2.371
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
Electronic versions: prod21382439575495.1746_6148_9_206.pdf
DOIs: 10.1186/1746-6148-9-206

Bibliographical note
This is an open access article distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/2.0), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Source: dtu
Source-ID: n::oai:DTIC-ART:bmc/409870126::33284
Research output: Research - peer-review › Journal article – Annual report year: 2013

Molekylær karakterisering af influenzavirus fra wilde fugle i Danmark i 2012
Aviær influenza (AI) virus indeholder 8 genom (RNA) segmenter, som koder for 13 proteiner. De mest variable proteiner er overflade glykoproteinerne hemagglutinin (HA) og neuraminidase (NA), der kodes af hhv. HA og NA genom segmenterne. HA og NA danner basis for subtypel klassificering af AI virus. Wilde vandfugle anses for at være den naturlige vært for AI virus, og i forbindelse med flere udbrud af højpatogen aviær influenza (HPAI) virus i fjerkræ er der fundet et tilsvarende lavpatoge aviær influenza (LPAI) virus i wilde vandfugle. AI virus kan spreds over lange afstande af wilde fugle, herunder potentielt også HPAI virus. Wilde fugle er derfor et oplagt mål for overvågning af AI virus, og Danmarks topologi med lange kyststrækninger og vadeområder er ideelle foder- og rastepladser for de mange wilde vandfugle, der trækker over Danmark eller overvintrer her.

General information
State: Published
Organisations: National Veterinary Institute
Number of pages: 24
Publication date: 2013

Publication information
Publisher: National Veterinary Institute
Original language: English
Source: PublicationPreSubmission
Source-ID: 93591605
Research output: Commissioned › Report – Annual report year: 2014

Novel reassortant swine influenza viruses are circulating in Danish pigs
The Danish surveillance program for influenza A virus in pigs has revealed that two novel reassortant swine influenza viruses may now be circulating in the Danish swine population, since they each have been detected in at least two submissions from different herds in 2011 as well as in 2012. One of the reassortant viruses comprised a HA gene similar to H1 of H1N1 avian-like swine influenza virus (SIV) and a NA gene most closely related to N2 gene of human H3N2 influenza virus that circulated in humans in the mid 1990s. The internal genes of this reassortant virus with the subtype H1avN2hu all belonged to the H1N1 avian-like SIV lineages. Until now this novel virus H1avN2hu has only been detected in Danish swine. The other novel reassortant virus contained the HA gene from H1N1pdm09 virus and a NA gene similar to the N2 gene of H3N2 SIV that have been circulating in European swine since the mid 1980s. The N2 gene of this new reassortant virus could also has been donated by the reassortant H1N2 SIV with an avian-like HA gene which is very common in Danish pigs and has been circulating since 2003. The internal genes of this reassortant virus with the subtype H1pdm09N2sw all belonged to the pandemic H1N1pdm09 influenza virus lineage. Swine influenza virus with a similar subtype to H1pdm09N2sw has previously been found in pigs in Italy and Germany. Detailed analyses of viral genes will further elucidate the relationship between these new swine influenza viruses found in the different countries. In addition, several sporadic reassortant swine influenza viruses comprising different constellations of internal genes from known circulating swine influenza viruses were found. Future full genome studies will reveal if some of these reassortant viruses also will be established in the Danish pig population.
Omfattende udbrud af hvalpesyge i danske mink (Neovison vison) og wilde rovdyr

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Kopenhagen Fur
Pages: 171-178
Publication date: 2013

Host publication information
Title of host publication: Faglig Årsberetning 2013 : Kopenhagen Fur
Place of publication: Aarhus N
Publisher: Kopenhagen Fur
Electronic versions:
CDV.pdf
URLs:
http://issuu.com/kopenhagenfur/docs/faglig__rsberetning
Research output: Research - peer-review › Book chapter – Annual report year: 2014

One health – One flu: Surveillance in pigs and mink has revealed extensive exchange of influenza A virus genes and viruses among animals and humans

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Section for Public sector service and commercial diagnostics
Pages: 26
Publication date: 2013

Host publication information
Place of publication: Lyngby
Electronic versions:
MVN2013ConfAbstractBook_v1.0.pdf
URLs:

Bibliographical note
DC11*
Research output: Research - peer-review › Conference abstract in proceedings – Annual report year: 2013

PMWS Development in Pigs from Affected Farms in Spain and Denmark
Postweaning multisystemic wasting syndrome (PMWS) is a worldwide spread condition that affects pigs in nursery and/or fattening units, and is considered to have a severe economic impact on swine production. The main clinical sign of PMWS
is wasting, but can also include pallor of the skin, icterus, respiratory distress and diarrhoea. The main essential infectious agent for PMWS development is porcine circovirus type 2 (PCV2), but the exact cause of PMWS is still unclear. PCV2 is present in most pig herds, but the occurrence of PMWS is more sporadic, and it is been difficult to reproduce PMWS by inoculating PCV2 alone. However, studies where co-infections have been applied have been more successful. Based on this, we modeled PMWS development based on longitudinal data on antibodies and PMWS status from herds in Denmark and Spain, where presence of a range of pathogens were considered as explanatory variables in the form of maternal immunity and the occurrence of seroconversion against the considered pathogens. However, maternal immunity could not be measured from mother animals due to cross fostering, no time points for seroconversion was available, and no case/control status could be assigned as PMWS do not have an ‘infectious period’ after which animals may be assigned control status. The talk will concentrate on the framework in which this was handled, which may be translated to similar settings for similar studies. We found that seroconversion towards PCV2 and Lawsonia intracellularis had a significant impact on PMWS in the Danish data, but it appears that the effect is positive, in the sense that seroconverted animals were less likely to develop PMWS. A number of maternal immunities also significantly affected PMWS development. Furthermore it was uncovered that most of these effects would not have been detected if pathogens were considered by themselves and not simultaneously.

**General information**

State: Published
Organisations: Department of Applied Mathematics and Computer Science, Statistics and Data Analysis, National Veterinary Institute, Section for Epidemiology, Section for Public sector service and commercial diagnostics, Section for Virology
Number of pages: 1
Publication date: 2013

**Host publication information**

Title of host publication: BIT’s 5th World Congress of Vaccine
Electronic versions:
prod11364940429509.WCV_Abstract_Anders_Stockmarr.pdf
Source: dtu
Source-ID: u::7344
Research output: Research - peer-review › Conference abstract in proceedings – Annual report year: 2013

**Spread of hepatitis E virus from pig slurry to the water environment**

**General information**

State: Published
Organisations: National Veterinary Institute, Section for Virology, National Food Institute, Division of Food Microbiology, University of Copenhagen
Pages: 25
Publication date: 2013

**Host publication information**

Place of publication: Lyngby
Electronic versions:
MVN2013ConfAbstractBook_v1.0.pdf
URLs:

**Bibliographical note**
DC09
Research output: Research - peer-review › Conference abstract in proceedings – Annual report year: 2013

**Swine Plasma Immunoglobulins for Prevention and Treatment of Post-Weaning Diarrhoea: Optimizing Stability Towards Gut Conditions**

**General information**

State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Section for Virology, Technical University of Denmark, Upfront Chromatography A/S, KiBif ApS, Multimerics ApS
Swine Plasma Immunoglobulins for Prevention and Treatment of Post-Weaning Diarrhoea: Optimizing Stability Towards Gut Conditions

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Section for Virology, Technical University of Denmark, Upfront Chromatography A/S, KiBif ApS, Multimerics ApS
Number of pages: 1
Publication date: 2013
Peer-reviewed: Yes
Event: Poster session presented at Mucosal Vaccines, Adjuvants & Delivery, Copenhagen, Denmark.

Swine plasma immunoglobulins for prevention and treatment of post-weaning diarrhoea: Optimizing stability towards gut conditions
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. We aim at developing products for protection against PWD based on natural antibodies (immunoglobulins) derived directly from inexpensive raw materials.

Swine immunoglobulins (Igs) were isolated directly from slaughterhouse swine plasma-waste by expanded bed chromatography. The immunoglobulin product is intended for enteral administration and thus has to pass through the digestive system, thus we consequently cross-linked the Igs by a periodate based method. The formation of high molecular weight complexes were demonstrated by size exclusion chromatography. By imitating the gastrointestinal system we subjected the Igs to pepsin or trypsin/chymotrypsin and observed the degradation patterns of the cross-linked Igs compared to unmodified Igs, and optimized coupling conditions to achieve maximal stability with concurrent retention of antigen binding activity. The availability of such an inexpensive, stable and highly active Ig product would allow swine producers to reduce expenses and cut down on antibiotics and zinc usage.
which consequently pose a great threat to human health. Therefore, sustainable alternatives for treating post-weaning diarrhoea without using antibiotics are in demand. Swine that are old (and big) enough for slaughter have during their upbringing been challenges by many different pathogens and thus have developed immunity towards these pathogens, which include pathogen-specific immunoglobulins (antibodies). We hypothesis that by harvesting natural immunoglobulins from porcine blood plasma, a waste product from swine slaughter, and feeding these immunoglobulins to the piglets this can subsequently (by passive immunisation) prevent and treat post-weaning diarrhoea.

Our challenge is to find a suitable method for stabilising the immunoglobulins for oral provision in order for the immunoglobulins to pass as unharmed as possible through the digestive system and still retaining their anti-pathogenic properties.

What we know:
It is possible to multimerise immunoglobulins, which results in an advantage when binding to their respective antigens in comparison to the non-multimerised immunoglobulins, but too high degree of multimerisation abates immunoglobulin reactivity. Unfortunately, a preliminary study showed that multimerisation destabilises the immunoglobulins. On the other hand, proteolytical resistance correlates with increased immunoglobulin concentration.

What we need:
To investigate the effect of increasing the concentration of multimerised immunoglobulins on proteolytical resistance.
To investigate multimerised immunoglobulins’ ability in inhibiting microbial (E. coli) adhesion on relevant matrices, such intestinal villi and/or intestinal cell lines.
A toxicological study on (if any) adverse side effects occurs when enteral providing immunoglobulins to piglets.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Section for Virology, Technical University of Denmark, Upfront Chromatography A/S, KiBif ApS, Multimerics ApS
Number of pages: 1
Publication date: 2013
Peer-reviewed: Yes
Event: Abstract from 10th Workshop in Protein.DTU, Kgs. Lyngby, Denmark.
Electronic versions:
Abstract_for_Protein_Workshop.pdf
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2013

The diversity of Porcine Reproductive and Respiratory Syndrome Virus Type 1 and 2 in Denmark
Both Type 1 and Type 2 PRRS viruses are circulating among Danish pigs. The first appearance of Type 1 PRRSV in Denmark was in 1992 whereas the Type 2 PRRSV was introduced in 1996 after the use of a live attenuated vaccine that reverted to virulence. Since then, vaccination to control the disease for both PRRSV genotypes has been widely used in Denmark and it is therefore highly relevant to monitor the diversity of currently circulating PRRSV strains. Only subtype 1 of the Type 1 PRRSV strains and vaccine-like Type 2 PRRSV strains were previously detected in Denmark, however, only few Danish PRRSV strains were sequenced. Denmark exports more than 50,000 living pigs each month. A portion of these pigs inevitably harbor PRRSV. Thus, the diversity of PRRSV in Denmark is of interest to other countries besides Denmark. The main objective of the present study was to close the gap in knowledge on the genetic diversity of currently circulating PRRSV strains in Danish pigs by sequencing ORF5 and ORF7 of approximately 41 Type 1 and 50 Type 2 strains isolated between 2003 and 2013. Furthermore, full genome analysis was performed on nine Type 1 and nine Type 2 selected strains. The preliminary assessment of the results showed that the Type 1 strains all belonged to subtype 1. Based on the ORF5 sequences, the Danish Type 1 viruses clustered into two groups. These two groups shared 84 % to 92 % and 94 % to 99% nucleotide identity to the Lelystad virus, respectively. The sequenced Type 2 viruses showed a significant higher level of identity in that the ORF5 sequences were 94 - >99 % identical at the nucleotide level. Most of the Type 2 viruses, shared high level of identity to the VR2332 vaccine strain (Ingelvac MLV), but a few more diverse isolates were also identified, including strains with interesting deletions in NSP2 and other genes. The full genome sequences of Danish strains showed an overall nucleotide identity of 88-98% (Type 1) and 94 % to >99 % (Type 2). The impact of these results will be discussed.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Section for Public sector service and commercial diagnostics, Danish Agriculture and Food Council, University of Hong Kong
Number of pages: 1
Association between average daily gain, faecal dry matter content and concentration of Lawsonia intracellularis in faeces

Background

The objective of this study was to investigate the association between average daily gain and the number of Lawsonia intracellularis bacteria in faeces of growing pigs with different levels of diarrhoea.

Methods

A longitudinal field study (n = 150 pigs) was performed in a Danish herd from day 29 to 47 post weaning. Every third day all pigs were weighed, subjected to a clinical examination and faecal samples were obtained. Faecal samples were subjected to dry matter determination and absolute quantification by PCR for L. intracellularis and porcine circovirus type 2 (PCV2). Association between average daily gain, faecal dry matter content, numbers of L. intracellularis bacteria and PCV2 genome copies in faeces was investigated in a multilevel mixed-effects linear model.

Results

Increasing numbers of L. intracellularis log10 bacteria/g faeces were significantly associated with decreasing average daily gain (P < 0.001). The association was decreasing with increasing faecal dry matter content (P < 0.01). The number of PCV2 log10 copies/g faeces was not significantly associated with average daily gain of the pigs (P > 0.5).

Conclusion

The results suggest a potential application of a PCR quantifying L. intracellularis in growing pigs. Faecal dry matter content must be taken into consideration in interpretation of such test results.
Clinical and laboratory studies on herds affected with postweaning multisystemic wasting syndrome in Denmark, France, Spain, and Sweden: Disease progression and a proposal for herd case definition

Objectives: To propose and evaluate a protocol to establish a diagnosis of postweaning multisystemic wasting syndrome (PMWS) at herd level.

Materials and methods: The data used included both laboratory data from previous epidemiological studies carried out in Italy, Denmark, and Spain and original postweaning mortality data collected from several herds in Denmark, France, Spain, and Sweden. Statistical process control techniques were used to analyze the longitudinal evolution of mortality in each herd.

Results: The analysis of data sets from three different countries showed that to diagnose at least one PMWS-affected pig with a probability > 95%, it is necessary to study a minimum of three to five pigs. Longitudinally collected data showed that when > 20 data points were available, a significant increase in mortality was always detected at close to the time of PMWS diagnosis. When <10 points were available, a significant increase in mortality was detected in four of six studied herds, although mortality percentages were always higher at the time of PMWS diagnosis than before diagnosis.

Implications: These results suggest that two conditions must be fulfilled to diagnose PMWS in a herd. Firstly, a significant increase in postweaning mortality, compared to the historical background in the herd, must be observed in association with clinical signs compatible with PMWS. Secondly, PMWS must be diagnosed in at least one of three to five necropsied pigs concurrently with the increase in mortality. Ruling out other potential causes of increased mortality is also necessary.

General information
State: Published
Organisations: National Veterinary Institute, Division of Veterinary Diagnostics and Research, Virology, Autonomous University of Barcelona, Danish Agriculture and Food Council, Agence Française de Sécurité Sanitaire des Aliments, National Veterinary Institute
Pages: 129-136
Publication date: 2012
Peer-reviewed: Yes

Publication information
Journal: Journal of Swine Health and Production
Volume: 20
Issue number: 3
ISSN (Print): 1537-209X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 0.45 SJR 0.341 SNIP 0.681
Web of Science (2017): Impact factor 0.978
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 0.57 SJR 0.515 SNIP 0.807
Web of Science (2016): Impact factor 0.562
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 0.43 SJR 0.453 SNIP 0.636
Web of Science (2015): Impact factor 1.277
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 0.46 SJR 0.457 SNIP 1.006
Web of Science (2014): Impact factor 1.205
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 0.44 SJR 0.366 SNIP 0.714
Web of Science (2013): Impact factor 0.771
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 0.27 SJR 0.263 SNIP 0.588
Web of Science (2012): Impact factor 0.625
ISI indexed (2012): ISI indexed yes
Consequences of outbreaks of influenza A virus in farmed mink (Neovison vison) in Denmark in 2009 and 2010

Influenza in mink (Neovison vison) is assumed to be rare, but outbreaks have previously been reported in farmed mink. The first report was from Swedish mink farms in 1984 which was caused by influenza A virus H10N4 of avian origin. In 2009 and 2010 outbreaks of respiratory disease were seen in several Danish mink farms. In all of the farms, the clinical symptoms were upper respiratory tract symptoms with sneezing and coughing as the most dominant symptoms. Peracute deaths were seen in mink without any clinical symptoms. Influenza H3N2 was found detected by PCR in the lungs from diseased mink. The mean mortality rate was 1.20% (95% confidence intervals: 0.58–1.82) during the outbreak period. Young mink and especially males were reported to be more likely to die. The outbreak in the farms varied from two to ten weeks. During the outbreak period most farms treated all mink with antimicrobials and four of these farms used feed medication in three weeks. The farmers, however, noted that the medication had little or no effect. The most plausible way of transmission of the influenza is from the raw untreated pig waste containing lungs used in the production of mink feed. Because the first clinical symptoms were observed few weeks after the raw pig waste was added to the wet mink feed.

General information

State: Published
Organisations: National Veterinary Institute, Section for Public sector service and commercial diagnostics, Division of Veterinary Diagnostics and Research, Virology, Section for Virology, Division of Poultry, Fish and Fur Animals, Section of Fur Animal Diseases and Wildlife, Holstebro Veterinary Clinic
Pages: 186-189
Publication date: 2012

Host publication information

Title of host publication: Proceedings of the Xth International Scientific Congress in fur animal production : Scientfur volume 36 (3/4)
Publisher: Wageningen Academic Publishers
DOIs: 10.3920/978-90-8686-760-8_27
Detection of PRRSV in 218 field samples using six molecular methods: What we are looking for?

Objectives
The purpose of this study was to determine the sensitivity and the specificity of six molecular methods used for the detection of porcine reproductive and respiratory syndrome virus (PRRSV).

Methods
218 field samples (serum, tissues) were collected between 2009 and 2011 from 50 PRRSV positive and 45 negative pig herds from Slovenia. Total viral RNA was extracted from original samples and stored in aliquots at -70 °C until analysis. RT-PCR and direct sequencing of positive samples was performed as described previously (Toplak et al., 2012). All field samples were analyzed with five commercial real-time RT-PCR kits (named as kit A to E) according to the instructions of producer.

Results
According to determined 258 nucleotides long sequences (ORF7) 102 PRRSV samples belong to Type I (identification of 12 different lineages of EU subtype 1 (a=1, b=8, c=1, d=1, e=61, f=8, g=2, h=4, i=3, j=4, k=1, m=8) with 85.7-93.8 % nucleotide identity between lineages and four samples belong to Type II. In total, 138 PRRSV positive samples were detected with broad range of PRRSV RNA in samples. The highest sensitivity was observed with kit E (96.3%) and with kit B (94.5%), followed by conventional RT-PCR (87.8%) and kit D (82.1%), while the lowest sensitivity was observed with kit A (55.3%) and kit C (53.8%). Reduced sensitivity was directly related to the genetic lineages.

Discussion and conclusion
The study showed that the performance of commercial RT-PCR assays are highly dependent on the genetic make-up of the target viruses and confirm findings of a previous study where we showed some commercial PCR kits failed to detect specific genetic linkages of PRRSV. Thus, these finding emphasise that it is cricial that the manifactors of diagnostic PCR kits (conventional and real-time) Continuesly follow the genetic evaluation of especially Type I PRRSV subtype viruses and regularly update their primer sequences.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, University of Ljubljana, ADIAGENE, Faculty of Veterinary Science, Tetracore, Inc.
Contributors: Toplak, I., Štukelj, M., Gracieux, P., Gyula, B., Larsen, L. E., Rauh, R.
Number of pages: 1
Publication date: 2012

Host publication information
Title of host publication: Proceedings of EuroPRRS2012 : Understanding and combating PRRS in Europe
Place of publication: Budapest, Hungary
Keywords: PRRSV, Diagnosis, Real-time RT-PCR, Sensitivity, Field samples
Electronic versions: prod21357491880578.Toplak_et_al_COST_abstract_08_08_2012_lael.pdf
URLs:
http://www.europrrs.net/events/europrrs2012/europrrs2012-proceedings.pdf
Source: dtu
Source-ID: u::5789
Research output: Research - peer-review › Article in proceedings – Annual report year: 2012

Diversity and zoonotic potential of rotaviruses in swine and cattle across Europe.

Group A rotaviruses can infect both humans and animals. Individual rotavirus strains can occasionally cross species barriers and might hereby contribute to the emergence of new genotypes in heterologous hosts. The incidence and impact of zoonotic rotavirus are not well defined, and one reason for this is a lack of data about strains circulating in suspected reservoir animal hosts. In this study we report the incidence, genetic diversity, and molecular epidemiology of rotaviruses detected in domestic cattle and swine in 6 European countries. From 2003 to 2007, 1101 and more than 2000 faecal specimens were collected from swine and cattle, both healthy and diarrhoeic, and tested for rotaviruses. Viruses from positive stools were genotyped and a subset of strains was characterized by nucleotide sequencing and phylogenetic analysis of the VP7 (G) and VP4 (P) genes. Rotaviruses were detected in 43% of bovine samples and in 14% of porcine samples. In cattle, 10 different combinations of G and P types were identified and the most common strains were G6P[11] and G6P[5]. In swine, the number of identified G–P combinations was higher (n = 21), however, no single combination was predominant across Europe. Newly described genotype specificities, P[27] and P[32], were identified in swine. When compared at the nucleotide sequence level, the identified porcine rotavirus strains and contemporary human strains grouped together phylogenetically, whereas bovine rotavirus strains formed separate clades. These data demonstrate large genetic diversity of porcine and bovine rotavirus strains across Europe, and suggest that livestock herds may serve as potential reservoirs for human infections.
Diversity of type i porcine reproductive and respiratory syndrome virus (PRRSV) in europe: A PRRSCon study

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Section for Public sector service and commercial diagnostics, Animal Health Service, Parco Technologico Padano, Animal Health and Veterinary Laboratories Agency, National Veterinary Research Institute, CReSA - Centre for Animal Health Research, Agence nationale de la sécurité sanitaire, alimentation, environnement et travail, Ghent University
Number of pages: 1
Publication date: 2012
Peer-reviewed: No
Event: Abstract from 22nd International Pig Veterinary Society Congress, Jeju, Korea, Republic of.

Bibliographical note
Oral presentation.
Source: dtu
Source-ID: u::6591
Research output: Research › Conference abstract for conference – Annual report year: 2012

Enabling Passive Immunization as an Alternative to Antibiotics for Controlling Enteric Infections in Production Animals

Enteric infections cause major problems in most intensive animal production sectors, including poultry, pigs and cattle, leading to disease, reduced production and compromised welfare. In addition some of these infections are zoonotic, and they are to a large extent responsible for the continued massive use of antibiotics in food animals. Thus there is a pressing need for economically feasible, efficient, non-antibiotics based means for controlling the problem. Passive immunization has been known for decades as an efficient way of endowing humans or animals with short-term (weeks) immunity. To control enteric infections by passive immunization a bolus of immunoglobulin may simply be administered orally. For this to work, large amounts of active immunoglobulins are needed. To be a real alternative to antibiotics the price of the
immunoglobulin product needs to be low. We combined an efficient and mild high-capacity method for extracting immunoglobulins directly from raw materials like milk, whey and blood plasma with a novel method for stabilizing activity. In a first experiment a total of 15 kg unstabilized bovine immunoglobulin was purified from whey (35,000 liters) and administered to colostrum-deprived calves (225-300 g pr calf during the first 24 hours after birth). No difference in resulting immunoglobulin serum concentration, weight gain or disease frequency were seen in this group of calves compared to a control group given full access to high-quality colostrum. The effect of orally administered bovine immunoglobulin is currently being tested in a calf herd with persistent diarrhea problems. Furthermore, it was shown in a Campylobacter challenge model in chickens that caecal and faecal counts of Campylobacter were between 0.5 and 1.0 logs lower in birds when given 200 mg avian immunoglobulins orally together with the challenge (at day 21 of age) compared to a placebo group receiving immunoglobulin with no reactivity against Campylobacter. While clearly preliminary, these results show that immunoglobulin can be produced from renewable sources at a price enabling passive immunization as a viable strategy for control of infectious diseases in the intensive animal production, with the potential to significantly reduce antibiotics consumption.

**General information**

State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, National Food Institute, Division of Food Microbiology, Section for Virology, Dianova A/S, Multimerics ApS, Upfront Chromatography A/S
Number of pages: 1
Publication date: 2012
Peer-reviewed: Yes
Event: Poster session presented at International Symposium: Alternatives to antibiotics (ATA), Paris, France.
Electronic versions:
IABS Poster2-29[1].pdf
Source: dtu
Source-ID: u::6569
Research output: Research - peer-review : Poster – Annual report year: 2012

**Epidemi af hvalpesyge i jyske mink: Nyt fra Veterinærinstituttet**

**General information**

State: Published
Organisations: National Veterinary Institute, Section for Public sector service and commercial diagnostics, Section for Virology, Section for Bacteriology, Pathology and Parasitology
Contributors: Larsen, G., Holm, E., Hjulsager, C. K., Larsen, L. E., Jensen, T. K., Hansen, M. S., Chréél, M.
Pages: 41
Publication date: 2012
Peer-reviewed: No

**Publication information**

Journal: Dansk Veterinaertidsskrift
Volume: 2012
Issue number: 16
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
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
European surveillance network for influenza in pigs 3 (ESNIP 3)

Objectives: The “European surveillance network for influenza in pigs (ESNIP) 3” continues a surveillance network previously established during concerted actions ESNIP 1 and ESNIP 2. Running from 2010-2013, ESNIP 3 represents the only organised surveillance network for influenza in pigs in Europe and seeks to strengthen formal interactions with human and avian surveillance networks.

Materials and Methods: The project consortium comprises 24 participants, contributing a variety of specialism’s and skills ensuring multi-disciplinary cutting-edge outputs. Most partners are actively working with swine influenza virus (SIV) experimentally and in the field. Three work packages aim to increase knowledge of the epidemiology and evolution of SIV in European pigs to inform changes in disease trends and variation in contemporary viruses through organised field surveillance programmes.

Results: An inventory of the programmes that are currently active in fifteen of the partners showed that passive surveillance was primarily used. Detected virus strains will be characterised by antigenic cartography (informing better evidence-based approaches for selection of vaccine strains) and genetically through full genome sequencing using the latest technology. The virus bank and electronic database will be expanded and formally curated with relevant SIV isolates together with information for global dissemination within and out with the consortium to the wider scientific and veterinary community.

Conclusions: All data will improve SI diagnosis by updating reagents employed in the recommended techniques to define minimum datasets for standardised epidemiological analyses. These approaches will aid pandemic preparedness and planning for human influenza whilst providing an evidence base for decisions relating to veterinary health.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, ESNIP 3 consortium, Animal Health and Veterinary Laboratories Agency, National Reference Laboratory for Swine Influenza, Wellcome Trust Sanger Institute, Ghent University
Contributors: Reid, S. M., Simon, G., Larsen, L. E., Kellam, P., Loeffen, W., van Reeth, K., Brown, I. H.
Number of pages: 1
Publication date: 2012
Peer-reviewed: Yes
Event: Abstract from 4th European Symposium of Porcine Health Management, Bruges, Belgium.
Electronic versions:
Reid et al ESNIP 3 Abstract for European.pdf
Source: dtu
Source-ID: u::6608
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2012

European surveillance network for influenza in pigs 3 (ESNIP 3)

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Ploufragan-Pluzané Laboratory, Animal Health and Veterinary Laboratories Agency, Wellcome Trust Sanger Institute, Ghent University, IZLER, National Veterinary Research Institute, Laboratorio Central Veterinario-Sanidad Animal, IDT Biologika GmbH, Finnish Food Safety Authority, Kimron Veterinary Institute, Veterinary Diagnostic Directorate, Central Veterinary Institute, University of Thessaly, Merial S.A.S., Hipra, University of Cambridge
Number of pages: 1
Publication date: 2012
Peer-reviewed: Yes
Event: Abstract from 22nd International Pig Veterinary Society Congress, Jeju, Korea, Republic of.
Electronic versions:
Simon et al European Surveillance network for influenza in pigs_Final.pdf
Source: dtu
Source-ID: u::6609
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2012
Genetic drift of HA and NA in Danish swine influenza virus from the period 2003-2012
The aim of this study is to analyze; the genetic drift in hemagglutinin (HA) and neuraminidase (NA) genes from influenza viruses isolated from Danish swine over the past decade; the antigenic evolution and relatedness between swine influenza virus strains of the H1 subtype by antigenic cartography.
Currently at least three influenza A subtypes (H1N1, H1N2 and H3N2) are endemic in the Danish swine population, and since 2010 the pandemic virus (H1N1pdm09) have also frequently been detected. The focus in this study will be on H1N1 and H1N2, since the prevalence of H3N2 have declined over the past years.
Obtained isolates derived from diagnostic samples submitted to the Danish National Veterinary Institute for influenza A virus detection. Approximately eight isolates from each of the years 2003 to 2012 are examined by HA and NA full length sequencing and phylogenetic analyses. In addition, HI-titers obtained by testing against a panel of reference swine influenza virus antisera are used for antigenic cartography. Preliminary phylogenetic analyses indicate a higher degree of drift for H1 genes than N1 genes.
The antigenic and genetic characterization of the swine influenza virus isolates in this study will provide a more complete picture of the molecular epidemiology of the H1N1 and H1N2 swine influenza viruses in Denmark.
A thorough knowledge of the antigenic drift in surface genes is very important concerning evaluation of the zoonotic potential of existing and future swine influenza virus strains and along with the monitoring of antigenic changes in hemagglutinin subtypes it will be possible to ensure a continuous efficacy of influenza virus vaccines.

Infectious risk factors for individual postweaning multisystemic wasting syndrome (PMWS) development in pigs from affected farms in Spain and Denmark
Two prospective longitudinal studies in 13 postweaning multisystemic wasting syndrome (PMWS)-affected farms from Spain (n = 3) and Denmark (n = 10) were performed. Blood samples from pigs were longitudinally collected from 1st week until the occurrence of the PMWS outbreak. Wasted and healthy age-matched pigs were euthanized, necropsied and histopathologically characterised. PMWS diagnosis was confirmed by means of lymphoid lesions and detection of porcine circovirus type 2 (PCV2) in these tissues by in situ hybridization or immunohistochemistry. Serological analyses were performed in longitudinally collected serum samples to detect antibodies against, PCV2, porcine reproductive and respiratory syndrome virus (PRRSV), porcine parvovirus (PPV), swine influenza virus (SIV) and Lawsonia intracellularis (law), Mycoplasma hyopneumoniae, Aujeszky's disease virus (ADV) and Salmonella spp. A Cox proportional hazards model was used to investigate the simultaneous effects of seroconversion and maternal immunity against the studied pathogens. Results showed that high levels of maternal immunity against PCV2 had a protecting effect in farms from both countries. Moreover, for the Danish dataset, seroconversion against law had an overall protecting effect, but for animals with very low levels of maternal antibody levels against this pathogen, the effect appeared neutral or aggravating. Otherwise, for the Spanish dataset, maternal immunity against PPV and PRRSV gave protective and aggravating effects, respectively. In conclusion, the present study reflects the complex interaction among different pathogens and their effects in order to trigger PMWS in PCV2 infected pigs.
In situ hybridization to detect porcine reproductive and respiratory syndrome virus

Porcine reproductive and respiratory syndrome (PRRS) has for nearly 3 decades been economically one of the most important swine diseases. Despite intensive research focus, many unanswered questions remain regarding the pathogenesis of PRRSV. In situ hybridization (ISH) is generally considered a more useful diagnostic tool than immunohystochemistry (IHC) and may be helpful in further research of pathogenesis. ISH is able to detect virus in non-progressive stages therefore the length of successful detection after infection is expected. It is not widely used, however, because of problems with specificity of the oligonucleotide probe due to the pronounced diversity of the PRRSV genome. The aim of the present study was to evaluate a PRRSV specific ISH protocol. Three, non-overlapping PRRSV specific 20 nucleotides, DIG labeled oligonucleotide probes were designed targeting the ORF7 region. The probes were specific designed to recognize PRRSV Type I isolates only. A total of 19 positive PRRSV paraffin blocks from different organs and infected with different strains were tested as well as a negative control. All samples were simultaneously tested by IHC using different anti-PRRSV monoclonal antibodies. Five experiments of ISH were performed, using a pool of 1 nmol of each of the three oligonucleotide probes with two different prehybridization temperature (105°C and 80°C) and time (5 and 10 min), using 0.5 nmol of each of the probes separately with prehybridization on 105°C during 5 min. Positive signals were detected in alveolar macrophages in lungs, in histiocytes in lymph nodes, Payer patches and tonsils, in macrophages, on inflamed area in ileum and in glomerular cells. 58 EuroPRRS2012 Budapest, Hungary ISH showed better sensitivity than IHC while there was an obvious discrepancy between sensitivity among the probes.

General information
State: Published
Organisations: National Veterinary Institute, Section for Public sector service and commercial diagnostics, Section for Virology, Section for Bacteriology, Pathology and Parasitology, Croatian Veterinary Institute
Pages: 57-58
Publication date: 2012

Host publication information
Title of host publication: Proceedings of EuroPRRS2012 : Understanding and combating PRRS in Europe
Place of publication: Budapest, Hungary
Keywords: Porcine reproductive and respiratory syndrome, In situ hybridization
Electronic versions: prod21357334490172.IN_SITU_HYBRIDIZATION_TO_DETECT_PORCINE_REPRODUCTIVE_AND_RESPIRATORY_SYNDROME_VIRUS_EuroPRRS2012.pdf
URLs: http://www.europrrs.net/events/europrrs2012/europrrs2012-proceedings.pdf
Source: dtu
Source-ID: u::6592
Research output: Research - peer-review › Article in proceedings – Annual report year: 2012

Investigation of the presence of human or bovine respiratory syncytial virus in the lungs of mink (Neovison vison) with hemorrhagic pneumonia due to Pseudomonas aeruginosa

Background
Hemorrhagic pneumonia is a disease of farmed mink (Neovison vison) caused by Pseudomonas aeruginosa. The disease is highly seasonal in Danish mink with outbreaks occurring almost exclusively in the autumn. Human respiratory syncytial virus (RSV) has been shown to augment infection with P. aeruginosa in mice and to promote adhesion of P. aeruginosa to human respiratory cells.

Findings
We tested 50 lung specimens from mink with hemorrhagic pneumonia for bovine RSV by reverse transcriptase polymerase chain reaction (PCR) and for human RSV by a commercial real-time PCR. RSV was not found.

Conclusions
This study indicates that human and bovine RSV is not a major co-factor for development of hemorrhagic pneumonia in Danish mink.
New influenza A virus reassortments have been found in Danish swine in 2011

In 2011 a passive surveillance for influenza A virus was conducted in Danish swine. Tested samples were clinical samples from affected pigs submitted to the Danish National Veterinary Institute for swine influenza virus detection. In total 713 samples from 276 herds were analysed and about 24% of the samples were positive for swine influenza virus. All influenza positive samples were tested for the H1N1pdm09 virus by a real time RT-PCR assay specific for the pandemic HA gene and 26% of the samples were positive. Subtyping of 90 samples by sequencing revealed the presence of: i) H1N1 "avian like" viruses which have been circulating in Danish pigs since it was found for the first time in 1981. ii) H1N2 reassortant viruses which comprise HA from "avian like" H1N1 and NA from swine H3N2. The reassortant H1N2 virus was discovered in Danish pig for the first time in 2003 and is now well established in the Danish pig population. iii) H1N1pdm09 viruses which were found the first time in Danish pigs in January 2010. iv) Three new subtype variants comprising H1 “avian like” together with N2 “human like”, H1 pandemic with N2 “human like” and finally H1 pandemic with N2 from swine H3N2. The presence of N2 “human like” gene in Danish swine is new and genetic analysis indicate that it is most closely related to NA of human H3N2 viruses. In addition, full genome characterization of 40 viruses from the surveillance revealed the presence of additional new reassortments of which some have internal genes from the pandemic H1N1 virus.

This study contribute significantly to our knowledge of the epidemiology of swine influenza A virus circulating in Danish swine and the potential role of swine in the emergence of novel reassortant viruses.
Outbreaks of Influenza A Virus in Farmed Mink (Neovison vison) in Denmark: Molecular characterization of the involved viruses

Influenza in mink (Neovison vison) is assumed to be rare, but outbreaks have previously been reported in farmed mink. The first report was from Swedish mink farms in 1984 and the second was reported from Canadian mink farms.

In 2009, influenza A of the subtype H3N2 was detected in several Danish mink farms with respiratory symptoms. Full-genome sequencing showed that the virus was a human/swine reassortant, with the H and N gene most related to human H3N2 viruses circulating in 2005. The remaining 6 genes were most closely related to H1N2 influenza viruses circulating in Danish swine. This virus had not previously been described in swine, mink nor humans. PCRs assays specifically targeting the new reassortant were developed and used to screen influenza positive samples from humans and swine in Denmark with negative results. Thus, there was no evidence that this virus had spread to humans or was circulating in Danish pigs.

In 2010 and 2011, influenza virus was again diagnosed in diseased mink in a few farms. The genetic typing showed that the virus was similar to the pandemic H1N1 virus circulating in humans and swine. The H3N2 virus was not detected in 2010 and 2011.

Taken together, these findings indicate that mink is highly susceptible for influenza A virus of human and swine origin and may therefore act as a potential host/reservoir for influenza A viruses.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Section for Public sector service and commercial diagnostics, Division of Poultry, Fish and Fur Animals, Section of Fur Animal Diseases and Wildlife, Statens Serum Institut, Holstebro Veterinary Clinic
Number of pages: 1
Publication date: 2012
Peer-reviewed: Yes
Event: Abstract from 10th International Scientific Congress in fur animal production (IFASA 2012), Copenhagen, Denmark.
Electronic versions:
prod21357491693004.IFASA2012_mink_influenza_Molekyl_r_lael_rev111220.pdf
Source: dtu
Source-ID: u::6611
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2012

Outbreaks of influenza A virus in farmed mink (Neovison vison) in Denmark: molecular characterization of the viruses

Influenza in mink (Neovison vison) is assumed to be rare, but several outbreaks have been described during recent years in Europe and the North America. In 2009, influenza A of the subtype H3N2 was detected in several Danish mink farms with respiratory symptoms. Full-genome sequencing showed that the virus was a human/swine reassortant, with the H and N gene most related to human H3N2 viruses circulating in 2005. The remaining 6 genes were most closely related to H1N2 influenza viruses circulating in Danish swine. This virus had not previously been described in swine, mink or humans. PCRs assays specifically targeting the new reassortant were developed and used to screen influenza positive samples from humans and swine in Denmark with negative results. Thus, there was no evidence that this virus had spread to humans or was circulating in Danish pigs. In 2010 and 2011, influenza virus was again diagnosed in diseased mink in a few farms. The genetic typing showed that the virus was similar to the pandemic H1N1 virus circulating in humans and swine. The H3N2 virus was not detected in 2010 and 2011. Taken together, these findings indicate that mink is highly susceptible for influenza A virus of human and swine origin and may therefore act as a potential host/reservoir for influenza A viruses.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Section for Public sector service and commercial diagnostics, Division of Veterinary Diagnostics and Research, Virology, Division of Poultry, Fish and Fur Animals, Section of Fur Animal Diseases and Wildlife, Statens Serum Institut, Holstebro Veterinary Clinic
Pages: 153-156
Publication date: 2012

Overvågning af influenza i svin 2011

PCR diagnosis of PRRS virus in oral fluids from weaned Danish pigs

Introduction

Oral fluid testing has been suggested as an alternative diagnostic approach for surveillance of pathogens in swine herds3. In Denmark oral fluid has been used for detection of PCV22 and swine veterinarians are eager to use it for diagnosis of other pathogens. The aim of the present study was to evaluate the diagnostic performance of oral fluid testing for PRRSV by PCR under Danish conditions.

Materials and Methods

Five herds with PRRS positive nursery pigs were selected for sampling by convenience. Oral fluid and blood samples were collected from each of 10 pens in each of the 5 herds. Oral fluid was collected by providing 1 cotton rope in each selected pen for 30 minutes. Blood samples from 5 systematic randomly selected pigs in each pen were taken and the separated serum was pooled penwise. Different purification methods were tested in order to decrease the content of PCR inhibitors in the RNA extract of oral fluid. QIAamp Viral RNA Mini Kit (QIAGEN) was selected for purification of RNA from oral fluid and serum. Purified RNA was tested for PRRSV by real-time RT-PCR by a modified previously published assay1.

Overall agreement, diagnostic sensitivity and diagnostic specificity were calculated in order to evaluate the performance of oral fluid as test material in comparison with penwise pooled sera. PCR results from serum samples were considered as gold standard.

Results
The detection of PRRSV in oral fluid and pooled serum is shown in figure 1 and 100% agreement was observed at the herd level. Pen level agreement between oral fluid and pooled serum samples for detection of PRRSV in the 50 pens is displayed in table 1. Overall agreement was 68%. The diagnostic sensitivity of oral fluid testing was 0.75 (95% CI= 0.55-0.89) and the diagnostic specificity of oral fluid testing was 0.95 (95% CI= 0.77-1.0).

Figure 1. Herd level detection of PRRSV based on samples from 50 pens

Table 1. 2x2 table of PRRSV real-time RT-PCR results, when testing pooled serum samples and oral fluid samples from 50 pens

Conclusions and Discussion
Agreement between oral fluid and serum testing at herd and pen level was promising. The present results indicate that oral fluid testing for PRRSV at pen level has a high diagnostic specificity and a somewhat lower, but acceptable diagnostic sensitivity. These findings suggest that oral fluid testing using the real-time RT-PCR procedure established in this study is applicable for PRRS surveillance and diagnosis under Danish conditions.

General information
State: Published
Organisations: National Veterinary Institute, Division of Veterinary Diagnostics and Research, Section for Veterinary Diagnostics, Virology, Danish Agriculture and Food Council, University of Copenhagen
Contributors: Heiselberg, P. R., Hjulsager, C. K., Pedersen, K. S., Kristensen, C. S., Breum, S. Ø., Larsen, L. E.
Publication date: 2012
Peer-reviewed: Yes
Event: Abstract from 22nd International Pig Veterinary Society Congress, Jeju, Korea, Republic of.
Electronic versions:
IPVS_2012_prh.pdf
URLs:
Source: dtu
Source-ID: u::3730
Research output: Research - peer-review » Conference abstract for conference – Annual report year: 2012

Porcine Circovirus Diseases: A review of PMWS
This article is a review on post‐weaning multisystemic wasting syndrome (PMWS), the first described disease among the porcine circovirus diseases (PCVD). Post-weaning multisystemic wasting syndrome has, since its appearance in Canada in 1991, been seen in all major pig producing countries. To diagnose PMWS at herd level typical clinical appearance consisting of wasting and increased mortality must be combined with finding at autopsy of diseased pigs, where typical microscopic findings in the lymphatic tissue must be present. Post-weaning multisystemic wasting syndrome significantly increases the mortality and reduces the daily weight gain in weaner pig and/or in finishing pigs. Post-weaning multisystemic wasting syndrome can be transmitted by pig‐to‐pig contact and some studies point at airborne transmission as a possibility. Studies in Europe have shown several risk factors that either increase or decrease the risk for a pig herd to be affected by PMWS. At the pig level, studies have shown the importance of maternal immunity as protection for subsequent development of PMWS. To control PMWS, good production management and control of other diseases are crucial. Since 2004, commercial vaccines against Porcine Circo Virus type 2 have been coming on the market and many studies have shown great benefits of these to control PMWS. Today, sow vaccines as well as piglet vaccines are available in most countries. An extensive meta-analysis of many of the vaccines has shown a comparable good efficacy of the vaccines in significantly reducing mortality and increasing weight gain of the pigs.

General information
State: Published
Organisations: National Veterinary Institute, Division of Veterinary Diagnostics and Research, Virology, Danish Agriculture and Food Council
Contributors: Baekbo, P., Kristensen, C. S., Larsen, L. E.
Pages: 60-67
Publication date: 2012
Peer-reviewed: Yes

Publication information
Journal: Transboundary and Emerging Diseases
Volume: 59
Issue number: Supplement s1
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): Impact factor 3.504
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): Impact factor 3.585
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.29 SJR 1.305 SNIP 1.249
Web of Science (2015): Impact factor 2.714
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.23 SJR 1.048 SNIP 1.207
Web of Science (2014): Impact factor 2.944
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.33 SJR 0.975 SNIP 1.123
Web of Science (2013): Impact factor 3.116
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.04 SJR 0.847 SNIP 1.178
Web of Science (2012): Impact factor 2.096
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.05 SJR 0.939 SNIP 1.124
Web of Science (2011): Impact factor 1.809
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.761 SNIP 0.983
Web of Science (2010): Impact factor 2.448
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
Keywords: PCV2, PMWS, Pigs, Review, Genotypes
DOIs:
10.1111/j.1865-1682.2011.01288.x

Bibliographical note
Special Issue: Emerging And Re-Emerging Pig Viral Infections.
Source: dtu
Source-ID: n::oai:DTIC-ART:blackwell/335196447::15145
Real-time PCR testing for Porcine Circovirus Type 2 and Lawsonia intracellularis to assess diarrhoea status

Introduction Real-time PCR tests have been developed to detect and quantify Porcine Circovirus type 2 (PCV2) and Lawsonia intracellularis in pigs’ faeces. Pooling of individual faecal samples is often used to reduce the costs of diagnostic testing. The objective of this study was to determine the association between quantities of PCV2 and L. intracellularis in pooled faecal samples and diarrhoea in pigs. Materials and Methods Forty individual faecal samples were collected from grower (>10 weeks) pigs on five farms in Denmark. Each pig was described as having diarrhoea +/- . Eighteen individual “diarrhoea” and 18 “non-diarrhoea” samples were randomly selected from each farm. Six “diarrhoea” and six “non-diarrhoea” pooled samples were made by combining three individual “diarrhoea/non-diarrhoea” samples. Individual and pooled samples were tested using real-time PCR specific for PCV2 and L. intracellularis. The associations between diarrhoea (+/-) and pooled faecal PCV2 and L. intracellularis quantity were analysed using logistic regression (Stata/IC 11.1). Results Low quantities of L. intracellularis were detected in six non-diarrhoeic pigs. There was no association between PCV2 or L. intracellularis quantity in pooled faecal samples and diarrhoea (p>0.05). However, when moderate/massive categories for L. intracellularis were combined, there was a tendency toward significance (OR=4.9; 95%CI 0.9 26.0). Conclusions PCV2 was not associated with diarrhoea in pigs on the five farms studied. Our results suggest that the quantity of L. intracellularis in pooled faecal samples may reflect diarrhoea status, however further research in this area is required. Subclinically-affected pigs shed low quantities of L. intracellularis.

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Virology, Bacteriology & Pathology, Department of Primary Industries, Queensland , Pig Research Centre, University of Copenhagen
Publication date: 2012
Peer-reviewed: Yes
Event: Abstract from 4th European Symposium of Porcine Health Management, Bruges, Belgium.
Electronic versions:
ESPHMabstract2.doc
URLs:
Source: orbit
Source-ID: 317433

Spread of Hepatitis E virus from pig slurry to the water environment

Objectives: Spread of pig slurry as an organic fertilizer is commonly used in Danish agriculture. The slurry is spread untreated so pathogens able to survive in slurry tanks will be widely distributed in the environment. The objective of this study was to examine if hepatitis E virus (HEV), which is known to be excreted in faeces from pigs, will be transported through the soil and into the drainage system of a field due to precipitation or will be retained in the soil matrix. Water from the drainage system is not treated before it is discharged into larger water reservoirs (lake, fjords, streams), and hence could present a risk for virus transmission to wildlife and shellfish. We tested the presence of HEV in water drained from a test field where slurry from a Danish pig farm had been applied and in mussels from different regions in Denmark with fields in close proximity.

Methods: Slurry from a Danish pig farm was spread on a tile-drained field of loamy soil. Water that arrived at the drainage system located 1 m below surface was collected over a time period of 4 month. Samples were collected on a weekly basis and when water flow in the drainage system exceeded a certain threshold (an event). In addition, samples of water collected from wells located along the field and groundwater. Archived mussels from different regions in Denmark were included in the study. Virus was concentrated from water using Poly Ethylene Glycol precipitation and virus from the digestive tissue of the mussels was extracted sing proteinase K treatment. Subsequently, viral genomic RNA, from both water and mussels, was purified using the NucliSENS miniMAG system and detection and quantification of HEV and mengovirus (used as process control) were performed by real time RT-PCR.

Results: Water samples representing a total of 14 events were tested. HEV was detected in the first event following spread of pig slurry. In agreement with this, the weekly sample of this period also tested positive. HEV was not found in any of the subsequent water samples. Of the 70 blue mussel samples, that mainly originated from fjords, none tested positive.

Conclusion: HEV is regarded as a zoonotic virus with pigs as the primary reservoir. The pathway to humans and other mammals is unclear. Here we show that under Danish conditions, spread of pig slurry can cause viral contamination of water reservoirs, making HEV accessible to the population and wildlife. This indicates a possible route of HEV transmission from pigs to other reservoirs. We also show that retention in soil matrix is at a minimum as HEV was
detected at first rainfall after application of pig slurry. The viability of the viruses found in this study is still unclear since HEV cannot be cultivated in cells. We did not find any HEV positive mussel samples indicating that the release of HEV from fields is not a concern for shellfish production.

**General information**

State: Published
Organisations: National Veterinary Institute, Section for Virology, National Food Institute, Division of Food Microbiology, University of Copenhagen
Contributors: Krog, J. S., Forslund, A., Breum, S. Ø., Larsen, L. E., Schultz, A. C.
Number of pages: 2
Publication date: 2012
Peer-reviewed: Yes
Event: Abstract from 9th International Congress of Veterinary Virology, Madrid, Spain.
Electronic versions: prod2135736377645.Abstract_ESVV.pdf

**Bibliographical note**

Oral presentation.
Source: dtu
Source-ID: u::6594
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2012

**Surveillance for avian influenza viruses in wild birds in Denmark and Greenland**

Avian influenza (AI) is a disease of major threat to poultry production. Surveillance of AI in wild birds contributes to the control of AI. In Denmark (DK) and Greenland (GL), extensive surveillance of AI viruses in the wild bird population has been conducted. The surveillance aimed at detecting viruses of both high pathogenic AI (HPAI) subtypes H5 and H7, and low pathogenic AI (LPAI). Captured live wild birds and shot game birds were sampled by swabbing of the oropharyngeal and/or cloacal tracts, or swabs were collected from faecal droppings. In DK, most samples were collected in major staging areas for migratory waterfowl, whereas in GL, samples were collected in breeding areas. Samples from birds found dead at scattered locations across DK were sampled by oropharyngeal swabbing. 17530 wild birds from DK were tested as part of the surveillance during 2006-2010, of which 1614 were birds found dead. During 2007-2010, 2926 live wild birds from GL were tested. Swab samples were tested by RT-PCR and culturing. Positive samples were subtyped and the pathogenicity was determined by HA cleavage site sequencing. HPAI H5N1 was detected only during spring 2006, in 44 wild birds from DK. LPAI H5 and H7 subtypes were detected throughout the period together with several other LPAI subtypes. In GL, HPAI was not detected, but few samples were PCR positive for AI. The occurrence of AI subtypes in the wild bird population correlates with concurrent outbreaks of LPAI in Danish poultry, which may suggest virus transmission between these populations.

**General information**

State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Virology, Aarhus University, United States Department of Agriculture, University of Copenhagen
Publication date: 2012
Peer-reviewed: Yes
Event: Abstract from 8th International Symposium on Avian Influenza, London, United Kingdom.
URLs:
Source: orbit
Source-ID: 317426
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2012

**Surveillance for Avian Influenza Viruses in Wild Birds in Denmark and Greenland, 2007–10**

In Denmark and Greenland, extensive surveillance of avian influenza (AI) viruses in wild bird populations has been conducted from 2007 through 2010. In Denmark, the surveillance consisted of passive surveillance of wild birds found dead or sick across Denmark and active surveillance of apparently healthy live birds in waterfowl reservoirs and along migratory flyways, birds living in proximity to domestic poultry, and hunted game birds. Dead birds were sampled by oropharyngeal swabbing. Healthy live wild birds were captured with nets, traps, or by hand and were sampled by swabbing of the oropharyngeal and cloacal tracts, or swabs were collected from fresh fecal droppings. Hunted game birds were delivered to game-handling establishments, where each bird was sampled by oropharyngeal and cloacal swabbing. During the 2007–10 period, a total of 11,055 wild birds were sampled in Denmark, of which 396 were birds that were found dead. In Greenland, samples were collected mainly from fecal droppings in breeding areas. Samples from 3555 live and apparently healthy wild birds were tested. All swab samples were tested by pan-influenza reverse transcriptase–PCR (RT-PCR), and the positive samples were further tested by H5/H7 specific RT-PCRs. H5/H7-positive samples were subjected
to hemagglutination cleavage site sequencing for pathotyping. In addition, all RT-PCR–positive samples were subjected
to virus isolation, and the virus isolates were subsequently subtyped. In Denmark, low pathogenic (LP) H5 viruses were
detected throughout the period, in addition to a few LPAI H7 and several other subtypes. In Greenland, very few samples
were positive for AI. None of them were found to be of the H5 or H7 subtypes by RT-PCR. Isolation of these viruses in
eggs was unsuccessful; thus, they were not subtyped further. The findings did, however, demonstrate the presence of
LPAI viruses in Greenland. For several water bird species overwintering in North America and northwest Europe,
respectively, Greenland constitutes a common breeding area. This raises the possibility that viruses could be transmitted
to North America via Greenland and vice versa. In Denmark, the screenings for AI showed LPAI viruses to be naturally
occurring in the wild bird population, particularly in waterfowl. The occurrence of AI viruses in the wild bird population may
pose a risk for AI infections in Danish poultry.
Suspected zoonotic transmission of rotavirus group A in Danish adults

Group A rotaviruses infect humans and a variety of animals. In July 2006 a rare rotavirus strain with G8P[14] specificity was identified in the stool samples of two adult patients with diarrhea, who lived in the same geographical area in Denmark. Nucleotide sequences of the VP7, VP4, VP6, and NSP4 genes of the identified strains were identical. Phylogenetic analyses showed that both Danish G8P[14] strains clustered with rotaviruses of animal, mainly, bovine and caprine, origin. The high genetic relatedness to animal rotaviruses and the atypical epidemiological features suggest that these human G8P[14] strains were acquired through direct zoonotic transmission events.
Scopus rating (2017): CiteScore 1.88 SJR 1.128 SNIP 0.807
Web of Science (2017): Impact factor 2.044
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): Impact factor 2.075
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.29 SJR 1.349 SNIP 1.052
Web of Science (2015): Impact factor 2.515
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.19 SJR 1.305 SNIP 1.016
Web of Science (2014): Impact factor 2.535
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.57 SJR 1.337 SNIP 1.113
Web of Science (2013): Impact factor 2.491
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.69 SJR 1.437 SNIP 1.17
Web of Science (2012): Impact factor 2.867
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.71 SJR 1.326 SNIP 1.214
Web of Science (2011): Impact factor 2.843
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.066 SNIP 1.042
Web of Science (2010): Impact factor 2.257
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.065 SNIP 1.197
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.082 SNIP 1.031
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 0.958 SNIP 1.047
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.022 SNIP 1.218
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.862 SNIP 0.948
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.944 SNIP 1.176
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.901 SNIP 1.184
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.926 SNIP 1.088
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.853 SNIP 1.08
Undersøgelse af PCV2-status i to danske besætninger - to års opfølgning

General information
State: Published
Organisations: National Veterinary Institute, Division of Veterinary Diagnostics and Research, Section for Veterinary Diagnostics, Virology
Contributors: Kristensen, C. S., Larsen, L. E., Hjulsager, C. K.
Number of pages: 8
Publication date: 2012

Publication information
Publisher: Videncenter for Svineproduktion
Original language: Danish
(Meddelelse; No. 933).
URLs:
http://vsp.lf.dk/da-DK/Publikationer/Kilder/lu_medd/2012/933.aspx

Bibliographical note
http://vsp.lf.dk/da-DK/Publikationer/Kilder/lu_medd/2012/933.aspx
Source: dtu
Source-ID: u::3592
Research output: Research › Report – Annual report year: 2012

Virus kan påvises i spyt fra grise

General information
State: Published
Organisations: National Veterinary Institute, Division of Veterinary Diagnostics and Research, Section for Veterinary Diagnostics, Virology, Svinepraksis.dk, Danish Veterinary and Food Administration, Videncenter for Svineproduktion, Landbrug & Fødevarer, University of Copenhagen
Contributors: Heiselberg, P. R., Christensen, S., Hjulsager, C. K., Petersen, K. S., Stege, H., Nielsen, J. P., Larsen, L. E., Kristensen, C. S.
Publication date: 2012
Peer-reviewed: Unknown

Publication information
Journal: Hyologisk
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
URLs:
http://www.hyologisk.dk/artikel?id=70374
Source: dtu
Source-ID: u::3729
Within-day repeatability for absolute quantification of Lawsonia intracellularis bacteria in feces from growing pigs

Absolute quantification of Lawsonia intracellularis by real-time polymerase chain reaction (PCR) is now possible on a routine basis. Poor repeatability of quantification can result in disease status misclassification of individual pigs when a single fecal sample is obtained. The objective of the current study was to investigate overall variation within a day for fecal numbers of L. intracellularis bacteria determined by real-time PCR in growing pigs. From each of 30 pigs with an infection of L. intracellularis, 5 fecal samples were collected within 1 day. A total of 150 fecal samples were obtained and subjected to quantitative PCR (qPCR) testing. Mean fecal dry matter content was 14.3% (standard deviation = 4.5%). Two pigs (6.7%) alternated between being L. intracellularis qPCR positive and negative. For 28 pigs, the excreting levels of L. intracellularis were within the dynamic range of the qPCR assay at all sampling points. For these 28 pigs, the mean excretion level of L. intracellularis was 6.1 log10 bacteria/g feces (standard deviation = 1.2 log10 bacteria/g feces). The maximum observed difference between 2 fecal samples from the same pig was 1.1 log10 bacteria/g feces. The average standard deviation for individual pigs was 0.27 log10 bacteria/g feces. The average coefficient of variation within pigs was 0.04, ranging from 0.006 to 0.08. The results imply that absolute quantification of L. intracellularis by qPCR has acceptable repeatability within 1 day. However, a population-specific proportion of pigs alternating between positive and negative test results must be expected.

General information
State: Published
Organisations: Adaptive Immunology & Parasitology, National Veterinary Institute, Division of Veterinary Diagnostics and Research, Bacteriology & Pathology, Section for Veterinary Diagnostics, Virology, University of Copenhagen
Pages: 968-970
Publication date: 2012
Peer-reviewed: Yes

Publication information
Journal: Journal of Veterinary Diagnostic Investigation
Volume: 24
Issue number: 5
ISSN (Print): 1040-6387
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.21 SJR 0.621 SNIP 0.842
Web of Science (2017): Impact factor 1.219
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.27 SJR 0.642 SNIP 0.855
Web of Science (2016): Impact factor 0.925
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 1.44 SJR 0.695 SNIP 0.886
Web of Science (2015): Impact factor 1.196
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 1.36 SJR 0.792 SNIP 0.912
Web of Science (2014): Impact factor 1.353
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 1.41 SJR 0.712 SNIP 0.955
Web of Science (2013): Impact factor 1.232
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 1.37 SJR 0.748 SNIP 1.023
Web of Science (2012): Impact factor 1.181
ISI indexed (2012): ISI indexed yes
You can pool faecal samples from individual pigs to test for Porcine Circovirus Type 2 and Lawsonia intracellularis using real-time PCRs

Introduction Real-time PCR tests have been developed to detect and quantify Porcine Circovirus type 2 (PCV2) and Lawsonia intracellularis in pigs’ faeces. Pooling of individual faecal samples is often used to reduce the costs of diagnostic testing. The objective of this study was to evaluate any change in the test sensitivity of PCV2 and L. intracellularis real-time PCR when individual faecal samples were pooled. Materials and Methods Forty eight faecal samples were collected from the rectum of individual pigs (>10 weeks) from four farms. Faecal samples were classified as diarrhoea +/- based on subjective assessment of consistency. Three individual samples were combined to make 16 pooled samples (8 diarrhoea; 8 non-diarrhoea). Individual and pooled samples were tested using real-time PCR tests specific for PCV2 and L. intracellularis. A positive result in any of the three individual samples was deemed “group positive”. Changes in test sensitivity after combining the three individual samples were evaluated. Results The sensitivity and specificity of the pooled faecal samples for L. intracellularis were 86.4% and 100%, respectively. The sensitivity and specificity of the pooled faecal samples for PCV2 were 97% and 100%, respectively. Conclusions These preliminary results suggest that three individual faecal samples may be pooled for PCV2 or L. intracellularis testing using real-time PCR with minimal loss of sensitivity. Under the conditions of this study, the sensitivity of pooling was reduced when quantities of L. intracellularis or PCV2 in individual samples were low.
Detection and quantification of porcine circovirus type 2 (PCV2) and PCV2-antibodies in oral fluid from finisher pigs.

General information
Distribution of influenza A viruses of avian and swine origin and their sialic acid receptors in experimentally influenza infected pigs

**General information**
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, University of Copenhagen
Contributors: Trebbien, R., Larsen, L. E., Viuff, B. M.
Publication date: 2011

**Host publication information**
Title of host publication: 6th International Symposium on Emerging and Re-emerging Pig Diseases: Proceedings
URLs:
http://www.emerging2011.com/

**Bibliographical note**
Oral presentation.
Source: orbit
Source-ID: 284118
Research output: Research - peer-review › Conference abstract in proceedings – Annual report year: 2011

**Distribution of sialic acid receptors and influenza A viruses of avian and swine origin and in experimentally infected pigs**
Background: Pigs are considered susceptible to influenza A virus infections from different host origins because earlier studies have shown that they have receptors for both avian (sialic acid-alpha-2,3-terminal saccharides (SA-2,3)) and swine/human (SA-alpha-2,6) influenza viruses in the upper respiratory tract. Furthermore, experimental and natural infections in pigs have been reported with influenza A virus from avian and human sources. Methods: This study investigated the receptor distribution in the entire respiratory tract of pigs using specific lectins Maackia Amurensis (MAA) I, and II, and Sambucus Nigra (SNA). Furthermore, the predilection sites of swine influenza virus (SIV) subtypes H1N1 and H1N2 as well as avian influenza virus (AIV) subtype H4N6 were investigated in the respiratory tract of experimentally infected pigs using immunohistochemical methods. Results: SIV antigen was widely distributed in bronchi, but was also present in epithelial cells of the nose, trachea, bronchioles, and alveolar type I and II epithelial cells in severely affected animals. AIV was found in the lower respiratory tract, especially in alveolar type II epithelial cells and occasionally in bronchiorial epithelial cells. SA-alpha- 2,6 was the predominant receptor in all areas of the respiratory tract with an average of 80-100% lining at the epithelial cells. On the contrary, the SA-alpha-2,3 was not present (0%) at epithelial cells of nose, trachea, and most bronchi, but was found in small amounts in bronchioles, and in alveoli reaching an average of 20-40% at the epithelial cells. Interestingly, the receptor expression of both SA-alpha-2,3 and 2,6 was markedly diminished in influenza infected areas compared to non-infected areas. Conclusions: A difference in predilection sites between SIV and AIV virus was found, and this difference was in accordance with the distribution of the SA-alpha-2,6 and SA-alpha-2,3 receptor, respectively. The results indicated that the distribution of influenza A virus receptors in pigs are similar to that of humans and therefore challenge the theory that the pig acts as a mixing vessel between human and avian influenza viruses. Furthermore, it was shown that AIV prefers to infect alveolar type II epithelial cells in pigs. This corresponds with findings in humans emphasising the resemblance between the two species.

**General information**
State: Published
Does PCV2 reduce the impact of subsequent infection with Lawosnia intracellularis?

**General information**
State: Published
Organisations: National Veterinary Institute, Bacteriology & Pathology, Division of Veterinary Diagnostics and Research, Section for Veterinary Diagnostics, Adaptive Immunology & Parasitology, Sektion for Eksotiske Virussygdomme, Division of Virology, Virology
Number of pages: 103
Pages: P.022
Publication date: 2011

**Host publication information**
Title of host publication: 6th International Symposium on Emerging and Re-emerging Pig Diseases: Proceedings
Electronic versions:
Identification.pdf
URLs:
Source: orbit
Source-ID: 282945
Research output: Research - peer-review » Conference abstract in proceedings – Annual report year: 2011

Identification of an antigenically different porcine parovirus (PPV) isolate in Denmark

**General information**
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics, Chinese Academy of Agricultural Sciences, Intervet Schering-Plough Animal Health Pty Ltd.
Number of pages: 52
Publication date: 2011

**Host publication information**
Title of host publication: Proceedings of the 6th International Symposium on Emerging and Re-emerging Pig Diseases
Electronic versions:
Identification.pdf
URLs:
Source: orbit
Source-ID: 282038
Research output: Research - peer-review » Conference abstract in proceedings – Annual report year: 2011

Investigation of PCV2-status in Danish herds - One year longitudinal study

**General information**
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Virology, Danish Agriculture and Food Council
Contributors: Kristensen, C. S., Hjulsager, C. K., Larsen, L. E.
Number of pages: 104
Pages: P.023
Publication date: 2011

**Host publication information**
Title of host publication: 6th International Symposium on Emerging and Re-emerging Pig Diseases: Proceedings
Electronic versions:
int02.pdf
URLs:

Bibliographical note
Pandemic H1N1 2009 virus in Danish pigs: Diagnosis and lack of surveillance

In March-April 2009, a novel pandemic H1N1 virus (H1N1v) of likely swine origin emerged in the human population globally. The first case in pigs was reported from Canada in May 2009 and presently almost all countries with pig production have reported cases. The emergence of a new influenza subtype in swine with a genetic profile similar to older circulating strains implied a challenge for the veterinary diagnostic laboratories. We report the development, validation and implementation of a diagnostic strategy for specific diagnosis of H1N1v in pigs and the results of tests of pigs performed in Denmark. Routinely, detection of swine influenza virus in clinical specimens is performed by real-time reverse transcriptase PCR assays (rRT-PCR) targeting the M and the NP genes. Alignment of the probe and primer sequences to available H1N1v gene sequences in GeneBank revealed that these assays most likely would recognize the H1N1v virus and this was further confirmed in the laboratory by test of samples from pH1N1 infected humans. However, these assays could not discriminate between the typical circulating strains and the H1N1v subtype. For specific detection of the H1N1v subtype, an rRT-PCR assay targeting the HA gene developed at the Staten Serum Institute for diagnosis of H1N1v in humans was validated for use on pig specimens. In silico analysis showed that the probe and primers had 100% identity to published H1N1v strains and 80-95% identity to classical-swine H1N1 which do not circulate in Denmark. In contrast, there was only 60-70% identity to the subtypes circulating in Denmark (H1N1, H3N2, and avian-like H1N2) indicating that these subtypes would not be detected by this assay. The negative outcome of the test of 76 Danish swine influenza virus positive samples in the H1N1v assay confirmed that the assay was specific for H1N1v. Test of dilution series of cell culture adapted strains revealed a sensitivity of 1-2 TCID50/ML. All influenza positive samples from swine submitted to NVI in 2009 (81 out of 299 submissions) have been tested for H1N1v with negative results. In 2010 (until the 24rd. of June) samples from 34 submissions have been tested and 5 herds were found positive for H1N1v (4 in January and 1 in June). The number of submissions for influenza diagnosis of swine have dropped significantly in 2010 compared to 2009 probably because the producers want to avoid the constraints put on the herd in case of a positive H1N1v result. In combination with the fact that Denmark does not have any formal surveillance program for swine influenza in place, we have currently no overview of the number of H1N1v positive swine in Denmark. However, the diagnosis of a positive herd in June 2010, outside the human influenza season, may indicate an ongoing swine to swine transmission of H1N1v in Denmark.

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics, Statens Serum Institut
Publication date: 2011
Peer-reviewed: Yes
Keywords: Swine, H1N1v, Influenza, Diagnosis
Electronic versions: abstract.pdf

Bibliographical note
Oral presentation by Solvej Østergaard Breum.
Source: orbit
Source-ID: 282036
Research output: Research - peer-review › Conference abstract for proceedings – Annual report year: 2011

Pandemic H1N1 2009 virus in Norwegian pigs naïve to influenza A viruses

In March-April 2009, a novel pandemic influenza A (H1N1) virus (pH1N1-09v) emerged in the human population. The first case of pH1N1v infection in pigs was reported from Canada in May 2009 and presently almost all countries with pig production have reported cases. The emergence of a new influenza subtype in swine with a genetic profile similar to older circulating strains implied a challenge for the veterinary diagnostic laboratories. We report the development, validation and implementation of a diagnostic strategy for specific diagnosis of H1N1v in pigs and the results of tests of pigs performed in Denmark. Routinely, detection of swine influenza virus in clinical specimens is performed by real-time reverse transcriptase PCR assays (rRT-PCR) targeting the M and the NP genes. Alignment of the probe and primer sequences to available H1N1v gene sequences in GeneBank revealed that these assays most likely would recognize the H1N1v virus and this was further confirmed in the laboratory by test of samples from pH1N1 infected humans. However, these assays could not discriminate between the typical circulating strains and the H1N1v subtype. For specific detection of the H1N1v subtype, an rRT-PCR assay targeting the HA gene developed at the Staten Serum Institute for diagnosis of H1N1v in humans was validated for use on pig specimens. In silico analysis showed that the probe and primers had 100% identity to published H1N1v strains and 80-95% identity to classical-swine H1N1 which do not circulate in Denmark. In contrast, there was only 60-70% identity to the subtypes circulating in Denmark (H1N1, H3N2, and avian-like H1N2) indicating that these subtypes would not be detected by this assay. The negative outcome of the test of 76 Danish swine influenza virus positive samples in the H1N1v assay confirmed that the assay was specific for H1N1v. Test of dilution series of cell culture adapted strains revealed a sensitivity of 1-2 TCID50/ML. All influenza positive samples from swine submitted to NVI in 2009 (81 out of 299 submissions) have been tested for H1N1v with negative results. In 2010 (until the 24rd. of June) samples from 34 submissions have been tested and 5 herds were found positive for H1N1v (4 in January and 1 in June). The number of submissions for influenza diagnosis of swine have dropped significantly in 2010 compared to 2009 probably because the producers want to avoid the constraints put on the herd in case of a positive H1N1v result. In combination with the fact that Denmark does not have any formal surveillance program for swine influenza in place, we have currently no overview of the number of H1N1v positive swine in Denmark. However, the diagnosis of a positive herd in June 2010, outside the human influenza season, may indicate an ongoing swine to swine transmission of H1N1v in Denmark.

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics, Statens Serum Institut
Publication date: 2011
Peer-reviewed: Yes
Keywords: Swine, H1N1v, Influenza, Diagnosis
Electronic versions: abstract.pdf

Bibliographical note
Oral presentation by Solvej Østergaard Breum.
Source: orbit
Source-ID: 282036
Research output: Research - peer-review › Conference abstract for proceedings – Annual report year: 2011
Pandemic Influenza A H1N1v circulates in Danish pigs

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Virology, Statens Serum Institut
Number of pages: 73
Publication date: 2011

Host publication information
Title of host publication: 6th International Symposium on Emerging and Re-emerging Pig Diseases : Proceedings
Electronic versions: 98FA82d01.pdf
URLs:

Bibliographical note
Oral presentation.
Source: orbit
Source-ID: 282207
Research output: Research - peer-review › Conference abstract in proceedings – Annual report year: 2011

PRRSV outbreak with high mortality in northern part of Denmark
Porcine reproductive and respiratory syndrome virus (PRRSV) belongs to the Arteriviridae family and is the cause of significant respiratory and reproductive disease in swine worldwide. Strains of PRRSV are divided into two genotypes: type 1 and type 2, also referred to as EU and US type, respectively, due to their geographical origin. In Denmark the type 1 virus was first recognized in 1992, and since 1996 both types of PRRSV are widely spread. Approximately 50 % of the herds are seropositive for PRRSV antibodies against either or both types of PRRSV.

In November 2010, a severe case of PRRSV with high mortality rate in piglets occurred in Northern Jutland. PRRSV type 2 was detected by real-time RT-PCR in lung tissue from 10 days old piglets. The outbreak was treated by extensive vaccination with Ingelvac® PRRS MLV and strict management procedures. 6 weeks later, the mortality of liveborn piglets had dropped to normal levels. From week 6 until week 14 after the initial outbreak, up to 75 % of fetuses were born as mummified. PCV2 and PPV have not been detected in the fetuses. 15 weeks after the initial outbreak, the number of liveborn piglets and the mortality until weaning was back to normal. Total losses of piglets until weaning for the 15 week period were about 50 %. Losses in the nursery and finisher barn are still substantial 15 weeks after the initial outbreak. Sequencing of ORF5 and ORF7 confirmed the type of PRRSV to be type 2, and revealed distinct nucleotide differences compared to other Danish PRRSV type 2 sequences in the ORF5 region. We speculate that the virus causing this outbreak is more pathogenic than previously recognized Danish PRRSV type 2 strains.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Section for Public sector service and commercial diagnostics, Boehringer Ingelheim Danmark A/S
Screening of reservoirs for hepatitis E virus

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics, Sektion for Eksotiske Virussygdomme, Division of Virology
Number of pages: 359
Pages: P.239
Publication date: 2011

Host publication information
Title of host publication: 6th International Symposium on Emerging and Re-emerging Pig Diseases : Proceedings
Electronic versions:
Screening of reservoirs for hepatitis E virus.pdf
URLs:
Source: orbit
Source-ID: 282018
Research output: Research - peer-review » Conference abstract in proceedings – Annual report year: 2011

The aetiological role of porcine circovirus type 2 in acute diarrhoea of weaners in Danish herds

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Virology, Universidade Federal de Minas Gerais, University of Copenhagen
Number of pages: 131
Pages: P.050
Publication date: 2011

Host publication information
Title of host publication: 6th International Symposium on Emerging and Re-emerging Pig Diseases : Proceedings
Electronic versions:
998FA82d01.pdf
URLs:
Source: orbit
Source-ID: 282208
Research output: Research - peer-review » Conference abstract in proceedings – Annual report year: 2011

Undersøgelse af PCV2-status i to danske besætninger - et års opfølgning.

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics
Contributors: Kristensen, C. S., Larsen, L. E., Hjulsager, C. K.
Number of pages: 7
Publication date: 2011
A preliminary study of the association between Porcine Circovirus Type 2, Lawsonia intracellularis and diarrhoea in growing pigs

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Virology, Bacteriology & Pathology, Wagga Wagga Agricultural Institute, Pig Research Centre, University of Copenhagen
Number of pages: 284
Pages: O.252
Publication date: 2010

Host publication information
Title of host publication: Proceedings of the 21st International Pig Veterinary Society Congress
URLs:
http://www.ipvs2010.com/
Source: orbit
Source-ID: 282422
Research output: Research - peer-review › Conference abstract in proceedings – Annual report year: 2011

A preliminary study of the effects of treating diarrhoeic pigs with oxytetracycline on shedding of Porcine Circovirus Type 2 and Lawsonia intracellularis

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Virology, Bacteriology & Pathology, Wagga Wagga Agricultural Institute, Pig Research Centre, University of Copenhagen
Number of pages: 464
Pages: P.158
Publication date: 2010

Host publication information
Title of host publication: Proceedings of the 21st International Pig Veterinary Society Congress
URLs:
http://www.ipvs2010.com/
Source: orbit
Source-ID: 282425
Research output: Research - peer-review › Conference abstract in proceedings – Annual report year: 2011

Detection of myxoma viruses encoding a defective M135R gene from clinical cases of myxomatosis; possible implications for the role of the M135R protein as a virulence factor

Background: Myxoma virus is a member of the Poxviridae and causes disease in European rabbits. Laboratory confirmation of the clinical disease, which occurs in the autumn of most years in Denmark, has been achieved previously using antigen ELISA and electron microscopy. Results: An unusually large number of clinically suspected cases of myxomatosis were observed in Denmark during 2007. Myxoma virus DNA was detected, using a new real time PCR assay which targets the M029L gene, in over 70% of the clinical samples submitted for laboratory confirmation. Unexpectedly, further analysis revealed that a high proportion of these viral DNA preparations contained a frame-shift mutation within the M135R gene that has previously been identified as a virulence factor. This frame-shift mutation results in expression of a greatly truncated product. The same frame-shift mutation has also been found recently within an
avirulent strain of myxoma virus (6918). However, three other frame-shift mutations found in this strain (in the genes M009L, M036L and M148R) were not shared with the Danish viruses but a single nucleotide deletion in the M138R/M139R intergenic region was a common feature. Conclusions: It appears that expression of the full-length myxoma virus M135R protein is not required for virulence in rabbits. Hence, the frame-shift mutation in the M135R gene in the nonpathogenic 6918 virus strain is not sufficient to explain the attenuation of this myxoma virus but one/some of the other frame-shift mutations alone or in conjunction with one/some of the thirty two amino acid substitutions must also contribute. The real time PCR assay for myxoma virus is a useful diagnostic tool for laboratory confirmation of suspected cases of myxomatosis.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Virology, Division of Veterinary Diagnostics and Research
Pages: 7
Publication date: 2010
Peer-reviewed: Yes

Publication information
Journal: Virology Journal
Volume: 7
Issue number: 1
ISSN (Print): 1743-422X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
Scopus rating (2017): CiteScore 2.43 SJR 1.053 SNIP 0.848
Web of Science (2017): Impact factor 2.465
Web of Science (2017): Indexed yes
Scopus rating (2016): CiteScore 2.43 SJR 1.154 SNIP 0.903
Web of Science (2016): Impact factor 2.139
Scopus rating (2015): CiteScore 2.47 SJR 1.196 SNIP 0.945
Web of Science (2015): Impact factor 2.362
Scopus rating (2014): CiteScore 2.27 SJR 1.057 SNIP 0.94
Web of Science (2014): Impact factor 2.181
Web of Science (2014): Indexed yes
Scopus rating (2013): CiteScore 2.44 SJR 1.051 SNIP 0.989
Web of Science (2013): Impact factor 2.089
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
Scopus rating (2012): CiteScore 2.37 SJR 0.973 SNIP 0.877
Web of Science (2012): Impact factor 2.092
ISI indexed (2012): ISI indexed yes
Scopus rating (2011): CiteScore 2.65 SJR 1.06 SNIP 0.882
Web of Science (2011): Impact factor 2.343
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): Impact factor 2.546
Web of Science (2010): Indexed yes
Scopus rating (2009): SJR 1.004 SNIP 0.793
Scopus rating (2008): SJR 0.65 SNIP 0.572
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
Diagnosis of Porcine Circovirus Diseases (PCVDs) by serology and qPCR

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics, Intervet Schering-Plough Animal Health Pty Ltd.
Number of pages: 105
Pages: 0.067
Publication date: 2010

Host publication information
Title of host publication: Proceedings of the 21st International Pig Veterinary Society Congress
URLs:
http://www.ipvs2010.com/
Source: orbit
Source-ID: 282420
Research output: Research - peer-review › Conference abstract in proceedings – Annual report year: 2011

Dynamics of swine influenza infections in the farrowing unit of a Danish sow herd

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics, Danish Agriculture and Food Council, Odder Dyreklinik, Merial Norden A/S, University of Copenhagen
Number of pages: 80
Pages: 0.042
Publication date: 2010

Host publication information
Title of host publication: Proceedings of the 21st International Pig Veterinary Society Congress
Source: orbit
Source-ID: 282419
Research output: Research - peer-review › Conference abstract in proceedings – Annual report year: 2011

Forskningsprojekt om ny spædgrisediarre i Danmark

General information
State: Published
Organisations: Bacteriology & Pathology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Microbial Ecology, Virology, Section for Veterinary Diagnostics, Videnscenter for svineproduktion
Pages: 31
Publication date: 2010
Peer-reviewed: Yes

Publication information
Journal: Dansk Veterinærtidsskrift
Volume: 93
Issue number: 1
Hepatitis E virus is highly prevalent in the Danish pig population

The objective of this study was to examine the prevalence of Hepatitis E virus (HEV) in the Danish pig population. Faecal samples from 97 pigs, 1–5 months of age were analysed for HEV RNA by a new PriProET real time RT-PCR assay. In addition, serum samples from 71 sow herds were screened for the presence of anti-HEV IgG antibodies by ELISA. The genotype of the detected HEV positive samples was estimated based on the melting temperature obtained by the PriProET real time RT-PCR assay. The HEV prevalence of faecal samples was 55.0% and 49.5% for herds and animals, respectively. A HEV IgG prevalence of 91.5% was found for the sow herds which correspond to 73.2% of the sows. The PriProET assay indicated that all HEV positive samples belonged to genotype 3 or 4, which is consistent with the observation of genotype 3 as dominant in European pigs. This is the first study showing that HEV is highly prevalent in the Danish pig population. The abundant presence of HEV in Danish pigs and the known high similarity between HEV isolates from pigs and humans support previous reports indicating possible zoonotic transmission of HEV.
Incidence, Diversity, and Molecular Epidemiology of Sapoviruses in Swine across Europe

Porcine sapovirus is an enteric calicivirus in domestic pigs that belongs to the family Caliciviridae. Some porcine sapoviruses are genetically related to human caliciviruses, which has raised public health concerns over animal reservoirs and potential cross-species transmission of sapoviruses. We report on the incidence, genetic diversity and molecular epidemiology of sapoviruses detected in domestic pigs in a comprehensive study conducted in six European countries (Denmark, Finland, Hungary, Italy, Slovenia and Spain) between 2004 and 2007. A total of 1,050 swine fecal samples from 88 pig farms were collected and tested by reverse transcription-PCR for sapoviruses, and positive findings were confirmed by sequencing. Sapoviruses were detected in 80 (7.6%) samples collected on 39 (44.3%) farms and in every country. The highest prevalence was seen among piglets aged 2 to 8 weeks, and there was no significant difference in the proportion of sapovirus positive findings in healthy animals or animals with diarrhea in Spain and Denmark (the only countries where both healthy animals and animals with diarrhea were tested). On the basis of the RNA polymerase region, highly heterogeneous populations of viruses representing six differential genogroups (genogroups III, VI, VII, and VIII, including potential new genogroups IX and X) were identified, with a predominance of genogroup GIII (50.6%). Genogroup VIII, found in five of the six countries, had the highest degree of homology (up to 66% at the amino acid level) to human sapovirus strains. Sapoviruses are commonly circulating and endemic agents in swine herds throughout Europe. Highly
heterogenous and potential new genogroups of sapoviruses were found in pigs; however, no "human-like" sapoviruses were detected.
Infection dynamics of Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) in vaccinated and non-vaccinated pigs

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Virology, Danvet K/S, Odder Dyreklinik, University of Copenhagen
Number of pages: 207
Pages: O.173
Publication date: 2010

Host publication information
Title of host publication: Proceedings of the 21st International Pig Veterinary Society Congress
Source: orbit
Source-ID: 282421
Research output: Research - peer-review › Conference abstract in proceedings – Annual report year: 2011

Infectious risk factors for postweaning multisystemic wasting syndrome (PMWS) development

General information
State: Published
Organisations: National Veterinary Institute, Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, Section for Veterinary Diagnostics, Virology, CReSA - Centre for Animal Health Research, Danish Agriculture and Food Council
Number of pages: 327
Pages: P.021
Publication date: 2010
Lung pathology in slaughtered pigs from Norwegian herds naturally infected with pandemic Influenza A (H1N1) 2009 virus

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, National Veterinary Institute
Contributors: Valheim, M., Gamlem, H., Gjerset, B., Larsen, L. E., Lium, B.
Number of pages: 588
Pages: P.282
Publication date: 2010

Outbreak of Influenza A Virus in Farmed Mink (Neovison vison) in Denmark

General information
State: Published
Organisations: Section of Fur Animal Diseases and Wildlife, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, Virology, Section of Poultry Diseases, Holstebro Veterinary Clinic
Publication date: 2010
Peer-reviewed: Yes
Event: Abstract from FAO/OIE OFFLU Annual Technical Meeting, Rome, Italy.
Source: orbit
Source-ID: 272074
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2010

Quantitative assessment of Lawsonia intracellularis in feces by real-time PCR

General information
State: Published
Organisations: Bacteriology & Pathology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics, Virology, University of Copenhagen
Number of pages: 1,216
Publication date: 2010
Replication, Pathogenesis and Transmission of Pandemic (H1N1) 2009 Virus in Non-Immune Pigs

The declaration of the human influenza A pandemic (H1N1) 2009 (H1N1/09) raised important questions, including origin and host range [1,2]. Two of the three pandemics in the last century resulted in the spread of virus to pigs (H1N1, 1918; H3N2, 1968) with subsequent independent establishment and evolution within swine worldwide [3]. A key public and veterinary health consideration in the context of the evolving pandemic is whether the H1N1/09 virus could become established in pig populations [4]. We performed an infection and transmission study in pigs with A/California/07/09. In combination, clinical, pathological, modified influenza A matrix gene real time RT-PCR and viral genomic analyses have shown that infection results in the induction of clinical signs, viral pathogenesis restricted to the respiratory tract, infection dynamics consistent with endemic strains of influenza A in pigs, virus transmissibility between pigs and virus-host adaptation events. Our results demonstrate that extant H1N1/09 is fully capable of becoming established in global pig populations. We also show the roles of viral receptor specificity in both transmission and tissue tropism. Remarkably, following direct inoculation of pigs with virus quasispecies differing by amino acid substitutions in the haemagglutinin receptor-binding site, only virus with aspartic acid at position 225 (225D) was detected in nasal secretions of contact infected pigs. In contrast, in lower respiratory tract samples from directly inoculated pigs, with clearly demonstrable pulmonary pathology, there was apparent selection of a virus variant with glycine (225G). These findings provide potential clues to the existence and biological significance of viral receptor-binding variants with 225D and 225G during the 1918 pandemic [5].

General information
State: Published
Organisations: Innate Immunology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Virology, Animal Health and Veterinary Laboratories Agency, University of Marburg, Agence Francaise de Sécurite des Aliments, Merial S.A.S., Hipra, Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia, Central Veterinary Institute, Ghent University
Pages: 1 - 9
Publication date: 2010
Peer-reviewed: Yes

Publication information
Journal: P L o S One
Volume: 5
Issue number: 2
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): CiteScore 3.32 SJR 1.427 SNIP 1.136
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 3.54 SJR 1.559 SNIP 1.148
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 3.94 SJR 1.772 SNIP 1.153
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 4.15 SJR 1.982 SNIP 1.156
Web of Science (2012): Impact factor 3.73
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
Selection of method is crucial for the diagnosis of porcine circovirus type 2 associated reproductive failures

During a 2-month period a newly repopulated Danish pig herd experienced an increase in numbers of stillborn and mummies, caused by porcine circovirus type 2 (PCV2) associated reproductive failure. Based on recordings of data over time, the progression of the clinical outbreak was studied and the diagnostic value of different techniques was evaluated.

Foetal hearts (38 cases and 13 controls) were examined by immunohistochemistry (IHC) and real-time polymerase chain reaction (PCR) for the detection of PCV2; and total immunoglobulin G (IgG) was measured in pleura cavity fluid. PCV2 IHC was positive in 14/38 of the case foetuses, which were delivered during a 9 days period early in the outbreak. On the basis of the results obtained by IHC and PCR, the foetuses were divided into 3 categories: PCV2 negative; moderately positive (10(4) to 10(7) copies per 500ng DNA); and massively positive for PCV2 (>10(7) copies per 500ng DNA). All control- and IHC positive foetuses were included in the negative and massively positive groups, respectively. Ten case foetuses had elevated IgG levels, which did not correlate with the IHC or PCR results. Based on the clustering of the IHC positive foetuses, it is suggested that IHC only is suited for diagnosing acute stages of reproductive failure, whereas quantitative PCR can be used as a sensitive diagnostic method within a wider time span. It seems that IgG measurements are unpredictable as indication of intrauterine infection with PCV2. Copyright © 2010 Elsevier B.V. All rights reserved.
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): Impact factor 2.524
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): Impact factor 2.628
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.56 SJR 1.413 SNIP 1.21
Web of Science (2015): Impact factor 2.564
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.54 SJR 1.291 SNIP 1.256
Web of Science (2014): Impact factor 2.511
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 3 SJR 1.459 SNIP 1.471
Web of Science (2013): Impact factor 2.726
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.18 SJR 1.441 SNIP 1.569
Web of Science (2012): Impact factor 3.127
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.27 SJR 1.56 SNIP 1.729
Web of Science (2011): Impact factor 3.327
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): Impact factor 3.256
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
Serological response and influence on virus load in pigs vaccinated with Porcilis PCV

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Virology, Intervet Schering-Plough Animal Health Pty Ltd., OE-Vet, Danvet K/S
Number of pages: 360
Pages: P.054
Publication date: 2010

Host publication information
Title of host publication: Proceedings of the 21st International Pig Veterinary Society Congress
URLs: http://www.ipvs2010.com/
Source: orbit
Source-ID: 258176
Research output: Research - peer-review > Journal article – Annual report year: 2010

Strategies for subtyping influenza viruses circulating in the Danish pig population
Influenza viruses are endemic in the Danish pig population and the dominant circulating subtypes are H1N1, a Danish H1N2 reassortant, and H3N2. Here we present our current and future strategies for influenza virus subtyping. For diagnostic and surveillance of influenza subtypes circulating in the Danish pig population functional and rapid subtyping assays are required. The conventional RT-PCR influenza subtyping assays developed by Chiapponi et al. (2003) have been implemented and used for typing of influenza viruses found positive in a pan influenza A real time RT-PCR assay. The H1 and N1 assays were specific when applied on Danish influenza positive samples, whereas the N2 assay consistently showed several unspecific PCR products. A subset of positive influenza samples detected by the real time RT-PCR screening assay could not be subtyped using these assays. Therefore, new influenza subtyping assays based on RT-PCR and subsequent sequencing were implemented for the four subtypes H1, H3, N1, and N2. The assays were based on primer sets published by the WHO, but slightly modified for improved detection of Danish subtype variants. Sequencing of circulating influenza viruses is beneficial since it provides information about the genetic drift of influenza in the Danish pig population. Finally, we will present preliminary results of the performance of new real time RT-PCR assays for rapid subtyping of the most common subtypes circulating in Danish pigs. These real time RT-PCR assays would provide a simpler and faster tool for routine diagnostic influenza subtyping.

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics
Contributors: Breum, S. Ø., Hjulsager, C. K., Trebbien, R., Larsen, L. E.
Pages: P-033
Publication date: 2010

Host publication information
Title of host publication: The International Symposium on Neglected Influenza Viruses: Final Programme & Abstracts
Volume: Poster Presentations
Svineinfluenza – status og afklaring af nomenklatur

**General information**
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics
Contributors: Larsen, L. E., Hjulsager, C. K.
Publication date: 2010
Peer-reviewed: Yes

**Publication information**
Journal: Dansk Veterinærtidsskrift
Volume: 93
Issue number: 10
ISSN (Print): 1600-2032
Ratings:
BFI (2008): BFI-level 1
Web of Science (2004): Indexed yes
Original language: Danish
Source: orbit
Source-ID: 265784

Vaccination med Porcilis PCV i to danske svinebesætninger: Vaccination gav et ensartet serologisk respons

In two pig farms with clinical symptoms of PCVD and circulation of PCV2, vaccination was instituted with 2 ml of Porcilis PCV given once at around 4 (3-5) weeks of age. Vaccinations resulted in a uniform serological response. In one farm, where vaccinated pigs were reared separated from non-vaccinated from weaning through to slaughter, the viraemia was prevented. In the other farm viraemia was reduced with at least 2 log(10) units, even though pigs were housed in the same pen as non-vaccinated and viraemic pigs. In this herd a statistically significant (+ 39 g) average daily weight gain was accomplished in vaccinated pigs compared to non-vaccinated during the period 8-16 weeks after weaning. It was concluded that vaccination with Porcilis PCV reduced the virus load in infected pigs, and vaccination had a positive impact on daily weight gain.

**General information**
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Virology, Intervet Schering-Plough Animal Health Pty Ltd., OE-Vet, Danvet K/S
Pages: 24-28
Publication date: 2010
Peer-reviewed: Yes

**Publication information**
Journal: Dansk Veterinærtidsskrift
Volume: 93
Issue number: 5
ISSN (Print): 0106-6854
Ratings:
BFI (2008): BFI-level 1
BFI (2004): BFI-level 1
Web of Science (2004): Indexed yes
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 (2012): ISI indexed no
ISI indexed (2013): ISI indexed no
Endemic Hepatitis E in two Nordic Countries
Antibodies against hepatitis E virus (anti-HEV) were found in 248 Swedish and Danish patients between 1993 and 2007. Most patients were symptomatic and tested for anti-HEV due to travel abroad. Among patients with known country of infection, most were infected in Asia, mainly on the Indian subcontinent. However, 29 patients were infected in Europe, nine of these had HEV IgM and/or HEV RNA in serum. In sera from 65 of 141 tested patients HEV RNA could be detected, and 63 strains could be typed by limited sequencing within ORF2. HEV RNA was found in sera from 71% of the patients with HEV IgM and IgG and in 18% of the patients with only detectable HEV IgG. It was also found up to three weeks after the onset of disease in 67% of the patients with known date of onset. Patients infected in Europe were infected by genotype 3, and were older than those infected by genotype 1 (mean age 55.3 vs 30 years, p

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics
Pages: 20-28
Publication date: 2009
Peer-reviewed: Yes

Publication information
Journal: Eurosurveillance (Online Edition)
Volume: 14
Issue number: 19
ISSN (Print): 1025-496X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 5.09 SJR 3.727 SNIP 2.087
Web of Science (2017): Impact factor 7.127
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.72 SJR 4.072 SNIP 2.311
Web of Science (2016): Impact factor 7.202
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 2.69 SJR 3.11 SNIP 1.864
Web of Science (2015): Impact factor 5.983
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 2.83 SJR 3.15 SNIP 1.75
Web of Science (2014): Impact factor 5.722
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.62 SJR 2.673 SNIP 1.766
Web of Science (2013): Impact factor 4.659
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 3.02 SJR 2.837 SNIP 2.262
Web of Science (2012): Impact factor 5.491
ISI indexed (2012): ISI indexed no
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 3.27 SJR 2.678 SNIP 2.5
ISI indexed (2011): ISI indexed no
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.831 SNIP 15.968
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.704 SNIP 4.554
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.461 SNIP 1.037
Scopus rating (2007): SJR 0.411 SNIP 0.185
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.384
Scopus rating (2005): SJR 0.78
Scopus rating (2004): SJR 0.457
Scopus rating (2003): SJR 0.309
Scopus rating (2002): SJR 0.231
Original language: English
Electronic versions:
Euros.pdf
URLs:
http://www.eurosurveillance.org/ViewArticle.aspx?ArticleId=19211
Source: orbit
Source-ID: 249535
Research output: Research - peer-review › Journal article – Annual report year: 2009

**H1N1 Influenza A hos mennesker og svin**

**General information**
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Larsen, L. E.
Pages: 80
Publication date: 2009
Peer-reviewed: Unknown

**Publication information**
Journal: Hyologisk
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: orbit
Source-ID: 252304
Research output: Communication › Journal article – Annual report year: 2009

**HEPATITIS E VIRUS IS PREVALENT IN THE DANISH PIG POPULATION**

**General information**
State: Published
Induction of porcine post-weaning multisystemic wasting syndrome (PMWS) in pigs from PMWS unaffected herds following mingling with pigs from PMWS-affected herds

In this paper we present the results from two experimental studies (I and II) investigating whether post-weaning multisystemic wasting syndrome (PMWS) can be induced in pigs from PMWS unaffected herds by mingling with pigs from PMWS-affected herds and to observe whether transportation and/or mingling of healthy pigs from unaffected herds could induce PMWS. The studies comprised pigs from 12 different herds. Eight herds had PMWS while four were unaffected. All 12 herds were found to be infected with PCV2. Pigs from PMWS-affected herds were mingled with pigs from unaffected herds in four separate compartments in both study I and study II. In addition, in study II, four groups of pigs from unaffected herds were included. Two groups with pigs transported and mingled from unaffected herds and two groups with pigs which were only transported. The PMWS diagnoses on the individual pigs were based on lymphoid depletion, histiocytic proliferation and the presence of giant cells or inclusion bodies together with the demonstration of PCV2 in lymphoid tissue. Healthy pigs, in both studies, developed PMWS 4–5 weeks after mingling with pigs clinically affected with PMWS. None of the pigs from unaffected herds which had no contact with pigs from PMWS-affected herds developed clinical signs of PMWS. Transportation and mingling of pigs from PMWS unaffected herds in combination or alone was insufficient to provoke PMWS.

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Sektion for Eksotiske Virussygdommne, Division of Virology, Division of Microbiology and Risk Assessment, National Food Institute, Section for Veterinary Epidemiology and public sector consultancy, Virology, Danish Pig Production
Pages: 244-250
Publication date: 2009
Peer-reviewed: Yes

Publication information
Journal: Veterinary Microbiology
Volume: 138
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): Impact factor 2.524
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): Impact factor 2.628
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.56 SJR 1.413 SNIP 1.21
Web of Science (2015): Impact factor 2.564
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.54 SJR 1.291 SNIP 1.256
Infection, excretion and seroconversion dynamics of porcine circovirus type 2 (PCV2) in pigs from post-weaning multisystemic wasting syndrome (PMWS) affected farms in Spain and Denmark

Longitudinal case-control studies were performed in post-weaning multisystemic wasting syndrome (PMWS) affected farms from Denmark and Spain using similar designs. Fourteen independent batches of 100-154 pigs per batch were
monitored from birth to PMWS outbreak occurrence. Pigs displaying PMWS-like signs and matched healthy cohorts were euthanized during the clinical outbreak. PMWS was diagnosed according to internationally accepted criteria and pigs were classified as: (i) PMWS cases, (ii) wasted non-PMWS cases and (iii) healthy pigs. Porcine circovirus type 2 (PCV2) quantitative PCR (qPCR) and serology techniques were applied to analyse longitudinally collected sera and/or nasal and rectal swabs. Results showed that PCV2 load increased in parallel to waning maternal antibody levels, reaching the maximum viral load concurrent with development of clinical signs. PMWS affected pigs had higher PCV2 prevalence and/or viral load than healthy pigs in all collected samples at necropsy (p < 0.0001-0.05) and even in sera and nasal swabs at the sampling prior to PMWS outbreak (p < 0.01-0.05). Danish farms had a higher PCV2 prevalence in young piglets as well as an earlier PMWS presentation compared to Spanish farms. PMWS diagnoses were confirmed by laboratory tests in only half of pigs clinically suspected to suffer from PMWS. Positive and significant correlations were found among PCV2 viral loads present in sera, nasal swabs, rectal swabs and lymphoid tissues (R = 0.289-0.827, p < 0.0001-0.01), which indicates that nasal and rectal swabs were suitable indicators of PCV2 excretion. Sensitivity and/or specificity values observed from both tests used separately or combined suggested that qPCR and/or serology tests are not apparently able to substitute histopathology plus detection of PCV2 in tissues for the individual PMWS diagnosis within PMWS affected farms. However, qPCR appears to be a potential reliable technique to diagnose PMWS on a population basis.

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Epidemiology and public sector consultancy, Sektion for Eksotiske Virussygdomme, Division of Virology, Virology
Pages: 272-282
Publication date: 2009
Peer-reviewed: Yes

Publication information
Journal: Veterinary Microbiology
Volume: 135
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): Impact factor 2.524
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): Impact factor 2.628
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.56 SJR 1.413 SNIP 1.21
Web of Science (2015): Impact factor 2.564
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.54 SJR 1.291 SNIP 1.256
Web of Science (2014): Impact factor 2.511
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 3 SJR 1.459 SNIP 1.471
Web of Science (2013): Impact factor 2.726
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.18 SJR 1.441 SNIP 1.569
Web of Science (2012): Impact factor 3.127
ISI indexed (2012): ISI indexed yes
Influenza A (H1N1) Infection in pigs

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Pages: 760-761
Publication date: 2009
Peer-reviewed: Yes

Publication information
Journal: Veterinary Record
Volume: 164
Issue number: 24
ISSN (Print): 0042-4900
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 0.39 SJR 0.464 SNIP 0.858
Web of Science (2017): Impact factor 2.05
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 0.3 SJR 0.482 SNIP 0.745
Web of Science (2016): Impact factor 1.737
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 0.39 SJR 0.521 SNIP 0.796
Web of Science (2015): Impact factor 1.741
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 0.41 SJR 0.489 SNIP 0.844
Web of Science (2014): Impact factor 1.493
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 0.5 SJR 0.506 SNIP 0.821
Web of Science (2013): Impact factor 1.633
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 0.52 SJR 0.505 SNIP 0.878
Web of Science (2012): Impact factor 1.803
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 0.62 SJR 0.569 SNIP 0.903
Web of Science (2011): Impact factor 1.248
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.576 SNIP 0.837
Web of Science (2010): Impact factor 1.482
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.64 SNIP 0.994
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 0.554 SNIP 0.842
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 0.499 SNIP 0.808
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.645 SNIP 0.94
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.585 SNIP 0.911
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.619 SNIP 0.944
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.56 SNIP 0.94
Web of Science (2003): Indexed yes
Influenzavirus hos svin

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Dansk Veterinærtidsskrift
Contributors: Dalsgård, A., Larsen, L. E.
Pages: 6-9
Publication date: 2009
Peer-reviewed: Unknown

Publication information
Journal: Dansk Veterinærtidsskrift
Issue number: 11
ISSN (Print): 1600-2032
Ratings:
BFI (2008): BFI-level 1
Web of Science (2004): Indexed yes
Original language: Danish
Source: orbit
Source-ID: 243397
Research output: Communication › Journal article – Annual report year: 2009

Inter-laboratory and inter-assay comparison on two real-time PCR techniques for quantification of PCV2 nucleic acid extracted from field samples

Several real-time PCR assays for quantification of PCV2 DNA (qPCR) have been described in the literature, and different in-house assays are being used by laboratories around the world. A general threshold of 10⁵ copies of PCV2 per millilitre serum for postweaning multisystemic wasting syndrome (PMWS) diagnosis has been suggested. However, neither inter-laboratory nor inter-assay comparisons have been published so far. In the present study two different qPCR probe assays Used routinely in two laboratories were compared on DNA extracted from serum, nasal and rectal swabs. Results showed a significant linear association between the assays (p <0.0001) and a systematic difference of 1.4 log(10) copies of PCV2 per millilitre of sample (p <0.0001). This difference indicated that the assay from laboratory 1 yielded a higher output than the one from laboratory 2. Results also showed that there was no linear association between the amount of PCV2 DNA and the amount of total DNA, neither in nasal (p = 0.86) nor in rectal (p=0.78) swabs, suggesting that normalizing of PCV2 DNA load in swab samples to total DNA concentration is not suitable. The present exploratory study highlights the need for the performance of ring trials on qPCV2 protocols between laboratories. Meanwhile, the proposed thresholds for PMWS diagnosis should only be considered reliable for each particular laboratory and each particular assay.

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Epidemiology and public sector consultancy, Virology
Pages: 172-178
Publication date: 2009
Peer-reviewed: Yes

Publication information
Journal: Veterinary Microbiology
Volume: 133
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): Impact factor 2.524
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): Impact factor 2.628
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.56 SJR 1.413 SNIP 1.21
Web of Science (2015): Impact factor 2.564
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.54 SJR 1.291 SNIP 1.256
Web of Science (2014): Impact factor 2.511
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 3 SJR 1.459 SNIP 1.471
Web of Science (2013): Impact factor 2.726
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.18 SJR 1.441 SNIP 1.569
Web of Science (2012): Impact factor 3.127
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.27 SJR 1.56 SNIP 1.729
Web of Science (2011): Impact factor 3.327
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): Impact factor 3.256
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
Keywords: Postweaning multisystemic wasting syndrome (PMWS), Inter-laboratory comparison, Porcine circovirus type 2 (PCV2), Quantitative real-time PCR
DOIs: 10.1016/j.vetmic.2008.06.014
Source: orbit
Source-ID: 237535
Research output: Research - peer-review › Journal article – Annual report year: 2009

Ny mulighed for at undersøge svinediarre

General information
State: Published
Organisations: Bacteriology & Pathology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics, Virology
Pages: 30
Publication date: 2009
Peer-reviewed: No

Publication information
Journal: Dansk Veterinærtidsskrift
Volume: 92
Issue number: 14
ISSN (Print): 1600-2032
Ratings:
BFI (2008): BFI-level 1
Web of Science (2004): Indexed yes
Original language: Danish
Source: orbit
Source-ID: 247157
Research output: Research › Journal article – Annual report year: 2009

PCV2 dynamik

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Virology, Dansk Svineproduktion, CReSA - Centre for Animal Health Research
Publication date: 2009
Peer-reviewed: No

Publication information
Journal: Dansk Svineproduktion
Issue number: 835
Original language: English
Source: orbit
Source-ID: 254888
Research output: Research › Journal article – Annual report year: 2009
Phylogenetic Analysis of PRRSV from Danish Pigs

Introduction and Objectives Porcine reproductive and respiratory syndrome virus (PRRSV) is a single-stranded RNA virus belonging to the Arteriviridae family. It is the causative agent of significant respiratory and reproductive disease in swine worldwide. The virus is a recently emerged pathogen, being first identified as a cause of clinical disease in 1991. The disease spread simultaneously in North America and Europe to gain global residence in a short time-span. Two genotypes of PRRSV are currently recognized due to profound genomic and antigenic differences: PRRSV EU type and PRRSV US type, named from their geographic origin of identification. Great diversity within the two genotypes exists, and further division of PRRSV EU type into at least 3 subtypes has been suggested (Stadejek et al. 2006, 2008). In Denmark PRRSV EU type was first identified in 1992 and a few years later the US type also was recognized. According to serologic testing, both types are prevalent in the Danish pig population. However, the genetic drift of the virus during the past 10 years has not been determined. The objective of this study was to examine the genetic diversity and evolution of PRRSV in Danish pigs by phylogenetic analysis, in order to assess the applicability of vaccines currently used to control PRRSV infection in Danish pig herds. Materials and methods Lung tissue from samples submitted to the National Veterinary Institute during 2003-2008 for PRRSV diagnosis were screened for PRRSV by real-time RT-PCR, essentially as described by Egli et al. 2001, on RNA extracted with RNeasy Mini Kit (QIAGEN). Complete open reading frames (ORF) ORF5 and ORF7 were PCR amplified as described (Oleksiewicz et al. 1998) and sequenced. Sequences were aligned and Neighbour-Joining trees were constructed with ClustalX. Trees were visualized with NJ-plot software. Genbank entries of Danish PRRSV sequences from the 1990'ties were included in the phylogenetic analysis. Translated sequences were aligned with current vaccine isolates. Results Both PRRSV EU and US type viruses were isolated from material submitted from Danish pigs in the period 2003 to 2008. Sequences were obtained from 14 viruses isolated from different herds. There was substantial sequence diversity within both types of viruses. All Danish PRRSV type EU viruses grouped with subtype EU1 viruses. Amino acid alignments of translated sequences showed that the protein sequences were highly conserved and match the vaccine strains without differences in predicted epitope regions of ORF5 and ORF7 proteins. Discussion and conclusions PRRSV of both EU and US types currently are co-circulating in the Danish pig population. The viruses are diverse within both groups with a slightly higher degree of diversity within the EU type group of viruses. However, for both types, sequences match the corresponding vaccine strains. Importantly, all viruses of the EU type group with subtype EU1 viruses. Subtype EU1 contains viruses from Asia and Europe, whereas the other subtypes represent viruses from East Europe only (Stadejek et al. 2006). Introduction of new subtype viruses or drift within the present viruses could potentially affect control of PRRSV infection. Diagnostic procedures could be impaired if mutations were in primer binding sites or if they caused changes in antigenicity of viruses. Antigenic differences between EU subtypes have been demonstrated (Stadejek et al. 2008). PRRSV is a very diverse virus with a high mutation rate. It is therefore extremely important to continuously monitor and sequence the virus. The present data suggests, that the PRRSV vaccines used for the moment are adequate for control of PRRSV infection in the Danish pig population. References 1.Egli et al. 2001 J.Vir.Methods 98:63-75. 2.Oleksiewicz et al. 1998, Vet.Microbiol. 64:7-22. 3.Stadejek et al. 2006, J.Gen.Vir. 87:1835-41. 4.Stadejek et al. 2008, Arch.Virol. 153:1479-88.
Pig major acute-phase protein and haptoglobin serum concentrations correlate with PCV2 viremia and the clinical course of postweaning multisystemic wasting syndrome

The aim of the present longitudinal study was to assess the evolution of two acute phase proteins (APPs), pig-major acute phase protein (pig-MAP) and haptoglobin (HPT), in serum from pigs that developed postweaning multisystemic wasting syndrome (PMWS) in comparison to healthy and wasted non-PMWS affected pigs. In addition, evidence of infection with other pathogens and its relation with variations in APP's concentrations was also assessed. Fourteen independent batches of 100 to 154 pigs were monitored from birth to PMWS outbreak occurrence in 11 PMWS affected farms. Pigs displaying PMWS-like signs and age-matched healthy controls were euthanized during the clinical outbreak. PMWS was diagnosed according to internationally accepted criteria and pigs were classified as: i) PMWS cases, ii) wasted non-PMWS cases and iii) healthy pigs. At the moment of PMWS occurrence, pig-MAP and HPT concentration in PMWS affected pigs were higher than in healthy ones (p>0.001). No differences in APPs serum concentrations between subclinically PCV2 infected pigs and healthy non-PCV2 infected pigs (based on quantitative PCR on serum results) were detected. Results showed a significant correlation between PCV2 loads and both pig-MAP (R=0.487 to 0.602, p>0.001) and HPT (R=0.326 to 0.550, p>0.05 to 0.0001) concentrations in serum of PMWS affected pigs, indicating that the acute phase response in PMWS affected pigs occurred concomitantly to PCV2 viremia. No other pathogen, apart from PCV2, was consistently related with variations in APP's concentrations. A ROC analysis, made to determine the capacity of discrimination of both APPs between PMWS affected and non-affected pigs, showed higher sensitivity and specificity values using pig-MAP compared to HPT. These results suggest that pig-MAP might be a better indicator of PMWS status than HPT. Moreover, the fact that APR occurred some days before the starting of clinical signs suggests that APPs could provide valuable prognostic information for PMWS development.

General information
State: Published
Organisations: Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics, Risø National Laboratory for Sustainable Energy, Virology, CReSA - Centre for Animal Health Research
Pages: 53-61
Publication date: 2009
Peer-reviewed: Yes

Publication information
Journal: Veterinary Microbiology
Volume: 138
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): Impact factor 2.524
  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): Impact factor 2.628
  Web of Science (2016): Indexed yes
  BFI (2015): BFI-level 2
  Scopus rating (2015): CiteScore 2.56 SJR 1.413 SNIP 1.21
  Web of Science (2015): Impact factor 2.564
  Web of Science (2015): Indexed yes
  BFI (2014): BFI-level 2
  Scopus rating (2014): CiteScore 2.54 SJR 1.291 SNIP 1.256
  Web of Science (2014): Impact factor 2.511
  Web of Science (2014): Indexed yes
  BFI (2013): BFI-level 2
  Scopus rating (2013): CiteScore 3 SJR 1.459 SNIP 1.471
  Web of Science (2013): Impact factor 2.726
  ISI indexed (2013): ISI indexed yes
Respiratory disease in calves: Microbiological investigations on trans-tracheally aspirated bronchoalveolar fluid and acute phase protein response

General information
State: Published
Organisations: Bacteriology & Pathology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Virology, Innate Immunology, Technical University of Denmark
Contributors: Angen, Ø., Thomsen, J., Larsen, L. E., Larsen, J., Kokotovic, B., Heegaard, P. M. H., Enemark, J. M. D.
Pages: 165-171
Publication date: 2009
Peer-reviewed: Yes
Transmission of different variants of PCV2 and viral dynamics in a research facility with pigs mingled from PMWS-affected herds and non-affected herds

Post-weaning Multisystemic Wasting Syndrome (PMWS) has been identified in most swine-producing countries worldwide. The disease has resulted in significant health challenges and economic damage to the swine industry. The aim of this study was to determine horizontal transmission of porcine circovirus type 2 (PCV2) and to examine viral dynamics in pigs in a controlled PMWS transmission study. In the study pigs from PMWS-affected herds and non-affected herds were permitted to have close contact (same pen), nose-to-nose contact (to pigs in neighbouring pens) or no physical contact (pen across the aisle and pens in other compartments). By DNA sequence analysis, eight variants of genotype PCV-2b were identified in the research facility. From the spread of these PCV2-variants it was concluded that PCV2 primarily infects through close contact and nose-to-nose contact. PCV2 genome sequences were obtained from selected pigs at arrival to the research facility and again when the same pigs developed PMWS. This analysis showed that pigs from PMWS-affected herds developed PMWS caused by the same variant of PCV2 as they carried when entering the research facility. In contrast, pigs from non-affected herds developed PMWS with PCV2-variants identified in pigs from PMWS-affected herds. This was probably connected to at least 103 higher mean serum titer of PCV2 in pigs from PMWS-affected herds as compared to pigs from non-affected herds at the beginning of the transmission study. The study further showed that pigs able to control the PCV2 infection, as measured by the PCV2-titer in serum, recovered clinically (pigs from PMWS-affected herds) or stayed healthy (pigs from non-affected herds). Likewise, pigs with a PCV2 titer below 5 10^8 copies/ml serum during the study period had a chance of recover from the PCV2 infection whereas pigs with PCV2 titers above 5 10^8 copies/ml serum at any time point generally died from PMWS.

General information
State: Published
Organisations: Microbial Ecology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics, Virology, Danish Pig Production
Pages: 219-226
Publication date: 2009
Peer-reviewed: Yes

Publication information
Journal: Veterinary Microbiology
Volume: 139
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): Impact factor 2.524
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): Impact factor 2.628
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.56 SJR 1.413 SNIP 1.21
Web of Science (2015): Impact factor 2.564
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.54 SJR 1.291 SNIP 1.215
Web of Science (2014): Impact factor 2.511
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 3 SJR 1.459 SNIP 1.471
Web of Science (2013): Impact factor 2.726
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.18 SJR 1.441 SNIP 1.569
Web of Science (2012): Impact factor 3.127
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.27 SJR 1.56 SNIP 1.729
Web of Science (2011): Impact factor 3.327
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): Impact factor 3.256
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
Vaccination af slagtekalve mod BRSV: Et feldforsøg i 16 danske slagtekalvebesætninger i perioden 2006 - 2008

Antibody titers against swine influenza subtypes determined by the hemagglutination inhibition test are highly dependent on the strain

Årsager til luftvejsinfektioner hos kalve
Årsager til luftvejsinfektioner hos kalve

**General information**
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, AgroTech AS, Dansk Kvæg
Contributors: Sloth, K. H., Fisker, I., Larsen, L. E.
Pages: 1 - 5
Publication date: 2008
Peer-reviewed: No

**Publication information**
Journal: Kvæginfo
Original language: Danish
Source: orbit
Source-ID: 223821
Research output: Research › Journal article – Annual report year: 2008

Comparison of two quantitative PCR techniques for porcine circovirus Type 2 (PCV2) nucleic acid in field samples

Porcine circovirus type 2 (PCV2) is considered the essential infectious agent of postweaning multisystemic wasting syndrome (PMWS), a global swine disease of devastating economic and animal welfare impact. Most pigs become infected with PCV2 during their life, but only a proportion of them develop PMWS (1). PMWS is associated with a high PCV2 load, and a general threshold of 10^7 copies of PCV2 per ml serum has been suggested for PMWS diagnosis (2,3).

The objective of this study was to compare the performance of two different real-time quantitative polymerase chain reaction (qPCR) assays for PCV2 used routinely in two laboratories located in Denmark (lab 1) and Spain (lab 2), respectively.

**General information**
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Epidemiology and public sector consultancy, Virology, Autonomous University of Barcelona
Publication date: 2008
Peer-reviewed: Yes
Event: Abstract from 20th International Pig Veterinary Society Congress, Durban, South Africa.
Source: orbit
Source-ID: 224289
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2008

Danske aktiviteter vedr. mitteovervågning og forskning

**General information**
State: Published
Organisations: National Veterinary Institute, Division of Veterinary Diagnostics and Research, Virology, Section for Veterinary Epidemiology and public sector consultancy
Contributors: Larsen, L. E., Bødker, R.
Publication date: 2008
Peer-reviewed: No
Event: Poster session presented at RUFF-møde om klimaændringer, Krogerup Avlsgård, Humlebæk, .
Source: orbit
Source-ID: 222701
Research output: Research › Poster – Annual report year: 2008
Dynamics of porcine circovirus type 2 infection and excretion in pigs from postweaning multisystemic wasting syndrome affected farms from Spain and Denmark

Sero-logical and non-quantitative DNA detection techniques (PCR) have been widely used to monitor porcine circovirus type 2 (PCV2) infection dynamics (1,2). In spite of available epidemiological information, very few data on PCV2 load dynamics of Postweaning multisystemic wasting syndrome (PMWS) affected and non-affected pigs in PMWS affected farms are available. The present longitudinal study describes the evolution of PCV2 infection and excretion in pathologically characterized pigs from PMWS affected farms from two different countries, namely Denmark and Spain.

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Epidemiology and public sector consultancy, Section of Swine fever etc., Division of Virology, Section for Veterinary Diagnostics, Autonomous University of Barcelona, Danish Meat Association, Institut de Recerca i Tecnologia Agroalimentàries
Publication date: 2008
Peer-reviewed: Yes
Event: Abstract from 20th International Pig Veterinary Society Congress, Durban, South Africa.
Source: orbit
Source-ID: 224295
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2008

Er der sammenhæng mellem PMWS og salmonella?

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Dansk Svineproduktion, CReSA - Centre for Animal Health Research
Contributors: Kristensen, C. S., Roma, L. G., Larsen, L. E.
Pages: 1-4
Publication date: 2008
Peer-reviewed: Unknown

Publication information
Journal: Dansk Svineproduktion
Issue number: Erfaring nr. 0806
Original language: English
Source: orbit
Source-ID: 231892
Research output: Communication › Journal article – Annual report year: 2008

Hepatitis E virus - en ny zoonose?

General information
State: Published
Organisations: National Veterinary Institute, Division of Veterinary Diagnostics and Research, Virology, Section for Veterinary Diagnostics
Contributors: Breum, S. Ø., Hjulsager, C. K., Larsen, L. E.
Publication date: 2008
Peer-reviewed: No
Source: orbit
Source-ID: 232979
Research output: Research › Conference abstract for conference – Annual report year: 2008

Hepatitis E Virus i danske grise

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics
Hepatitis E. virus is prevalent in the Danish pig population

Hepatitis E virus (HEV) is responsible for major outbreaks of acute hepatitis in humans from developing countries, but evidence increases that also in industrialized countries locally acquired HEV infections occur. The disease usually affects young adults and has a relatively high mortality in infected pregnant women. HEV sequences worldwide can be classified into four major genotypes. Genotypes 1 and 2 are causing the majority of HEV infections in humans in hyper-endemic areas. In contrast, HEV genotypes 3 and 4 identified in cases of human hepatitis with increasing prevalence in countries such as USA, Europe, Japan and China. There is increasing evidence for the zoonotic origin of infections with HEV genotypes 3 and 4. Swine HEV sequences closely related to human HEV sequences have been detected in many countries and in several cases the source of infection has been linked to contact with swine or ingestion of undercooked swine meat. The aim of this study was to clarify if HEV is prevalent in the Danish pig population. Presence of HEV was examined by detection of HEV by real time RT-PCR or serological screening for HEV antibodies.
countries and in several cases the source of infection has been linked to contact with swine or ingestion of undercooked swine meat. The aim of this study was to clarify if HEV is prevalent in the Danish pig population. Presence of HEV was examined by detection of HEV by real time RT-PCR or serological screening for HEV antibodies.

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics, Section for Veterinary Epidemiology and public sector consultancy, Autonomous University of Barcelona
Publication date: 2008
Peer-reviewed: Yes
Event: Poster session presented at 20th International Pig Veterinary Society Congress, Durban, South Africa.
Source: orbit
Source-ID: 224310
Research output: Research - peer-review › Poster – Annual report year: 2008

Identification of a new porcine circovirus type 2 (PCV2) genotype in Danish archive pigsamples
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.

General information
State: Published
Organisations: Microbial Ecology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Virology
Contributors: Dupont, K., Larsen, L. E.
Publication date: 2008
Peer-reviewed: Yes
Event: Abstract from 20th International Pig Veterinary Society Congress, Durban, South Africa.
Source: orbit
Source-ID: 224413
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2008

Longitudinal determination of haptoglobin and pigmap concentrations in PMWS affected and non-affected pigs

General information
State: Published
Organisations: Innate Immunology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics, Virology
Publication date: 2008
Peer-reviewed: No
Event: Abstract from colloquim on animal acute phase proteins, Barcelona, Spain, .
Source: orbit
Source-ID: 240817
Research output: Research › Conference abstract for conference – Annual report year: 2008

PCV-2 genotype definition and nomenclature

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Autonomous University of Barcelona, Merial S.A.S., Ghent University, Institute of Virology and Immunoprophylaxis, University of Saskatchewan, The Ohio State University, Robert Koch Institute, Lund University, Devenish Nutrition, AHDB Pork, Agence Française de Sécurité Sanitaire des Aliments, Danish Pig Production, University of Copenhagen, Queen's University Belfast, Wageningen University & Research
Pages: 867-868
Publication date: 2008
Real-time onestep RT-PCR for the detection and differentiation of European and North American types of PRRSV in boar semen

Porcine Reproductive and respiratory syndrome virus (PRRSV) is a single-stranded RNA virus and a worldwide cause of significant respiratory disease and reproductive failure in swine. Two different types of PRRSV, the European (EU) and North American (US) type exist. Boar semen can harbor PRRSV (1) and the virus can be transmitted by this route, creating a need for diagnostic tests to ensure a PRRSV-free semen supply. PCR is an obvious method for such testing, and especially nested and TwoStep RT-PCR methods have been extensively used for this purpose. However, OneStep RT-PCR offers a more convenient and safe diagnostic procedure, since cDNA synthesis and PCR is performed sequentially without inbetween opening of the PCR-tubes, thus eliminating a substantial contamination risk. The aim of the present study was to validate a real-time OneStep RT-PCR assay for the simultaneous detection and discrimination of PRRSV EU and US types in semen.
Real-time onestep RT-PCR for the detection and differentiation of European and North American types of PRRSV in boar semen

Porcine Reproductive and respiratory syndrome virus (PRRSV) is a single-stranded RNA virus and a worldwide cause of significant respiratory disease and reproductive failure in swine. Two different types of PRRSV, the European (EU) and North American (US) type exist. Boar semen can harbor PRRSV (1) and the virus can be transmitted by this route, creating a need for diagnostic tests to ensure a PRRSV-free semen supply. PCR is an obvious method for such testing, and especially nested and TwoStep RT-PCR methods have been extensively used for this purpose. However, OneStep RT-PCR offers a more convenient and safe diagnostic procedure, since cDNA synthesis and PCR is performed sequentially without inbetween opening of the PCR-tubes, thus eliminating a substantial contamination risk. The aim of the present study was to validate a real-time OneStep RT-PCR assay for the simultaneous detection and discrimination of PRRSV EU and US types in semen.

Sapovirus fundet i danske grise

Publication information
Journal: Dansk Veterinærtidsskrift
Issue number: 18
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
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
Vacciner til kvæg - status og perspektiver

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Adaptive Immunology & Parasitology
Contributors: Larsen, L. E., Jungersen, G.
Pages: 12-14
Publication date: 2008
Peer-reviewed: Unknown

Publication information
Journal: Danske Maelkeproducenter
Volume: december
ISSN (Print): 1395-878X
Original language: Danish
Source: orbit
Source-ID: 231639
Research output: Communication › Journal article – Annual report year: 2008

Validation of real time PCR assays for use in routine diagnostics of pig diarrhoea

At the National Veterinary Institute in Denmark we want to optimize routine diagnostic analyses by screening samples simultaneously for several agents by real time PCR. Here we present the validation of real time PCR assays for E. coli F4, E. coli F18 and Lawsonia intracellularis2 in pig feces. The validation is based on feces samples spiked with a serial dilution of the respective bacteria for determination of PCR efficiencies, dynamic ranges and detection limits. In addition, the effect of the PCR assays of different concentrations of feces and pig to pig variation have been evaluated.

General information
State: Published
Organisations: Bacteriology & Pathology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Virology, Section for Veterinary Diagnostics
Publication date: 2008
Peer-reviewed: Yes
Event: Poster session presented at Advances in qPCR, Stockholm, Sweden.
Source: orbit
Source-ID: 224219
Research output: Research - peer-review › Poster – Annual report year: 2008

Airborne transmission of PMWS between pig units located at close range

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Epidemiology and public sector consultancy, Virology
Contributors: Kristensen, C., Bille-Hansen, V., Vestergaard, K., Jorsal, S. E. L., Bækbo, P., Enøe, C., Larsen, L. E.
Publication date: 2007
Peer-reviewed: No
Event: Abstract from 5th International Symposium on Emerging and Re-emerging Pig Diseases, Krakow, Poland.
Source: orbit
Source-ID: 240807
Research output: Research › Conference abstract for conference – Annual report year: 2007
**Airborn transmission of PMWS between pig units located at close range**

**General information**
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Virology
Contributors: Kristensen, C. S., Bille-Hansen, V., Vestergaard, K., Jorsal, S. E. L., Bækbo, P., Larsen, L. E.
Publication date: 2007
Peer-reviewed: Yes
Event: Abstract from 5th International Symposium on Emerging and Re-emerging Pig Diseases, Krakow, Poland.
Source: orbit
Source-ID: 241482
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2007

**Calves health and welfare**

**General information**
State: Published
Organisations: National Veterinary Institute, Division of Veterinary Diagnostics and Research, Virology
Contributors: Larsen, L. E.
Publication date: 2007
Peer-reviewed: No
Event: Abstract from CCDays, Nyborg, Denmark.
Source: orbit
Source-ID: 242164
Research output: Research › Conference abstract for conference – Annual report year: 2007

**Dynamics in PMWS positive herds**

**General information**
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Microbial Ecology, Division of Microbiology and Risk Assessment, National Food Institute, Section for Veterinary Epidemiology and public sector consultancy, Virology
Publication date: 2007
Peer-reviewed: Yes
Event: Abstract from 5th International Symposium on Emerging and Re-emerging Pig Diseases, Krakow, Poland.
Source: orbit
Source-ID: 241481
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2007

**Faktorer af betydning for sundheden hos kalve**

**General information**
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Larsen, L. E.
Publication date: 2007
Peer-reviewed: No

**Publication information**
Journal: KvægInfo
Volume: 1808
Original language: Danish
Source: orbit
Source-ID: 242199
Research output: Research › Journal article – Annual report year: 2007
Mingling of PMWS-affected pigs with non-affected pigs: a PCV2 sequence study

General information
State: Published
Organisations: Microbial Ecology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics, Virology
Publication date: 2007
Peer-reviewed: Yes
Event: Poster session presented at 5th International Symposium on Emerging and Re-emerging Pig Diseases, Krakow, Poland.
Source: orbit
Source-ID: 240808
Research output: Research - peer-review » Poster – Annual report year: 2007

Myxomatose hos kaniner

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Larsen, L. E.
Publication date: 2007
Peer-reviewed: No

Publication information
Journal: Dansk Veterinaærtidsskrift
Volume: 21
ISSN (Print): 1600-2032
Ratings:
BFI (2008): BFI-level 1
Web of Science (2004): Indexed yes
Original language: Danish
Source: orbit
Source-ID: 242189
Research output: Research » Journal article – Annual report year: 2007

Norovirus hyppig hos kalve

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Virology
Contributors: Kristensen, S. L. S., Hjulsager, C. K., Larsen, L. E.
Publication date: 2007
Peer-reviewed: No

Publication information
Journal: Norovirus hyppig hos kalve
Volume: 10
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
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
Norovirus, Sapovirus, rotavirus and hepeviruses in animal samples. Norovirus surveillance humans. Sapovirus surveillance humans

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Virology
Contributors: Böttiger, B., Johnsen, C. K., Midgley, S., Hjulsager, C. K., Larsen, L. E.
Publication date: 2007
Peer-reviewed: Yes
Event: Poster session presented at EVENT meeting, Pesc, Hungary.
Source: orbit
Source-ID: 240986
Research output: Research - peer-review » Poster – Annual report year: 2007

PCV2 dynamics in PMWS positive Herds

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Microbial Ecology, Division of Microbiology and Risk Assessment, National Food Institute, Section for Veterinary Epidemiology and public sector consultancy, Virology
Publication date: 2007
Peer-reviewed: Yes
Event: Paper presented at 5th International Symposium on Emerging and Re-emerging Pig Diseases, Krakow, Poland.
Source: orbit
Source-ID: 240510
Research output: Research - peer-review » Paper – Annual report year: 2007

Seological testing for Porcine circovirus type 2 in Danish pig herds with and without PMWS

General information
State: Published
Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Virology, Section for Veterinary Diagnostics
Publication date: 2007
Peer-reviewed: No
Event: Abstract from 5th International Symposium on Emerging and Re-emerging Pig Diseases, Krakow, Poland.
Source: orbit
Source-ID: 240809
Research output: Research » Conference abstract for conference – Annual report year: 2007

Validation of real-time one-step RT-PCR assays for detection of influenza a virus subtypes H5 and H7 in pigs

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics, Section of Poultry Diseases, Division of Poultry, Fish and Fur Animals
Contributors: Trebbien, R., Hjulsager, C. K., Handberg, K., Larsen, L. E.
Publication date: 2007
What do we know on epidemiology, control and prevention of porcine circovirus diseases

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Publication date: 2007
Peer-reviewed: No
Event: Abstract from 5th International Symposium on Emerging and Re-emerging Pig Diseases, Krakow, Poland.
Source: orbit
Source-ID: 240811
Research output: Research › Conference abstract for conference – Annual report year: 2007

Aviær influenza i svin

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics
Contributors: Larsen, L. E., Hjulsager, C. K.
Pages: 2-4
Publication date: 2006
Peer-reviewed: No

Publication information
Journal: Dyrlaegemagasinet for Praktiserende Dyrlæger
Volume: 1/6 2006
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: English
Source: orbit
Source-ID: 240506
Research output: Research › Journal article – Annual report year: 2006

Circulation of bovine respiratory syncytial virus in Brazil

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Almeida, R., Domingues, H., Spilki, F., Larsen, L. E., Hagglund, S., Belak, S., Arns, C.
Pages: 632-634
Publication date: 2006
Peer-reviewed: Yes

Publication information
Journal: Veterinary Record
Volume: 158
Issue number: 18
ISSN (Print): 0042-4900
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 0.39 SJR 0.464 SNIP 0.858
Web of Science (2017): Impact factor 2.05
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 0.3 SJR 0.482 SNIP 0.745
Web of Science (2016): Impact factor 1.737
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 0.39 SJR 0.521 SNIP 0.796
Web of Science (2015): Impact factor 1.741
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 0.41 SJR 0.489 SNIP 0.844
Web of Science (2014): Impact factor 1.493
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 0.5 SJR 0.506 SNIP 0.821
Web of Science (2013): Impact factor 1.633
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 0.52 SJR 0.505 SNIP 0.878
Web of Science (2012): Impact factor 1.803
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 0.62 SJR 0.569 SNIP 0.903
Web of Science (2011): Impact factor 1.248
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.576 SNIP 0.837
Web of Science (2010): Impact factor 1.482
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.64 SNIP 0.994
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 0.554 SNIP 0.842
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 0.499 SNIP 0.808
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.645 SNIP 0.94
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.585 SNIP 0.911
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.619 SNIP 0.944
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.56 SNIP 0.94
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.607 SNIP 1.078
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.589 SNIP 1.143
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 0.621 SNIP 1.16
Diagnosis and epidemiology of bovine coronavirus in Swedish neonatal dairy and beef calves

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Tråvén, M., Verdier, K., Larsen, L. E., Thorén, P.
Publication date: 2006
Peer-reviewed: No
Event: Abstract from 7th International Congress of Veterinary Virology, Lisboa, Portugal.
Source: orbit
Source-ID: 230105
Research output: Research - peer-review » Journal article – Annual report year: 2006

Molecular epidemiology of bovine coronavirus on the basis of comparative analyses of the S gene

Bovine coronavirus (BCoV), a group 2 member of the genus Coronavirus in the family Coronaviridae, is an important pathogen in cattle worldwide. It causes diarrhea in adult animals (winter dysentery), as well as enteric and respiratory diseases in calves. The annual occurrence of BCoV epidemics in Sweden and Denmark led to this investigation, with the aim to deepen the knowledge of BCoV epidemiology at the molecular level. A total of 43 samples from outbreaks in both countries were used for PCR amplification and direct sequencing of a 624-nucleotide fragment of the BCoV S gene. Sequence comparison and phylogenetic studies were performed. The results showed (i) identical sequences from different animals in the same herds and from paired nasal and fecal samples, suggesting a dominant virus circulating in each herd at a given time; (ii) sequence differences among four outbreaks in different years in the same herd, indicating new introduction of virus; (iii) identical sequences in four different Danish herds in samples obtained within 2 months, implying virus transmission between herds; and (iv) that at least two different virus strains were involved in the outbreaks of BCoV in Denmark during the spring of 2003. This study presents molecular data of BCoV infections that will contribute to an increased understanding of BCoV epidemiology in cattle populations.

General information
New swine influenza A H1N2 re-assortment found in Danish swine

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, Division of Microbiology and Risk Assessment, National Food Institute, Section for Veterinary Epidemiology and public sector consultancy, Virology
Publication date: 2006
Peer-reviewed: No
Event: Abstract from 19th International Pig Veterinary Society Congress, Copenhagen, Denmark.
Source: orbi
Source-ID: 240801
Research output: Research › Conference abstract for conference – Annual report year: 2006

Norovirus i danske køer

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Virology

New swine influenza A H1N2 reassortment found in Danish swine

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, Division of Microbiology and Risk Assessment, National Food Institute, Section for Veterinary Epidemiology and public sector consultancy, Virology
Publication date: 2006
Peer-reviewed: Yes
Event: Paper presented at 19th International Pig Veterinary Society Congress, Copenhagen, Denmark.
Source: orbi
Source-ID: 240512
Research output: Research › Paper – Annual report year: 2006
Contributors: Kristensen, S. S., Hjulsager, C. K., Larsen, L. E.
Publication date: 2006
Peer-reviewed: No

**Publication information**
Journal: Dansk Veterinærtidsskrift
Volume: 18
ISSN (Print): 1600-2032
Ratings:
BFI (2008): BFI-level 1
Web of Science (2004): Indexed yes
Original language: English
Source: orbit
Source-ID: 242186
Research output: Research › Journal article – Annual report year: 2006

**PMWS in Denmark: Epidemiology, diagnosis and control**

**General information**
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Division of Microbiology and Risk Assessment, National Food Institute, Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, Virology, Section for Veterinary Epidemiology and public sector consultancy
Publication date: 2006

**Host publication information**
Title of host publication: PCVD...Coming Full Circle
Place of publication: Merial Write Book
Source: orbit
Source-ID: 242195
Research output: Research › Book chapter – Annual report year: 2006

**The use of different diagnostic tests in a herd with an unexpected case of a BVD virus positive calf.**

**General information**
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Virology, Sektion for Eksotiske Virussygdomme, Division of Virology
Contributors: Holm, E., Voss, H., Jensen, N., Larsen, L. E., Uttenthal, Å.
Publication date: 2006
Peer-reviewed: No
Source: orbit
Source-ID: 240805
Research output: Research › Conference abstract for conference – Annual report year: 2006

**Transmission of PMWS between pen mates**

**General information**
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, Section for Veterinary Epidemiology and public sector consultancy, Virology
Publication date: 2006
Peer-reviewed: No
Event: Abstract from 19th International Pig Veterinary Society Congress, Copenhagen, Denmark.
Source: orbit
Source-ID: 240802
Research output: Research › Conference abstract for conference – Annual report year: 2006
Vertical transmission of bovine viral diarrhoea virus (BVDV) in mousedeer (Tragulus javanicus) and spread to domestic cattle

This study investigates the transmission of bovine viral diarrhoea virus (BVDV) 1f from a persistently infected (PI) lesser Malayan mousedeer to two bovine calves. Different contact routes to two calves were analysed: 1) aerosol contact between two adjacent pens without physical contact; 2) indirect contact by use of common utensils; 3) direct nose-to-nose contact for 30 seconds. One of the calves was infected either by aerosol or indirect contact. The virus sequence in 247 nucleotides in the 5'-UTR was 100% identical in mousedeer and calf. To elucidate the distribution of BVDV within the affected mousedeer family the captive population in a Zoo was analysed. The maternal line of PI animals was maintained, whereas a PI male was able to reproduce and have a non-PI calf. As a consequence of this, six female PI mousedeer were killed; subsequent autopsies did not reveal any lesions. Sequencing mousedeer BVD virus in the E2 region (420 nucleotides) through 4 generations showed only 7 mutations, which were maintained from mother to offspring.
Veterinary and medical aspects of abortion in Danish sheep

The Danish sheep population totals around 144,000 animals, but little is known of the causes and prevalence of diseases. This study focuses on the causes of abortion in Danish sheep. During one breeding season, aborted foetuses and stillbirths with signs of intrauterine death or malformation were submitted for laboratory examination from a population of 3,758 breeding ewes. Samples from 24 incidents of abortion and 21 ewes delivering malformed lambs or lambs with ante partum decomposition were submitted. A specific aetiology was established in 66.7% and 14.3% of the cases, respectively. Bacterial pathogens were the most prevalent cause of abortion. Several of the abortifacients were zoonotic microorganisms, for example Listeria monocytogenes, Campylobacter fetus subsp. fetus, Yersinia pseudotuberculosis and Toxoplasma gondii. The identified microorganisms probably represent the most common causes of abortion in Danish sheep but occurrence in Denmark of other pathogens such as Coxiella burnetii and Chlamydophila abortus cannot be excluded. Due to the high prevalence of zoonotic microorganisms, precautions must be taken in handling abortions or assisting lambing, especially for pregnant women.
Age-dependent differences in cytokine and antibody responses after experimental RSV infection in a bovine model

Respiratory syncytial virus (RSV) causes severe respiratory disease in both infants and calves. As in humans, bovine RSV (BRSV) infections are most severe in the first 6 months of life. In this study, experimental infection with BRSV was performed in calves aged 1-5, 9-16 or 32-37 weeks. Compared to younger animals, older calves showed significantly less fever and lower TNFα levels and less virus-specific IFN γ release. In addition, blood from older animals had more mononuclear cells, more B cells and stronger BRSV-specific IgA and neutralising antibody responses to infection. A strong "inflammatory" but weak humoral antiviral response in very young animals suggests that enhanced inflammation contributes to disease during RSV infection during the early postnatal period.

General information

State: Published
Organisations: Adaptive Immunology & Parasitology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, Virology, Innate Immunology, Technical University of Denmark
Contributors: Grell, S., Riber, U., Tjørnehøj, K., Larsen, L. E., Heegaard, P. M. H.
Pages: 3412-3423
Publication date: 2005
Peer-reviewed: Yes
Diagnostik af svineinfluenza

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Sektion for Eksotiske Virussygdomme, Division of Virology
Contributors: Larsen, L. E., Bøtner, A.
Publication date: 2005
Peer-reviewed: No

Publication information
Evaluation of a single-tube fluorogenic RT-PCR assay for detection of bovine respiratory syncytial virus in clinical samples

Bovine respiratory syncytial virus (BRSV) causes severe disease in naive cattle of all ages and is a common pathogen in the respiratory disease complex of calves. Simplified methods for rapid BRSV diagnosis would encourage sampling during outbreaks and would consequently lead to an extended understanding of the virus. In this study, a BRSV fluorogenic reverse transcription PCR (fRT-PCR) assay, based on TaqMan principle, was developed and evaluated on a large number of clinical samples, representing various cases of natural and experimental BRSV infections. By using a single-step closed-tube format, the turn-around time was shortened drastically and results were obtained with minimal risk for cross-contamination. According to comparative analyses, the detection limit of the fRT-PCR was on the same level as that of a nested PCR and the sensitivity relatively higher than that of a conventional PCR, antigen ELISA (Ag-ELISA) and virus isolation (VI). Interspersed negative control samples, samples from healthy animals and eight symptomatically or genetically related viruses were all negative, confirming a high specificity of the assay. Taken together, the data indicated that the fRT-PCR assay can be applied to routine virus detection in clinical specimens and provides a rapid and valuable tool in BRSV research.

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Hakhverdyan, M., Hägglund, S., Larsen, L. E., Belák, S.
Pages: 195-202
Publication date: 2005
Peer-reviewed: Yes

Publication information
Journal: Journal of Virological Methods
Volume: 123
Issue number: 2
ISSN (Print): 0166-0934
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.82 SJR 0.858 SNIP 0.817
Web of Science (2017): Impact factor 1.756
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.78 SJR 0.873 SNIP 0.729
Web of Science (2016): Impact factor 1.693
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 1.68 SJR 0.87 SNIP 0.802
Web of Science (2015): Impact factor 1.508
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 1.87 SJR 0.898 SNIP 0.933
Web of Science (2014): Impact factor 1.781
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 1.99 SJR 0.866 SNIP 0.9
Web of Science (2013): Impact factor 1.883
ISI indexed (2013): ISI indexed yes
Marked induction of IL-6, haptoglobin and IFN gamma following experimental BRSV infection in young calves

Bovine respiratory syncytial virus (BRSV) has been identified worldwide as an important pathogen associated with acute respiratory disease in calves. An infection model has been developed reflecting accurately the clinical course and death development of pathological signs during a natural BRSV-infection. In the experiments described in the present study, calves were infected at 13-21 weeks of age and reinfected 14 weeks later. Blood samples from the entire infection period were analysed for acute phase protein (haptoglobin) by ELISA and for expression (mRNA level in peripheral blood mononuclear cells) of the cytokines interleukin-2 (IL-2), interleukin-4 (IL-4), interleukin-6 (IL-6) and interferon-gamma (IFN gamma) by quantitative real-time reverse transcribed polymerase chain reaction (RT-PCR). IFN gamma, interleukin-6 and haptoglobin were markedly induced to-ether with development of clinical signs in response to the first infection with BRSV. The IFN gamma response was biphasic, with an early peak at day 1-3 post infection (p.i.) and a later increase between day 5 and 8 p.i. Reinfection also resulted in an induction of IFN gamma, but without induction of clinical signs, IL-6 and haptoglobin. These results indicate that early mediators connected with the innate responses are induced on a first encounter with the pathogen, but not on a second encounter (reinfection) where the adaptive immune system may act as
the first line defence.

**General information**
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Virology, Division of Veterinary Diagnostics and Research, Innate Immunology
Contributors: Grell, S. N., Tjørnehøj, K., Larsen, L. E., Heegaard, P. M. H.
Pages: 235-245
Publication date: 2005
Peer-reviewed: Yes

**Publication information**
Journal: Veterinary Immunology and Immunopathology
Volume: 103
Issue number: 3-4
ISSN (Print): 0165-2427
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 1.7 SJR 0.68 SNIP 0.71
Web of Science (2017): Impact factor 1.632
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): Impact factor 1.718
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 1.67 SJR 0.862 SNIP 0.749
Web of Science (2015): Impact factor 1.664
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 1.6 SJR 0.777 SNIP 0.718
Web of Science (2014): Impact factor 1.535
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 1.89 SJR 0.834 SNIP 0.797
Web of Science (2013): Impact factor 1.748
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 2.15 SJR 0.841 SNIP 0.913
Web of Science (2012): Impact factor 1.877
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 2.16 SJR 0.859 SNIP 0.995
Web of Science (2011): Impact factor 2.076
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): Impact factor 2.176
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 0.784 SNIP 0.851
Persistent BVDV infection in mousedeer infects calves - Do we know the reservoirs for BVDV?
Bovine virus diarrhoea virus (BVDV)-1f was isolated from a Lesser Malayan Mousedeer in Copenhagen Zoo during a routine screening. Analysis of animals related to the Copenhagen mousedeer revealed that its mother and all siblings were virus positive, a pattern also seen for persistently infected (PI) cattle. BVDV could be transmitted from the PI mousedeer to a calf after indirect contact. The host spectrum for BVDV seems to be even wider than expected; the implications for BVDV control are discussed. (c) 2005 Elsevier B.V. All rights reserved.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Division of Microbiology and Risk Assessment, National Food Institute, Virology, Division of Veterinary Diagnostics and Research
Contributors: Uttenthal, Å., Grøndahl, M., Houe, H., Van Maanen, C., Rasmussen, T. B., Larsen, L. E.
Pages: 87-91
Publication date: 2005
Peer-reviewed: Yes

Publication information
Journal: Preventive Veterinary Medicine
Volume: 72
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): CiteScore 2.26 SJR 1.144 SNIP 1.31
Web of Science (2017): Impact factor 1.924
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.2 SJR 1.249 SNIP 1.361
<table>
<thead>
<tr>
<th>Year</th>
<th>Impact Factor</th>
<th>SJR</th>
<th>SNIP</th>
</tr>
</thead>
<tbody>
<tr>
<td>2016</td>
<td>1.987</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2015</td>
<td>2.182</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2014</td>
<td>2.389</td>
<td>1.265</td>
<td>1.436</td>
</tr>
<tr>
<td>2013</td>
<td>2.389</td>
<td>1.265</td>
<td>1.436</td>
</tr>
<tr>
<td>2012</td>
<td>2.389</td>
<td>1.265</td>
<td>1.436</td>
</tr>
<tr>
<td>2011</td>
<td>2.389</td>
<td>1.265</td>
<td>1.436</td>
</tr>
<tr>
<td>2010</td>
<td>2.389</td>
<td>1.265</td>
<td>1.436</td>
</tr>
<tr>
<td>2009</td>
<td>2.389</td>
<td>1.265</td>
<td>1.436</td>
</tr>
<tr>
<td>2008</td>
<td>2.389</td>
<td>1.265</td>
<td>1.436</td>
</tr>
<tr>
<td>2007</td>
<td>2.389</td>
<td>1.265</td>
<td>1.436</td>
</tr>
<tr>
<td>2006</td>
<td>2.389</td>
<td>1.265</td>
<td>1.436</td>
</tr>
<tr>
<td>2005</td>
<td>2.389</td>
<td>1.265</td>
<td>1.436</td>
</tr>
<tr>
<td>2004</td>
<td>2.389</td>
<td>1.265</td>
<td>1.436</td>
</tr>
<tr>
<td>2003</td>
<td>2.389</td>
<td>1.265</td>
<td>1.436</td>
</tr>
<tr>
<td>2002</td>
<td>2.389</td>
<td>1.265</td>
<td>1.436</td>
</tr>
<tr>
<td>2001</td>
<td>2.389</td>
<td>1.265</td>
<td>1.436</td>
</tr>
<tr>
<td>2000</td>
<td>2.389</td>
<td>1.265</td>
<td>1.436</td>
</tr>
<tr>
<td>1999</td>
<td>2.389</td>
<td>1.265</td>
<td>1.436</td>
</tr>
</tbody>
</table>

Original language: English
Persistent BVDV infection in Mousedeer infects calves. Do we know the reservoirs for BVDV?

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Virology, Division of Veterinary Diagnostics and Research
Publication date: 2005
Peer-reviewed: No
Event: Abstract from European symposium on BVDV control, Portugal, .
Source: orbit
Source-ID: 242303
Research output: Research › Conference abstract for conference – Annual report year: 2005

Porcine Circovirus Type 2 Enteritis is an Important Differential Diagnosis to Porcine Proliferative Enteropathy caused by Lawsonia Intracellularis

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Division of Microbiology and Risk Assessment, National Food Institute, Virology
Publication date: 2005
Peer-reviewed: Yes
Source: orbit
Source-ID: 241475
Research output: Research › Conference abstract for conference – Annual report year: 2005

Smittetrisiko ved separatring af gylle

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Adaptive Immunology & Parasitology, Section for Veterinary Epidemiology and public sector consultancy
Publication date: 2005
Peer-reviewed: No

Publication information
Journal: Forskning i bioenergi
Volume: 6
ISSN (Print): 1604-6331
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Original language: Danish

Bibliographical note
Translated title: Infection risk in relation to manure separation
Source: orbit
Source-ID: 241862
Research output: Research › Journal article – Annual report year: 2005
A real-time RT-PCR SYBR Green-I assay for detection of porcine reproductive and respiratory syndrome virus

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section of Poultry Diseases, Division of Poultry, Fish and Fur Animals, Virology, Stald/vægterservice, Division of Virology, Sektion for Eksotiske Virussygdomme
Contributors: Hjulsager, C. K., Jørgensen, P. H., Larsen, L. E., Storgaard, T., Bøtner, A.
Publication date: 2004
Peer-reviewed: Yes
Event: Poster session presented at International qPCR Symposium & Application Workshop, Freising-Weihenstephan, Germany.
Source: orbit
Source-ID: 240993
Research output: Research - peer-review ▶ Poster – Annual report year: 2004

Bestemmelse af immunoglobulin (IgG) niveau i kalve med henblik på evaluering af råmælksoptagelse

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Laboratory Service, Division of Virology
Contributors: Larsen, L. E., Pedersen, R. E., Lauridsen, B. H., Steffensen, M. A., Trinderup, M., Jensen, A. M.
Publication date: 2004
Peer-reviewed: No

Publication information
Journal: Dansk Veterinærtidsskrift
ISSN (Print): 1600-2032
Ratings:
BFI (2008): BFI-level 1
Web of Science (2004): Indexed yes
Original language: Danish
Source: orbit
Source-ID: 242181
Research output: Research ▶ Journal article – Annual report year: 2004

Bovine respiratory syncytial virus ISCOMs - protection in the presence of maternal antibodies
The protection induced by immunostimulating complexes (ISCOMs) against bovine respiratory syncytial virus (BRSV) was evaluated and compared to that of a commercial inactivated vaccine (CV) in calves with BRSV-specific maternal antibodies. Following experimental challenge, controls (n = 4) and animals immunized with CV (n = 5) developed moderate to severe respiratory disease, whereas calves immunized with ISCOMS (17 = 5) remained clinically healthy. BRSV was re-isolated from the nasopharynx of all controls and from all calves immunized with CV, but from none of the calves immunized with ISCOMs. BRSV-RNA was detected by real-time PCR from a single animal in this group. Significantly higher BRSV-specific nasal IgG, serum IgG(1) and IgG(2) titers were detected before and after challenge in animals immunized with ISCOMs versus CV. In conclusion, the ISCOMs overcame the suppressive effect of maternal antibodies in calves and induced strong clinical and virological protection against a BRSV challenge.

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Pages: 646-655
Publication date: 2004
Peer-reviewed: Yes

Publication information
Journal: Vaccine
Volume: 23
Issue number: 5
ISSN (Print): 0264-410X
Ratings:
Microbiological investigations on trans-tracheal aspirated bronchoalveolar fluid from clinically normal calves and calves with pneumonia

General information
State: Published
Organisations: Bacteriology & Pathology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Virology
Contributors: Angen, Ø., Enemark, J. M., Larsen, L. E., Thomsen, J.
Publication date: 2004
Peer-reviewed: Yes
Event: Abstract from ASM General Meeting.
Source: orbit
Source-ID: 229506
Research output: Research - peer-review › Conference abstract for conference – Annual report year: 2004

An experimental infection model for reproduction of calf pneumonia with bovine respiratory syncytial virus (BRSV) based on one combined exposure of calves

Bovine respiratory syncytial virus (BRSV) has been recognised as an important pathogen in calf pneumonia for 30 years, but surprisingly few effective infection models for studies of the immune response and the pathogenesis in the natural host have been established. We present a reproducible experimental infection model for BRSV in 2-5-month-old, conventionally reared Jersey calves. Thirty-four colostrum-fed calves were inoculated once by aerosol and intratracheal injection with BRSV. Respiratory disease was recorded in 91% of the BRSV-inoculated calves, 72% had an accompanying rise in rectal temperature and 83% exhibited >5%, consolidation of the lung tissue. The disease closely resembled natural outbreaks of BRSV-related pneumonia, and detection of BRSV in nasal secretions and lung tissues confirmed the primary role of BRSV. Nine mock-inoculated control calves failed to develop respiratory disease. This model is a valuable tool for the study of the pathogenesis of BRSV and for vaccine efficacy studies.

General information
State: Published
Organisations: Sektion for Eksotiske Virusssygdomme, Division of Virology, National Veterinary Institute, Virology, Division of Veterinary Diagnostics and Research
Contributors: Tjørnehøj, K., Uttenthal, Å., Viuff, B., Larsen, L. E., Rontved, C., Ronsholt, L.
Pages: 55-65
Publication date: 2003
Peer-reviewed: Yes
**Bovine respiratory syncytial virus immunostimulating complexes (BRSV-ISCOMS) provided protection against a virulent challenge**

**General information**
- State: Published
- Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute
- Publication date: 2003
- Peer-reviewed: No
- Event: Abstract from 6th International Congress of Veterinary Virology, St. Malo, France.
- Source: orbit
- Source-ID: 240800
- Research output: Research › Conference abstract for conference – Annual report year: 2003

**Characterisation of a pestivirus isolated from persistently infected mousedeer (Tragulus javanicus)**

Serum samples from the male Mousedeer A and the mother, father and sister of A were tested for bovine virus diarrhoea viruses (BVDV) by isolation, and for BVDV antibodies by blocking ELISA and homologous neutralisation test. Further, RNA was extracted and tested by RT-PCR protocol analysing the 5'-untranslated region and the E2 gene of pestivirus. The RT-PCR products were subsequently sequenced. Mousedeer A was positive in virus isolation on three occasions (days 1, 19 and 40) and by RT-PCR. The sister and mother of Mousedeer A were also found virus positive by isolation and RT-PCR. Mousedeer A, its sister and its mother, all had an antibody neutralisation titer below 10. The father of A was virus negative but was positive in the blocking antibody ELISA and had a high neutralisation antibody titer. The repeated detection of BVDV in Mousedeer A, the high amount of virus in serum, the lack of antibodies and the virus positive family members documented that the mousedeer were persistently infected with a pestivirus. The father of A probably had an acute infection resulting in antibodies to pestivirus and viral clearance. Sequence analysis and phylogenetic analysis revealed that the mousedeer pestivirus was closely related to BVDV Type 1f. The existences of persistently infected animals in non-domestic species have great implications for BVDV eradication campaigns in cattle.

**General information**
- State: Published
- Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Virology, Division of Veterinary Diagnostics and Research
- Contributors: Grøndahl, C., Uttenthal, Å., Houe, H., Rasmussen, T. B., Hoyer, M., Larsen, L. E.
- Pages: 1455-1463
- Publication date: 2003
- Peer-reviewed: Yes

**Publication information**
- Journal: Archives of Virology
- Volume: 148
- Issue number: 8
- ISSN (Print): 0304-8608
- Ratings:
  - BFI (2018): BFI-level 1
  - Web of Science (2018): Indexed yes
  - BFI (2017): BFI-level 1
  - Scopus rating (2017): CiteScore 2.25 SJR 0.973 SNIP 0.989
  - Web of Science (2017): Impact factor 2.16
  - Web of Science (2017): Indexed yes
  - BFI (2016): BFI-level 1
  - Scopus rating (2016): CiteScore 2.16 SJR 0.969 SNIP 0.896
  - Web of Science (2016): Impact factor 2.058
  - BFI (2015): BFI-level 1
  - Scopus rating (2015): CiteScore 2.16 SJR 1.096 SNIP 0.889
  - Web of Science (2015): Impact factor 2.255
  - BFI (2014): BFI-level 1
  - Scopus rating (2014): CiteScore 2.37 SJR 1.098 SNIP 1.028
  - Web of Science (2014): Impact factor 2.39
  - BFI (2013): BFI-level 1
Detection of persistent infection with pestivirus (BVDV) in a mousedeer (Tragulus Javanicus) and experimental transmission to cattle

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Virology, Division of Veterinary Diagnostics and Research
Contributors: Grøndahl, C., Uttenthal, Å., Houec, H., Rasmussen, T. B., Høyer, M. J., Larsen, L. E.
Publication date: 2003
Peer-reviewed: No
Event: Abstract from International Congress for Zoo Animals, Rom, Italy.
Source: orbit
BRSV - danske erfaringer

General information
State: Published
Organisations: National Veterinary Institute, Division of Veterinary Diagnostics and Research, Virology
Contributors: Larsen, L. E.
Publication date: 2002
Peer-reviewed: Yes
Source: orbit
Source-ID: 242162
Research output: Research - peer-review » Conference abstract for conference – Annual report year: 2002

Immune response to bovine respiratory syncytial virus (BRSV) following immunisation with a commercial inactivated BRSV vaccine

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, Adaptive Immunology & Parasitology, Innate Immunology
Contributors: Larsen, L. E., Tjørnehøj, K., Riber, U., Heegaard, P. M. H., Røntved, C., Viuff, B.
Publication date: 2002
Peer-reviewed: No
Event: Abstract from Buiatric Congres, Hannover, Germany.
Source: orbit
Source-ID: 240798
Research output: Research » Conference abstract for conference – Annual report year: 2002

Replication and clearance of respiratory syncytial virus - Apoptosis is an important pathway of virus clearance after experimental infection with bovine respiratory syncytial virus

Human respiratory syncytial virus is an important cause of severe respiratory disease in young children, the elderly, and in immunocompromised adults. Similarly, bovine respiratory syncytial virus (BRSV) is causing severe, sometimes fatal, respiratory disease in calves. Both viruses are pneumovirus and the infections with human respiratory syncytial virus and BRSV have similar clinical, pathological, and epidemiological characteristics. In this study we used experimental BRSV infection in calves as a model of respiratory syncytial virus infection to demonstrate important aspects of viral replication and clearance in a natural target animal. Replication of BRSV was demonstrated in the luminal part of the respiratory epithelial cells and replication in the upper respiratory tract preceded the replication in the lower respiratory tract. Virus excreted to the lumen of the respiratory tract was cleared by neutrophils whereas apoptosis was an important way of clearance of BRSV-infected epithelial cells. Neighboring cells, which probably were epithelial cells, phagocytized the BRSV-infected apoptotic cells. The number of both CD4+ and CD8+ T cells increased during the course of infection, but the T cells were not found between the epithelial cells of the bronchi up until apoptosis was no longer detected, thus in the bronchi there was no indication of direct contact-dependent T-cell-mediated cytotoxicity in the primary infection.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Virology, Division of Veterinary Diagnostics and Research
Pages: 2195-2207
Publication date: 2002
Peer-reviewed: Yes

Publication information
Journal: American Journal of Pathology
Volume: 161
Issue number: 6
ISSN (Print): 0002-9440
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
Bovine respiratory syncytial virus (BRSV) pneumonia in beef calf herds despite vaccination

The present report describes the clinical, pathological, serological and virological findings in calves from 2 larger Danish beef herds experiencing outbreaks of pneumonia. The calves had been vaccinated with an inactivated bovine respiratory syncytial virus (BRSV) vaccine 2 months prior to the outbreak. The clinical signs comprised nasal discharge, pyrexia, cough and increased respiratory rates. A total of 28 calves died in the 2 herds. The laboratory investigations revealed that BRSV was involved and probably initiated both outbreaks. Furthermore, the serological results suggested that the vaccine induced only sparse levels of antibodies probably due to the presence of maternally derived antibodies at the time of vaccination. Necropsy findings in 5 calves revealed changes typical for infectious pneumonia with involvement of BRSV. In conclusion, vaccination of calves against BRSV in 2 Danish beef herds failed to protect the calves against severe or even
fatal BRSV mediated respiratory disease 2 months later.

**General information**
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Technical University of Denmark
Contributors: Larsen, L. E., Tegtmeier, C., Pedersen, E.
Pages: 113-121
Publication date: 2001
Peer-reviewed: Yes

**Publication information**
Journal: Acta Veterinaria Scandinavica (Print Edition)
Volume: 42
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): CiteScore 1.45 SJR 0.655 SNIP 1.077
Web of Science (2017): Impact factor 1.497
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): Impact factor 1.472
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 0.98 SJR 0.644 SNIP 1.641
Web of Science (2015): Impact factor 1.23
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 1.54 SJR 0.753 SNIP 1.21
Web of Science (2014): Impact factor 1.377
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 1.41 SJR 0.539 SNIP 1.11
Web of Science (2013): Impact factor 1.382
ISI indexed (2013): ISI indexed no
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 1.26 SJR 0.591 SNIP 0.789
Web of Science (2012): Impact factor 1.345
ISI indexed (2012): ISI indexed no
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 1.42 SJR 0.664 SNIP 0.997
Web of Science (2011): Impact factor 1.367
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): Impact factor 1.196
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
Scopus rating (2008): SJR 0.338 SNIP 0.588
Scopus rating (2007): SJR 0.295 SNIP 0.378
Scopus rating (2006): SJR 0.272 SNIP 0.342
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.208 SNIP 0.292
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.322 SNIP 0.543
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.277 SNIP 0.501
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.328 SNIP 0.454
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.49 SNIP 0.757
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 0.463 SNIP 0.912
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 0.393 SNIP 0.903
Original language: English
Keywords: bovine respiratory syncytial virus, enzootic pneumonia, BRSV, serology, vaccination, calves
DOIs:
10.1186/1751-0147-42-113
Source: orbit
Source-ID: 230707
Research output: Research - peer-review › Journal article – Annual report year: 2001

BRSV Infektionsdynamik - perspektiver for sundhedsstyringen
General information
State: Published
Organisations: National Veterinary Institute, Division of Veterinary Diagnostics and Research, Virology
Contributors: Larsen, L. E.
Publication date: 2001
Peer-reviewed: No
Event: Abstract from Boologisk Selskab : Efterårsseminar, Brædstrup, .
Source: orbit
Source-ID: 242158
Research output: Research › Conference abstract for conference – Annual report year: 2001

Does BRSV persist in calves
General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Sektion for Ekstern Virussygdomme, Division of Virology
Contributors: Larsen, L. E., Tjømehøj, K., Viuff, B., Røntved, C.
Publication date: 2001
Peer-reviewed: No
Event: Abstract from RSV after 45 Years Symposium, Sergovia, Spanien, .
Source: orbit
Source-ID: 240797
Research output: Research › Conference abstract for conference – Annual report year: 2001

Forekomst og betydning af bovin coronavirus
General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Larsen, L. E.
Pages: 6-7
Herpeslammelse og vaccination

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Larsen, L. E., Hoff-Jørgensen, R.
Publication date: 2001
Peer-reviewed: No

Publication information
Journal: DANSK VETERINÆRTIDSSKRIFT
Volume: 84
Issue number: 16
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
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
Source: orbit
Source-ID: 242175
Research output: Research › Journal article – Annual report year: 2001

Immunitetsstyring i slagtekalvebesætninger

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Sektion for
Ekotsiske Virussygdomme, Division of Virology
Contributors: Larsen, L. E., Viuff, B., Tjørnehøj, K., Røntved, C.
Pages: 1-6
Publication date: 2001
Peer-reviewed: No

Publication information
Journal: Kalveproducenten
Volume: 19
Phylogenetic characterisation of the G(L) sequences of equine arteritis virus isolated from semen of asymptomatic stallions and fatal cases of equine viral arteritis in Denmark

The study describes for the first time the phylogenetic relationship between equine arteritis virus (EAV) isolated from asymptomatic virus-shedding stallions and fatal cases of equine viral arteritis (EVA) in an European country. EAV was isolated from three dead foals and an aborted foetus during three different outbreaks of EVA. From these fatalities, the complete open reading frame 5, encoding the EAV GL protein, was amplified by reverse transcription-polymerase chain reaction and subjected to nucleotide sequence analysis. Furthermore, DNA sequences were obtained from virus isolated from semen samples of seven virus-shedding, but clinically healthy, Danish stallions. DNA sequence alignment revealed an overall divergence of 0-14 and 0-10% at the nucleotide and amino acid levels, respectively. Phylogenetic analysis including 24 previously published sequences revealed that European as well as North American "types" of EAV were present in the semen of asymptomatic carrier stallions and in fatal cases of EVA. Our results reveal that the presence of EAV-shedding stallions in Denmark represents a potential source of severe EVA.
Web of Science (2016): Impact factor 2.628
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.56 SJR 1.413 SNIP 1.21
Web of Science (2015): Impact factor 2.564
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.54 SJR 1.291 SNIP 1.256
Web of Science (2014): Impact factor 2.511
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 3 SJR 1.459 SNIP 1.471
Web of Science (2013): Impact factor 2.726
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.18 SJR 1.441 SNIP 1.569
Web of Science (2012): Impact factor 3.127
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 3.27 SJR 1.56 SNIP 1.729
Web of Science (2011): Impact factor 3.327
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): Impact factor 3.256
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
Antibody dynamics in BRSV-infected Danish dairy herds as determined by isotype-specific immunoglobulins

Using specific ELISAs, antibody levels of four different isotypes to bovine respiratory syncytial virus (BRSV) were determined in calves, following experimental BRSV infection. Most calves experienced an increase in the specific IgM and IgG1 titres about 6-10 days after infection with BRSV. The IgM titre was transient showing positive titres for only 5-10 days, while specific IgG1 was present for a longer time. IgA was detected concomitantly with IgM but at a lower level. Production of IgG2 anti-BRSV antibodies was detected from 3 weeks after infection. In two closed herds, repeated blood samplings were performed on young stock to analyse maternal immunity. The passively transferred antibodies were mainly of the IgG1 isotype and the half-life of IgG1 to BRSV was estimated to be 26.6 days. One of the herds had an outbreak of enzootic pneumonia, diagnosed to be caused by BRSV. Furthermore, another herd with acute BRSV was followed by weekly blood samples in six calves; in both herds IgM and IgG1 was detected shortly after the appearance of clinical signs. Serum samples from 50 Danish dairy herds (453 samples) were tested for immunoglobulins of the isotypes IgG1, IgG2 and IgM. The presence of antibodies to BRSV was widespread and more than 54% of the samples had BRSV antibodies of both the IgG1 and IgG2 isotypes indicating a high herd prevalence to BRSV. Test samples from two herds out of 50 were free from all isotypes to BRSV.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Virology, Division of Veterinary Diagnostics and Research, Secretariat
Pages: 329-341
Publication date: 2000
Peer-reviewed: Yes

Publication information
Journal: Veterinary Microbiology
Volume: 76
Issue number: 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): Impact factor 2.524
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): Impact factor 2.628
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.56 SJR 1.413 SNIP 1.21
Web of Science (2015): Impact factor 2.564
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.54 SJR 1.291 SNIP 1.256
Web of Science (2014): Impact factor 2.511
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 3 SJR 1.459 SNIP 1.471
Web of Science (2013): Impact factor 2.726
ISI indexed (2013): ISI indexed yes
Bovine respiratory syncytial virus (BRSV): A review

Bovine respiratory syncytial virus (BRSV) infection is the major cause of respiratory disease in calves during the first year of life. The study of the virus has been difficult because of its lability and very poor growth in cell culture. However, during the last decade, the introduction of new immunological and biotechnological techniques has facilitated a more extensive study of BRSV as illustrated by the increasing number of papers published. Despite this growing focus, many aspects of the pathogenesis, epidemiology, immunology etc, remain obscure. The course and outcome of the infection is very complex and unpredictable which makes the diagnosis and subsequent therapy very difficult. BRSV is closely related to human respiratory syncytial virus (HRSV) which is an important cause of respiratory disease in young children. In contrast to BRSV, the recent knowledge of HRSV is regularly extensively reviewed in several books and journals. The present paper contains an updated review on BRSV covering most aspects of the structure, molecular biology, pathogenesis, pathology, clinical features, epidemiology, diagnosis and immunology based on approximately 140 references from...
international research journals.

**General information**

State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Larsen, L. E.
Pages: 1+-
Publication date: 2000
Peer-reviewed: Yes

**Publication information**

Journal: Acta Veterinaria Scandinavica
Volume: 41
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): CiteScore 1.45 SJR 0.655 SNIP 1.077
Web of Science (2017): Impact factor 1.497
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): Impact factor 1.472
Web of Science (2016): Indexed yes

BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 0.98 SJR 0.644 SNIP 1.641
Web of Science (2015): Impact factor 1.23

BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 1.54 SJR 0.753 SNIP 1.21
Web of Science (2014): Impact factor 1.377

BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 1.41 SJR 0.539 SNIP 1.11
Web of Science (2013): Impact factor 1.382

ISI indexed (2013): ISI indexed no
Web of Science (2013): Indexed yes

BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 1.26 SJR 0.591 SNIP 0.789
Web of Science (2012): Impact factor 1.345

ISI indexed (2012): ISI indexed no
Web of Science (2012): Indexed yes

BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 1.42 SJR 0.664 SNIP 0.997
Web of Science (2011): Impact factor 1.367

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): Impact factor 1.196
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
Scopus rating (2008): SJR 0.338 SNIP 0.588
Extensive sequence divergence among bovine respiratory syncytial viruses isolated during recurrent outbreaks in closed herds

The nucleotides coding for the extracellular part of the G glycoprotein and the full SH protein of bovine respiratory syncytial virus (BRSV) were sequenced from viruses isolated from numerous outbreaks of BRSV infection. The isolates included viruses isolated from the same herd (closed dairy farms and veal calf production units) in different years and from all confirmed outbreaks in Denmark within a short period. The results showed that identical viruses were isolated within a herd during outbreaks and that viruses from recurrent infections varied by up to 11% in sequence even in closed herds. It is possible that a quasispecies variant swarm of BRSV persisted in some of the calves in each herd and that a new and different highly fit virus type (master and consensus sequence) became dominant and spread from a single animal in connection with each new outbreak. Based on the high level of diversity, however, the most likely explanation was that BRSV was (re)introduced into the herd prior to each new outbreak. These findings are highly relevant for the understanding of the transmission patterns of BRSV among calves and human respiratory syncytial virus among humans.
Increased pulmonary secretion of tumor necrosis factor-alpha in calves experimentally infected with bovine respiratory syncytial virus

Bovine respiratory syncytial virus (BRSV) is an important cause of respiratory disease among calves in the Danish cattle industry. An experimental BRSV infection model was used to study the pathogenesis of the disease in calves. Bronchoalveolar lung lavage (BAL) was performed on 28 Jersey calves, of which 23 were experimentally infected with BRSV and five were given a mock inoculum. The presence of the cytokine tumor necrosis factor alpha (TNF-alpha) in the BAL fluids was detected and quantified by a capture ELISA. TNF-alpha was detected in 21 of the infected animals. The amount of TNF-alpha in the BAL fluid of calves killed post inoculation day (PID) 2 and 4 was at the same very low level as in the uninfected control animals. Large amounts of TNF-alpha were detected on PID 6, maximum levels of TNF-alpha were reached on PID 7, and smaller amounts of TNF-alpha were seen on PID 8. The high levels of TNF-alpha appeared on the days where severe lung lesions and clinical signs were obvious and the amounts of BRSV-antigen were at their greatest. Although Pasteurellaceae were isolated from some of the BRSV-infected calves, calves treated with antibiotics before and through the whole period of the infection, as well as BRSV-infected calves free of bacteria reached the same level of TNF-alpha as animals from which bacteria were isolated from the lungs. It is concluded that significant quantities of TNF-alpha are produced in the lungs of the calves on PID 6-7 of BRSV infection. The involvement of TNF-alpha in the pathogenesis of, as well as the anti-viral immune response against, BRSV infection is discussed.
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 1.6 SJR 0.777 SNIP 0.718
Web of Science (2014): Impact factor 1.535
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 1.89 SJR 0.834 SNIP 0.797
Web of Science (2013): Impact factor 1.748
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 2.15 SJR 0.841 SNIP 0.913
Web of Science (2012): Impact factor 1.877
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 2.16 SJR 0.859 SNIP 0.995
Web of Science (2011): Impact factor 2.076
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): Impact factor 2.176
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
Keywords: bovine respiratory syncytial virus, experimental calf pneumonia, pathogenesis, tumor necrosis factor-alpha
DOIs:
10.1016/S0165-2427(00)00214-2
Source: orbit
Source-ID: 230772
Research output: Research - peer-review ; Journal article – Annual report year: 2000
Infection with bovine respiratory syncytial virus in calves is accompanied by a significant pulmonary secretion of tumor necrosis factor-alpha

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Virology, Division of Veterinary Diagnostics and Research
Contributors: Rontved, C., Tjørnehøj, K., Viuff, B., Larsen, L. E., Godson, D., Ronsholt, L., Alexandersen, S.
Pages: A1039-A1039
Publication date: 2000
Peer-reviewed: Yes

Publication information
Journal: Faseb Journal
Volume: 14
Issue number: 6
ISSN (Print): 0892-6638
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 4.53 SJR 2.438 SNIP 1.2
Web of Science (2017): Impact factor 5.595
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 4.68 SJR 2.694 SNIP 1.239
Web of Science (2016): Impact factor 5.498
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 4.68 SJR 2.831 SNIP 1.273
Web of Science (2015): Impact factor 5.299
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 4.92 SJR 3.049 SNIP 1.355
Web of Science (2014): Impact factor 5.043
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 5.5 SJR 3.188 SNIP 1.431
Web of Science (2013): Impact factor 5.48
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 5.6 SJR 3.147 SNIP 1.469
Web of Science (2012): Impact factor 5.704
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): CiteScore 5.4 SJR 3.141 SNIP 1.581
Web of Science (2011): Impact factor 5.712
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 3.519 SNIP 1.605
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 2.933 SNIP 1.344
BFI (2008): BFI-level 2
Serological responses of calves to experimental infection and reinfection with bovine respiratory syncytial virus (BRSV)

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Sektion for Ekotiske Virusssygdomme, Division of Virology
Contributors: Larsen, L. E., Tjørnehøj, K., Viuff, B., Røntved, C., Blixenkrone-Møller, M., Rønsholt, L.
Publication date: 2000
Peer-reviewed: No
Event: Abstract from international Congress of Veterinary Virology, Bresia, Italien.
Source: orbit
Source-ID: 240796
Research output: Research › Conference abstract for conference – Annual report year: 2000

The acute phase response of haptoglobin and serum amyloid A (SAA) in cattle undergoing experimental infection with bovine respiratory syncytial virus

The ability of a pure virus infection to induce an acute phase protein response is of interest as viral infections are normally considered to be less efficient in inducing an acute phase protein response than bacterial infections. This was studied in a bovine model for infection with bovine respiratory syncytial virus (BRSV), analysing the induction of the two most dominant bovine acute phase proteins haptoglobin and serum amyloid A (SAA). Strong and reproducible acute phase responses were detected for both proteins, peaking at around 7-8 days after inoculation of BRSV, while no response was seen in mock-inoculated control animals. The serum concentrations reached for SAA and haptoglobin during the BRSV-induced acute phase response were generally the same or higher than previously reported for bacterial infections in calves. The magnitude and the duration of the haptoglobin response was found to correlate well with the severity of clinical signs (fever) and with the extent of lung consolidation while SAA responded most rapidly to infection.

General information
State: Published
Organisations: Innate Immunology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Sektion for Ekotiske Virusssygdomme, Division of Virology, Virology
Contributors: Heegaard, P. M. H., Godson, D., Toussaint, M., Tjørnehøj, K., Larsen, L. E., Viuff, B., Rønsholt, L.
Pages: 151-159
Publication date: 2000
Peer-reviewed: Yes

Publication information
Journal: Veterinary Immunology and Immunopathology
Volume: 77
Issue number: 1-2
ISSN (Print): 0165-2427
Ratings:
BFI (2018): BFI-level 2
Diagnosis of enzootic pneumonia in Danish cattle: reverse transcription-polymerase chain reaction assay for detection of bovine respiratory syncytial virus in naturally and experimentally infected cattle

A reverse transcription-polymerase chain reaction (RT-PCR) assay was developed for detection of bovine respiratory syncytial virus (BRSV) in lung tissue of naturally and experimentally infected cattle. Primers were selected from the gene coding the F fusion protein, which is relatively conserved among BRSV isolates. The RT-PCR assay was highly specific, it yielded positive reactions only when performed on BRSV-infected cell cultures or tissues. The detection limit of the RT-PCR assay was assessed as 5 TCID50. BRSV was detected in tissues of the respiratory tract and in the tracheobronchial lymph node of calves euthanized 2-8 days after experimental infection with BRSV, whereas samples of other tissues and samples from mock-infected animals were negative at all time points. Examination of lung samples from 8 different regions of the lungs revealed that although the virus was most often found in the cranioventral lobules, it was frequently present in all lung lobules. Microbiologic examinations of all acute fatal cases of pneumonia (135 animals) in cattle submitted for diagnostic purposes during 1 year revealed that Actinomyces pyogenes (11%), Haemophilus somnus (10%), Pasteurella sp. (7%), and Pasteurella haemolytica (7%) were the most common bacterial agents found in the lungs. BRSV was identified using a conventional antigen enzyme-linked immunosorbent assay (ELISA) in 23 (17%) animals. The established BRSV-specific RT-PCR assay yielded positive results for the same 23 animals, in addition, 10 animals that were negative with the ELISA were positive with the RT-PCR assay. These results indicates that the RT-PCR assay can be a sensitive, reliable alternative to conventional diagnostic procedures.
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 1.21 SJR 0.621 SNIP 0.842
Web of Science (2017): Impact factor 1.219
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.27 SJR 0.642 SNIP 0.855
Web of Science (2016): Impact factor 0.925
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 1.44 SJR 0.695 SNIP 0.886
Web of Science (2015): Impact factor 1.196
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 1.36 SJR 0.792 SNIP 0.912
Web of Science (2014): Impact factor 1.353
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 1.41 SJR 0.712 SNIP 0.955
Web of Science (2013): Impact factor 1.232
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 1.37 SJR 0.748 SNIP 1.023
Web of Science (2012): Impact factor 1.181
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 1.34 SJR 0.714 SNIP 0.93
Web of Science (2011): Impact factor 1.214
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.739 SNIP 1.033
Web of Science (2010): Impact factor 1.381
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.728 SNIP 1.023
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.798 SNIP 0.958
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 0.616 SNIP 0.78
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.718 SNIP 0.908
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.593 SNIP 0.769
Scopus rating (2004): SJR 0.621 SNIP 0.799
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.806 SNIP 1.098
Scopus rating (2002): SJR 0.915 SNIP 1.036
Scopus rating (2001): SJR 0.806 SNIP 1.071
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 0.941 SNIP 0.936
Web of Science (2000): Indexed yes
Eksperimentel afprøvning af Triangle RSV vaccine mod bovint respiratorisk syncytial virus (BRSV) i konventionelt opdrættede kalve: Foreløbige resultater

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Sektion for Ekstotiske Virussygdomme, Division of Virology
Contributors: Larsen, L. E., Tjørnehøj, K., Rønsholt, L., Viuff, B.
Pages: 13-15
Publication date: 1999
Peer-reviewed: No

Publication information
Journal: SVS/SVIV Information
Volume: 67
Original language: Danish
Source: orbit
Source-ID: 241785
Research output: Research - Journal article – Annual report year: 1999

Geno-epidemiological investigations of bovine respiratory syncytial virus (brsv) strain differences and quasispecies during recurrent outbreaks: no evidence of herd persistence, but high level of identity between virus strains isolated in the same geographic region at a given time.

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Sektion for Ekstotiske Virussygdomme, Division of Virology, Secretariat
Contributors: Larsen, L. E., Tjørnehøj, K., Viuff, B., Nielsen, T. K.
Publication date: 1999
Peer-reviewed: No
Event: Abstract from "RSV after 43 Years" Symposium, Florida, USA.
Source: orbit
Source-ID: 240795
Research output: Research - Conference abstract for conference – Annual report year: 1999

Lungebetændelse hos kalve og BRS-virus: Fup eller fakta?

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Larsen, L. E.
Pages: 4-8
Publication date: 1999
Peer-reviewed: Unknown
Muligheder for at vaccination af danske kalve mod respirationsvejs virus

General information
State: Published
Organisations: National Veterinary Institute, Division of Veterinary Diagnostics and Research, Virology
Contributors: Larsen, L. E.
Publication date: 1999
Peer-reviewed: No
Source: orbit
Source-ID: 242155
Research output: Research › Conference abstract for conference – Annual report year: 1999

Påvisning af equin arteritis virus i et aborteret hestefoster

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Virology
Contributors: Holm, E., Larsen, L. E.
Pages: 12-14
Publication date: 1999
Peer-reviewed: No

Publication information
Journal: SVS/SVIV Information
Volume: 65
Original language: Danish
Source: orbit
Source-ID: 241784
Research output: Research › Journal article – Annual report year: 1999

Afprøvning af vacciner mod bovint respiratorisk syncytial virus (BRSV) hos kalve

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Virology, Division of Veterinary Diagnostics and Research
Contributors: Tjørnehøj, K., Rønsholt, L., Larsen, L. E., Viuff, B.
Pages: 3-7
Publication date: 1998
Peer-reviewed: No

Publication information
Journal: SVS/SVIV Information
Volume: 62
Original language: Danish
Source: orbit
Source-ID: 241773
Research output: Research › Journal article – Annual report year: 1998

Isotype specifikke ELISAs for BRSV antistoffer

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics
Contributors: Larsen, L. E., Holm, E.
Pages: 2
Publication date: 1998
Peer-reviewed: No
Luftvejslidelser hos kalve, ætiologi og diagnostik

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Tegtmeier, C., Larsen, L. E.
Pages: 35-38
Publication date: 1998
Peer-reviewed: No

Publication information
Journal: Dansk Veterinær Tidsskrift
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
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
Source: orbit
Source-ID: 241771
Research output: Research › Journal article – Annual report year: 1998

Molecular biological studies on Bovint Respiratory Syncytial Virus Infections in Calves

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Contributors: Larsen, L. E.
Publication date: 1998

Publication information
Original language: English
Source: orbit
Source-ID: 241782

Serological and genetic characterisation of bovine respiratory syncytial virus (BRSV) indicates that Danish isolates belong to the intermediate subgroup: no evidence of a selective effect on the variability of G protein nucleotide sequence by prior cell culture adaption and passages in cell culture or calves

Danish isolates of bovine respiratory syncytial virus (BRSV) were characterised by nucleotide sequencing of the G glycoprotein and by their reactivity with a panel of monoclonal antibodies (MAbs). Among the six Danish isolates, the
overall sequence divergence ranged between 0 and 3% at the nucleotide level and between 0 and 5% at the amino acid level. Sequence divergences of 7-8%, 8-9% and 2-3% (nucleotide) and 9-11%, 12-16% and 4-6% (amino acid) were observed in the comparison made between the group of Danish isolates and the previously sequenced 391-2USA, 127UK and 220-69Bel isolates, respectively. Phylogenetic analysis showed that the Danish isolates formed three lineages within a separate branch of the phylogenetic tree. Nevertheless, the Danish isolates were closely related to the 220-69Bel isolate, the prototype of the intermediate antigenic subgroup. The sequencing of the extracellular part of the G gene of additional 11 field BRSV viruses, processed directly from lung samples without prior adaption to cell culture growth, revealed sequence variabilities in the range obtained with the propagated virus. In addition, several passages in cell culture and in calves had no major impact on the nucleotide sequence of the G protein. These findings indicated that the previously established variabilities of the G protein of RS virus isolates were not attributable to mutations induced during the propagation of the virus. The reactivity of the Danish isolates with G protein-specific MAbs were similar to that of the 220-69Bel isolate. Furthermore, the sequence of the immunodominant region was completely conserved among the Danish isolates on one side and the 220-69Bel isolate on the other. When combined, these data strongly suggested that the Danish isolates belong to the intermediate subgroup.

**General information**

State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Sektion for Eksotiske Virussygdomme, Division of Virology
Contributors: Larsen, L. E., Uttenthal, Å., Arctander, P., Tjørnehøj, K., Viuff, B., Røntved, C., Rønsholt, L., Alexandersen, S., Blixenkrone-Moller, M.
Pages: 265-279
Publication date: 1998
Peer-reviewed: Yes

**Publication information**

Journal: Veterinary Microbiology
Volume: 62
Issue number: 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): Impact factor 2.524
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): Impact factor 2.628
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 2.56 SJR 1.413 SNIP 1.21
Web of Science (2015): Impact factor 2.564
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 2.54 SJR 1.291 SNIP 1.256
Web of Science (2014): Impact factor 2.511
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 3 SJR 1.459 SNIP 1.471
Web of Science (2013): Impact factor 2.726
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 3.18 SJR 1.441 SNIP 1.569
Web of Science (2012): Impact factor 3.127
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
Vaccination af slagtekalve mod bovint respiratorisk syncytial virus (BRSV)

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Sektion for Eksotiske Virussygdomme, Division of Virology
Contributors: Larsen, L. E., Tjærnehøj, K.
Pages: 4-6
Publication date: 1998
Peer-reviewed: No

Publication information
Journal: SVS/SVIV Information
Volume: 63
Original language: Danish
Source: orbit
Source-ID: 241779
Variability of the G-protein of Bovine respiratory syncytial virus

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Sektion for Ekstosiske Virusygdomme, Division of Virology
Contributors: Larsen, L. E., Jensen, N. E., Tjørnehøj, K., Viuff, B., Nielsen, T., Uttenhal, Å.
Publication date: 1997
Peer-reviewed: No
Event: Abstract from 4th International Congress of Veterinary Virology, Edinburgh, United Kingdom.
Source: orbit
Source-ID: 240791

Variability of the G-protein of Bovine respiratory syncytial virus

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Sektion for Ekstosiske Virusygdomme, Division of Virology
Contributors: Larsen, L. E., Uttenhal, Å., Archtander, P., Tjørnehøj, K., Viuff, B., Røntved, C., Rønsholt, L., Alexandersen, S., Blixenkrone-Møller, M.
Publication date: 1997
Peer-reviewed: No
Event: Abstract from International Congress on Negative Strand Viruses, Dublin, Ireland.
Source: orbit
Source-ID: 240793

Diagnosis of BRSV infections in calves

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Sektion for Ekstosiske Virusygdomme, Division of Virology
Contributors: Larsen, L. E., Uttenhal, Å., Viuff, B., Røntved, C., Rønsholt, L., Tjørnehøj, K., Alexandersen, S.
Publication date: 1996
Peer-reviewed: No
Event: Abstract from First Nordic Veterinary Immunology Meeting, Copenhagen, Denmark.
Source: orbit
Source-ID: 241770

Projects:

Redskaber til kontrol af virusinfektioner i danske svin
Aktivitet 1. Konsekvenser af blitzvaccination mod PRRSV under danske forhold Formålet med denne aktivitet er at undersøge, om massevaccination 3-4 gange årligt giver anledning til reproduktionsproblemer, fødsel af viræmiske grise og forekomst af rekombinante stammer Massevaccinationen inkluderer vaccinati-on af avlsdyr i sidste trimester, hvilket betyder, at vaccinationen vil kunne give anledning til overførsel af virus til fosteret, som eventuelt kan resultere i kastninger og fødsel af PRRS virus positive pattegrise. En anden ulempe ved denne procedure er risikoen for, at der sker blanding (rekombination) mellem vaccinevir-us og vildtvirus-stammer, så der opstår nye stammer af PRRS, som potentielt kan være mere aggressive. Undersøgelsen udføres i første omgang i 1 dansk PRRSV positive besætning I forbindelse med den første massevaccination udtages blodprøver fra 10 søer i 3 ugehold i henholdsvis 1, 2 og 3 trimester (dag 20-30, 60-70 og 90-100 efter løbning). Der udtages endvidere blodprøver fra de samme søer i forbindelse med faring og der indsamles PUCS, foretages yveraftørring af søerne og haler og testikler indsamles kuldvis fra alle pattegrise fra de inkluderede søer og fryses. Spytprøver indsamles ved fravænning.<br/>Prøverne undersøges for PRRSV. Prøverne undersøges for PRRSV. Aktivitet 2. Overvågning af diversite-ten af danske PRRSV stammer. Formålet er at undersøge om der udvikles nye varianter af PRRSV der ikke dækkes af de eksisterende vacciner. I samarbejde med praktiserende dyrlæger og SEGES Svineprodukti-on virus fra atypiske udbrud af PRRSV blive fuld genom sektventeret og undersøgt ved bioinformatiske værktøjer. Det tilstræbes at sektvende 20 danske isolater fra problembesætninger i 2019.<br/>På
Kort sigt får svineproducenterne og deres rådgivere adgang til nyeste viden om, hvordan nye og gamle virus opfører sig i besætningerne og påvises hos grisene, og på mellemlang sigt vil det medføre bedre rådgivning ude på staldgangen, når virus skal kontrolleres.<br/>

Larsen, L. E., PI, National Veterinary Institute, Virology
Kvisgaard, L. K., Project Participant, Virology, National Veterinary Institute
Kristensen, C. S., Project Participant, Videncenter for Svineproduktion, Landbrug & Fødevarer
01/01/2019 → 31/12/2019
Nature of activity type: Research
Collaborators: Videncenter for Svineproduktion, Landbrug & Fødevarer
Project: Research

**Optimeret sygdomsforebygglelse i slægtesvinebesætninger**


**Finansiering Svineafgiftsfonden**


Jorsal, S. E. L., Project Manager, National Veterinary Institute, Diagnostic & Development
Goecke, N. B., PhD Student, National Veterinary Institute, Virology
Larsen, L. E., Project Participant, National Veterinary Institute, Virology
Hjulsager, C. K., Project Participant, National Veterinary Institute, Virology
Skovgaard, K., Project Participant, National Veterinary Institute, Innate Immunology
Svineafgiftsfonden: DKK1,776,000.00
01/01/2015 → 31/12/2017
Collaborators: SEGES Pig Research Center
Documents:

**Impact of low-grade inflammation on influenza**

Starbæk, S. M. R., PhD Student, National Veterinary Institute
Skovgaard, K., Main Supervisor, National Veterinary Institute
Heegaard, P. M. H., Supervisor, National Veterinary Institute
Jungersen, G., Supervisor, National Veterinary Institute
Larsen, L. E., Supervisor, National Veterinary Institute
Institut stipendie (DTU)
01/12/2016 → 30/11/2019
Award relations: Impact of low-grade inflammation on influenza
Project: PhD

**Host range selection, virulence determinants and pathogenesis of influenza A viruses: Towards the identification of new antiviral drugs and vaccines**

Andersen, M. R., PhD Student, National Veterinary Institute
Larsen, L. E., Main Supervisor, National Veterinary Institute
Kvisgaard, L. K., Supervisor, National Veterinary Institute
Institut stipendie (DTU)
01/08/2015 → 31/12/2018
Award relations: Host range selection, virulence determinants and pathogenesis of influenza A viruses: Towards the identification of new antiviral drugs and vaccines
Project: PhD

Animal Influenza Viruses - Impacts of influenza virus in Danish swine herds
Ryt-Hansen, P., PhD Student, National Veterinary Institute
Larsen, L. E., Main Supervisor, National Veterinary Institute
Plösz, B. G., Supervisor, Department of Environmental Engineering
Krog, J. S., Supervisor, National Veterinary Institute
Larsen, I., Supervisor
Sonne Kristensen, C., Supervisor
Samfinansierede - Virksomhed
01/10/2016 → 30/09/2019
Award relations: Animal Influenza Viruses - Impacts of influenza virus in Danish swine herds
Project: PhD

Diagnostic methods for veterinary pathogens
Goekce, N. B., PhD Student, National Veterinary Institute
Larsen, L. E., Main Supervisor, National Veterinary Institute
Hjulsager, C. K., Supervisor, National Veterinary Institute
Skovgaard, K., Supervisor, National Veterinary Institute
Bøtner, A., Examiner, National Veterinary Institute
Salicio, S. C., Examiner
Simon, G., Examiner
Salicio, S. C., Examiner
Samfinansieret - Andet
15/12/2014 → 30/09/2018
Award relations: Diagnostic methods for veterinary pathogens
Project: PhD

Molecular biology of foot-and-mouth disease virus
Kjær, J., PhD Student, National Veterinary Institute
Belsham, G., Main Supervisor, National Veterinary Institute
Rasmussen, T. B., Supervisor, National Veterinary Institute
Larsen, L. E., Examiner, National Veterinary Institute
Bukh, J., Examiner
Ryan, M. D., Examiner
Offentlig finansiering
15/12/2014 → 20/06/2018
Award relations: Molecular biology of foot-and-mouth disease virus
Project: PhD

Development of methods for in-line detection and identification of viruses in water
Uhrbrand, K., PhD Student, National Food Institute
Christensen, L. S., Main Supervisor, National Food Institute
Hedlund, K., Supervisor
Myrmel, M., Supervisor
Larsen, L. E., Examiner
Cook, N., Examiner
Simonsson, M., Examiner
Offentlig finansiering
01/08/2008 → 27/06/2012
Award relations: Development of methods for in-line detection and identification of viruses in water
Project: PhD

Identification of risk factors for acquiring ADV in Danish mink farms
Hagberg, E. E., PhD Student, Department of Bio and Health Informatics
Pedersen, A. G., Main Supervisor, Department of Bio and Health Informatics
Krarup, A., Supervisor
Larsen, L. E., Supervisor
Sicheritz-Pontén, T., Examiner, Department of Bio and Health Informatics
Decaro, N., Examiner
Kølsen Fischer, T., Examiner
Industrial PhD
01/08/2013 → 06/06/2017
Award relations: Identification of risk factors for acquiring ADV in Danish mink farms
Project: PhD

Lab-on-chip system for virus detection in water
Kirkegaard, J., PhD Student, Department of Micro- and Nanotechnology
Rozlosnik, N., Main Supervisor, Risø National Laboratory for Sustainable Energy
Larsen, L. E., Supervisor, National Veterinary Institute
Svendsen, W. E., Supervisor, Department of Micro- and Nanotechnology
Emnéus, J., Examiner, Department of Micro- and Nanotechnology
Heegaard, N. H. H., Examiner
Merkoçi, A., Examiner
Heegaard, N. H. H., Examiner
Merkoçi, A., Examiner
Anden EU-finansiering
01/10/2013 → 11/01/2017
Award relations: Lab-on-chip system for virus detection in water
Project: PhD

Hepatitis E virus i svin
Krog, J. S., PhD Student, National Veterinary Institute
Larsen, L. E., Main Supervisor, National Veterinary Institute
Breum, S. Ø., Supervisor, National Veterinary Institute
Schultz, A. C., Supervisor
Ethelberg, S., Examiner
van der Poel, W. H., Examiner
Institut stipendie (DTU) Samf.
01/06/2010 → 30/09/2013
Award relations: Hepatitis E virus i svin
Project: PhD

Animale influenza virus
Fobian, K., PhD Student, National Veterinary Institute
Larsen, L. E., Main Supervisor, National Veterinary Institute
Breum, S. Ø., Supervisor, National Veterinary Institute
Belsham, G., Examiner, National Veterinary Institute
Bragstad, K., Examiner
Harder, T. C., Examiner
Institut stipendie (DTU) Samf.
01/06/2010 → 05/11/2014
Award relations: Animale influenza virus
Project: PhD

Optimizing the bulk milk tank surveillance in Danish dairy cattle
Foddai, A., PhD Student, National Veterinary Institute
Lind, P., Main Supervisor, National Veterinary Institute
Hisham Beshara Halasa, T., Supervisor, National Veterinary Institute
Utenthal, Å., Supervisor, National Veterinary Institute
Larsen, L. E., Examiner, National Veterinary Institute
Houe, H., Examiner
Lindberg, A., Examiner
Houe, H., Examiner
Institut, samfinansiering
01/07/2010 → 09/03/2015
Award relations: Optimizing the bulk milk tank surveillance in Danish dairy cattle
Project: PhD
Identification of the determinants of efficient pestivirus replication
Risager, P. C., PhD Student, National Veterinary Institute
Belsham, G., Main Supervisor, National Veterinary Institute
Rasmussen, T. B., Supervisor, National Veterinary Institute
Larsen, L. E., Examiner, National Veterinary Institute
Becher, P., Examiner
Lindberg, M., Examiner
Institut, samfinansiering
01/01/2010 → 18/12/2013
Award relations: Identification of the determinants of efficient pestivirus replication
Project: PhD

Porcine Reproductive and respiratory Syndrome Virus (PRRSV)
Kvisgaard, L. K., PhD Student, National Veterinary Institute
Larsen, L. E., Main Supervisor, National Veterinary Institute
Hjulsager, C. K., Supervisor, National Veterinary Institute
Rasmussen, T. B., Examiner, National Veterinary Institute
Bækbo, P., Examiner
Stadejek, T., Examiner
Anden EU-finansiering
01/07/2010 → 30/09/2013
Award relations: Porcine Reproductive and respiratory Syndrome Virus (PRRSV)
Project: PhD

Functional analysis of replication determinants in classical swine fever virus
Hadsbjerg, J., PhD Student, National Veterinary Institute
Belsham, G., Main Supervisor, National Veterinary Institute
Rasmussen, T. B., Supervisor, National Veterinary Institute
Larsen, L. E., Examiner, National Veterinary Institute
Becher, P., Examiner
Knudsen, C. R., Examiner
Institut stipendie (DTU)
01/09/2013 → 05/04/2017
Award relations: Functional analysis of replication determinants in classical swine fever virus
Project: PhD

Tailored Design of Innovative Vaccine against PRRSV
Welner, S., PhD Student, Section for Public sector service and commercial diagnostics
Larsen, L. E., Main Supervisor, National Veterinary Institute
Jungersen, G., Supervisor, National Veterinary Institute
Lund, O., Supervisor, Department of Bio and Health Informatics
Rasmussen, T. B., Examiner, National Veterinary Institute
Graham, S. P., Examiner
Lundegaard, C., Examiner, Center for Biological Sequence Analysis
Graham, S. P., Examiner
Institut stipendie (DTU)
01/09/2013 → 20/12/2017
Award relations: Tailored Design of Innovative Vaccine against PRRSV
Project: PhD

Non-coding RNA mediated gene regulation during in fluenza infection
Brogaard, L., PhD Student, National Veterinary Institute
Skovgaard, K., Main Supervisor, National Veterinary Institute
Larsen, L. E., Supervisor, National Veterinary Institute
Lorenzen, N., Examiner, National Veterinary Institute
Salicio, S. C., Examiner
Tchilian, E. Z., Examiner
Salicio, S. C., Examiner
Tchilian, E. Z., Examiner
Institut stipendie (DTU)
15/07/2013 → 31/01/2018
Award relations: Non-coding RNA mediated gene regulation during in fluenza infection
Project: PhD
**Pigvac: A plant-produced immunoenhanced pig vaccine against PRRS**

Projektet skal udvikle en vaccine mod den problematiske svinesygdom PRRS. PRRS virus er den mest betydningsfulde smitsomme sygdom hos svin på verdensplan - herunder Danmark. Sygdommen, der blandt andet medfører aborter hos søer og høj dødelighed blandt smågrise, har stor indvirknings på dyrevelfærd samt landbrugsøkonomi, og der bliver brugt store mængder antibiotika på at behandle PRRS-associerede vejrtrækningsproblemer. Derfor vil vi lave en vaccine med viruslignende partikler med virusproteinet GP5 på overfladen, som kan påvirke immunforsvaret, så grisen bliver beskyttet mod PRRS. Planen er, at de viruslignende partikler med GP5-proteinerne på overfladen skal produceres i planter, da det giver fordele i forhold til omkostninger, opskalerbarhed og sikkerhed.

Sørensen, M. R., Project Participant, National Veterinary Institute, Section for Immunology and Vaccinology
Jungersen, G., Approving Authority, National Veterinary Institute, Section for Immunology and Vaccinology
Larsen, L. E., Project Participant, National Veterinary Institute, Section for Virology
01/01/2014 → 31/12/2018
Collaborators: Aarhus University, Boehringer Ingelheim GmbH
Project: Research

**Swine plasma immunoglobulins against post-weaning diarrhoea**

Fravænningsdiarré medfører nedsat velfærd og økonomiske tab som følge af sygdom og dødsfald og udgifter til behandling (antibiotika og zink) og er en udbredt lidelse i intensiv svineproduktion. I projektet udvikles nye metoder og produkter til beskyttelse mod infektioner, der indebærer at indføre immunoglobulin direkte fra plasma til åbningen til en pris, der er økonomisk bæredygtig for svineproducenter. Det virker ved lokalt i tarmen at forhindre vikingsomkring af smittefremkaldende mikroorganismer. Den midlertidige lokale immunitet, der hermed etableres, i tilfælde af svinevelfærd og produktivitet ved at formindske forekomsten af sygdom og dødsfald væsentligt i den sygdomsbelastede fravænngsperiode under samtidig minimering af behovet for behandling med antibiotika og zink.

Heegaard, P. M. H., Project Applicant, National Veterinary Institute, Division of Veterinary Diagnostics and Research, Innate Immunology
Larsen, L. E., Project Participant, National Veterinary Institute, Division of Veterinary Diagnostics and Research, Virology
Hedegaard, C. J., Project Participant, National Veterinary Institute, Section for Immunology and Vaccinology
Project ID: 22619
GUDP - Projekt. Udviklings- og demonstrationsprojekt med forskningsandel: DKK5.017.193.00
01/10/2012 → 30/09/2015
Collaborators: KibiF ApS, Videncenter for Svineproduktion, Landbrug & Fødevarer
Award relations: Swine plasma immunoglobulins against post-weaning diarrhoea
Project: Research

**Bayesian statistical analysis to assess serological testing strategies for avian influenza surveillance in Europe**

Club 5 Joint Research 2012
Larsen, L. E., Project Participant, National Veterinary Institute, Division of Veterinary Diagnostics and Research, Virology
Project ID: 22531
01/10/2012 → 31/10/2013
Collaborators: National Veterinary Institute, Animal Health and Veterinary Laboratories Agency, CVI Lelystad
Project: Research

**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 investigative 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.
Larsen, L. E., Project Participant, National Veterinary Institute, Division of Veterinary Diagnostics and Research, Virology
Project ID: 22523
01/09/2011 → 30/09/2012
Keywords: Club5 Microarray virus
Collaborators: Animal Health and Veterinary Laboratories Agency, CVI Lelystad, Agence nationale de la sécurité sanitaire, alimentation, environnement et travail
ESNIP 3: 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.

Larsen, L. E., Project Manager, National Veterinary Institute, Division of Veterinary Diagnostics and Research, Virology
Project ID: 22492
01/10/2010 → 31/10/2013
Keywords: ESNIP3
Documents:
ESNIP3_part_B.pdf
Project: Research

PCV2 award 2008 fra Boehringer Ingelheim
Larsen, L. E., Project Manager, National Veterinary Institute, Division of Veterinary Diagnostics and Research, Section for Veterinary Diagnostics
Jensen, T. K., Project Participant, National Veterinary Institute, Division of Veterinary Diagnostics and Research, Section for Veterinary Diagnostics
Project ID: 22335
Gaver, Udenlandske offentlige og private: DKK186,238.00
01/12/2008 → 31/12/2015
Award relations: PCV2 award 2008 fra Boehringer Ingelheim
Project: Research

Indsættelsesstrategi, lungebetændelse eller intensiv fodring som årsag til leverbylder
Jungersen, M. V., Project Manager
Larsen, L. E., Project Participant, National Veterinary Institute, Division of Veterinary Diagnostics and Research, Virology
Graumann, A. M., Project Participant, AgroTech AS
Project ID: 22393
Forsk. Private danske - Fonde: DKK168,000.00
01/01/2009 → 12/07/2014
Collaborators: Aarhus University, AgroTech AS
Award relations: Indsættelsesstrategi, lungebetændelse eller intensiv fodring som årsag til leverbylder
Project: Research

Ny spædgrisediarre i Danmark. Afklaering af årsagsforhold og diagnostik samt effekt af behandlinger.
Angen, Ø., Project Manager, National Veterinary Institute, Division of Veterinary Diagnostics and Research
Jensen, T. K., Project Manager, National Veterinary Institute, Division of Veterinary Diagnostics and Research
Mølbak, L., Project Manager, National Veterinary Institute, Division of Veterinary Diagnostics and Research
Kokotovic, B., Project Manager, National Veterinary Institute, Division of Veterinary Diagnostics and Research
Jorsal, S. E. L., Project Manager, National Veterinary Institute, Division of Veterinary Diagnostics and Research Bækbo, P., Project Manager, Landbrug & Fødevarer, Videncenter for Svineproduktion,
Project ID: 22438
**New tools and approaches to control Porcine Reproductive and Respiratory Syndrome in the EU and Asia**

Nauwynck, H., Project Manager, University Gent

Rodrigo, R., Contact Person, Consejo Superior de Investigaciones Cientificas

Sanchez-Serrano, J. J., Contact Person, Consejo Superior de Investigaciones Cientificas

Domingo, M., Contact Person, CReSA - Centre for Animal Health Research

Taranzi, L., Contact Person, Parco Technologico Padano S.R.L.

Piatti, G., Contact Person, Parco Technologico Padano S.R.L.

Griot, C., Contact Person, Eidgenoessisches Volkswirtschaftsdepartement

Summermatter, K., Contact Person, Eidgenoessisches Volkswirtschaftsdepartement

Larsen, L. E., Project Manager, National Veterinary Institute, Division of Veterinary Diagnostics and Research, Virology

Trebbien, R., Project Participant, National Veterinary Institute, Division of Veterinary Diagnostics and Research, Virology

Wijaszka, T., Contact Person, Panstwowy Instytut Weterynaryjny

Kotelba, B., Contact Person, Panstwowy Instytut Weterynaryjny

Waddell, D., Contact Person, The University of Edinburgh, Old College

Campbell, F., Contact Person, The University of Edinburgh, Old College

Boriello, P., Contact Person, The Secretary of State for Environment, Food and Rural Affairs, Nobel House

Thorns, C., Contact Person, The Secretary of State for Environment, Food and Rural Affairs, Nobel House

Bianchi, A., Contact Person, Stichting Dienst Landbouwkundig Onderzoek

vn Zijderfeld, F., Contact Person, Stichting Dienst Landbouwkundig Onderzoek

Tong, G., Contact Person, Shanghai Veterinary Research Institute, Chinese Academy of Agricultural Sciences

Lin, J., Contact Person, Shanghai Veterinary Research Institute, Chinese Academy of Agricultural Sciences

Bui, Q. A., Contact Person, Ministry of Agriculture and Rural Development

Seidler, R., Contact Person, Boehringer Ingelheim GmbH

Papp, H., Contact Person, Boehringer Ingelheim GmbH

External Project ID: info:eu-repo/grantAgreement/EC/FP7/245141

**Forsk. EU - Rammeprogram: DKK1.92**

01/01/2010 → 31/12/2014

Collaborators: Ministry of Agriculture and Rural Development, Stichting Dienst Landbouwkundig Onderzoek, Chinese Academy of Agricultural Sciences, Boehringer Ingelheim GmbH, CReSA - Centre for Animal Health Research, The University of Edinburgh, Old College, Parco Technologico Padano S.R.L., Parco Technologico Padano, The Secretary of State for Environment, Food and Rural Affairs, Nobel House, , Federal Department of Economic Affairs, Education and Research, Secretary of State for Environment, Food and Rural Affairs, Consejo Superior de Investigaciones Cientificas, Eidgenoessisches Volkswirtschaftsdepartement, Shanghai Veterinary Research Institute, Chinese Academy of Agricultural Sciences, , Panstwowy Instytut Weterynaryjny, University of Edinburgh, University Gent, Ghent University

Award relations: New tools and approaches to control Porcine Reproductive and Respiratory Syndrome in the EU and Asia

Project: Research

---

**Velfærdsmæssige behov omkring kælvning og umiddelbart efter fødsel hos malkekvæg**

Larsen, L. E., Project Manager, National Veterinary Institute, Division of Veterinary Diagnostics and Research

Heegaard, P. M. H., Project Manager, National Veterinary Institute, Division of Veterinary Diagnostics and Research

Jungersen, G., Project Manager, National Veterinary Institute, Division of Veterinary Diagnostics and Research

Project ID: 22441

Forskningsprojekter - Fødevareministeriet: DKK727,799.00

01/01/2009 → 31/12/2012

Award relations: Velfærdsmæssige behov omkring kælvning og umiddelbart efter fødsel hos malkekvæg

Project: Research

---

**Betydning af tidlig kontakt for kalvens velfærd**

Projektet vil klargøre virkningen af forskellige typer af social kontakt på kalves adfærd og sundhed, samt sammenhængen mellem kalvens alder og virkningen af social kontakt mellem andre kalve. Projektet vil således tilvejebringe den viden, der savnes i den aktuelle debat om, hvorvidt kalve i enkeltekasse skal kunne røre hinanden. Ud over dette klargøres virkningen af at reducere den sociale kontakt mellem kalve til visuel kontakt gennem den første del af måløkeperioden frem for hele måløkeperioden.

Jensen, M. B., Project Manager, Aarhus University

Larsen, L. E., Project Participant, National Veterinary Institute, Division of Veterinary Diagnostics and Research, Virology
Zoonotiske aspekter af Hepatitis E i Danmark


Larsen, L. E., Project Manager, National Veterinary Institute, Division of Veterinary Diagnostics and Research, Virology
Christensen, L. S., Project Participant, National Food Institute
Böttiger, B., Project Participant, Statens Serum Institut
Larsen, H. H., Project Participant, Statens Serum Institut

Project ID: 22442
Forskningsprojekter - Fødevareministeriet: DKK917,000.00
01/01/2010 → 31/12/2012
Collaborators: Statens Serum Institut
Award relations: Zoonotiske aspekter af Hepatitis E i Danmark
Project: Research

Activities:

**Immunitetsstyring i kvægbesætninger**
Period: 21 Mar +2018
Lars Erik Larsen (Invited speaker)
Virology
National Veterinary Institute

Related event

**Danske kvæfgadlyægser Forening - Årsrøde 2018**
21/03/2018 → 22/03/2018
Kolding, Denmark
Activity: Talks and presentations › Conference presentations

**Influenza - det nye sort**
Period: 24 Oct 2018
Lars Erik Larsen (Invited speaker)
Charlotte Sonne Kristensen (Invited speaker)
Virology
National Veterinary Institute

Related event

**Svinekongressen**
23/10/2018 → 24/10/2018
Herning, Denmark
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations
Control of influenza in a One Health perspective – do we have the tools and are they used properly?
Period: 4 Oct 2018
Lars Erik Larsen (Invited speaker)
Jesper Schak Krog (Other)
Virology
National Veterinary Institute

Related event
NBVCG seminar: Contingency Planning – focus on: vaccination, animal welfare, wildlife and costs
04/10/2018 → 05/10/2018
Riga, Latvia
Activity: Talks and presentations » Talks and presentations in private or public companies and organisations

Virus’ overlevelse i forskellige miljøer med fokus på Hepatitis E
Period: 29 Aug 2018
Lars Erik Larsen (Invited speaker)
Virology
National Veterinary Institute
Degree of recognition: National

Related event
Den Danske Dyrlægeforeningens årsmøde 2018
27/10/2018 → 29/10/2018
Nyborg, Denmark
Activity: Talks and presentations » Talks and presentations in private or public companies and organisations

PRRSV CONTROL – THE DANISH WAY
Period: 17 Jun 2018
Lars Erik Larsen (Keynote speaker)
Virology
National Veterinary Institute
Section for Public sector service and commercial diagnostics

Related event
26th International Pig Veterinary Society (IPVS) Congres
18/06/2018 → 22/06/2018
Quipeng
Activity: Talks and presentations » Conference presentations

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 part, 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.

DVHS (Event)
Period: 1 Nov 2016 → 1 Nov 2019
Lars Erik Larsen (Member)
Virology
National Veterinary Institute

Description
Dansk veterinær Hyologisk Forening

Related event

DVHS
01/01/1999 → …
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

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.

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.

**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

**Press clippings:**

**Svin smitter svin med influenza**
Lars Erik Larsen
01/08/2009
National Veterinary Institute, Division of Veterinary Diagnostics and Research, Virology

**Media contribution (1)**

**Svin smitter svin med influenza**
01/08/2009
Print
http://www.dyrlaegemagasinet.dk
PUB-OA
Lars Erik Larsen
National Veterinary Institute, Division of Veterinary Diagnostics and Research, Virology
Press/Media: Press / Media

**Valle mod Kalvediarré**
Lars Erik Larsen
01/01/2008
National Veterinary Institute, Division of Veterinary Diagnostics and Research, Virology

**Media contribution (1)**
Valle mod Kalvediarré
01/01/2008
Print
Lars Erik Larsen
National Veterinary Institute, Division of Veterinary Diagnostics and Research, Virology
Press/Media: Press / Media