Determinants of the VP1/2A junction cleavage by the 3C protease in foot-and-mouth disease virus infected cells

The foot-and-mouth disease virus (FMDV) capsid precursor, P1-2A, is cleaved by FMDV 3C protease to yield VP0, VP3, VP1 and 2A. Cleavage of the VP1/2A junction is the slowest. Serotype O FMDVs with uncleaved VP1-2A (having a K210E substitution in VP1; at position P2 in cleavage site) have been described previously and acquired a second site substitution (VP1 E83K) during virus rescue. Furthermore, introduction of the VP1 E83K substitution alone generated a second site change at the VP1/2A junction (2A L2P, position P2' in cleavage site). These virus adaptations have now been analysed using Next Generation Sequencing to determine sub-consensus level changes in the virus; this revealed other variants within the E83K mutant virus population that changed residue VP1 K210. The construction of serotype A viruses with a blocked VP1/2A cleavage site (containing K210E) has now been achieved. A collection of alternative amino acid substitutions were made at this site and the properties of the mutant viruses determined. Only the presence of a positively charged residue at position P2 in the cleavage site permitted efficient cleavage of the VP1/2A junction, consistent with analyses of diverse FMDV genome sequences. Interestingly, in contrast to the serotype O virus results, no second site mutations occurred within the VP1 coding region of serotype A viruses with the blocked VP1/2A cleavage site. However, some of these viruses acquired changes in the 2C protein that is involved in enterovirus morphogenesis. These results have implications for the testing of potential antiviral agents targeting the FMDV 3C protease.
Distinct roles for the IIId2 sub-domain in pestivirus and picornavirus internal ribosome entry sites

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

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Genome organization, translation and replication of foot-and-mouth disease virus RNA

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Organisations: National Veterinary Institute, Section for Virology
Authors: Martinez-Salas, E. (Ekstern), Belsham, G. (Intern)
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Chapter: 2
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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, saffoldivirus, 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.
Validation of a serum neutralization test for detection of antibodies specific to cyprinid herpesvirus 3 in infected common and koi carp (Cyprinus carpio)

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

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Pages: 687-701
Publication date: 2017
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.
A novel multiplex RT-qPCR method based on dual-labelled probes suitable for typing all known genotypes of viral haemorrhagic septicaemia virus

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

General information

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Organisations: National Veterinary Institute, Section for Virology, University of Santiago de Compostela
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Foot-and-mouth disease (FMD) remains one of the most economically important infectious diseases of production animals globally. Vaccination can successfully control this disease, however, current vaccines are imperfect. They are made using chemically inactivated FMD virus (FMDV) that is produced in large-scale mammalian cell culture under high containment conditions. Here, we have expressed the FMDV capsid protein precursor (P1-2A) of strain O1 Manisa alone or with the FMDV 3C protease (3Cpro) using a "single cycle" packaged alphavirus self-replicating RNA based on Semliki Forest virus (SFV). When the FMDV P1-2A was expressed with 3Cpro then processing of the FMDV capsid precursor protein is observed within cells and the proteins assemble into empty capsid particles. The products interact with anti-FMDV antibodies in an ELISA and bind to the integrin αvβ6 (a cellular receptor for FMDV). In cattle vaccinated with these rSFV-FMDV vectors alone, anti-FMDV antibodies were elicited but the immune response was insufficient to give protection against FMDV challenge. However, the prior vaccination with these vectors resulted in a much stronger immune response against FMDV post-challenge and the viremia observed was decreased in level and duration. In subsequent experiments, cattle were sequentially vaccinated with a rSFV-FMDV followed by recombinant FMDV empty capsid particles, or vice versa, prior to challenge. Animals given a primary vaccination with the rSFV-FMDV vector and then boosted with FMDV empty capsids showed a strong anti-FMDV antibody response prior to challenge, they were protected against disease and...
no FMDV RNA was detected in their sera post-challenge. Initial inoculation with empty capsids followed by the rSFV-FMDV was much less effective at combating the FMDV challenge and a large post-challenge boost to the level of anti-FMDV antibodies was observed. This prime-boost system, using reagents that can be generated outside of high-containment facilities, offers significant advantages to achieve control of FMD by vaccination.

**General information**

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Organisations: National Veterinary Institute, Section for Virology, Karolinska Institutet, The Pirbright Institute
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BFI (2008): BFI-level 1
Scopus rating (2008): SJR 2.323 SNIP 0.96
Web of Science (2008): Indexed yes
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Web of Science (2006): Indexed yes
Assessing the potential spread and maintenance of foot-and-mouth disease virus infection in wild ungulates: general principles and application to a specific scenario in Thrace

Foot-and-mouth disease (FMD), due to infection with serotype O virus, occurred in wild boar and within eleven outbreaks in domestic livestock in the south-east of Bulgaria, Thrace region, in 2011. Hence, the issue of the potential for the spread and maintenance of FMD virus (FMDV) infection in a population of wild ungulates became important. This assessment focused on the spread and maintenance of FMDV infection within a hypothetical wild boar and deer population in an environment, which is characterized by a climate transitional between Mediterranean and continental and variable wildlife population densities. The assessment was based on three aspects: (i) a systematic review of the literature focusing on experimental infection studies to identify the parameters describing the duration of FMDV infection in deer and wild boar, as well as observational studies assessing the occurrence of FMDV infection in wild deer and wild boar populations, (ii) prevalence survey data of wild boar and deer in Bulgaria and Turkey and (iii) an epidemiological model, simulating the host-to-host spread of FMDV infections. It is concluded, based on all three aspects, that the wildlife population in Thrace, and so wildlife populations in similar ecological settings, are probably not able to maintain FMD in the long term in the absence of FMDV infection in the domestic host population. However, limited spread of FMDV infection in time and space in the wildlife populations can occur. If there is a continued crossover of FMDV between domestic and wildlife populations or a higher population density, virus circulation may be prolonged.
During a severe outbreak of diarrhoea and vomiting in a pig herd in Central Eastern Europe, faecal samples were tested positive for porcine epidemic diarrhoea virus (PEDV) and negative for transmissible gastroenteritis virus (TGEV) using a commercial RT-qPCR assay that can detect both of these coronaviruses. However, further analyses, using other TGEV- and PEDV-specific RT-qPCR assays, provided results inconsistent with infection by either of these viruses. Sequencing of an amplicon (ca. 1.6 kb), generated by an RT-PCR specific for the PEDV S-gene, indicated a very close similarity (ca. 99% identity) to recently described chimeric viruses termed swine enteric coronaviruses (SeCoVs). These viruses (with an RNA genome of ca. 28 kb) were first identified in Italy in samples from 2009 but have not been detected there since 2012. A closely related virus was detected in archived samples in Germany from 2012, but has not been detected subsequently. Building on the initial sequence data, further amplicons were generated and over 9 kb of sequence corresponding to the 3′-terminus of the new SeCoV genome was determined. Sequence comparisons showed that the three known SeCoVs are ≥98% identical across this region and contain the S-gene and 3a sequences from PEDV within a backbone of TGEV, but the viruses are clearly distinct from each other. It is demonstrated, for the first time, that pigs from within the SeCoV-infected herd seroconverted against PEDV but tested negative in a TGEV-specific ELISA that detects antibodies against the S protein. These results indicate that SeCoV is continuing to circulate in Europe and suggest it can cause a disease that is very similar to PED. Specific detection of the chimeric SeCoVs either requires development of a new diagnostic RT-qPCR assay or the combined use of assays targeting the PEDV S-gene and another part of the TGEV genome.
Conserved elements within the genome of foot-and-mouth disease virus; their influence on virus replication

Objectives:
Several conserved elements within the genome of foot-and-mouth disease virus (FMDV) have been identified, e.g. the IRES. Such elements can be crucial for the efficient replication of the genomic RNA. Previously, SHAPE analysis of the entire FMDV genome (Poulsen et al., 2016 submitted) has identified a conserved RNA structure within the 3Dpol coding region (the RNA-dependent RNA polymerase) which might have an important role in virus replication. The FMDV 2A peptide, another conserved element, is responsible for the primary “cleavage” at its own C-terminus (2A/2B junction). It is believed that this “cleavage” is achieved by ribosomal skipping, in which the 2A peptide prevents the ribosome from linking the next amino acid (aa) to the growing polypeptide. The nature of this “cleavage” has so far not been investigated in the context of the full-length FMDV RNA within cells.

Through reverse genetics, this study aims to identify how these distinct conserved elements influence the replication of FMDV RNA.

Methods:
Changes were made within the predicted 3Dpol RNA structure and the 2A peptide coding sequence which were expected to be detrimental for their function. These were:
1) Silent mutations, to disrupt the 3Dpol RNA secondary structure, were generated in a FMDV replicon containing Gaussia luciferase.
2) Sequence changes encoding selected modifications of the 2A peptide (as described by Donnelly et al., 2001) were introduced into a full-length FMDV cDNA and in a FMDV replicon cDNA containing Gaussia luciferase.

RNA transcripts were generated in vitro from the plasmids, and introduced into BHK cells by electroporation. The replication efficiency was assessed by measurement of luciferase activity or by rescue of mutant viruses. The rescued viruses derived from the 2A mutant cDNAs were passaged 3 times and the rescued RNAs were sequenced.

Results:
Initial results indicate that 3 different replicon mutants, with the disrupted 3Dpol RNA structure, had very similar RNA replication efficiencies as the wt FMDV replicon.
Furthermore, the replicon system showed that the 2A mutants were also able to undergo replication, although at a lower rate than for the wt FMDV replicon. One mutant which previously (Donnelly et al., 2001) was found not to undergo “cleavage” was still replication competent. Analysis of rescued viruses by sequencing of the third passage revealed that the 2A mutants with the lowest “cleavage” activity had reverted to the wt but some mutants with defective “cleavage” activity were viable.

Conclusions:
Initial results confirm that efficient “cleavage” at the 2A/2B junction is required for optimal replication. Rescue of viable mutant viruses with mutants previously characterized as “non-cleaving” indicates a discrepancy between in vitro and cell-based experiments.
Detrimental changes to the 3Dpol RNA structure did not change the replication efficiency in a replicon system. However these results do not eliminate a possible effect of this structure on virus replication; such analyses are in progress. Further study of these two conserved elements will provide more valuable insights into mechanisms underlying FMDV virus replication.

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Development and evaluation of tailored specific real-time RT-PCR assays for detection of foot-and-mouth disease virus serotypes circulating in East Africa

Rapid, reliable and accurate diagnostic methods provide essential support to programmes that monitor and control foot-and-mouth disease (FMD). While pan-specific molecular tests for FMD virus (FMDV) detection are well established and widely used in endemic and FMD-free countries, current serotyping methods mainly rely either on antigen detection ELISAs or nucleotide sequencing approaches. This report describes the development of a panel of serotype-specific real-time RT-PCR assays (rRT-PCR) tailored to detect FMDV lineages currently circulating in East Africa. These assays target sequences within the VP1-coding region that share high intra-lineage identity, but do not cross-react with FMD viruses from other serotypes that circulate in the region. These serotype-specific assays operate with the same thermal profile as the pan-diagnostic tests making it possible to run them in parallel to produce CT values comparable to the pan-diagnostic
test detecting the 3D-coding region. These assays were evaluated alongside the established pan-specific molecular test using field samples and virus isolates collected from Tanzania, Kenya and Ethiopia that had been previously characterised by nucleotide sequencing. Samples (n = 71) representing serotype A (topotype AFRICA, lineage G-I), serotype O (topotypes EA-2 and EA-4), serotype SAT 1 (topotype I (NWZ)) and serotype SAT2 (topotype IV) were correctly identified with these rRT-PCR assays. Furthermore, FMDV RNA from samples that did not contain infectious virus could still be serotyped using these assays. These serotype-specific real-time RT-PCR assays can detect and characterise FMDVs currently circulating in East Africa and hence improve disease control in this region.

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Scopus rating (2012): SJR 0.869 SNIP 0.935 CiteScore 2.08
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Scopus rating (2009): SJR 0.964 SNIP 1.061
Web of Science (2009): Indexed yes
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Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 0.955 SNIP 1.029
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. Polyepitope 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.
Experimental infection of piglets with an early European strain of PED virus and a recent US PEDV strain

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Experimental pig-to-pig transmission study with a recent European African Swine Fever virus isolate

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Organisations: National Veterinary Institute, Section for Epidemiology, Section for Virology
Authors: Olesen, A. S. (Intern), Lohse, L. (Intern), Boklund, A. (Intern), Hisham Beshara Halasa, T. (Intern), Rasmussen, T. B. (Intern), Bøtner, A. (Intern)
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Experimental Treatment of Ebola Virus Disease with TKM-130803: A Single-Arm Phase 2 Clinical Trial

BACKGROUND:
TKM-130803, a small interfering RNA lipid nanoparticle product, has been developed for the treatment of Ebola virus disease (EVD), but its efficacy and safety in humans has not been evaluated.

METHODS AND FINDINGS:
In this single-arm phase 2 trial, adults with laboratory-confirmed EVD received 0.3 mg/kg of TKM-130803 by intravenous infusion once daily for up to 7 d. On days when trial enrolment capacity was reached, patients were enrolled into a concurrent observational cohort. The primary outcome was survival to day 14 after admission, excluding patients who died within 48 h of admission. After 14 adults with EVD had received TKM-130803, the pre-specified futility boundary was reached, indicating a probability of survival to day 14 of ≤0.55, and enrolment was stopped. Pre-treatment geometric mean Ebola virus load in the 14 TKM-130803 recipients was 2.24 × 109 RNA copies/ml plasma (95% CI 7.52 × 108, 6.66 × 109). Two of the TKM-130803 recipients died within 48 h of admission and were therefore excluded from the primary outcome analysis. Of the remaining 12 TKM-130803 recipients, nine died and three survived. The probability that a TKM-130803 recipient who survived for 48 h will subsequently survive to day 14 was estimated to be 0.27 (95% CI 0.06, 0.58). TKM-130803 infusions were well tolerated, with 56 doses administered and only one possible infusion-related reaction observed. Three patients were enrolled in the observational cohort, of whom two died.

CONCLUSIONS:
Administration of TKM-130803 at a dose of 0.3 mg/kg/d by intravenous infusion to adult patients with severe EVD was not shown to improve survival when compared to historic controls.

TRIAL REGISTRATION:
Pan African Clinical Trials Registry PACTR201501000997429.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Dunning, J. (Ekstern), Sahr, F. (Ekstern), Rojek, A. (Ekstern), Gannon, F. (Ekstern), Carson, G. (Ekstern), Idriss, B. (Ekstern), Massaquoi, T. (Ekstern), Gandi, R. (Ekstern), Joseph, S. (Ekstern), Osman, H. K. (Ekstern), Brooks, T. J. G.
Extraction and analysis of signatures from the Gene Expression Omnibus by the crowd

Gene expression data are accumulating exponentially in public repositories. Reanalysis and integration of themed collections from these studies may provide new insights, but requires further human curation. Here we report a crowdsourcing project to annotate and reanalyze a large number of gene expression profiles from Gene Expression Omnibus (GEO). Through a massive open online course on Coursera, over 70 participants from over 25 countries identify and annotate 2,460 single-gene perturbation signatures, 839 disease versus normal signatures, and 906 drug perturbation signatures. All these signatures are unique and are manually validated for quality. Global analysis of these signatures confirms known associations and identifies novel associations between genes, diseases and drugs. The manually curated signatures are used as a training set to develop classifiers for extracting similar signatures from the entire GEO repository. We develop a web portal to serve these signatures for query, download and visualization.
In late February 2014, unusually high numbers of wild birds, thick-billed murre (Uria lomvia), were found dead at the coast of South Greenland. To investigate the cause of death, 45 birds were submitted for laboratory examinations in Denmark. Avian influenza viruses (AIVs) with subtypes H11N2 and low pathogenic (LP) H5N1 were detected in some of the birds. Characterization of the viruses by full-genome sequencing revealed that all the gene segments belonged to the North American lineage of AIVs.

The seemingly sparse and mixed subtype occurrence of LP AIVs in these birds, in addition to an emaciated appearance of birds, suggests that the murre die-off was not due to infection with AIV, but could be the mere cause of sparse food availability or stormy weather. Here we present the first characterization of AIVs isolated in Greenland, and our results support the idea that wild birds in Greenland may be involved in the movement of AIV between North America and Europe.
First evidence of infectious hematopoietic necrosis virus (IHNV) in the Netherlands

In spring 2008, infectious hematopoietic necrosis virus (IHNV) was detected for the first time in the Netherlands. The virus was isolated from rainbow trout, Oncorhynchus mykiss (Walbaum), from a put-and-take fishery with angling ponds. IHNV is the causative agent of a serious fish disease, infectious hematopoietic necrosis (IHN). From 2008 to 2011, we diagnosed eight IHNV infections in rainbow trout originating from six put-and-take fisheries (symptomatic and asymptomatic fish), and four IHNV infections from three rainbow trout farms (of which two were co-infected by infectious pancreatic necrosis virus, IPNV), at water temperatures between 5 and 15 °C. At least one farm delivered trout to four of these eight IHNV-positive farms. Mortalities related to IHNV were mostly <40%, but increased to nearly 100% in case of IHNV and IPNV co-infection. Subsequent phylogenetic analysis revealed that these 12 isolates clustered into two different monophyletic groups within the European IHNV genogroup E. One of these two groups indicates a virus-introduction event by a German trout import, whereas the second group indicates that IHNV was already (several years) in the Netherlands before its discovery in 2008.

**General information**

State: Published

Organisations: National Veterinary Institute, Section for Virology, Wageningen University & Research, Friedrich Loeffler Institute, Netherlands Food and Consumer Product Safety Authority


Number of pages: 9

Publication date: 2016

Main Research Area: Technical/natural sciences

**Publication information**

Journal: Journal of Fish Diseases

Volume: 39

Issue number: 8

ISSN (Print): 0140-7775

Ratings:

BFI (2018): BFI-level 1

Web of Science (2018): Indexed yes

BFI (2017): BFI-level 1

Web of Science (2017): Indexed yes

BFI (2016): BFI-level 1

Scopus rating (2016): CiteScore 2.12

Web of Science (2016): Indexed yes

BFI (2015): BFI-level 1

Scopus rating (2015): CiteScore 1.71

Web of Science (2015): Indexed yes

BFI (2014): BFI-level 1

Scopus rating (2014): CiteScore 1.99

Web of Science (2014): Indexed yes

BFI (2013): BFI-level 1

Scopus rating (2013): CiteScore 1.74

ISI indexed (2013): ISI indexed yes

Web of Science (2013): Indexed yes
Fish health in Mediterranean Aquaculture, past mistakes and future challenges

General information
State: Published
Organisations: Section for Virology, National Veterinary Institute
Authors: Vendramin, N. (Intern), Zmčic, S. (Ekstern), Padros, F. (Ekstern), Oraic, D. (Ekstern), Le Breton, A. (Ekstern), Zarza, C. (Ekstern), Olesen, N. J. (Intern)
Number of pages: 8
Pages: 38-45
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Bulletin of the European Association of Fish Pathologists
Volume: 36
Issue number: 1
ISSN (Print): 0108-0288
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 0.49 SJR 0.234 SNIP 0.421
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.27 SNIP 0.496 CiteScore 0.64
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.32 SNIP 0.414 CiteScore 0.68
Foot-and-mouth disease virus capsid proteins; analysis of protein processing, assembly and utility as vaccines

Foot-and-mouth disease (FMD) remains one of the most economically important infectious diseases of production animals globally. The infection is caused by foot-and-mouth disease virus (FMDV), a member of the picornavirus family. The positive sense RNA genome of the virus includes a single, large, open reading frame that encodes a polyprotein. The intact polyprotein is never observed as it is processed, both during and after translation, to 15 different mature proteins plus a variety of precursors. The FMDV capsid protein precursor, P1-2A, is cleaved by the virus encoded 3C protease (3Cpro) to generate VP0, VP3, VP1 and the peptide 2A. Sixty copies of each of the capsid proteins “self-assemble” into empty capsid particles or with the RNA genome into infectious viruses. These particles normally lack 2A but it is possible to construct and isolate mutant FMDVs in which the cleavage of the VP1/2A junction is greatly inhibited, leading to the production of “self-tagged” virus particles that retain the 2A peptide. Interestingly, such mutant viruses acquire “second site” changes elsewhere within VP1.

Recent studies have shown that reducing the expression level of the 3Cpro relative to the P1-2A capsid precursor enhances the yield of processed capsid proteins and their assembly into empty capsid particles within mammalian cells. Such particles can potentially form the basis of a vaccine but they may only have the same properties as the current inactivated vaccines. We have expressed the FMDV P1-2A alone or with FMDV 3Cpro using a “single cycle” alphavirus vector based on Semliki Forest virus (SFV). Cattle vaccinated with these rSFV-FMDV vectors alone, produced anti-FMDV antibodies but the immune response was insufficient to give protection against FMDV challenge. However, vaccination with these vectors primed a much stronger immune response against FMDV post-challenge. In subsequent experiments, cattle were sequentially vaccinated with a rSFV-FMDV followed by recombinant FMDV empty capsid particles, or vice versa, prior to challenge. Animals given a primary vaccination with the rSFV-FMDV vector and then boosted with FMDV empty capsids showed a strong anti-FMDV antibody response prior to challenge; they were protected against disease and
no FMDV RNA was detected in their sera post-challenge. Initial inoculation with empty capsids followed by the rSFV-FMDV was much less effective at combating the FMDV challenge. This prime-boost system, using reagents that can be generated outside of high-containment facilities, offers significant advantages to achieve control of FMD by vaccination.

**General information**

State: Published  
Organisations: National Veterinary Institute, Section for Virology  
Authors: Belsham, G. (Intern)  
Number of pages: 1  
Publication date: 2016  
Main Research Area: Technical/natural sciences  
Electronic versions:  
SKoreaAbstractGRBE.pdf  
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2016

**Forbedret diagnostik af mink enteritis virus (MEV)**

**General information**  
State: Published  
Organisations: National Veterinary Institute, Section for Virology  
Authors: Kvisgaard, L. K. (Intern), Holm, E. (Intern), Chriél, M. (Intern), Larsen, L. E. (Intern), Hjulsager, C. K. (Intern)  
Pages: 101-104  
Publication date: 2016  
Host publication information  
Title of host publication: Faglig årsberetning 2015 : Kopenhagen Fur  
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Publisher: Kopenhagen Fur  
Main Research Area: Technical/natural sciences  
Electronic versions:  
Faglig_arsberetning_2015.pdf  
Publication: Research › Report chapter – Annual report year: 2016

**Functional role of intestinal dendritic cell subsets in the mucosal IgA response to rotavirus**

**General information**  
State: Published  
Organisations: Section for Virology, National Veterinary Institute, Lund University, Stanford University  
Authors: Hütter, J. (Intern), Nakawesi, J. (Ekstern), Feng, N. (Ekstern), Greenberg, H. (Ekstern), Butcher, E. (Ekstern), Lahl, K. (Intern)  
Number of pages: 1  
Pages: 776-776  
Publication date: 2016  
Conference: ICI 2016 International Congress of Immunology, Melbourne, Australia, 21/08/2016 - 21/08/2016  
Main Research Area: Technical/natural sciences  
Publication information  
Journal: European Journal of Immunology  
Volume: 46  
Issue number: S1  
ISSN (Print): 0014-2980  
Ratings:  
BFI (2018): BFI-level 1  
Web of Science (2018): Indexed yes  
BFI (2017): BFI-level 1  
Web of Science (2017): Indexed Yes  
BFI (2016): BFI-level 1  
Scopus rating (2016): CiteScore 3.61 SJR 2.47 SNIP 0.935  
Web of Science (2016): Indexed yes  
BFI (2015): BFI-level 1
Generation and transcriptional programming of intestinal dendritic cells: essential role of retinoic acid

Vitamin A metabolite retinoic acid (RA) regulates adaptive immunity in the intestines, with well-characterized effects on IgA responses, Treg induction, and gut trafficking of T- and B-effector cells. It also controls the generation of conventional dendritic cell (cDC) precursors in the bone marrow and regulates cDC subset representation, but its roles in the specialization of intestinal cDC subsets are understudied. Here we show that RA acts cell intrinsically in developing gut-tropic pre-mucosal dendritic cell (pre-μDC) to effect the differentiation and drive the specialization of intestinal CD103+CD11b- (cDC1) and of CD103+CD11b+ (cDC2). Systemic deficiency or DC-restricted antagonism of RA signaling resulted in altered phenotypes of intestinal cDC1 and cDC2, and reduced numbers of cDC2. Effects of dietary deficiency were most apparent in the proximal small intestine and were rapidly reversed by reintroducing vitamin A. In cultures of pre-μDC with Flt3L and granulocyte-macrophage colony-stimulating factor (GM-CSF), RA induced cDC with characteristic phenotypes of intestinal cDC1 and cDC2 by controlling subset-defining cell surface receptors, regulating subset-specific transcriptional programs, and suppressing proinflammatory nuclear factor-κB-dependent gene expression. Thus, RA is required for transcriptional programming and maturation of intestinal cDC, and with GM-CSF and Flt3L provides a minimal environment for in vitro generation of intestinal cDC1- and cDC2-like cDC from specialized precursors.
Genomic Sequence of a Ranavirus Isolated from Short-Finned Eel (Anguilla australis)

The short-finned eel ranavirus (SERV) was isolated from short-finned eel imported to Italy from New Zealand. Phylogenomic analyses revealed that SERV is a unique member of the genus Ranavirus, family Iridoviridae, branching at the base of the tree near other fish ranaviruses.

General information
State: Published
Organisations: Section for Virology, National Veterinary Institute, University of Florida, Instituto Zooprofilattico Sperimentale delle Venezie, James Cook University
Authors: Subramaniam, K. (Ekstern), Toffan, A. (Ekstern), Cappellozza, E. (Ekstern), Steckler, N. K. (Ekstern), Olesen, N. J. (Intern), Ariel, E. (Ekstern), Waltzek, T. B. (Ekstern)
Number of pages: 2
Publication date: 2016
Main Research Area: Technical/natural sciences
Publication information
Journal: Genome Announcements
Volume: 4
Issue number: 4
Article number: e00843-16
ISSN (Print): 2169-8287
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Genomic Sequencing of Ranaviruses Isolated from Turbot (Scophthalmus maximus) and Atlantic Cod (Gadus morhua)

Ranaviruses have been isolated from Atlantic cod (Gadus morhua) and turbot (Scophthalmus maximus) in Denmark. Phylogenomic analyses revealed that these two ranaviruses are nearly identical and form a distinct clade at the base of the ranavirus tree branching off near other fish ranaviruses.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, James Cook University, University of Florida
Authors: Ariel, E. (Ekstern), Steckler, N. K. (Ekstern), Subramaniam, K. (Ekstern), Olesen, N. J. (Intern), Waltzek, T. B. (Ekstern)
Number of pages: 2
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Genome Announcements
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ISSN (Print): 2169-8287
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BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Scopus rating (2016): CiteScore 0.41 SJR 0.217 SNIP 0.233
Web of Science (2016): Indexed yes
Scopus rating (2015): SJR 0.199 SNIP 0.077
Scopus rating (2014): SJR 0.218 SNIP 0.089
ISI indexed (2013): ISI indexed no
Original language: English
Electronic versions:
Genome_Announc_2016_Ariel_.pdf
DOIs:
10.1128/genomeA.01393-16
Source: Findit
Source-ID: 2350264279
Publication: Research - peer-review › Journal article – Annual report year: 2016

High diversity of picornaviruses in rats from different continents revealed by deep sequencing

Outbreaks of zoonotic diseases in humans and livestock are not uncommon, and an important component in containment of such emerging viral diseases is rapid and reliable diagnostics. Such methods are often PCR-based and hence require the availability of sequence data from the pathogen. Rattus norvegicus (R. norvegicus) is a known reservoir for important zoonotic pathogens. Transmission may be direct via contact with the animal, for example, through exposure to its faecal matter, or indirectly mediated by arthropod vectors. Here we investigated the viral content in rat faecal matter (n=29) collected from two continents by analyzing 2.2 billion next-generation sequencing reads derived from both DNA and RNA. Among other virus families, we found sequences from members of the Picornaviridae to be abundant in the microbiome of
all the samples. Here we describe the diversity of the picornavirus-like contigs including near-full-length genomes closely related to the Boone cardiovirus and Theiler's encephalomyelitis virus. From this study, we conclude that picornaviruses within R. norvegicus are more diverse than previously recognized. The virome of R. norvegicus should be investigated further to assess the full potential for zoonotic virus transmission.

**General information**

State: Published

Organisations: Department of Systems Biology, National Veterinary Institute, Section for Virology, University of Copenhagen, University of Illinois at Urbana-Champaign, Curtin University, State Serum Institute


Number of pages: 8

Publication date: 2016

Main Research Area: Technical/natural sciences

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**Immunity raised by recent European subtype 1 PRRSV strains allows better replication of East European subtype 3 PRRSV strain Lena than that raised by an older strain**

Stable spatial distribution of porcine reproductive and respiratory syndrome (PRRSV)-1 subtypes in Europe is accompanied by a strong population immunity induced by local PRRSV strains. In the present study, it was examined if the immunity induced by three West European subtype 1 PRRSV strains (2007 isolate 07V063 and 2013 isolates 13V091 and 13V117) offers protection against the highly virulent East European subtype 3 PRRSV strain Lena. The number of fever days was greater (p < 0.05) in the control group (7.6 ± 1.7 days) compared to the immune groups (07V063-immune: 4.0 ± 1.2 days, 13V091-immune: 4.6 ± 1.1 days, 13V117-immune: 4.0 ± 2.9 days). In all groups, protection was characterized by reduction (p < 0.05) of AUC values of nasal shedding (control: 14.6, 07V063-immune: 3.4, 13V091-immune: 8.9, 13V117-immune: 8.0) and viremia (control: 28.1, 07V063-immune: 5.4, 13V091-immune: 9.0, 13V117-immune: 8.3). Reduction of respiratory disease, nasal shedding (mean AUC and mean peak values) and viremia (mean AUC and mean peak values) was more pronounced in 07V063-immune (p < 0.05) than in 13V091-immune and 13V117-immune animals. Inoculation with subtype 1 PRRSV strains caused priming of the Lena-specific virus neutralization antibody response. Upon challenge with Lena, we observed a very strong serological booster effect for neutralizing antibodies against strains used for the first inoculation. Our results indicate that inoculation with subtype 1 PRRSV strains can partially protect against antigenically divergent subtype 3 strains. The lower protection level elicited by recently isolated subtype 1 PRRSV strains may impair the outcome of the spatial expansion of subtype 3 strains from East Europe to West Europe.

**General information**

State: Published

Organisations: National Veterinary Institute, Section for Virology, Ghent University

Authors: Trus, I. (Ekstern), Frydas, I. S. (Ekstern), Reddy, V. R. A. P. (Ekstern), Bonckaert, C. (Ekstern), Li, Y. (Ekstern), Kvisgaard, L. K. (Intern), Larsen, L. E. (Intern), Nauwynck, H. J. (Ekstern)

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Inter-laboratory study to characterize the detection of serum antibodies against porcine epidemic diarrhoea virus

Porcine epidemic diarrhea virus (PEDV) has caused extensive economic losses to pig producers in many countries. It was recently introduced, for the first time, into North America and outbreaks have occurred again in multiple countries within Europe as well. To assess the properties of various diagnostic assays for the detection of PEDV infection, multiple panels of porcine sera have been shared and tested for the presence of antibodies against PEDV in an inter-laboratory ring trial. Different laboratories have used a variety of “in house” ELISAs and also one commercial assay. The sensitivity and specificity of each assay has been estimated using a Bayesian analysis applied to the ring trial results obtained with the different assays in the absence of a gold standard. Although different characteristics were found, it can be concluded that each of the assays used can detect infection of pigs at a herd level by either the early European strains of PEDV or the recently circulating strains (INDEL and non-INDEL). However, not all the assays seem suitable for demonstrating freedom from disease in a country. The results from individual animals, especially when the infection has occurred within an
experimental situation, show more variation.

**General information**
State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Strandbygaard, B. (Intern), Lavazza, A. (Ekstern), Lelli, D. (Ekstern), Blanchard, Y. (Ekstern), Grasland, B. (Ekstern), Poder, S. L. (Ekstern), Rose, N. (Ekstern), Steinbach, F. (Ekstern), van der Poel, W. H. (Ekstern), Widén, F. (Ekstern), Belsham, G. (Intern), Bøtner, A. (Intern)
Number of pages: 10
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Main Research Area: Technical/natural sciences

**Publication information**
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BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.326 SNIP 1.208
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.393 SNIP 1.21 CiteScore 2.56
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.281 SNIP 1.262 CiteScore 2.54
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.438 SNIP 1.484 CiteScore 3
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.437 SNIP 1.579 CiteScore 3.18
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.562 SNIP 1.738 CiteScore 3.27
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.371 SNIP 1.476
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.29 SNIP 1.472
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.169 SNIP 1.3
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.043 SNIP 1.322
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.022 SNIP 1.401
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.078 SNIP 1.262
International ring trials for adoption and validation of real-time RT-PCR protocols for sub-typing European swine influenza viruses

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Reid, S. M. (Ekstern), Russell, C. (Ekstern), Williamson, S. (Ekstern), Simon, G. (Ekstern), Loeffen, W. (Ekstern), Larsen, L. E. (Intern), Zohari, S. (Ekstern), Chiapponi, C. (Ekstern), Harder, T. (Ekstern), Gorin, S. (Ekstern), Queguiner, S. (Ekstern), Krog, J. S. (Intern), Foni, E. (Ekstern), Brookes, S. (Ekstern), Brown, I. (Ekstern)
Pages: 600-600
Publication date: 2016
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-PT2-094
Main Research Area: Technical/natural sciences
Conference: 24th International Pig Veterinary Society (IPVS) Congress, Dublin, Ireland, 07/06/2016 - 07/06/2016
Electronic versions:
Book of abstracts
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2016

Introduction of replacement gilts to PRRS-positive sow herds

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, SEGES Pig Research Center
Authors: Hoelstad, B. E. (Intern), Larsen, L. E. (Intern), Hjulsager, C. K. (Intern), Kristensen, C. (Ekstern)
Pages: 568-568
Publication date: 2016
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
Main Research Area: Technical/natural sciences
Conference: 24th International Pig Veterinary Society (IPVS) Congress, Dublin, Ireland, 07/06/2016 - 07/06/2016
Electronic versions:
Book of abstracts
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 luftrum med øvrige staldafsnit, havde separat indgang og kørte alt ind/altsud. 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
Authors: Hoelstad, B. E. (Intern), Sonne Kristensen, C. (Ekstern), Qvist Pawlowski, M. (Ekstern), Hjulsager, C. K. (Intern), Kvisgaard, L. K. (Intern), Lauritsen, K. T. (Intern), Larsen, L. E. (Intern)
Number of pages: 4
Publication date: 2016
Norovirus Polymerase Fidelity Contributes to Viral Transmission In Vivo

Intrahost genetic diversity and replication error rates are intricately linked to RNA virus pathogenesis, with alterations in viral polymerase fidelity typically leading to attenuation during infections in vivo. We have previously shown that norovirus intrahost genetic diversity also influences viral pathogenesis using the murine norovirus model, as increasing viral mutation frequency using a mutagenic nucleoside resulted in clearance of a persistent infection in mice. Given the role of replication fidelity and genetic diversity in pathogenesis, we have now investigated whether polymerase fidelity can also impact virus transmission between susceptible hosts. We have identified a high-fidelity norovirus RNA-dependent RNA polymerase mutant (I391L) which displays delayed replication kinetics in vivo but not in cell culture. The I391L polymerase mutant also exhibited lower transmission rates between susceptible hosts than the wild-type virus and, most notably, another replication defective mutant that has wild-type levels of polymerase fidelity. These results provide the first experimental evidence that norovirus polymerase fidelity contributes to virus transmission between hosts and that
maintaining diversity is important for the establishment of infection. This work supports the hypothesis that the reduced polymerase fidelity of the pandemic GII.4 human norovirus isolates may contribute to their global dominance.

**General information**
State: Published
Organisations: National Veterinary Institute, Section for Virology, University of Cambridge, University of Birmingham
Authors: Arias Esteban, A. (Intern), Thorne, L. (Ekstern), Ghurburrun, E. (Ekstern), Bailey, D. (Ekstern), Goodfellow, I. (Ekstern)
Number of pages: 11
Publication date: 2016
Main Research Area: Technical/natural sciences

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Journal: mSphere
Volume: 1
Issue number: 5
Article number: 00279-16
ISSN (Print): 2379-5042
Ratings:
Web of Science (2018): Indexed yes
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3 SJR 1.543 SNIP 1.053
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.878 SNIP 0.858 CiteScore 3.12
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.801 SNIP 0.902 CiteScore 3.13
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 2.062 SNIP 1.003 CiteScore 3.58
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 2.148 SNIP 1.008 CiteScore 3.81
ISI indexed (2012): ISI indexed no
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 2.026 SNIP 0.934 CiteScore 3.71
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.112 SNIP 0.942
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 2.267 SNIP 0.948
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 2.632 SNIP 0.936
Scopus rating (2007): SJR 2.458 SNIP 0.883
Scopus rating (2006): SJR 2.667 SNIP 0.912
Scopus rating (2005): SJR 3.013 SNIP 1.001
Scopus rating (2004): SJR 2.64 SNIP 1.032
Scopus rating (2003): SJR 2.649 SNIP 0.65
Original language: English

RNA polymerases, Noroviruses, Polymerase fidelity, Quasispecies, Virus transmission

Electronic versions:
Arias_et_al_2016_mSphere.pdf
DOIs:
10.1128/mSphere.00279-16
Source: PublicationPreSubmission
Source-ID: 126745432
Occurrence of Swine Enteric Coronavirus (SeCoV) infection during 2016 within Central Eastern Europe

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Bøtner, A. (Intern), Rasmussen, T. B. (Intern), Strandbygaard, B. (Intern), Belsham, G. (Intern)
Pages: 103-103
Publication date: 2016

Host publication information
Title of host publication: EPIZONE 10th annual meeting: Programme & abstracts
Place of publication: Madrid, Spain
Main Research Area: Technical/natural sciences
porcine coronavirus, PEDV, TGEV, SeCoV

Bibliographical note
Poster 13

Oral fluid samples for the monitoring of PRRSV status and dynamics

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Danvet K/S, Boehringer Ingelheim AH
Authors: Holmgren, S. (Ekstern), Kvisgaard, L. K. (Intern), Bak, H. (Ekstern), Larsen, L. E. (Intern)
Pages: 578-578
Publication date: 2016

Host publication information
Title of host publication: 24th International Pig Veterinary Society Congress - abstracts book
Place of publication: Dublin, Ireland
Publisher: Royal Dublin Society
Article number: PO-PW1-087
Main Research Area: Technical/natural sciences
Conference: 24th International Pig Veterinary Society (IPVS) Congress, Dublin, Ireland, 07/06/2016 - 07/06/2016
Electronic versions:
Book of abstracts

Outbreaks of Aleutian mink disease in farmed mink (Neovison vison) in Denmark: molecular characterization by partial NS1 gene sequencing

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Department of Systems Biology, Center for Biological Sequence Analysis, Molecular Evolution, Department of Bio and Health Informatics, Kopenhagen Fur
Pages: 85-87
Publication date: 2016

Host publication information
Title of host publication: Proceedings of the XIth International Scientific Congress in Fur Animal Production
Place of publication: Helsinki, Finland
Publisher: Libris
Editors: Mäki-Tanila, A., Valaja, J., Mononen, J., Sironen, T., Vapalahti, O.
Series: Scientifur
Volume: 40
Number: 3/4
ISSN: 2445-6292
Overførsel af Aleutian Mink Disease Virus med lopper

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Section for Virology, KSL Consulting ApS, Kopenhagen Diagnostics, Aalborg University
Authors: Hartby, C. M. (Intern), Hammer Jensen, T. (Ekstern), Søholt Larsen, K. (Ekstern), Hansen, M. S. (Intern), Chriël, M. (Intern), Larsen, L. E. (Intern), Struve, T. (Ekstern), Hjulsager, C. K. (Intern)
Pages: 91-94
Publication date: 2016

Host publication information
Title of host publication: Faglig årsberetning 2015 : Kopenhagen Fur
Place of publication: Aarhus N
Publisher: Kopenhagen Fur
Main Research Area: Technical/natural sciences
Electronic versions:
Faglig_årsberetning_2015.pdf
Publication: Research › Report chapter – Annual report year: 2016

Overvågning af aviær influenza i vilde fugle i Danmark 2015

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, University of Copenhagen
Authors: Hjulsager, C. K. (Intern), Krog, J. S. (Intern), Madsen, J. J. (Ekstern), Thorup, K. (Ekstern), Larsen, L. E. (Intern)
Number of pages: 33
Publication date: 2016

Publication information
Place of publication: Frederiksberg C
Publisher: Veterinærinstituttet, Danmarks Tekniske Universitet
Original language: Danish
Main Research Area: Technical/natural sciences
Electronic versions:
AI_overvaagning_vilde_fugle_2015_rapport.pdf
Source: FindIt
Source-ID: 2305680084
Publication: 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
Authors: Krog, J. S. (Intern), Hjulsager, C. K. (Intern), Larsen, L. E. (Intern)
Number of pages: 29
Publication date: 2016

Publication information
Place of publication: Frederiksberg C
Publisher: DTU Veterinærinstituttet
Original language: Danish
Main Research Area: Technical/natural sciences
Electronic versions:
Phylogeny of the Viral Hemorrhagic Septicemia Virus in European Aquaculture

One of the most valuable aquaculture fish in Europe is the rainbow trout, Oncorhynchus mykiss, but the profitability of trout production is threatened by a highly lethal infectious disease, viral hemorrhagic septicemia (VHS), caused by the VHS virus (VHSV). For the past few decades, the subgenogroup Ia of VHSV has been the main cause of VHS outbreaks in European freshwater-farmed rainbow trout. Little is currently known, however, about the phylogenetic radiation of this Ia lineage into subordinate Ia clades and their subsequent geographical spread routes. We investigated this topic using the largest Ia-isolate dataset ever compiled, comprising 651 complete G gene sequences: 209 GenBank Ia isolates and 442 Ia isolates from this study. The sequences come from 11 European countries and cover the period 1971-2015. Based on this dataset, we documented the extensive spread of the Ia population and the strong mixing of Ia isolates, assumed to be the result of the Europe-wide trout trade. For example, the Ia lineage underwent a radiation into nine Ia clades, most of which are difficult to allocate to a specific geographic distribution. Furthermore, we found indications for two rapid, large-scale population growth events, and identified three polytomies among the Ia clades, both of which possibly indicate a rapid radiation. However, only about 4% of Ia haplotypes (out of 398) occur in more than one European country. This apparently conflicting finding regarding the Europe-wide spread and mixing of Ia isolates can be explained by the high mutation rate of VHSV. Accordingly, the mean period of occurrence of a single Ia haplotype was less than a full year, and we found a substitution rate of up to 7.813 × 10-4 nucleotides per site per year. Finally, we documented significant differences between Germany and Denmark regarding their VHS epidemiology, apparently due to those countries’ individual handling of VHS.

General information

State: Published
Organisations: Section for Virology, National Veterinary Institute, Friedrich-Loeffler-Institute, Aarhus University, Université europeenne de Bretagne, University of Bern, Wageningen University, Istituto Zooprofilattico Sperimentaledelle Venezie
Authors: Cieslak, M. (Ekstern), Mikkelsen, S. S. (Intern), Skall, H. F. (Ekstern), Baud, M. (Ekstern), Diserens, N. (Ekstern), Engelsma, M. Y. (Ekstern), Haenen, O. L. M. (Ekstern), Mousakhani, S. (Ekstern), Panzarin, V. (Ekstern), Wahl, T. (Ekstern), Olesen, N. J. (Intern), Schütze, H. (Ekstern)
Number of pages: 18
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information

Journal: P L o S One
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BFI (2018): BFI-level 1
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Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.11 SJR 1.201 SNIP 1.092
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.414 SNIP 1.131 CiteScore 3.32
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.545 SNIP 1.141 CiteScore 3.54
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.74 SNIP 1.147 CiteScore 3.94
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Pooling of faecal samples for quantitative virus diagnostics by real-time PCR

General information
State: Published
Organisations: National Veterinary Institute, Virology, Section for Virology
Authors: Hartby, C. M. (Intern), Andersen, M. R. (Intern), Kvisgaard, L. K. (Intern), Chriél, M. (Intern), Larsen, L. E. (Intern), Hjulsager, C. K. (Intern)
Pages: 27-30
Publication date: 2016

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Place of publication: Helsinki, Finland
Publisher: Libris
Editors: Mäki-Tanila, A., Valaja, J., Mononen, J., Sironen, T., Vapalahti, O.

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Volume: 40
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Electronic versions: IFASA2016_Vol.40_1_.pdf
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Prevention of foot-and-mouth disease in cattle using a prime-boot-vaccination strategy
Foot-and-mouth disease (FMD) is one of the most economically important infectious diseases of production animals globally. Vaccination can help to control this disease, however, current vaccines are imperfect. They are made using chemically inactivated FMD virus (FMDV) that is produced in mammalian cell culture under high containment. Here, we have expressed the FMDV capsid protein precursor (P1-2A) of strain O1 Manisa alone or with the FMDV 3C protease
(3Cpro) using a “single cycle” packaged alphavirus self-replicating RNA based on Semliki Forest virus (SFV). When the FMDV P1-2A was expressed with 3Cpro then processing of the FMDV capsid precursor protein is observed within cells and the proteins assemble into empty capsid particles. In cattle vaccinated once with these rSFV-FMDV vectors alone, anti-FMDV antibodies were elicited but the immune response was insufficient to give protection against FMDV challenge. However, the prior vaccination with these vectors resulted in a much stronger immune response against FMDV post-challenge and the viremia observed was decreased in level and duration. In subsequent experiments, cattle were sequentially vaccinated with a rSFV-FMDV followed by recombinant FMDV empty capsid particles, or vice versa, prior to challenge. Animals given a primary vaccination with the rSFV-FMDV vector and then boosted with FMDV empty capsids showed a strong anti-FMDV antibody response prior to challenge. Following challenge with FMDV, the cattle were protected against disease and no FMDV RNA was detected in their sera. Initial inoculation with empty capsids followed by the rSFV-FMDV was much less effective at combating the FMDV challenge and a large post-challenge boost to the level of anti-FMDV antibodies was observed and clinical disease occurred. This prime-boost system, using reagents that can be generated outside of high-containment facilities, offers significant advantages to achieve control of FMD by vaccination.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, The Pirbright Institute, Karolinska Institutet
Authors: Gullberg, M. (Intern), Lohse, L. (Intern), Betner, A. (Intern), McInerney, G. (Ekstern), Burman, A. (Ekstern), Jackson, T. (Ekstern), Polacek, C. (Intern), Belsham, G. (Intern)
Number of pages: 2
Publication date: 2016
Event: Abstract from 19th European Study group on the molecular Biology of Picornaviruses (Europic 2016), Switzerland.
Main Research Area: Technical/natural sciences
Electronic versions:
Europic_Abstract2016Vaccine.pdf
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2016

QA prime-boost vaccination strategy in prevent serotype O FMDV infection using a "single-cycle" alphavirus vector and empty capsid particles

Introduction
Foot-and-mouth disease (FMD) remains one of the most economically important infectious diseases of production animals globally. Vaccination can help to control this disease, however, current vaccines based on chemically inactivated FMDV, are imperfect and there is a need for new, safe and effective vaccines to control FMD. There is no cross protection between the 7 serotypes but serotype O is the most abundant globally.

Material and methods
The FMDV capsid protein precursor (P1-2A) of strain O1 Manisa has been expressed with the FMDV 3C protease (3Cpro) using a “single cycle” packaged alphavirus self-replicating RNA based on Semliki Forest virus (SFV). Purified O1 Manisa empty capsid particles (ECs) have been prepared using a recombinant vaccinia virus expression system. Cattle have been vaccinated with the SFV-FMDV vectors and boosted subsequently with the ECs and then challenged with serotype O FMDV. The immune response against FMDV achieved by vaccination and infection status following challenge has been determined.

Results
In cattle vaccinated once with these rSFV-FMDV vectors alone, anti-FMDV antibodies were elicited but the immune response was insufficient to give protection against FMDV challenge. However, the vaccination with these vectors resulted in a much stronger immune response against FMDV post-challenge than in naïve animals. In subsequent experiments, cattle were sequentially vaccinated with the rSFV-FMDV followed by recombinant FMDV empty capsid particles prior to challenge. Animals given a primary vaccination with the rSFV-FMDV vector and then boosted with FMDV empty capsids showed a strong anti-FMDV antibody response prior to challenge. Following challenge with serotype O FMDV, the cattle were protected against disease and no FMDV RNA was detected in their sera.

Discussion
This prime-boost system, using reagents that can be generated outside of high-containment facilities, offers significant advantages to achieve control of FMD by vaccination.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Karolinska Institutet, The Pirbright Institute
Authors: Gullberg, M. (Intern), Lohse, L. (Intern), Betner, A. (Intern), McInerney, G. (Ekstern), Burman, A. (Ekstern), Jackson, T. (Ekstern), Polacek, C. (Intern), Belsham, G. (Intern)
Number of pages: 1
Publication date: 2016
Event: Abstract from European Commission for the control of Foot-and-Mouth Disease (EuFMD) 2016 : Open Session, Cascais, Portugal.
Main Research Area: Technical/natural sciences
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.
Recommended reporting standards for test accuracy studies of infectious diseases of finfish, amphibians, molluscs and crustaceans: the STRADAS-aquatic checklist

Complete and transparent reporting of key elements of diagnostic accuracy studies for infectious diseases in cultured and wild aquatic animals benefits end-users of these tests, enabling the rational design of surveillance programs, the assessment of test results from clinical cases and comparisons of diagnostic test performance. Based on deficiencies in the Standards for Reporting of Diagnostic Accuracy (STARD) guidelines identified in a prior finfish study (Gardner et al. 2014), we adapted the Standards for Reporting of Animal Diagnostic Accuracy Studies-paratuberculosis (STRADAS-paraTB) checklist of 25 reporting items to increase their relevance to finfish, amphibians, molluscs, and crustaceans and provided examples and explanations for each item. The checklist, known as STRADAS-aquatic, was developed and refined by an expert group of 14 transdisciplinary scientists with experience in test evaluation studies using field and experimental samples, in operation of reference laboratories for aquatic animal pathogens, and in development of international aquatic animal health policy. The main changes to the STRADAS-paraTB checklist were to nomenclature related to the species, the addition of guidelines for experimental challenge studies, and the designation of some items as relevant only to experimental studies and ante-mortem tests. We believe that adoption of these guidelines will improve reporting of primary studies of test accuracy for aquatic animal diseases and facilitate assessment of their fitness-for-purpose. Given the importance of diagnostic tests to underpin the Sanitary and Phytosanitary agreement of the World Trade Organization, the principles outlined in this paper should be applied to other World Organisation for Animal Health (OIE)-relevant species.

General information
State: Published
Organisations: Section for Virology, National Veterinary Institute, University of Prince Edward Island, University of Sydney, University of Adelaide, CSIRO Australian Animal Health Laboratory, Fisheries and Oceans Canada, National Veterinary Services Laboratories, IFREMER, U.S. Geological Survey, University of Florida
Authors: Gardner, I. A. (Ekstern), Whittington, R. J. (Ekstern), Caraguel, C. G. B. (Ekstern), Hick, P. (Ekstern), Moody, N. J. G. (Ekstern), Corbel, S. (Ekstern), Garver, K. A. (Ekstern), Warg, J. V. (Ekstern), Arzul, I. (Ekstern), Purcell, M. K. (Ekstern), Crane, M. S. J. (Ekstern), Waltzek, T. B. (Ekstern), Olesen, N. J. (Intern), Gallardo Lagno, A. (Ekstern)
Number of pages: 21
Pages: 91-111
Publication date: 2016
Main Research Area: Technical/natural sciences

Publication information
Journal: Diseases of Aquatic Organisms
Volume: 118
Issue number: 2
ISSN (Print): 0177-5103
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BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.95 SJR 0.858 SNIP 0.929
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.949 SNIP 0.935 CiteScore 1.96
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.889 SNIP 0.881 CiteScore 1.86
Sequence adaptations during growth of rescued classical swine fever viruses in cell culture and within infected pigs

Classical swine fever virus (CSFV) causes an economically important disease of swine. Four different viruses were rescued from full-length cloned cDNAs derived from the Paderborn strain of CSFV. Three of these viruses had been modified by mutagenesis (with 7 or 8 nt changes) within stem 2 of the subdomain IIIf of the internal ribosome entry site (IRES) that directs the initiation of protein synthesis. Rescued viruses were inoculated into pigs. The rescued vPader10 virus, without modifications in the IRES, induced clinical disease in pigs that was very similar to that observed previously with the parental field strain and transmission to in-contact pigs occurred. Two sequence reversions, in the NS2 and NSSB

Original language: English
Reporting standards, Sensitivity, Specificity, Finfish, Amphibians, Molluscs, Crustaceans, STRADAS-paraTB, Diagnostic validation, Aquatic Science, Ecology, Evolution, Behavior and Systematics

Electronic versions:
d118p091.pdf
DOIs:
10.3354/dao02947
Links:
http://www.int-res.com/abstracts/dao/v118/n2/p91-111
Source: FindIt
Source-ID: 2289357999
Publication: Research - peer-review › Journal article – Annual report year: 2016
coding regions, became dominant within the virus populations in these infected pigs. Rescued viruses, with mutant IRES elements, did not induce disease and only very limited circulation of viral RNA could be detected. However, the animals inoculated with these mutant viruses seroconverted against CSFV. Thus, these mutant viruses were highly attenuated in vivo. All 4 rescued viruses were also passaged up to 20 times in cell culture. Using full genome sequencing, the same two adaptations within each of four independent virus populations were observed that restored the coding sequence to that of the parental field strain. These adaptations occurred with different kinetics. The combination of reverse genetics and in depth, full genome sequencing provides a powerful approach to analyse virus adaptation and to identify key determinants of viral replication efficiency in cells and within host animals.

**General information**

State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Hadsbjerg, J. (Intern), Friis, M. B. (Intern), Fahnøe, U. (Intern), Nielsen, J. (Intern), Belsham, G. (Intern), Rasmussen, T. B. (Intern)
Number of pages: 12
Pages: 123-134
Publication date: 2016
Main Research Area: Technical/natural sciences

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Journal: Veterinary Microbiology
Volume: 192
ISSN (Print): 0378-1135
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BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.326 SNIP 1.208
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.393 SNIP 1.21 CiteScore 2.56
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.281 SNIP 1.262 CiteScore 2.54
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.438 SNIP 1.484 CiteScore 3
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.437 SNIP 1.579 CiteScore 3.18
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.562 SNIP 1.738 CiteScore 3.27
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.371 SNIP 1.476
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.29 SNIP 1.472
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.169 SNIP 1.3
Web of Science (2008): Indexed yes
Significantly increased numbers of foetuses positive for porcine parvovirus (PPV) in Denmark in 2015 coincided with a shift in genotype

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, SEGES Pig Research Center
Authors: Krog, J. S. (Intern), Hjulsager, C. K. (Intern), Haugegaard, S. (Ekstern), Larsen, L. E. (Intern)
Pages: 452-452
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Place of publication: Dublin, Ireland
Publisher: Royal Dublin Society
Article number: PO-PF3-156
Main Research Area: Technical/natural sciences
Conference: 24th International Pig Veterinary Society (IPVS) Congress, Dublin, Ireland, 07/06/2016 - 07/06/2016
Electronic versions:
Book of abstracts
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2016

Simultaneous vaccination with PRRS MLV against both PRRSV type 1 and type 2: PRRSV in lungs following challenge

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, SEGES Pig Research Center, Technical University of Denmark, Warsawa University
Authors: Kristensen, C. S. (Ekstern), Kvisgaard, L. K. (Intern), Haugegaard, S. (Ekstern), Pawlowski, M. (Ekstern), Carlsen, S. H. (Ekstern), Stadejek, T. (Ekstern), Larsen, L. E. (Intern)
Pages: 577-577
Publication date: 2016

Host publication information
Title of host publication: 24th International Pig Veterinary Society Congress - abstracts book
Place of publication: Dublin, Ireland
Spatio-temporal Analysis of the Genetic Diversity of Arctic Rabies Viruses and Their Reservoir Hosts in Greenland

There has been limited knowledge on spatio-temporal epidemiology of zoonotic arctic fox rabies among countries bordering the Arctic, in particular Greenland. Previous molecular epidemiological studies have suggested the occurrence of one particular arctic rabies virus (RABV) lineage (arctic-3), but have been limited by a low number of available samples preventing in-depth high resolution phylogenetic analysis of RABVs at that time. However, an improved knowledge of the evolution, at a molecular level, of the circulating RABVs and a better understanding of the historical perspective of the disease in Greenland is necessary for better direct control measures on the island. These issues have been addressed by investigating the spatio-temporal genetic diversity of arctic RABVs and their reservoir host, the arctic fox, in Greenland using both full and partial genome sequences. Using a unique set of 79 arctic RABV full genome sequences from Greenland, Canada, USA (Alaska) and Russia obtained between 1977 and 2014, a description of the historic context in relation to the genetic diversity of currently circulating RABV in Greenland and neighboring Canadian Northern territories has been provided. The phylogenetic analysis confirmed delineation into four major arctic RABV lineages (arctic 1–4) with viruses from Greenland exclusively grouping into the circumpolar arctic-3 lineage. High resolution analysis enabled distinction of seven geographically distinct subclades (3.I – 3.VII) with two subclades containing viruses from both Greenland and Canada. By combining analysis of full length RABV genome sequences and host derived sequences encoding mitochondrial proteins obtained simultaneously from brain tissues of 49 arctic foxes, the interaction of viruses and their hosts was explored in detail. Such an approach can serve as a blueprint for analysis of infectious disease dynamics and virus-host interdependencies. The results showed a fine-scale spatial population structure in Greenland arctic foxes based on mitochondrial sequences, but provided no evidence for independent isolated evolutionary development of RABV in different arctic fox lineages. These data are invaluable to support future initiatives for arctic fox rabies control and elimination in Greenland.
Sublethal concentrations of ichthyotoxic alga Prymnesium parvum affect rainbow trout susceptibility to viral haemorrhagic septicaemia virus

Ichthyotoxic algal blooms are normally considered a threat to maricultured fish only when blooms reach lethal cell concentrations. The degree to which sublethal algal concentrations challenge the health of the fish during blooms is practically unknown. In this study, we analysed whether sublethal concentrations of the ichthyotoxic alga Prymnesium parvum affect the susceptibility of rainbow trout Oncorhynchus mykiss to viral haemorrhagic septicaemia virus (VHSV). During exposure to sublethal algal concentrations, the fish increased production of mucus on their gills. When fish were exposed to the algae for 12 h prior to the addition of virus, a marginal decrease in the susceptibility to VHSV was observed compared to fish exposed to VHSV without algae. If virus and algae were added simultaneously, inclusion of the algae increased mortality by 50% compared to fish exposed to virus only, depending on the experimental setup. We concluded that depending on the local exposure conditions, sublethal concentrations of P. parvum could affect susceptibility of fish to infectious agents such as VHSV.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, University of Copenhagen, Aarhus University
Authors: Andersen, N. G. (Ekstern), Lorenzen, E. (Ekstern), Boutrup, T. S. (Intern), Hansen, P. J. (Ekstern), Lorenzen, N. (Ekstern)
Number of pages: 9
Pages: 187-195
Publication date: 2016
Main Research Area: Technical/natural sciences

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Journal: Diseases of Aquatic Organisms
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BFI (2018): BFI-level 1
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BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.95 SJR 0.858 SNIP 0.929
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.949 SNIP 0.935 CiteScore 1.96
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.889 SNIP 0.881 CiteScore 1.86
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.812 SNIP 0.918 CiteScore 1.77
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.912 SNIP 1.092 CiteScore 2.04
Subtyping of influenza på danske minkfarmer i 2014

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Hjulsager, C. K. (Intern), Krog, J. S. (Intern), Chriél, M. (Intern), Larsen, G. (Intern), Larsen, L. E. (Intern)
Pages: 109-113
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Title of host publication: Faglig årsberetning 2015 : Kopenhagen Fur
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Publication: Research › Report chapter – Annual report year: 2016

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Viral haemorrhagic septicaemia virus, Susceptibility, Harmful algal blooms, Fish Disease, Oncorhynchus mykiss, VHSV, Aquatic Science, Ecology, Evolution, Behavior and Systematics, Fish disease
DOIs:
10.3354/dao02946
Source: Findit
Source-ID: 2288696639
Publication: Research - peer-review › Journal article – Annual report year: 2016
The future of antiviral immunotoxins

There is a constant need for new therapeutic interventions in a wide range of infectious diseases. Over the past few years, the immunotoxins have entered the stage as promising antiviral treatments. Immunotoxins have been extensively explored in cancer treatment and have achieved FDA approval in several cases. Indeed, the design of new anticancer immunotoxins is a rapidly developing field. However, at present, several immunotoxins have been developed targeting a variety of different viruses with high specificity and efficacy. Rather than blocking a viral or cellular pathway needed for virus replication and dissemination, immunotoxins exert their effect by killing and eradicating the pool of infected cells. By targeting a virus-encoded target molecule, it is possible to obtain superior selectivity and drastically limit the side effects, which is an immunotoxin-related challenge that has hindered the success of immunotoxins in cancer treatment. Therefore, it seems beneficial to use immunotoxins for the treatment of virus infections. One recent example showed that targeting of virus-encoded 7 transmembrane (7TM) receptors by immunotoxins could be a future strategy for designing ultraspecific antiviral treatment, ensuring efficient internalization and hence efficient eradication of the pool of infected cells, both in vitro and in vivo. In this review, we provide an overview of the mechanisms of action of immunotoxins and highlight the advantages of immunotoxins as future anti-viral therapies.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, University of Copenhagen
Authors: Spiess, K. (Ekstern), Høy Jakobsen, M. (Ekstern), Kledal, T. N. (Intern), Rosenkilde, M. M. (Ekstern)
Number of pages: 15
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Journal: Journal of Leukocyte Biology
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Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4 SJR 2.402 SNIP 1.095
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.452 SNIP 1.149 CiteScore 3.95
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.58 SNIP 1.186 CiteScore 3.94
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 2.647 SNIP 1.188 CiteScore 4.22
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 2.593 SNIP 1.271 CiteScore 4.6
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 2.508 SNIP 1.3 CiteScore 4.5
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.52 SNIP 1.221
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 2.461 SNIP 1.185
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 2.586 SNIP 1.084
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.

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Organisations: National Veterinary Institute, Section for Virology
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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
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 5.41 SJR 5.984 SNIP 1.377
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 6.127 SNIP 1.512 CiteScore 4.91
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 6.835 SNIP 1.507 CiteScore 4.85
The Non-structural Protein 5 and Matrix Protein Are Antigenic Targets of T Cell Immunity to Genotype 1 Porcine Reproductive and Respiratory Syndrome Viruses

The porcine reproductive and respiratory syndrome virus (PRRSV) is the cause of one of the most economically important diseases affecting swine worldwide. Efforts to develop a next-generation vaccine have largely focused on envelope glycoproteins to target virus-neutralizing antibody responses. However, these approaches have failed to demonstrate the necessary efficacy to progress toward market. T cells are crucial to the control of many viruses through cytolysis and cytokine secretion. Since control of PRRSV infection is not dependent on the development of neutralizing antibodies, it has been proposed that T cell-mediated immunity plays a key role. Therefore, we hypothesized that conserved T cell antigens represent prime candidates for the development a novel PRRS vaccine. Antigens were identified by screening a proteome-wide synthetic peptide library with T cells from cohorts of pigs rendered immune by experimental infections with a closely related (subtype 1) or divergent (subtype 3) PRRSV-1 strain. Dominant T cell IFN-gamma responses were directed against the non-structural protein 5 (NSP5), and to a lesser extent, the matrix (M) protein. The majority of NSP5-specific CD8 T cells and M-specific CD4 T cells expressed a putative effector memory phenotype and were polyfunctional as assessed by coexpression of TNF-alpha and mobilization of the cytotoxic degranulation marker CD107a. Both antigens were generally well conserved among strains of both PRRSV genotypes. Thus, M and NSP5 represent attractive vaccine candidate T cell antigens, which should be evaluated further in the context of PRRSV vaccine development.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Animal and Plant Health Agency, University of Veterinary Medicine, University of Surrey, University College London
Authors: Mokhtar, H. (Ekstern), Pedrera, M. (Ekstern), Frossard, J. (Ekstern), Biffar, L. (Ekstern), Hammer, S. E. (Ekstern), Kvisgaard, L. K. (Intern), Larsen, L. E. (Intern), Stewart, G. R. (Ekstern), Somavarapu, S. (Ekstern), Steinbach, F. (Ekstern), Graham, S. P. (Ekstern)
Number of pages: 14
Publication date: 2016
Main Research Area: Technical/natural sciences

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Journal: Frontiers in Immunology
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Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
Scopus rating (2016): CiteScore 5.37 SJR 2.963 SNIP 1.483
Web of Science (2016): Indexed yes
Scopus rating (2015): SJR 2.818 SNIP 1.29 CiteScore 5.09
Web of Science (2015): Indexed yes
Scopus rating (2014): SJR 2.382 SNIP 1.056 CiteScore 4.24
Web of Science (2014): Indexed yes
Scopus rating (2013): SJR 1.842 SNIP 0.837 CiteScore 3.55
ISI indexed (2013): ISI indexed no
Scopus rating (2012): SJR 0.785 SNIP 0.193 CiteScore 1.38
ISI indexed (2012): ISI indexed no
Scopus rating (2011): SJR 0.121
The pig as a large preclinical model for therapeutic human anti-cancer vaccine development

Development of therapeutic cancer vaccines has largely been based on rodent models and the majority failed to establish therapeutic responses in clinical trials. We therefore used pigs as a large animal model for human cancer vaccine development due to the large similarity between the porcine and human immunome. We administered peptides derived from porcine IDO, a cancer antigen important in human disease, formulated in Th1-inducing adjuvants to outbred pigs. By in silico prediction 136 candidate IDO-derived peptides were identified and peptide-SLA class I complex stability measurements revealed 89 stable (t½ ≥ 0.5 hour) complexes with expressed SLA alleles. By IFN-γ ELISpot we showed that it was possible to break the peripheral tolerance and induce a cell-mediated response to an endogenous antigen. Mounting a proper Th1 response is highly dependent on peptide dose; we therefore designed a dose titration study with 15 Göttingen minipigs receiving intraperitoneal injections of either 1 µg, 10 µg or 100 µg of 30-31mer peptides covering the majority of IDO-derived potential cytotoxic T lymphocyte (CTL) epitopes. Peptides were formulated in CAF09, an adjuvant comprised of cationic DDA liposomes decorated with poly (I:C) and MMG as immune modulators. Interestingly, the 1 µg group was the only one showing responses to all immunization peptides following seven injections as determined by IFN-γ ELISpot. These data show that a reduction in dose can result in a highly specific Th1-biased response. To test the CTL functionality we designed an in vivo cytotoxicity assay, where purified autologous PBMCs fluorescently labelled and pulsed with IDO-derived target peptides were administered intravenously into each donor and killing capacity was measured by flow cytometry. All animals receiving 10 µg peptide immunizations showed specific killing of peptide-pulsed target cells one week post i.v. transfer with certain animals reaching close to 60% specific killing capacity in vivo.
The pig as a large preclinical model for therapeutic human anti-cancer vaccine development

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Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Section for Virology, State Serum Institute, University of Copenhagen, Technical University of Denmark, Statens Serum Institut
Number of pages: 1
Publication date: 2016
Event: Abstract from 11th International Veterinary Immunology Symposium, Gold Coast, Australia.
Main Research Area: Technical/natural sciences
Source: PublicationPreSubmission
Source-ID: 127762619
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2016
Tracking the elusive cytotoxic T cell response in pigs

Quantitative and qualitative assessment of antigen-specific cytotoxic T cell (CTL) responses in pigs is not a straightforward process. Through the years we have developed a series of reagents, tools and protocols to characterize peptide-specific CTL responses in pigs.

The most common recombinant SLA heavy chains were produced and peptide binding motifs were determined by assays measuring the affinity and stability of the peptide-SLA complex (pSLA) interaction. These results have been used to train neural networks to predict the binding of any pSLA (http://www.cbs.dtu.dk/services/). Recombinant SLA molecules complexed with verified binding peptides can be assembled to SLA multimers for staining of peptide-specific CTLs, and measured by flow cytometry, as we have shown with FMDV and influenza. This, however, requires SLA-matched pigs for which we have developed two methods: a sequence-based, high-resolution SLA genotyping method by standard PCR for specific detection of eight in-house SLA molecules; and a next-generation sequencing method for parallel detection of up to 50 samples of barcoded cDNA PCR products spanning exon 2 and 3. The latter for a wider characterization of expressed alleles in candidate pigs.

The in vivo generation of CTL responses to antigens following peptide immunizations is thought to require cross-presentation in appropriate dendritic cells (DC). In mice this was linked to targeting of CD103+DCs recruited after intraperitoneal immunizations. We have therefore developed a protocol for intraperitoneal delivery of peptides formulated in poly(I:C)/MMG-decorated liposomes (CAF09) to investigate the influence of peptide dose on the generation of CTL vs. antibody responses. Finally, the induced CTL killing was assessed by an in vivo cytotoxicity assay, where purified autologous PBMCs, fluorescently labeled and pulsed with target peptides, were reinjected into the donor. The in vivo killing of peptide-pulsed cells was measured by flow cytometry relative to non-pulsed PBMCs at different time points after cell transfer.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Section for Virology, Section for Bacteriology, Pathology and Parasitology, Department of Systems Biology, Center for Biological Sequence Analysis, Department of Bio and Health Informatics, University of Copenhagen, United States Department of Agriculture
Number of pages: 1
Publication date: 2016
Event: Abstract from 11th International Veterinary Immunology Symposium, Gold Coast, Australia.
Main Research Area: Technical/natural sciences
Electronic versions: Jungersen_et_al_IVIS_Abstract.pdf
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2016

Udvikling af antistoffer efter vaccination mod og podning med PRRSV: Meddelelser nr. 1067

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Technical University of Denmark
Authors: Sonne Kristensen, C. (Ekstern), Qvist Pawlowski, M. (Ekstern), Thoning, H. (Ekstern), Haugegaard, S. (Ekstern), Holmgaard Carlsen, S. (Ekstern), Lauritsen, K. T. (Intern), Hjulsager, C. K. (Intern), Larsen, L. E. (Intern)
Number of pages: 19
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Publisher: Videncenter for Svineproduktion
Original language: Danish
Main Research Area: Technical/natural sciences
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Links: http://vsp.dk/Publikationer/Kilder/lu_medd/2016/1067.aspx
Source: PublicationPreSubmission
Source-ID: 127552278
Publication: Commissioned › Report – Annual report year: 2016

Unrecognized circulation of SAT 1 foot-and-mouth disease virus in cattle herds around Queen Elizabeth National Park in Uganda

Foot-and-mouth disease (FMD) is endemic in Uganda in spite of the control measures used. Various aspects of the maintenance and circulation of FMD viruses (FMDV) in Uganda are not well understood; these include the role of the African buffalo (Syncerus caffer) as a reservoir for FMDV. To better understand the epidemiology of FMD at the livestock-
wildlife-interface, samples were collected from young, unvaccinated cattle from 24 pastoral herds that closely interact with wildlife around Queen Elizabeth National Park in Uganda, and analysed for evidence of FMDV infection. In total, 37 (15 %) of 247 serum samples had detectable antibodies against FMDV non-structural proteins (NSPs) using a pan-serotypic assay. Within these 37 sera, antibody titres ≥80 against the structural proteins of serotypes O, SAT 1, SAT 2 and SAT 3 were detected by ELISA in 5, 7, 4 and 3 samples, respectively, while neutralizing antibodies were only detected against serotype O in 3 samples. Two FMDV isolates, with identical VP1 coding sequences, were obtained from probang samples from clinically healthy calves from the same herd and are serotype SAT 1 (topotype IV (EA-I)). Based on the VP1 coding sequences, these viruses are distinct from previous cattle and buffalo SAT 1 FMDV isolates obtained from the same area (19-30 % nucleotide difference) and from the vaccine strain (TAN/155/71) used within Uganda (26 % nucleotide difference). Eight herds had only one or a few animals with antibodies against FMDV NSPs while six herds had more substantial evidence of prior infection with FMDV. There was no evidence for exposure to FMDV in the other ten herds. The two identical SAT 1 FMDV VP1 sequences are distinct from former buffalo and cattle isolates from the same area, thus, transmission between buffalo and cattle was not demonstrated. These new SAT 1 FMDV isolates differed significantly from the vaccine strain used to control Ugandan FMD outbreaks, indicating a need for vaccine matching studies. Only six herds had clear serological evidence for exposure to O and SAT 1 FMDV. Scattered presence of antibodies against FMDV in other herds may be due to the occasional introduction of animals to the area or maternal antibodies from past infection and/or vaccination. The evidence for asymptomatic FMDV infection has implications for disease control strategies in the area since this obstructs early disease detection that is based on clinical signs in FMDV infected animals.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Dhikusooka, M. T. (Ekstern), Ayebazibwe, C. (Ekstern), Namatovu, A. (Ekstern), Belsham, G. (Intern), Siegismund, H. R. (Ekstern), Wekesa, S. N. (Ekstern), Balinda, S. N. (Ekstern), Muwanika, V. B. (Ekstern), Tjørnehøj, K. (Intern)
Number of pages: 13
Publication date: 2016
Main Research Area: Technical/natural sciences

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Journal: B M C Veterinary Research
Volume: 12
Issue number: 1
ISSN (Print): 1746-6148
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BFI (2018): BFI-level 1
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BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.83 SJR 0.847 SNIP 0.983
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.925 SNIP 0.97 CiteScore 1.86
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.885 SNIP 0.987 CiteScore 1.81
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.829 SNIP 0.833 CiteScore 1.85
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.743 SNIP 1.043 CiteScore 1.94
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.157 SNIP 1.455 CiteScore 2.66
ISI indexed (2011): ISI indexed no
Virulence determinants within the E2 glycoprotein of Classical Swine Fever Virus

Classical Swine Fever is a highly contagious disease of pigs caused by Classical Swine Fever Virus (CSFV), a member of the pestivirus genus within the family Flaviviridae. The E2 glycoprotein of CSFV has been shown to be an important factor for the virulence of the virus. In a recent study, we have identified a specific motif within the E2 glycoprotein that contributes to the virulence of the highly virulent CSFV strain Koslov (Fahnøe et al. 2014). This motif comprises residues S74 and L75 in the N-terminal domain of E2 (S763 and L764 in the polyprotein). Evidence points towards involvement of this motif in virulence. CSFV strains encoding L763 and P764 represent the predominant alleles across all published full-length CSFV genomes, whereas the S763/L764 combination is only seen in highly virulent strains. In this study, mutations were introduced into the consensus cDNA clone of the highly virulent CSFV strain Koslov to evaluate the virulence of a set of E2 mutants with modifications in the encoded residues 763 and 764; these mutants are termed; vKos_SP, vKos_LP and vKos_LL, respectively. Animal infection experiments were performed to compare virulence of these E2 mutants in comparison to vKos (with the SL motif). The results indicate that the E2 residues 763-64 play an important role in CSFV virulence.
Virulence of viral haemorrhagic septicaemia virus (VHSV) genotype III in rainbow trout

In general, viral haemorrhagic septicaemia virus (VHSV) isolates from marine fish species in European waters (genotypes GIb, GII and GIII) are non- to low virulent in rainbow trout. However, a VHSV isolation was made in 2007 from a disease outbreak in sea farmed rainbow trout in Norway. The isolate, named NO-2007-50-385, was demonstrated to belong to GIII. This isolate has attracted attention to assess which of the viral genome/proteins might be associated with the virulence in rainbow trout. In this study, we describe the difference of virulence in rainbow trout between the NO-2007-50-385 and 4p168 isolates as representatives of virulent and non-virulent GIII isolates, respectively. Rainbow trout were bath challenged with VHSV NO-2007-50-385 for 1 and 6 h, resulting in cumulative mortalities of 5 and 35%, respectively. No mortality was observed in the rainbow trout groups immersed with the genotype III VHSV isolate 4p168 for 1 and 6 h. The viral titre in organs from fish challenged with NO-2007-50-385 for 6 h increased more rapidly than those exposed for 1 h. By in vitro studies it was demonstrated that the final titres of VHSV DK-3592B (GI), NO-2007-50-385 and 4p168 inoculated on EPC cells were very similar, whereas when inoculated on the rainbow trout cell line RTG-2 the titre of the non-virulent 4p168 isolate was 3-4 logs below the two other VHSV isolates. Based on a comparative analysis of the entire genome of the genotype III isolates, we suggest that substitutions of amino acids in positions 118-123 of the nucleo-protein are candidates for being related to virulence of VHSV GIII in rainbow trout.

General information

State: Published
Organisations: National Veterinary Institute, Section for Virology, Fisheries Research Agency
Authors: Ito, T. (Ekstern), Kurita, J. (Ekstern), Mori, K. (Ekstern), Olesen, N. J. (Intern)
Number of pages: 13
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Main Research Area: Technical/natural sciences

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Article number: 4
ISSN (Print): 0928-4249
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): SJR 1.281 SNIP 1.142
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.342 SNIP 1.006 CiteScore 2.66
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.189 SNIP 1.197 CiteScore 2.46
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.353 SNIP 1.457 CiteScore 3.13
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.254 SNIP 1.279 CiteScore 2.97
Vis jeres værd, universiteter

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Kledal, T. N. (Intern)
Pages: 2-2
Publication date: 2016
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Publication information
Journal: Boersen
ISSN (Print): 0105-0729
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Original language: Danish
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West Nile fever: A virus disease spreading in Europe
Status over West Nile virus in Europe and the Danish surveillance program.

General information
State: Published
Organisations: National Veterinary Institute, Section for Epidemiology, Section for Virology, Fødevarestyrelsen, University of Copenhagen
Authors: Lohse, L. (Intern), Madsen, J. J. (Ekstern), Huda, A. (Ekstern), Bædker, R. (Intern), Thorup, K. (Ekstern), Polacek, C. (Intern), Bøtner, A. (Intern)
Pages: 10-13
Publication date: 2016
Main Research Area: Technical/natural sciences

Publications information
Journal: Dansk Veterinaertidsskrift
Volume: 2016
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ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
ISI indexed (2012): ISI indexed no
BFI (2011): BFI-level 1
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
BFI (2009): BFI-level 1
BFI (2008): BFI-level 1
Original language: English
Electronic versions:
West_Nile_fever_DVT_08_2016.pdf
Links:
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Publication: Research › Journal article – Annual report year: 2016

A cell culture-adapted Classical swine fever virus phenotype does not require the 476Arg Ems mutation

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Friedrich Loeffler Institute
Authors: Drager, C. (Ekstern), Blome, S. (Ekstern), Beer, M. (Ekstern), Reimann, I. (Ekstern), Rasmussen, T. B. (Intern)
Number of pages: 1
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Main Research Area: Technical/natural sciences

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EPIZONE_Abstract_Cell_culture_Adapted_CSFV_TBRUR.pdf
Aleutian Mink Disease Virus in Free-Ranging Mink from Sweden

Aleutian mink disease (AMD) is a chronic viral disease in farmed mink and the virus (AMDV) has been found in many free-ranging mink (Neovison vison) populations in Europe and North America. In this study, AMDV DNA and AMDV antibodies were analysed in 144 free-ranging mink hunted in Sweden. Associations between being AMDV infected (defined as positive for both viral DNA and antibodies) and the weight of the spleen, liver, kidneys, adrenal glands and body condition were calculated and the sequences of ten AMDV isolates were analysed in order to characterize the genetic relationships. In total, 46.1% of the mink were positive for AMDV antibodies and 57.6% were positive for AMDV DNA. Twenty-two percent of the mink tested on both tests (n = 133) had dissimilar results. The risk of having AMDV antibodies or being positive for AMDV DNA clearly increased with age and the majority of the mink that were two years or older were infected. Few macroscopic changes were found upon necropsy. However, the relative weight of the spleen was sexually dimorphic and was found to be slightly, but significantly (rho = 0.006), heavier in AMDV infected male mink than uninfected. No association between AMDV infection and body condition, weight of the kidneys, liver or adrenal glands were found. Several different strains of AMDV were found across the country. Two of the AMDV sequences from the very north of Sweden did not group with any of the previously described groups of strains. In summary, AMDV seems to be prevalent in wild mink in Sweden and may subtly influence the weight of the spleen.
Analysis of Recent Serotype O Foot-and-Mouth Disease Viruses from Livestock in Kenya: Evidence of Four Independently Evolving Lineages

Foot-and-mouth disease (FMD) is endemic in Kenya where four serotypes (O, A, SAT 1 and SAT 2) of the virus are currently in circulation. Within 2010 and 2011, the National Laboratory recorded an increase in the number of FMD outbreaks caused by serotype O virus. The characteristics of these viruses were determined to ascertain whether these were independent outbreaks or one single strain spreading throughout the country. The sequences of the complete VP1-coding region were analysed from viruses sampled within different areas of Kenya during 2010 and 2011. The results indicated that the 2010 to 2011 outbreaks in Kenya were caused by four independent strains. By comparison with earlier type O isolates from Eastern Africa, it was apparent that the outbreaks were caused by viruses from three different lineages of topotype EA-2 and a fourth virus strain belonging to topotype EA-4. The topotypes EA-1 and EA-3 were not detected from these outbreaks. Implications of these results for FMD control in Eastern Africa are discussed.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, The Pirbright Institute, Makerere University, University of Copenhagen, Ministry of Livestock Development
Authors: Wekesa, S. N. (Ekstern), Muwanika, V. B. (Ekstern), Siegismund, H. R. (Ekstern), Sangula, A. K. (Ekstern), Namatovu, A. (Ekstern), Dhikusooka, M. T. (Ekstern), Tjørnehøj, K. (Intern), Balinda, S. N. (Ekstern), Wadsworth, J. (Ekstern), Knowles, N. J. (Ekstern), Belsham, G. (Intern)
Number of pages: 10
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Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
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 calciviruses 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
Authors: Hartby, C. M. (Intern), Kvisgaard, L. K. (Intern), Larsen, L. E. (Intern), Chriél, M. (Intern), Hjulsager, C. K. (Intern)
Number of pages: 3
Publication date: 2015
Event: Abstract from Nordic Association of Agricultural Scientists, Turku, Finland.
Main Research Area: Technical/natural sciences
Electronic versions:
NJF_qPCR_assays_for_viral_mink_diarrhea_endelig_version.pdf
Source: PublicationPreSubmission
Source-ID: 116757331
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2015

Bat Coronavirus circulating in Danish bats

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, University of Copenhagen, Central Veterinary Institute
Authors: Rasmussen, T. B. (Intern), Chriél, M. (Intern), Baagøe, H. J. (Ekstern), Fjederholt, E. (Ekstern), Kooi, E. A. (Ekstern), Belsham, G. (Intern), Batner, A. (Intern)
Number of pages: 1
Pages: 252-252
Publication date: 2015
Event: Poster session presented at 10th International Congress for Veterinary Virology, Montpellier, France.
Main Research Area: Technical/natural sciences
Electronic versions:
EPIZONE_Poster_Coronavirus_in_bats_TBRUR_150825_final.pdf
Source: PublicationPreSubmission
Source-ID: 116892687
Publication: Research - peer-review › Poster – Annual report year: 2015

Beskytter de eksisterende vacciner godt nok mod PCV2-mutant (PCV2d)?

General information
State: Published
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
Organisations: National Veterinary Institute, Section for Virology, Center for Biological sequence analysis, Department of Systems Biology, Center for Biological Sequence Analysis, Immunological Bioinformatics, Section for Immunology and Vaccinology
Publication date: 2015
Main Research Area: Technical/natural sciences
Challenges for Serology-Based Characterization of Foot-and-Mouth Disease Outbreaks in Endemic Areas; Identification of Two Separate Lineages of Serotype O FMDV in Uganda in 2011

Control of foot-and-mouth disease (FMD) in Uganda by ring vaccination largely depends on costly trivalent vaccines, and use of monovalent vaccines could improve the cost effectiveness. This, however, requires application of highly specific diagnostic tests. This study investigated outbreaks of FMD in seven Ugandan districts, during 2011, using the PrioCHECK(R) FMDV NS ELISA, solid-phase blocking ELISAs (SPBEs) and virus neutralization tests (VNTs), together with virological analyses for characterization of the responsible viruses. Two hundred and eighteen (218) cattle and 23 goat sera as well as 82 oropharyngeal fluid/epithelial tissue samples were collected. Some 50% of the cattle and 17% of the goat sera were positive by the PrioCHECK(R) FMDV NS ELISA, while SPBEs identified titres 80 for antibodies against serotype O FMD virus (FMDV) in 51% of the anti-NSP positive cattle sera. However, 35% of the anti-NSP positive cattle sera had SPBE titres 80 against multiple serotypes, primarily against serotypes O, SAT 1 and SAT 3. Comparison of SPBEs and VNTs for the detection of antibodies against serotypes O, SAT 1 and SAT 3 in 72 NSP positive cattle sera showed comparable results against serotype O (P=0.181), while VNTs detected significantly fewer samples positive for antibodies against SAT 1 and SAT 3 than the SPBEs (P
Characterisation of recent foot-and-mouth disease viruses from African buffalo (Syncerus caffer) and cattle in Kenya is consistent with independent virus populations

Background
Understanding the epidemiology of foot-and-mouth disease (FMD), including roles played by different hosts, is essential for improving disease control. The African buffalo (Syncerus caffer) is a reservoir for the SAT serotypes of FMD virus (FMDV). Large buffalo populations commonly intermingle with livestock in Kenya, yet earlier studies have focused on FMD in the domestic livestock, hence the contribution of buffalo to disease in livestock is largely unknown. This study analysed 47 epithelia collected from FMD outbreaks in Kenyan cattle between 2008 and 2012, and 102 probang and serum samples collected from buffalo in three different Kenyan ecosystems; Maasai-Mara (MME) (n=40), Tsavo (TSE) (n=33), and Meru (ME) (n=29).

Results
Antibodies against FMDV non-structural proteins were found in 65 of 102 (64%) sera from buffalo with 44/102 and 53/102 also having neutralising antibodies directed against FMDV SAT 1 and SAT 2, respectively. FMDV RNA was detected in 42% of the buffalo probang samples by RT-qPCR (Cycle Threshold (Ct) ≤32). Two buffalo probang samples were positive by VI and were identified as FMDV SAT 1 and SAT 2 by Ag-ELISA, while the latter assay detected serotypes O (1), A (20), SAT 1 (7) and SAT 2 (19) in the 47 cattle epithelia. VP1 coding sequences were generated for two buffalo and 21 cattle samples. Phylogenetic analyses revealed SAT 1 and SAT 2 virus lineages within buffalo that were distinct from those detected in cattle.

Conclusions
We found that FMDV serotypes O, A, SAT 1 and SAT 2 were circulating among cattle in Kenya and cause disease, but only SAT 1 and SAT 2 viruses were successfully isolated from clinically normal buffalo. The buffalo isolates were genetically distinct from isolates obtained from cattle. Control efforts should focus primarily on reducing FMDV circulation among livestock and limiting interaction with buffalo. Comprehensive studies incorporating additional buffalo viruses are recommended.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Foot-and-Mouth Disease Laboratory, Makerere University, Kenya Wildlife Service, University of Copenhagen
Authors: Nabalayo Wekesa, S. (Ekstern), Kiprotich Sangula, A. (Ekstern), Belsham, G. (Intern), Tjørnehej, K. (Intern), Muwanika, V. B. (Ekstern), Gakuya, F. (Ekstern), Mijele, D. (Ekstern), Redlef Siegismund, H. (Ekstern)
Number of pages: 15
Publication date: 2015

To investigate the foot-and-mouth disease virus (FMDV) serotypes circulating in Uganda’s cattle population, both serological and virological analyses of samples from outbreaks that occurred during 2012-2013 were performed. Altogether, 79 sera and 60 oropharyngeal fluid (OP)/tissue/oral swab samples were collected from herds with reported FMD outbreaks in seven different Ugandan districts. Overall, 61/79 (77%) of the cattle sera were positive for antibodies against FMDV by PrioCHECK® FMDV NS ELISA and solid phase blocking ELISA detected titres ≥ 80 for serotypes O, SAT 1, SAT 2 and SAT 3 in 41, 45, 30 and 45 of these 61 seropositive samples, respectively. Virus neutralisation tests detected the highest levels of neutralising antibodies (titres ≥ 45) against serotype O in the herds from Kween and Rakai districts, against SAT 1 in the herd from Nwoya district and against SAT 2 in the herds from Kiruhura, Isingiro and Ntungamo districts. Consistent with the detection of high levels of neutralising antibodies against SAT 2, was the isolation of a SAT 2 FMDV from Isingiro; sequencing (for the VP1 coding region) indicated that this virus belonged to lineage I within this serotype, like the currently used vaccine strain. From the Wakiso district 11 tissue/swab samples were collected; serotype A FMDV, genotype Africa (G-I), was isolated from the epithelial samples. This study shows that within a period of less than one year, FMD outbreaks in Uganda were caused by four different serotypes namely O, A, SAT 1 and SAT 2. Therefore, to enhance the control of FMD in Uganda, there is need for efficient and timely determination of outbreak virus strains/serotypes and vaccine matching. The value of incorporating serotype A antigen into the imported vaccines along with the current serotype O, SAT 1 and SAT 2 strains should be considered.
Characterization of the PRRSV strain circulating in a PRRSV type 1 positive herd before, during and after vaccination with a PRRSV type 1 vaccine

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Danish Pig Production
Authors: Kvisgaard, L. K. (Intern), Kristensen, C. S. (Ekstern), Hjulsager, C. K. (Intern), Larsen, L. E. (Intern)
Number of pages: 1
Publication date: 2015
Event: Abstract from 7th International Symposium on Emerging and Re-emerging Pig Diseases, Kyoto, Japan.
Main Research Area: Technical/natural sciences
Electronic versions:
iserpd2015abstract_FINAL.pdf
Source: PublicationPreSubmission
Source-ID: 119057195
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2015

Characterizing novel endogenous retroviruses from genetic variation inferred from short sequence reads
From Illumina sequencing of DNA from brain and liver tissue from the lion, Panthera leo, and tumor samples from the pike-perch, Sander lucioperca, we obtained two assembled sequence contigs with similarity to known retroviruses.
Phylogenetic analyses suggest that the pike-perch retrovirus belongs to the epsilonretroviruses, and the lion retrovirus to the gammaretroviruses. To determine if these novel retroviral sequences originate from an endogenous retrovirus or from a recently integrated exogenous retrovirus, we assessed the genetic diversity of the parental sequences from which the short Illumina reads are derived. First, we showed by simulations that we can robustly infer the level of genetic diversity from short sequence reads. Second, we find that the measures of nucleotide diversity inferred from our retroviral sequences significantly exceed the level observed from Human Immunodeficiency Virus infections, prompting us to conclude that the novel retroviruses are both of endogenous origin. Through further simulations, we rule out the possibility that the observed elevated levels of nucleotide diversity are the result of co-infection with two closely related exogenous retroviruses.

**General information**

State: Published
Organisations: National Veterinary Institute, Section for Virology, University of Copenhagen, Statens Seruminstitute
Authors: Mourier, T. (Ekstern), Mollerup, S. (Ekstern), Vinner, L. (Ekstern), Kjartansdóttir, K. R. (Ekstern), Guldberg Fröslev, T. (Ekstern), Boutrup, T. S. (Intern), Nielsen, L. P. (Ekstern), Willerslev, E. (Ekstern), Hansen, A. J. (Ekstern)
Number of pages: 11
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Main Research Area: Technical/natural sciences

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Web of Science (2016): Indexed yes
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Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.103 SNIP 1.544 CiteScore 4.75
Web of Science (2014): Indexed yes
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Scopus rating (2013): SJR 1.886 SNIP 1.51 CiteScore 4.06
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.458 SNIP 0.896 CiteScore 2.44
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http://www.nature.com/articles/srep15644
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Source-ID: 2287348912
Publication: Research - peer-review › Journal article – Annual report year: 2015
Complete genome sequence of eelpout rhabdovirus (ERV) identified by deep sequencing of viral RNA

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, National Veterinary Institute, Swedish Agency for Marine and Water Management
Authors: Hakhverdyan, M. (Ekstern), Areskog, M. (Ekstern), Blomkvist, E. (Ekstern), Alfjorden, A. (Ekstern), Boutrup, T. S. (Intern), Ahola, H. (Ekstern), Ljunghager, F. (Ekstern), Hagström, Å. (Ekstern), Olesen, N. J. (Intern), Juremalm, M. (Ekstern), Valarcher, J. (Ekstern), Axen, C. (Ekstern), Leijon, M. (Ekstern)
Pages: 341-341
Publication date: 2015

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Place of publication: Las Palmas
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Article number: P-117
Main Research Area: Technical/natural sciences
Conference: 17th International Conference on Diseases of Fish and Shellfish, Las Palmas, Spain, 07/09/2015 - 07/09/2015
Electronic versions:
Book_of_abstracts_17th_International_conference_on_Diseases_of_Fish_and_Shellfish.pdf
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2015

Creation of Functional Viruses from Non-Functional cDNA Clones Obtained from an RNA Virus Population by the Use of Ancestral Reconstruction
RNA viruses have the highest known mutation rates. Consequently it is likely that a high proportion of individual RNA virus genomes, isolated from an infected host, will contain lethal mutations and be non-functional. This is problematic if the aim is to clone and investigate high-fitness, functional cDNAs and may also pose problems for sequence-based analysis of viral evolution. To address these challenges we have performed a study of the evolution of classical swine fever virus (CSFV) using deep sequencing and analysis of 84 full-length cDNA clones, each representing individual genomes from a moderately virulent isolate. In addition to here being used as a model for RNA viruses generally, CSFV has high socioeconomic importance and remains a threat to animal welfare and pig production. We find that the majority of the investigated genomes are non-functional and only 12% produced infectious RNA transcripts. Full length sequencing of cDNA clones and deep sequencing of the parental population identified substitutions important for the observed phenotypes. The investigated cDNA clones were furthermore used as the basis for inferring the sequence of functional viruses. Since each unique clone must necessarily be the descendant of a functional ancestor, we hypothesized that it should be possible to produce functional clones by reconstructing ancestral sequences. To test this we used phylogenetic methods to infer two ancestral sequences, which were then reconstructed as cDNA clones. Viruses rescued from the reconstructed cDNAs were tested in cell culture and pigs. Both reconstructed ancestral genomes proved functional, and displayed distinct phenotypes in vitro and in vivo. We suggest that reconstruction of ancestral viruses is a useful tool for experimental and computational investigations of virulence and viral evolution. Importantly, ancestral reconstruction can be done even on the basis of a set of sequences that all correspond to non-functional variants.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Department of Systems Biology, Center for Biological Sequence Analysis, Molecular Evolution, Friedrich Loeffler Institute, University of Glasgow
Authors: Fahne, U. (Intern), Pedersen, A. G. (Intern), Dräger, C. (Ekstern), Orton, R. J. (Ekstern), Blome, S. (Ekstern), Höper, D. (Ekstern), Beer, M. (Ekstern), Rasmussen, T. B. (Intern)
Number of pages: 10
Publication date: 2015
Main Research Area: Technical/natural sciences

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Journal: PLoS One
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Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
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.

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.
Detection of African Swine Fever Virus DNA in Blood Samples Stored on FTA Cards from Asymptomatic Pigs in Mbeya Region, Tanzania

The aim of the study was to assess whether blood samples collected onto FTA® cards could be used in combination with real-time PCR for the detection of African swine fever virus (ASFV) DNA in samples from resource-poor settings under the assumption that asymptomatically (sub-clinically) infected pigs may be present. Blood samples were collected from clinically healthy pigs from Mbeya Region, Tanzania. The blood samples were stored on FTA® cards and analysed by real-time PCR assays in duplicate; three pigs had high levels of viral DNA (Ct values of 27-29), and three pigs had a low level of viral DNA (Ct 36-45). Four pigs were positive in one of the duplicate samples only, but clear products of the expected size were obtained when the reactions were analysed by gel electrophoresis. For comparison, blood samples from pigs experimentally infected with either a pathogenic (OURT T88/1) or a non-pathogenic (OURT T88/3) isolate of ASFV were collected, stored on FTA® cards and analysed in the same way. The blood from pigs infected with the OURT T88/1 isolate showed high levels of viral DNA (Ct 22-33), whereas infection with non-pathogenic OURT T88/3 isolate resulted in only low levels of viral DNA (Ct 39) in samples collected at 10-14 days after inoculation.
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.

Detection of antibodies specific to koi herpesvirus (KHV) by serum neutralization test

State: Published
Organisations: National Veterinary Institute, Section for Virology, ANSES - French Agency for Food, Environmental and Occupational Health & Safety, Friedrich Loeffler Institute, Instituto Zooprofilattico Sperimentale delle Venezie, National Veterinary Research Institute, Wageningen University & Research
Authors: Cabon, J. (Ekstern), Louboutin, L. (Ekstern), Castric, J. (Ekstern), Bergmann, S. M. (Ekstern), Bovo, G. (Ekstern), Matras, M. (Ekstern), Haenen, O. (Ekstern), Olesen, N. J. (Intern), Morin, T. (Ekstern)
Pages: 115-115
Publication date: 2015

Detection of PRRSV in air sampled inside and outside PRRSV-positive herds in Denmark

State: Published
Organisations: National Veterinary Institute, Section for Virology, Technical University of Denmark, Svinevet Pig Practise, Boehringer Ingelheim Danmark A/S
Authors: Priebe, A. (Ekstern), Kvisgaard, L. K. (Intern), Rathkjen, P. H. (Ekstern), Hjulsager, C. K. (Intern), Havn, K. (Ekstern), Larsen, L. E. (Intern)
Number of pages: 1
Publication date: 2015
Event: Abstract from International Porcine Reproductive And Respiratory Syndrome Congress, Ghent, Belgium.
Development and Characterization of Probe-Based Real Time Quantitative RT-PCR Assays for Detection and Serotyping of Foot-And-Mouth Disease Viruses Circulating in West Eurasia.

Rapid and accurate diagnosis of foot-and-mouth disease (FMD) and virus serotyping are of paramount importance for control of this disease in endemic areas where vaccination is practiced. Ideally this virus characterization should be achieved without the need for virus amplification in cell culture. Due to the heterogeneity of FMD viruses (FMDVs) in different parts of the world, region specific diagnostic tests are required. In this study, hydrolysable probe-based real time reverse transcription quantitative polymerase chain reaction (RTqPCR) assays were developed for specific detection and serotyping of the FMDVs currently circulating in West Eurasia. These assays were evaluated, in parallel with pan-FMDV diagnostic assays and earlier serotype-specific assays, using field samples originating from Pakistan and Afghanistan containing FMD viruses belonging to different sublineages of OPanAsia.A-Iran05 and Asia-1 (Group-II and Group-VII (Sindh-08)). In addition, field samples from Iran and Bulgaria, containing FMDVs belonging to the O-PanAsia sublineages were also tested. Each of the three primer/probe sets was designed to be specific for just one of the serotypes O, A and Asia-1 of FMDV and detected the RNA from the target viruses with cycle threshold (CT) values comparable with those obtained with the serotype independent pan-FMDV diagnostic assays. No cross-reactivity was observed in the assays between the heterotypic viruses circulating in the region. The assays reported here have higher diagnostic sensitivity (100% each for serotypes O and Asia-1, and 92% [95%CI = 81.4–100%] for serotype A positive samples) and specificity (100% each for serotypes O, A and Asia-1 positive samples) for the viruses currently circulating in West Eurasia compared to the serotyping assays reported earlier. Comparisons of the sequences of the primers and probes used in these assays and the corresponding regions of the circulating viruses provided explanations for the poor recognition of some of the viruses by the earlier assays. These new assays should help in the early detection and typing of serotype O, A and Asia-1 FMDVs circulating in West Eurasia to enable improved disease control.
Development of a real-time RT-PCR assay that detects a broad range of Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) Type 1 subtypes

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Parco Technologico Padano
Authors: Kvisgaard, L. K. (Intern), Hjulsager, C. K. (Intern), Botti, S. (Ekstern), Larsen, L. E. (Intern)
Number of pages: 1
Publication date: 2015
Event: Abstract from International Porcine Reproductive And Respiratory Syndrome Congress, Ghent, Belgium.
Main Research Area: Technical/natural sciences
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Source: PublicationPreSubmission
Source-ID: 119055993
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2015

Different clinical, virological, serological and tissue tropism outcomes of two new and one old Belgian type 1 subtype 1 porcine reproductive and respiratory virus (PRRSV) isolates

In this study, the pathogenic behavior of PRRSV 13V091 and 13V117, isolated in 2013 from two different Belgian farms with enzootic respiratory problems shortly after weaning in the nursery, were compared with the Belgian strain 07V063 isolated in 2007. Full-length genome sequencing was performed to identify their origin. Twelve weeks-old pigs were inoculated intranasally (IN) with 13V091, 13V117 or 07V063 (9 pigs/group). At 10 days post inoculation (dpi), 4 animals from each group were euthanized and tissues were collected for pathology, virological and serological analysis. 13V091 infection resulted in the highest respiratory disease scores and longest period of fever. Gross lung lesions were more pronounced for 13V091 (13%), than for 13V117 (7%) and 07V063 (11%). The nasal shedding and viremia was also most extensive with 13V091. The 13V091 group showed the highest virus replication in conchae, tonsils and retropharyngeal lymph nodes. 13V117 infection resulted in the lowest virus replication in lymphoid tissues. 13V091 showed higher numbers of sialoadhesin-infected cells/mm(2) in conchae, tonsils and spleen than 13V117 and 07V063. Neutralizing antibody response with 07V063 was stronger than with 13V091 and 13V117. It can be concluded that (i) 13V091 is a
highly pathogenic type 1 subtype 1 PRRSV strain that replicates better than 07V063 and 13V117 and has a strong tropism for sialoadhesin-cells and (ii) despite the close genetic relationship between 13V117 and 07V063, 13V117 has an increased nasal replication and shedding, but a decreased replication in lymphoid tissues compared to 07V063.

**General information**

**State:** Published

**Organisations:** National Veterinary Institute, Section for Virology, Ghent University

**Authors:** Frydas, I. S. (Ekstern), Trus, I. (Ekstern), Kvisgaard, L. K. (Intern), Bonckaert, C. (Ekstern), Reddy, V. R. A. P. (Ekstern), Li, Y. (Ekstern), Larsen, L. E. (Intern), Nauwynck, H. J. (Ekstern)

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

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BFI (2016): BFI-level 2

Scopus rating (2016): SJR 1.281 SNIP 1.142

Web of Science (2016): Indexed yes

BFI (2015): BFI-level 2

Scopus rating (2015): SJR 1.342 SNIP 1.006 CiteScore 2.66

Web of Science (2015): Indexed yes

BFI (2014): BFI-level 2

Scopus rating (2014): SJR 1.189 SNIP 1.197 CiteScore 2.46

Web of Science (2014): Indexed yes

BFI (2013): BFI-level 2

Scopus rating (2013): SJR 1.353 SNIP 1.457 CiteScore 3.13

ISI indexed (2013): ISI indexed yes

Web of Science (2013): Indexed yes

BFI (2012): BFI-level 2

Scopus rating (2012): SJR 1.254 SNIP 1.279 CiteScore 2.97

ISI indexed (2012): ISI indexed yes

Web of Science (2012): Indexed yes

BFI (2011): BFI-level 2

Scopus rating (2011): SJR 1.593 SNIP 1.645 CiteScore 3.85

ISI indexed (2011): ISI indexed yes

Web of Science (2011): Indexed yes

BFI (2010): BFI-level 2

Scopus rating (2010): SJR 1.506 SNIP 1.602

BFI (2009): BFI-level 2

Scopus rating (2009): SJR 1.472 SNIP 1.702

Web of Science (2009): Indexed yes

BFI (2008): BFI-level 2

Scopus rating (2008): SJR 1.557 SNIP 2.009

Web of Science (2008): Indexed yes

Scopus rating (2007): SJR 1.745 SNIP 2.184

Web of Science (2007): Indexed yes

Scopus rating (2006): SJR 1.348 SNIP 1.946

Scopus rating (2005): SJR 0.879 SNIP 1.593

Web of Science (2005): Indexed yes
Disease management mitigates risk of pathogen transmission from farmed salmon

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Section for Virology, Pacific Biological Station, Marine Scotland Science, Cefas
Authors: Jones, S. R. M. (Ekstern), Bruno, D. W. (Ekstern), Madsen, L. (Intern), Peeler, E. J. (Ekstern)
Pages: 50-50
Publication date: 2015

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Title of host publication: 17th International Conference on Diseases of Fish And Shellfish : Abstract book
Place of publication: Las Palmas
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Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2015

Elucidating the T-cell reactivity against porcine IDO and RhoC to establish the pig as an animal model for vaccine development against human cancer

Immune therapy of cancer has recently experienced a great breakthrough with prolonged overall survival in patients with metastatic disease following the use of checkpoint inhibitors and T cell therapy with ex vivo expanded CD8+ cytotoxic T cells (CTLs). In the further development of immune therapies against cancer, vaccine formulations tailored to mount in vivo CTL responses towards co-delivered cancer antigens will be an important hallmark. Recognition of antigen-derived peptides presented in the context of major histocompatibility complex (MHC) class I molecules on cancer cells is a requirement for activation of CTLs. Previously, the development of therapeutic anti-cancer vaccines have largely been based on rodent models, in particular mice; however the majority of these fail to establish a therapeutic response once put into clinical trials. Pigs have the potential of serving as a model superior to rodents as they are more closely related to humans in terms of immunology and physiology. Here, we introduce pigs as a supplementary large animal model for human cancer vaccine development via the use of our unique technology for swine leukocyte antigen (SLA) production. IDO and RhoC, two tumor antigens previously identified as important players in human cancer development and progression, were used as vaccine targets. Using peptide-MHC-I binding predictors we identified IDO-derived and RhoC-derived candidate peptides potentially binding to five different broadly distributed SLA molecules. We measured the peptide-SLA complex stability of these and found a total of 89 stable (t½ ≥ 0.5 hours) peptide-MHC complexes with SLA-1*04:01, -1*07:02, -2*04:01, -2*05:02 and/or -3*04:01. For a pilot study, 12 pigs were immunized with overlapping 20-mer peptides spanning the entire IDO and RhoC sequences formulated in a panel of CTL-inducing adjuvants. Vaccine and adjuvant efficacy will be evaluated through immunological assays among others including ex vivo stimulation of whole blood with identified stable SLA-binding peptides and quantification of peptide-specific CTLs. Hence, these data elucidate the potential in using pigs as a large animal model for human anti-cancer vaccine development.
Establishing the pig as a large animal model for vaccine development against human cancer

Immunotherapy has increased overall survival of metastatic cancer patients, and cancer antigens are promising vaccine targets. To fulfill the promise, appropriate tailoring of the vaccine formulations to mount in vivo cytotoxic T cell (CTL) responses toward co-delivered cancer antigens is essential. Previous development of therapeutic cancer vaccines has largely been based on studies in mice, and the majority of these candidate vaccines failed to induce therapeutic responses in the subsequent human clinical trials. Given that antigen dose and vaccine volume in pigs are translatable to humans and the porcine immunome is closer related to the human counterpart, we here introduce pigs as a supplementary large animal model for human cancer vaccine development. IDO and RhoC, both important in human cancer development and progression, were used as vaccine targets and 12 pigs were immunized with overlapping 20mer peptides spanning the entire porcine IDO and RhoC sequences formulated in CTL-inducing adjuvants: CAF09, CASAC, Montanide ISA 51 VG, or PBS. Taking advantage of recombinant swine MHC class I molecules (SLAs), the peptide-SLA complex stability was measured for 198 IDO- or RhoC-derived 9-11mer peptides predicted to bind to SLA-1*04:01, −1*07:02, −2*04:01, −2*05:02, and/or −3*04:01. This identified 89 stable (t½ ≥ 0.5 h) peptide-SLA complexes. By IFN-γ release in PBMC cultures we monitored the vaccine-induced peptide-specific CTL responses, and found responses to both IDO- and RhoC-derived peptides across all groups with no adjuvant being superior. These findings support the further use of pigs as a large animal model for vaccine development against human cancer.
Evaluation of the effect of percolation and NaCl solutions on viral haemorrhagic septicaemia virus (VHSV) under experimental conditions

In the present Danish "Ministerial order no. 965 of 18/07/2013 regarding authorisation and operation of aquaculture farms and sale of aquatic organisms and products thereof" fish cutting plants have according to 20 the possibility to get rid of their wastewater by percolation. To examine the effect of percolation on viral haemorrhagic septicaemia virus (VHSV) a sand column experiment has been performed. VHSV was infused onto a column packed with gravel as top and bottom layer (in total 22 cm) and dug sand (76 cm). Over a period of 18 h 3.9 x 10(10) TCID50 VHSV was pumped onto the column where after tap water was added over the rest of the experimental period. The experiment ran over 7 days. During that period samples were collected from the outlet for virological examination. The sampling was most intense in the period where there was the highest risk of VHSV escaping the column. VHSV was not isolated from any of the outlet samples. As the sensitivity of the virological examination was 13.9 TCID50/ml a reduction of >4 log was shown at the outlet. Percolation thus seems to be a usable method for sanitation of water contaminated with VHSV. Changes in temperature, pH, earth types etc. may potentially change the reduction. Some of the fish cutting plants also produce smoked trout fillets using brine in the process. It was tested whether a high NaCl solution will inactivate VHSV. After 20 h with a salinity of 20.9% no inactivation was observed.

Statement of relevance
Fish processing plants slaughtering VHS diseased fish may discharge wastewater containing the disease causing virus. In order to protect both farmed and wild fish it is important that this virus does not get into contact with other fish. This manuscript concerns the faith of VHSV when percolated through the ground. In Denmark this is an approved method to get rid of the wastewater. To our knowledge, for fish pathogenic viruses, this kind of investigation has never been published before and the presented knowledge is therefore new and valuable. (C) 2015 Elsevier B.V. All rights reserved.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, DHI Denmark
Authors: Skall, H. F. (Intern), Jørgensen, C. (Ekstern), Olesen, N. J. (Intern)
Number of pages: 5
Pages: 507-511
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Aquaculture
Volume: 448
ISSN (Print): 0044-8486
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Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.75 SJR 1.101 SNIP 1.524
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.103 SNIP 1.254 CiteScore 2.12
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.002 SNIP 1.34 CiteScore 2.16
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.136 SNIP 1.3 CiteScore 2.18
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
First detection of bonamia ostreae in native flat oysters from the limfjord in denmark

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Section for Virology
Authors: Madsen, L. (Intern), Thomassen, H. E. H. (Intern)
Pages: 92-92
Publication date: 2015

Host publication information
Title of host publication: 17th International Conference on Diseases of Fish And Shellfish : Abstract book
Place of publication: Las Palmas
Publisher: European Association of Fish Pathologists
Fishpathogens.eu/noda: a free and handy online platform for Betanodavirus targeted research and data sharing

Viral nervous necrosis (VNN) is a severe neuropathological disease affecting a broad variety of finfish species worldwide. The causative agents of VNN are small viruses with a bi-segmented RNA genome known as betanodaviruses. At least four species with distinct but yet insufficiently characterized epidemiological features are recognized. The spread of VNN to an increasing number of host species, its wide geographic extent and its economical and ecological impacts justify the importance of collating as much molecular data as possible for tracing the origin of viral isolates and highlight the need for a freely accessible tool for epidemiological and molecular data sharing and consultation. For this purpose, we established a web-based specific database using the www.fishpathogens.eu platform, with the aim of collecting molecular and epidemiological information on VNN viruses, with relevance to their control, management and research studies.
Foot-and-Mouth Disease

Foot-and-mouth disease (FMD) is an economically important, highly contagious disease of cloven-hoofed animals characterised by the appearance of vesicles (blisters) on the feet and in, and around, the mouth. The causative agent, foot-and-mouth disease virus (FMDV), was the first mammalian virus to be discovered. It has a ribonucleic acid (RNA) genome enclosed within a protein coat (capsid). The virus replicates very rapidly within the cytoplasm of cells. The RNA genome has to function both as a messenger RNA (mRNA) and as a template for RNA replication. The RNA encodes a single large polyprotein that is processed, by virus-encoded proteases, to about 12 mature products (plus functionally important precursors) that are required for virus replication and assembly. Some of these viral proteins modify host cell activities to block antivirus defence systems. Thus, this small virus displays a remarkably complex array of biological activities.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, The Pirbright Institute
Authors: Belsham, G. (Intern), Charleston, B. (Ekstern), Jackson, T. (Ekstern), Paton, D. J. (Ekstern)
Number of pages: 9
Publication date: 2015

Host publication information
Title of host publication: Encyclopedia of Life Sciences
Publisher: Wiley
Main Research Area: Technical/natural sciences
Animals, Virus, Vesicles, Picornavirus, RNA, Integrins
DOIs:
10.1002/9780470015902.a0001024.pub
Source: PublicationPreSubmission
Source-ID: 105956609
Publication: Research - peer-review › Encyclopedia chapter – Annual report year: 2015

Foot-and-Mouth Disease Virus Serotype SAT 3 in Long-Horned Ankole Calf, Uganda

After a 16-year interval, foot-and-mouth disease virus serotype SAT 3 was isolated in 2013 from an apparently healthy long-horned Ankole calf that grazed close to buffalo in Uganda. The emergent virus strain is ≈20% different in nucleotide sequence (encoding VP1 [viral protein 1]) from its closest relatives isolated previously from buffalo in Uganda.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Ministry of Agriculture, Animal Industry and Fisheries, University of Copenhagen, Ministry of Livestock Development
Fugleinfluenzavirus H10N7 spredte sig blandt danske sæler i 2014

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Section for Virology
Authors: Hjulsager, C. K. (Intern), Krog, J. S. (Intern), Hansen, M. S. (Intern), Chriél, M. (Intern), Larsen, L. E. (Intern)
Pages: 42-42
Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information
Journal: Dansk Veterinaertidsskrift
Issue number: 9
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
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
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ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
BFI (2009): BFI-level 1
BFI (2008): BFI-level 1
Original language: Danish
Electronic versions:
Hjulsager_2015_H10N7_i_s_ler_DVT.pdf
Source: PublicationPreSubmission
Source-ID: 118962262
Publication: Research - peer-review » Journal article – Annual report year: 2015

Genetics of VHSV in Europe

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Friedrich Loeffler Institute, University of Bern, Wageningen University & Research, Aarhus University, ANSES - French Agency for Food, Environmental and Occupational Health & Safety, Instituto Zooprofilattico Sperimentale delle Venezie
High-throughput Gene Expression Analysis In Pigs As Model For Respiratory Infections

Influenza A virus infections have great impact on human health and welfare and significant resources are linked to influenza epidemics due to excess hospitalizations and lost productivity. Up to 15% of the human population is affected when Influenza spreads around the world in seasonal epidemics (WHO).

Animal models are essential in understanding the mechanisms involved in human infectious disease and for the development of effective prevention and treatment strategies. It is increasingly realized that large animal models like the pig are exceptionally human like and serve as an excellent model for disease and inflammation. Pigs are fully susceptible to human influenza, and have been demonstrated to be involved in influenza evolution and ecology. Pigs share many similarities with humans regarding lung physiology and innate immune cell infiltration of the respiratory system and thus seem to be an obvious large animal model for respiratory infections. This study aimed at providing a better understanding of the involvement of circulating non-coding RNA and innate immune factors in porcine blood leukocytes during influenza virus infection. By employing the pig as a model we were able to perform highly controlled experimental infections and to study changes of symptoms, viral titer, and expression of microRNAs/mRNAs as the influenza infection progresses in time, generating information that would be difficult to obtain from human patients.

The Gram-negative bacterium Actinobacillus pleuropneumoniae causes pneumonia in pigs, a disease which is associated with high morbidity and mortality, as well as impaired animal welfare. The rapidly evolving pneumonia is characterized by large areas of lung necrosis resulting from the combined effect of tissue damage caused by the bacteria, and a strong proinflammatory immune response. To obtain in-depth understanding of this infection, concurrent gene expression of host and pathogen in lung samples collected from pigs experimentally infected with A. pleuropneumoniae was studied. We applied high-throughput RT-qPCR for the simultaneous analysis of host and pathogen gene expression. This parallel analysis was done in lung tissue samples as well as in the immediate surroundings of infection loci after laser capture microdissection. Regulation of gene expression of several immune factors was observed in agreement with protein levels of these factors in lung tissue, infection status and histopathological findings.
General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Section for Bacteriology, Pathology and Parasitology, Section for Virology, IDT-Biologika GmbH, Technical University of Denmark
Authors: Skovgaard, K. (Intern), Brogaard, L. (Intern), Schou, K. K. (Intern), Larsen, L. E. (Intern), Mortensen, S. (Ekstern), Dürwald, R. (Ekstern), Schengel, M. (Ekstern), Heegaard, P. M. H. (Intern)
Number of pages: 1
Publication date: 2015
Event: Abstract from 7th international qPCR & NGS Event Symposium & Industrial Exhibition & Application Workshops, Germany.
Main Research Area: Technical/natural sciences
Electronic versions:
2._High_throughput_gene_expression_analysis_in_pigs_as_model_for_respiratory_infections.pdf
Source: PublicationPreSubmission
Source-ID: 122152957
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2016

Hvordan ser afrikansk svinepest ud i danske grise II?: Rapport over smitteforsøg i drægtige søer 2014

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Lohse, L. (Intern), Strandbygaard, B. (Intern), Nielsen, J. (Intern), Uttenthal, Å. (Intern), Rasmussen, T. B. (Intern), Belsham, G. (Intern), Bøtner, A. (Intern)
Pages: 21-23
Publication date: 2015
Main Research Area: Technical/natural sciences
Publication information
Journal: Dansk Veterinaertidsskrift
Volume: 9
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
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BFI (2013): BFI-level 1
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
ISI indexed (2012): ISI indexed no
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ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
BFI (2009): BFI-level 1
BFI (2008): BFI-level 1
Original language: English
Electronic versions:
Hvordan_ser_afrikansk_svinepest_ud_i_danske_grise_II_Lohse_et_al.pdf
Source: PublicationPreSubmission
Source-ID: 114766961
Identification and complete genome analysis of novel picornavirus in bovine in Japan

We identified novel viruses in feces from cattle with diarrhea collected in 2009 in Hokkaido Prefecture, Japan, by using a metagenomics approach and determined the (near) complete sequences of the virus. Sequence analyses revealed that they had a standard picornavirus genome organization, i.e. 5' untranslated region (UTR) - L- P1 (VP4- VP3- VP2- VP1) - P2 (2A- 2B- 2C) - P3 (3A- 3B- 3C-3D) - 3'UTR- poly(A). They are closely related to other unclassified Chinese picornaviruses; bat picornaviruses group 1-3, feline picornavirus, and canine picornavirus, sharing 45.4-51.4% (P1), 38.0-44.9% (P2), and 49.6-53.3% (P3) amino acid identities, respectively. The phylogenetic analyses and detailed genome characterization showed that they, together with the unclassified Chinese picornaviruses, grouped as a cluster for the P1, 2C, 3CD and VP1 coding regions. These viruses had conserved features (e.g. predicted protein cleavage sites, presence of a leader protein, 2A, 2C, 3C, and 3D functional domains), suggesting they have a common ancestor. Reverse-transcription-PCR assays, using specific primers designed from the 5'UTR sequence of these viruses, showed that 23.0% (20/87) of fecal samples from cattle with diarrhea were positive, indicating the prevalence of these picornavirus in the Japanese cattle population in Hokkaido Prefecture. However, further studies are needed to investigate the pathogenic potential and etiological role of these viruses in cattle.

General information

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Organisations: National Veterinary Institute, Section for Virology, Tokyo University of Agriculture and Technology, Nippon Veterinary and Life Science University, National Institute of Infectious Diseases
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Publication date: 2015
Main Research Area: Technical/natural sciences

Publication information

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Volume: 210
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Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 1.179 SNIP 0.915 CiteScore 2.55
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.257 SNIP 0.915 CiteScore 2.56
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.213 SNIP 0.933 CiteScore 2.63
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.293 SNIP 1.113 CiteScore 2.94
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.202 SNIP 1.059 CiteScore 2.9
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.265 SNIP 1.216 CiteScore 3.04
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.217 SNIP 1.075
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.292 SNIP 1.038
Inactivation of vhsv by infiltration and salt under experimental conditions

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, DHI Denmark
Authors: Skall, H. F. (Ekstern), Jørgensen, C. (Ekstern), Olesen, N. J. (Intern)
Pages: 149-149
Publication date: 2015

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Main Research Area: Technical/natural sciences
Conference: 17th International Conference on Diseases of Fish and Shellfish, Las Palmas, Spain, 07/09/2015 - 07/09/2015
Electronic versions:
O_141_17th_EAFP_2015.pdf
Source: FindIt
Source-ID: 2286531291
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2015

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
Main Research Area: Technical/natural sciences

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Journal: Emerging Infectious Diseases
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<td>SJR 1.607 SNIP 2.297</td>
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<td>2004</td>
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<td>2003</td>
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<td>SJR 1.607 SNIP 2.297</td>
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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.
Isolation of VHS and IHN from recent outbreaks on croatian rainbow trout farms

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Croatian Veterinary Institute, Instituto Zooprofilattico Sperimentale delle Venezie
Authors: Oraic, D. (Ekstern), Zrncic, S. (Ekstern), Brnic, D. (Ekstern), Vendramin, N. (Intern), Mikkelsen, S. S. (Intern), Bruun, M. S. (Intern), Toffan, A. (Ekstern), Olesen, N. J. (Intern)
Pages: 241-241
Publication date: 2015

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Place of publication: Las Palmas
Publisher: European Association of Fish Pathologists
Article number: P-017
Main Research Area: Technical/natural sciences
Conference: 17th International Conference on Diseases of Fish and Shellfish, Las Palmas, Spain, 07/09/2015 - 07/09/2015
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2015

Long Range RNA-RNA interactions with the genome of classical swine fever virus

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Hadsbjerg, J. (Intern), Rasmussen, T. B. (Intern), Belsham, G. (Intern)
Number of pages: 1
Publication date: 2015
Event: Poster session presented at 10th International Congress for Veterinary Virology, Montpellier, France.
Main Research Area: Technical/natural sciences
Electronic versions: PosterEpiESVV_final300dpi.pdf
Publication: Research - peer-review › Poster – Annual report year: 2015

Long Range RNA-RNA interactions with the genome of classical swine fever virus

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Hadsbjerg, J. (Intern), Rasmussen, T. B. (Intern), Belsham, G. (Intern)
Number of pages: 1
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Event: Poster session presented at 9th Annual Meeting of EPIZONE, Montpellier, France.
Main Research Area: Technical/natural sciences
Electronic versions: PosterEpiESVV_final300dpi.pdf
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Mass mortalities in baltic sea eelpout (zoarces viviparous) caused by a new rhabdovirus

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, National Veterinary Institute, Swedish Agency for Marine and Water Management
Authors: Areskog, M. (Ekstern), Blomkvist, E. (Ekstern), Alfjorden, A. (Ekstern), Hakhverdyan, M. (Ekstern), Boutrup, T. S. (Intern), Ahola, H. (Ekstern), Ljunghager, F. (Ekstern), Hagström, Å. (Ekstern), Olesen, N. J. (Intern), Juremalm, M. (Ekstern), Leijon, M. (Ekstern), Valarcher, J. (Ekstern), Axen, C. (Ekstern)
Host publication information
Title of host publication: 17th International Conference on Diseases of Fish And Shellfish : Abstract book
Place of publication: Las Palmas
Publisher: European Association of Fish Pathologists
Article number: O-059
Main Research Area: Technical/natural sciences
Conference: 17th International Conference on Diseases of Fish and Shellfish, Las Palmas, Spain, 07/09/2015 - 07/09/2015
Electronic versions:
Book_of_abstracts_17th_International_conference_on_Diseases_of_Fish_and_Shellfish.pdf
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2015

MicroRNA regulation of TLRs in a post-influenza animal model
Introduction
Substantial morbidity and mortality is caused by secondary bacterial infections occurring in individuals after influenza A virus (IAV) infection. Results from studies in mice suggest that this may in part be due to a lack of responsiveness to Toll-like receptor (TLR) ligands in the post-IAV infected individual. Using the pig as an animal model, we have identified microRNAs (miRNAs) that are differentially expressed in lung tissue two weeks after challenge compared to uninfected controls, i.e. well after the infection has cleared. The role for differential expression of miRNA at this late time point remains unclear. We therefore seek to examine the potential involvement of miRNAs in the translational regulation of TLRs and associated proteins, thus contributing to the lowered responsiveness to bacterial TLR ligands at this late time point, making the individual vulnerable to secondary infections.

Methods and outcome
Pigs were experimentally challenged with a Danish reassortant IAV strain (A/sw/Denmark/12687/03(H1N2)). Lung tissue was harvested 14 days after challenge, as well as from uninfected control animals. Using RNAseq and high-throughput RT-qPCR, we quantified the expression of relevant miRNAs (e.g. miR-335 and miR-146a-5p) and mRNA levels of relevant miRNA targets.

Transcriptional analysis at the site of infection reveals a set of miRNAs to be regulated one week after the pigs had cleared the IAV infection (i.e. two weeks after challenge). This set included miRNAs experimentally validated or in silico predicted to bind to and regulate transcripts of TLRs and relevant co-factors and transcription factors (online tools). The antiviral immune response elicited by IAV infection thus includes late miRNA regulation, which in turn may be at the expense of host responsiveness to bacterial TLR ligands.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Section for Virology, IDT-Biologika GmbH
Authors: Brogaard, L. (Intern), Heegaard, P. M. H. (Intern), Larsen, L. E. (Intern), Dürrwald, R. (Ekstern), Schlegel, M. (Ekstern), Skovgaard, K. (Intern)
Number of pages: 1
Publication date: 2015
Main Research Area: Technical/natural sciences
Electronic versions:
Abstract_TOLL2015_Louise_Brogaard_1.pdf

Bibliographical note
Poster presentation
Source: PublicationPreSubmission
Source-ID: 118949835
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2015

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 the time of sampling within the same year, although there was a tendency to grouping according to the year of sampling. Similar results were observed for H5 sequences. M and H5/H7 gene sequences from poultry showed a high degree of similarity to Danish wild bird sequences, suggesting exchange of viruses between geographically close wild birds and poultry. Significant drift was observed in both M and H5 gene sequences that are important for adequate molecular diagnostics, thus highlighting the importance of continuous surveillance and molecular characterization of AI viruses.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, University of Copenhagen
Authors: Larsen, L. E. (Intern), Krog, J. S. (Intern), Madsen, J. J. (Ekstern), Thorup, K. (Ekstern), Hjulsager, C. K. (Intern)
Publication date: 2015
Event: Abstract from 9th International Symposium on Avian Influenza, Athens, Georgia, United States.
Main Research Area: Technical/natural sciences
Electronic versions:
Molecular_characterization_of_AI_viruses_from_poultry_and_wild_bird_surveillance_in_Denmark_til_ORBIT.pdf

Bibliographical note
Abstract for oral presentation by Charlotte K Hjulsager at 9th International Symposium on Avian Influenza, Athens, Georgia, US. April 12-15, 2015.
Source: PublicationPreSubmission
Source-ID: 112051314
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2015

Molecular Epidemiology and Evolution of Influenza Viruses Circulating within European Swine between 2009 and 2013
The emergence in humans of the A(H1N1)pdm09 influenza virus, a complex reassortant virus of swine origin, highlighted the importance of worldwide influenza virus surveillance in swine. To date, large-scale surveillance studies have been reported for southern China and North America, but such data have not yet been described for Europe. We report the first large-scale genomic characterization of 290 swine influenza viruses collected from 14 European countries between 2009 and 2013. A total of 23 distinct genotypes were identified, with the 7 most common comprising 82% of the incidence. Contrasting epidemiological dynamics were observed for two of these genotypes, H1huN2 and H3N2, with the former showing multiple long-lived geographically isolated lineages, while the latter had short-lived geographically diffuse lineages. At least 32 human-swine transmission events have resulted in A(H1N1)pdm09 becoming established at a mean frequency of 8% across European countries. Notably, swine in the United Kingdom have largely had a replacement of the endemic Eurasian avian virus-like ("avian-like") genotypes with A(H1N1)pdm09-derived genotypes. The high number of reassortant genotypes observed in European swine, combined with the identification of a genotype similar to the A(H3N2)v genotype in North America, underlines the importance of continued swine surveillance in Europe for the purposes of maintaining public health. This report further reveals that the emergences and drivers of virus evolution in swine differ at the global level.

IMPORTANCE The influenza A(H1N1)pdm09 virus contains a reassortant genome with segments derived from separate virus lineages that evolved in different regions of the world. In particular, its neuraminidase and matrix segments were derived from the Eurasian avian virus-like ("avian-like") lineage that emerged in European swine in the 1970s. However, while large-scale genomic characterization of swine has been reported for southern China and North America, no equivalent study has yet been reported for Europe. Surveillance of swine herds across Europe between 2009 and 2013 revealed that the A(H1N1)pdm09 virus is established in European swine, increasing the number of circulating lineages in the region and increasing the possibility of the emergence of a genotype with human pandemic potential. It also has implications for veterinary health, making prevention through vaccination more challenging. The identification of a genotype similar to the A(H3N2)v genotype, causing zoonoses at North American agricultural fairs, underlines the importance of continued genomic characterization in European swine.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Wellcome Trust Sanger Institute, Animal and Plant Health Agency, University of Oxford, Ghent University, Ploufragan-Pluzané Laboratory, Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia, Kimron Veterinary Institute, National Food Chain Safety Office, Merial S.A.S., Laboratori HIPRA SA, Panstwowy Instytut Weterinaryjnyj, IDT-Biologika GmbH, Finnish Food Safety Authority, Central Veterinary Institute
Pages: 9920-9931
Publication date: 2015
Molecular tracing of VHS in Denmark

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Norwegian Veterinary Institute, Friedrich Loeffler Institute, Danish Veterinary and Food Administration
Authors: Mikkelsen, S. S. (Intern), Schuetze, H. (Ekstern), Korsholm, H. (Ekstern), Jensen, B. B. (Ekstern), Bruun, M. S. (Intern), Olesen, N. J. (Intern)
Pages: 194-194
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Place of publication: Las Palmas
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Article number: O-186
Main Research Area: Technical/natural sciences
Conference: 17th International Conference on Diseases of Fish and Shellfish, Las Palmas, Spain, 07/09/2015 - 07/09/2015
Electronic versions:
Book_of_abstracts_17th_International_conference_on_Diseases_of_Fish_and_Shellfish.pdf
Source: PublicationPreSubmission
Source-ID: 118580288
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2015

Mutant stamme af PCV2: opdatering af tilgængelig viden

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

Publication information
Publisher: DTU Veterinaerinstituttet
Original language: Danish
Main Research Area: Technical/natural sciences
Electronic versions:
mutant_PCV2_opdatering_150513.pdf
Source: PublicationPreSubmission
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Publication: 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
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.
Next Generation Sequencing of Classical Swine Fever Virus

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Rasmussen, T. B. (Intern)
Pages: 14-14
Publication date: 2015

Host publication information
Title of host publication: Workshop of the African and Classical Swine Fever National Reference Laboratories (ASF and CSF) : Abstract book
Place of publication: Madrid, Spain
Main Research Area: Technical/natural sciences
Overvågning af avier influenza i vilde fugle i Danmark 2014

gråændebesætninger, da virus kan persistere i længere tid i besætningerne, hvilken er en velkendt risikofaktor for udvikling af HPAI fra LPAI med subtyperne H5 og H7.

**General information**

**State:** Published
**Organisations:** National Veterinary Institute, Section for Virology, University of Copenhagen
**Authors:** Hjulsager, C. K. (Intern), Krog, J. S. (Intern), Madsen, J. J. (Ekstern), Thorup, K. (Ekstern), Larsen, L. E. (Intern)
**Number of pages:** 32
**Publication date:** 2015

**Publication information**

**Publisher:** DTU Veterinærinstituttet
**Original language:** English
**Main Research Area:** Technical/natural sciences
**Electronic versions:**

Overvågning af avi_r_influenza_i_vilde_fugle_i_Danmark_2014_til_ORBIT.pdf

**Bibliographical note**

**Scientific report**
**Source:** PublicationPreSubmission
**Source-ID:** 112051265
**Publication:** Research - peer-review › Report – 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 influenzavirusundersøgelse på DTU-VET 2) Test af influenza 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 generne) 5) Komplet genom karakterisering af udvalgte virusisolater Der blev totalt i 2014 iværksat undersøgelse for influenza A virus på 1173 prøver fordelt på 538 indsendelser fra 422 besætninger. I alt var 435 (37 %) af prøverne positive og 239 (44 %) af indsendelserne havde minimum en positiv prøve fordelt på 199 forskellige besætninger. Indsendelserne fordelte sig over hele landet og over hele året. Der var flest indsendelser til undersøgelse i de kolde måneder, men influenza virus blev påvist med næsten samme hyppighed hele året. I alt blev 80 influenza 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” H1N1 subtype er faldet drastisk og forekom i 2014 tilsyneladende mindre hyppigt end H1N1pdm09 subtypen. Influenzavirus af subtypen H3N2, der har cirkuleret i Danmark siden 1990, blev påvist i en enkelt indsendelse i 2014, hvilket også var tilfældet i 2013. Den centraleuropæiske variant af H1N2, der har et human-like HA gen, er i lighed med tidligere år ikke påvist i danske svin. Virus med subtypen H1pdm09 blev påvist i 60 indsendelser fra 55 besætninger og udgjorde således 24 % af de influenzavirus positive indsendelser. Dette er næsten en fordobling i forhold til 2013. Hos mennesker var 2014 dominerer af H1N1pdm09 subtypen, men det er uklaert om stigningen hos svin i 2014 skyldes øget smitteoverførsel fra mennesker til svin. Resultaterne af overvågningen i 2014 underbygger antagelsen om at de nye reassortments fra de foregående år: H1N2hu, H1pdmN2hu og H1pdmN2sw, nu er fast etableret i de danske

Overvågningen har endvidere påvist adskillige nye virus reassortments, hvor gener fra H1N1pdm09 indgår, bl.a. tyder det på at H1N2 virus med interne gener fra H1N1pdm09 har etableret sig i den danske svinepopulation. Overvågningen har endvidere påvist adskillige nye virus reassortments, hvor gener fra H1N1pdm09 indgår, bl.a. tyder det på at H1N2 virus med interne gener fra H1N1pdm09 har etableret sig i den danske svinepopulation. Der er global bevågenhed omkring svineinfluenzavirus med interne gener fra H1N1pdm09, da der i flere tilfælde er vist smitte med sådanne virus til mennesker, fx H3N2v i USA. Overvågningen har også bidraget til, at vi tidligt har påvist et nyt virus med zoontotisk potentiale som H3hu05N2sw. Dette betyder, at der kan foretages en nærmere genetisk og biologisk karakterisering af dette virus, hvilket kan danne evidens-baseret baggrundsviden for riskohåndtering, i det tilfælde at der konstateres human smitte med dette virus. Den fremtidige overvågning vil bl.a. have fokus på at undersøge om dette virus bliver etableret i danske svin. Fra et veterinært synspunkt er det vigtigt at få fastlagt hvilke(n) subtype(r), der cirkulerer i besætningen, da valg af vaccine er afhængig af denne information. Det er derfor positivt, at der over de senere år er sket en stigning i antal indsendelser til influenzapåvisning i Danmark, da det øger muligheden for at vaccinere korrekt og derved nedbringe risikoen for antibiotika krævende sekundære infektioner. Det er også positivt at det er et nyt subtyper (med human-like HA-gen), der er dominerende i andre dele af Europa, stadig ikke findes i Danmark. Introduktion af dette virus kan frygtes at få epizootisk karakter, da immuniteten i populationen mod dette virus er meget lille. Det kan konkluderes, at den iværksatte overvågning har givet et godt indblik i hvilke influenza A virus, der cirkulerer i danske svin, og at denne information dagligt bruges proaktivt ved håndtering af sygdom i besætningerne. Overvågningen har endvidere vist, at virus med nye gen kombinationer er blevet etableret i danske svin, og der bør de kommende år holdes øje med, om disse virus smitter til mennesker.

**General information**

State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Krog, J. S. (Intern), Hjulsager, C. K. (Intern), Larsen, L. E. (Intern)
Publication date: 2015

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Publisher: DTU Veterinærinstituttet
Original language: English
Main Research Area: Technical/natural sciences
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**Overvågning af influenza A virus i svin i 2014 ORBIT.pdf**
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**Piscirickettsia salmonis infection in european sea bass - an emerging disease in mediterranean mariculture**

**General information**

State: Published
Organisations: National Veterinary Institute, Section for Virology, Section for Bacteriology, Pathology and Parasitology, AquaPri Innovation, Croatian Veterinary Institute
Authors: Zrncic, S. (Ekstern), Vendramin, N. (Intern), Boutrup, T. S. (Ekstern), Boye, M. (Intern), Bruun, M. S. (Intern), Brnic, D. (Ekstern), Oraic, D. (Ekstern)
Pages: 153-153
Publication date: 2015

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Title of host publication: 17th International Conference on Diseases of Fish And Shellfish : Abstract book
Place of publication: Las Palmas
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Article number: O-145
Main Research Area: Technical/natural sciences
Conference: 17th International Conference on Diseases of Fish and Shellfish, Las Palmas, Spain, 07/09/2015 - 07/09/2015
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Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2015
PRRS-virus meget stabilt over tid

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Danish Pig Production
Authors: Kristensen, C. S. (Ekstern), Kvisgaard, L. K. (Intern)
Number of pages: 1
Pages: 38-38
Publication date: 2015
Main Research Area: Technical/natural sciences

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Journal: Svin
Issue number: April
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Ratings:
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Publication: Research › Journal article – 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 Vetmedica, Inc., Svinevet Pig Practise
Authors: Priebe, A. (Ekstern), Rathkjen, P. H. (Ekstern), Larsen, L. E. (Intern), Kvisgaard, L. K. (Intern), Hjulsager, C. K. (Intern), Angulo, J. (Ekstern), Havn, K. (Ekstern)
Number of pages: 1
Publication date: 2015

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Article number: PO85
Main Research Area: Technical/natural sciences
Conference: 7th European Symposium of Porcine Health Management, Nantes, France, 22/04/2015 - 22/04/2015
Source: PublicationPreSubmission
Source-ID: 119056467
Publication: Research - 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 Vetmedica, Inc., Technical University of Denmark, Boehringer Ingelheim Danmark A/S, Svinevet Pig Practise
Authors: Priebe, A. (Ekstern), Rathkjen, P. H. (Ekstern), Larsen, L. E. (Intern), Kvisgaard, L. K. (Intern), Hjulsager, C. K. (Intern), Angulo, J. (Ekstern), Havn, K. (Ekstern)
Pages: 171-171
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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
Rationally designed chemokine-based toxin targeting the viral G protein-coupled receptor US28 potently inhibits cytomegalovirus infection in vivo

The use of receptor-ligand interactions to direct toxins to kill diseased cells selectively has shown considerable promise for treatment of a number of cancers and, more recently, autoimmune disease. Here we move the fusion toxin protein (FTP) technology beyond cancer/autoimmune therapeutics to target the human viral pathogen, human cytomegalovirus (HCMV), on the basis of its expression of the 7TM G protein-coupled chemokine receptor US28. The virus origin of US28 provides an exceptional chemokine-binding profile with high selectivity and improved binding for the CX3C chemokine, CX3CL1. Moreover, US28 is constitutively internalizing by nature, providing highly effective FTP delivery. We designed a synthetic CX3CL1 variant engineered to have ultra-high affinity for US28 and greater specificity for US28 than the natural sole receptor for CX3CL1, CX3CR1, and we fused the synthetic variant with the cytotoxic domain of Pseudomonas Exotoxin A. This novel strategy of a rationally designed FTP provided unparalleled anti-HCMV efficacy and potency in vitro and in vivo.

General information
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Organisations: National Veterinary Institute, Section for Virology, INAGEN Aps, University of Copenhagen, Rutgers New Jersey Medical School, Xiamen University, Stanford University School of Medicine, University of Plymouth
Number of pages: 6
Pages: 8427-8432
Publication date: 2015
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Volume: 112
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Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 8.56 SJR 6.321 SNIP 2.629
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 6.767 SNIP 2.682 CiteScore 8.84
Web of Science (2015): Indexed yes
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Scopus rating (2014): SJR 6.853 SNIP 2.725 CiteScore 8.86
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 6.989 SNIP 2.73 CiteScore 9.5
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 6.792 SNIP 2.682 CiteScore 9.49
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 6.771 SNIP 2.636 CiteScore 9.31
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 6.769 SNIP 2.529
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 6.913 SNIP 2.544
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 6.899 SNIP 2.445
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 6.766 SNIP 2.441
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 6.734 SNIP 2.434
Web of Science (2006): Indexed yes
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Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 7.026 SNIP 2.622
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 7.018 SNIP 2.501
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 7.183 SNIP 2.471
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 7.192 SNIP 2.463
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 7.731 SNIP 2.475
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 8.271 SNIP 2.446
Selective Expression of the MAPK Phosphatase Dusp9/MKP-4 in Mouse Plasmacytoid Dendritic Cells and Regulation of IFN-beta Production

Plasmacytoid dendritic cells (pDCs) efficiently produce large amounts of type I IFN in response to TLR7 and TLR9 ligands, whereas conventional DCs (cDCs) predominantly secrete high levels of the cytokines IL-10 and IL-12. The molecular basis underlying this distinct phenotype is not well understood. In this study, we identified the MAPK phosphatase Dusp9/MKP-4 by transcriptome analysis as selectively expressed in pDCs, but not cDCs. We confirmed the constitutive expression of Dusp9 at the protein level in pDCs generated in vitro by culture with Flt3 ligand and ex vivo in sorted splenic pDCs. Dusp9 expression was low in B220(-) bone marrow precursors and was upregulated during pDC differentiation, concomitant with established pDC markers. Higher expression of Dusp9 in pDCs correlated with impaired phosphorylation of the MAPK ERK1/2 upon TLR9 stimulation. Notably, Dusp9 was not expressed at detectable levels in human pDCs, although these displayed similarly impaired activation of ERK1/2 MAPK compared with cDCs. Enforced retroviral expression of Dusp9 in mouse GM-CSF-induced cDCs increased the expression of TLR9-induced IL-12p40 and IFN-beta, but not of IL-10. Conditional deletion of Dusp9 in pDCs was effectively achieved in Dusp9(flox/flox); CD11c-Cre mice at the mRNA and protein levels. However, the lack of Dusp9 in pDC did not restore ERK1/2 activation after TLR9 stimulation and only weakly affected IFN-beta and IL-12p40 production. Taken together, our results suggest that expression of Dusp9 is sufficient to impair ERK1/2 activation and enhance IFN-beta expression. However, despite selective expression in pDCs, Dusp9 is not essential for high-level IFN-beta production by these cells.

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Web of Science (2017): Indexed Yes
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Scopus rating (2016): CiteScore 4.79 SJR 3.368 SNIP 1.177
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 3.568 SNIP 1.267 CiteScore 5.05
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 3.716 SNIP 1.279 CiteScore 5.03
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 3.844 SNIP 1.345 CiteScore 5.61
Simultaneous vaccination with PRRS mlv against both PRRSV type 1 and type 2: duration of viraemia and level of clinical protection

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Technical University of Denmark, Danish Pig Production
Authors: Kristensen, C. S. (Ekstern), Kvisgaard, L. K. (Intern), Pawlowski, M. (Ekstern), Holmgaard Carlsen, S. (Ekstern), Hjulsager, C. K. (Intern), Larsen, L. E. (Intern)
Number of pages: 1
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Event: Abstract from 7th International Symposium on Emerging and Re-emerging Pig Diseases, Kyoto, Japan.
Main Research Area: Technical/natural sciences
Electronic versions:
ISERPD2015_Abstract_Lindholm_final.pdf
Source: PublicationPreSubmission
Source-ID: 119057308
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2015
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
Authors: Lopes Antunes, A. C. (Intern), Hisham Beeshara Halasa, T. (Intern), Lauritsen, K. T. (Intern), Kristensen, C. S. (Ekstern), Larsen, L. E. (Intern), Toft, N. (Intern)
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Web of Science (2017): Indexed yes
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Scopus rating (2016): CiteScore 1.83 SJR 0.847 SNIP 0.983
Web of Science (2016): Indexed yes
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Scopus rating (2015): SJR 0.925 SNIP 0.97 CiteScore 1.86
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.885 SNIP 0.987 CiteScore 1.81
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.829 SNIP 0.833 CiteScore 1.85
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.743 SNIP 1.043 CiteScore 1.94
Web of Science (2012): Indexed yes
Strain-specific serological response after simultaneous vaccination with PRRS MLV against

Swine influenza viruses in circulation in European pigs exhibit an increasing genetic diversity since last pandemic 2009
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 Chromotography A/S
Authors: Hedegaard, C. J. (Intern), Strube, M. L. (Intern), Bendix Hansen, M. (Ekstern), Kjær Lindved, B. (Ekstern), Larsen, L. E. (Intern), Lihme, A. (Ekstern), Boye, M. (Intern), Heegaard, P. M. H. (Intern)
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Event: Poster session presented at 5th European Veterinary Immunology Workshop, Vienna, Austria.
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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 Enterobactericea in immunoglobulin fed piglets as compared to the control group. Thus pig slaughterhouse plasma is indicated as a potential source resource of antibodies for the control of PWD.

Sygdom og sundhed

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 Chromotography A/S
Authors: Hedegaard, C. J. (Intern), Strube, M. L. (Intern), Bendix Hansen, M. (Ekstern), Kjær Lindved, B. (Ekstern), Larsen, L. E. (Intern), Lihme, A. (Ekstern), Boye, M. (Intern), Heegaard, P. M. H. (Intern)
Number of pages: 1
Publication date: 2015
Event: Abstract from 5th European Veterinary Immunology Workshop, Vienna, Austria.
Main Research Area: Technical/natural sciences
Electronic versions:
Abstract_EVIW_2015_CJHE.pdf
Source: PublicationPreSubmission
Source-ID: 115562559
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2015

Sygdom og sundhed
The immunity raised by recent European subtype 1 PRRSV strains allows a better replication of East European subtype 3 PRRSV strain Lena than the immunity raised by an older strain - increased risk for spatial expansion of PRRSV Lena-like strains

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Ghent University
Authors: Trus, I. (Ekstern), Frydas, I. S. (Ekstern), Reddy, V. R. A. P. (Ekstern), Bonckaert, C. (Ekstern), Li, Y. (Ekstern), Kvisgaard, L. K. (Intern), Larsen, L. E. (Intern), Nauwynck, H. J. (Ekstern)
Number of pages: 1
Publication date: 2015
Event: Abstract from International Porcine Reproductive And Respiratory Syndrome Congress, Ghent, Belgium.
Main Research Area: Technical/natural sciences
Electronic versions:
Ivan_Trus_abstract.pdf
Source: PublicationPreSubmission
Source-ID: 119057016
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2015

The pig as a large animal model for influenza a virus infection
It is increasingly realized that large animal models like the pig are exceptionally human like and serve as an excellent model for disease and inflammation. Pigs are fully susceptible to human influenza, share many similarities with humans regarding lung physiology and innate immune cell infiltration of the respiratory system.

This study aimed at providing a better understanding of the involvement of innate immune factors and non-coding RNA in blood leukocytes during influenza A virus infection. By using the pig as a model we were able to perform highly controlled experimental infections and study early clinical signs of disease, viral titer, and transcriptional response of coding and non-coding RNA. This was completed during the first two weeks after experimental viral infection, generating information that would be difficult to obtain from human patients.

Expression of a wide range of immune factors including several genes known to be centrally involved in the viral defence was quantified by high throughput qPCR (BioMark, Fluidigm). Likewise, miRNAs were quantified using the BioMark (Fluidigm) as well as by MiRCURY LNATM (Exiqon).

During the first 24 hours of infection we found the expression of several antiviral genes, including interferon and interferon-related genes, to mimic key findings from human studies. Finally, several circulating miRNAs isolated from blood leukocytes was found to hold great potential as biomarkers for progression of viral lung infection. These results further consolidate the pig as a valuable model for influenza A virus infection.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Section for Virology, Technical University of Denmark, IDT-Biologika GmbH
Authors: Skovgaard, K. (Intern), Brogaard, L. (Intern), Larsen, L. E. (Intern), Mortensen, S. (Ekstern), Dürrwald, R. (Ekstern), Schengel, M. (Ekstern), Heegaard, P. M. H. (Intern)
Number of pages: 1
Publication date: 2015
Main Research Area: Technical/natural sciences
The pig as a model for therapeutic human anti-cancer vaccine development, elucidating the T-cell reactivity against IDO and RhoC

Immunotherapy against cancer has shown increased overall survival of metastatic cancer patients and is a promising new vaccine target. For this to succeed, appropriate tailoring of vaccine formulations to mount in vivo cytotoxic T cell (CTL) responses towards co-delivered cancer antigens is important. Previous development of therapeutic cancer vaccines has largely been based on studies in mice and the majority of these candidate vaccines failed to establish therapeutic responses in subsequent human clinical trials. Since the porcine immunome is more closely related to the human counterpart, we here introduce pigs as a superior large animal model for human cancer vaccine development via the use of our unique technology for swine leukocyte antigen (SLA) production. IDO and RhoC, both known to be important in human cancer development and progression, were used as vaccine targets. Pigs were immunized with overlapping 20-mer peptides spanning the entire porcine IDO and RhoC sequences formulated in a panel of CTL-inducing adjuvants. 198 candidate IDO- and RhoC-derived 9-11mer peptides potentially binding to SLA- 1*04:01, -1*07:02, -2*04:01, -2*05:02 and/or -3*04:01 were identified in silico, and peptide-SLA complex stability measurements revealed 89 stable (t½ ≥ 0.5 hour) complexes. Vaccine-induced peptide-specific CTL responses were monitored using IFN-γ release as a read out. We found responses to IDO- and RhoC-derived peptides across all groups; surprisingly non-stably binding peptides also induced responses. None of the adjuvants was found to be superior as they were all capable of generating CTL responses to IDO and RhoC hence supporting the further use of pigs as a large animal model for vaccine development against human cancer.

General information
State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Section for Virology, University of Copenhagen, Technical University of Denmark, Copenhagen University Hospital
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Main Research Area: Technical/natural sciences
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Use of recombinant capsid proteins in the development of a vaccine against foot-and-mouth disease virus (FMDV).

Foot-and-mouth disease remains one of the world’s most economically important diseases of livestock. It is caused by foot-and-mouth disease virus, a member of the picornavirus family. The virus replicates very rapidly and can be efficiently transmitted between hosts by a variety of routes. The disease has been effectively controlled in some parts of the world but remains endemic in many others, thus there is a constant risk of introduction of the disease into areas that are normally free of foot-and-mouth disease with potentially huge economic consequences. To reduce the need for large-scale culling of infected, and potentially infected, animals there has been significant effort to develop new vaccines against this disease which avoid some, or all, of the deficiencies of current vaccines. A major focus has been on the use of systems that express the structural proteins of the virus that self-assemble to generate “empty capsid” particles which share many features with the intact virus but lack the ribonucleic acid genome and are therefore non-infectious. Such particles can be “designed” to improve their stability or modify their antigenicity and can be produced without “high containment” facilities. The development and use of such improved vaccines should assist in the global efforts to control this important disease.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Belsham, G. (Intern), Bøtner, A. (Intern)
Pages: 11-23
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Main Research Area: Technical/natural sciences
VHS virus - present situation

Geographic distribution: VHSV can be divided into 4 genotypes and at least 8 subtypes and there is a close linkage between genotypes, geographic range and affected fish species. VHS is still only reported from the Northern hemisphere and while countries like Denmark, Norway and England have freed themselves for VHS, several countries are still struggling with the disease. An update on the recent VHS outbreaks in rainbow trout in Iran, in olive flounder in Korea, in wrasse in Scotland, in turbot in Turkey, in a number of fish species in the great lakes in USA and Canada, and a general overview of the worldwide distribution of the disease will be given. Virus evolution: Recent studies indicate that only a few amino acid changes in the structural proteins of VHSV can change the virulence patterns significantly, thereby coming closer to assessing the risk of none to low virulent viruses becoming high virulent. Virulence factors both depend on the ability of VHSV to enter a cell and on the speed and efficiency of virus replication in the cells. Apparently the viral nucleocapsid protein plays a very important role for the later and seems to be the target for determination of a virulence marker.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Aarhus University
Authors: Skall, H. F. (Ekstern), Olesen, N. J. (Intern)
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Main Research Area: Technical/natural sciences
Conference: DAFINET and ProFish Workshop, København, Denmark, 17/11/2015 - 17/11/2015
Electronic versions:
DAFINET_November_2015_Abstract_Book_1_.pdf
Source: FindIt
Source-ID: 2289246351
Publication: Research - peer-review » Conference abstract in proceedings – Annual report year: 2015

Viral haemorrhagic septicaemia virus (VHSV): on the search for determinants important for virulence in rainbow trout oncorhynchus mykiss
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).


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 produktionssystemer, 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 besætningsjerne formodede, at de havde et PRRS-stabilt sohold (ingen cirkulation af PRRS-virus blandt søerne), så grisene var PRRS-fri (grise uden PRRS-virus) ved 30 kg. I hver besætning blev der taget blodprøver af 10 hold grise ved 30 kg.
Analysis of ORF5 and Full-Length Genome Sequences of Porcine Reproductive and Respiratory Syndrome Virus Isolates of Genotypes 1 and 2 Retrieved Worldwide Provides Evidence that Recombination Is a Common Phenomenon and May Produce Mosaic Isolates

Recombination is currently recognized as a factor for high genetic diversity, but the frequency of such recombination events and the genome segments involved are not well known. In the present study, we initially focused on the detection of recombinant porcine reproductive and respiratory syndrome virus (PRRSV) isolates by examining previously published data sets of ORF5 sequences (genotypes 1 and 2) obtained worldwide. We then examined full-length genome sequences in order to determine potential recombination breakpoints along the viral genome. For ORF5, 11 sets of genotype 1 sequences from different geographical areas, including 2 Asian, 1 American, and 7 European regions, and three sets of genotype 2, including sets from China, Mexico, and the United States, were analyzed separately. Potential recombination breakpoints were detected in 10/11 genotype 1 sets, including 9 cases in which the clustering of at least one isolate was different before and after the breakpoints. In genotype 2, potential breakpoints and different tree clustering of at least one strain before and after the breakpoint were observed in 2 out of 3 sets. The results indicated that most of the ORF5 data sets contained at least one recombinant sequence. When the full-length genome sequences were examined, both genotype 1 and 2 sets presented breakpoints (10 and 9, respectively), resulting in significantly different topologies before and after the breakpoints. Mosaic genomes were detected in genotype 1 sequences. These results may have significant implications for the understanding of the molecular epidemiology of PRRSV. IMPORTANCE PRRSV is one of the most important viruses affecting swine production worldwide, causing big economic losses and sanitary problems. One of the key questions on PRRSV arises from its genetic diversity, which is thought to have a direct impact on immunobiology, epidemiology, diagnosis, and vaccine efficacy. One of the causes of this genetic diversity is recombination among strains. This study provides evidence that recombinant PRRSV isolates are common in most of the countries with significant swine production, especially PRRSV genotype 1. This observation has implications in the proper characterization of PRRSV strains, in the future development of phylogenetic studies, and in the development of new PRRSV control strategies. Moreover, the present paper emphasizes the need for a deeper understanding of the mechanisms and circumstances involved in the generation of genetic diversity of PRRSV.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Universidad Autonoma de Barcelona, The Pirbright Institute, Centro de Investigacion en Alimentacion y Desarrollo
Authors: Martín-Valls, G. E. (Ekstern), Kvisgaard, L. K. (Intern), Tello, M. (Forskerdatabase), Darwich, L. (Ekstern), Cortey, M. (Ekstern), Burgara-Estrella, A. J. (Ekstern), Hernández, J. (Forskerdatabase), Larsen, L. E. (Intern), Mateu, E. (Ekstern)
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Scopus rating (2016): SJR 3.052 SNIP 1.131 CiteScore 4.42
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Web of Science (2015): Indexed yes
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Scopus rating (2014): SJR 3.168 SNIP 1.219 CiteScore 4.4
Web of Science (2014): Indexed yes
A Single Amino Acid Mutation (I1012F) of the RNA Polymerase of Marine Viral Hemorrhagic Septicemia Virus Changes In Vitro Virulence to Rainbow Trout Gill Epithelial Cells

Viral hemorrhagic septicemia virus (VHSV) is separated into four different genotypes (I to IV) with different sublineages (K. Einer-Jensen, P. Ahrens, R. Forsberg, and N. Lorenzen, J. Gen. Virol. 85: 1167-1179, 2004; K. Einer-Jensen, J. Winton, and N. Lorenzen, Vet. Microbiol. 106: 167-178, 2005). European marine VHSV strains (of genotypes I to III) are, in general, nonpathogenic or have very low pathogenicity to rainbow trout after a waterborne challenge, and here we also show that genotype IVa is nonpathogenic to trout. Despite several attempts, it has not been possible to link genomic variation to in vivo virulence. In vitro virulence to gill epithelial cells (GECs) has been used as a proxy for in vivo virulence, and here we extend these studies further with the purpose of identifying residues associated with in vitro virulence.

Genotype Ia (DK-3592B) and III (NO/650/07) isolates, which are pathogenic to rainbow trout (O. B. Dale, I. Orpetveit, T.
M. Lyngstad, S. Kahns, H. F. Skall, N. J. Olesen, and B. H. Dannevig, Dis. Aquat. Organ. 85: 93-103, 2009), were compared to two marine strains that are nonpathogenic to trout, genotypes lb (strain 1p8 [H. F. Mortensen, O. E. Heuer, N. Lorenzen, L. Otte, and N. J. Olesen, Virus Res. 63: 95-106, 1999]) and Iv (JF-09). DK-3592 and NO/650/07 were pathogenic to GECs, while marine strains 1p8 and JF-09 were nonpathogenic to GECs. Eight conserved amino acid substitutions contrasting high-and low-virulence strains were identified, and reverse genetics was used in a gain-of-virulence approach based on the JF-09 backbone. Mutations were introduced into the G, NV, and L genes, and seven different virus clones were obtained. For the first time, we show that a single amino acid mutation in conserved region IV of the L protein, I1012F, rendered the virus able to replicate and induce a cytopathic effect in trout GECs. The other six mutated variants remained nonpathogenic.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Norwegian University of Life Sciences, Aarhus University
Authors: Kim, S. (Ekstern), Thu, B. J. (Ekstern), Skall, H. F. (Ekstern), Vendramin, N. (Intern), Evensen, O. (Ekstern)
Number of pages: 10
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Scopus rating (2016): SJR 3.052 SNIP 1.131 CiteScore 4.42
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
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Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 3.168 SNIP 1.219 CiteScore 4.4
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 3.468 SNIP 1.26 CiteScore 4.92
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 3.154 SNIP 1.227 CiteScore 5.2
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 3.399 SNIP 1.288 CiteScore 5.37
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 3.532 SNIP 1.278
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 3.595 SNIP 1.307
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 3.803 SNIP 1.264
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
Authors: Fobian, K. (Intern), P. Fabrizio, T. (Ekstern), Yoon, S. (Ekstern), Hansen, M. S. (Intern), Webby, R. J. (Ekstern), Larsen, L. E. (Intern)
Publication date: 2014
Event: Abstract from Influenza 2014, Oxford, United Kingdom.
Main Research Area: Technical/natural sciences
Source: PublicationPreSubmission
Source-ID: 103646129
Publication: Research - peer-review ▶ Conference abstract for conference – Annual report year: 2014

Characteristics of a foot-and-mouth disease virus with a partial VP1 G-H loop deletion in experimentally infected cattle

Previous work in cattle illustrated the protective efficacy and negative marker potential of a A serotype foot-and-mouth disease virus (FMDV) vaccine prepared from a virus lacking a significant portion of the VP1 G-H loop (termed A(−)). Since this deletion also includes the arginine-glycine-aspartate (RGD) motif required for virus attachment to the host cell in vivo, it was hypothesised that this virus would be attenuated in naturally susceptible animals. The A(−) virus was passaged three times in cattle via needle inoculation of virus suspension delivered into the intradermal space of the tongue.
(intradermolingual: IDL). Included in the study were three direct contact cattle, two of which were used for the third cattle passage (by inoculation) after direct contact exposure for three days. Cattle were monitored for clinical signs and samples were collected for sequencing as well as antibody and viral genome detection by ELISA and qRT-PCR. Following needle inoculation with the A(−) virus, naïve cattle developed typical clinical signs of FMDV infection, diagnostic assays also provided positive serological and virological results. However, the contact cattle did not develop clinical signs or generate serological or virological markers indicative of FMDV infection even when the cattle were subsequently needle inoculated with 105 TCID50 A(−) FMDV delivered IDL following three days of direct contact exposure. The results suggest that the A(−) virus is not attenuated in cattle when inoculated IDL. This virus could be useful as a tool to understand further the natural pathogenesis, receptor usage and internalisation pathways of FMDV.
Clinical characterization of a type 2 PRRSV causing significant clinical disease in the field in Denmark

General information
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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
Authors: Larsen, L. E. (Intern), Kvisgaard, L. K. (Intern), Hjulsager, C. K. (Intern), Bøtner, A. (Intern), Rathkjen, P. H. (Ekstern), Heegaard, P. M. H. (Intern), Bisgaard, N. (Ekstern), Hansen, M. S. (Intern), Nielsen, J. (Ekstern)
Publication date: 2014

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Comparative analysis of sequences from PT 2013
Every year The European reference Laboratory offers two proficiency tests for all national Reference Laboratories in Europe as well as any other country that wants to participate. In 2013 43 laboratories participated in at least one of the two proficiency tests that cover all the listed fish diseases in Europe.
As part of the EURL proficiency test for fish diseases it is required to sequence any RANA virus isolates found in any of the samples. It is also highly recommended to sequence the ISA virus to determine whether it be HPRΔ or HPR0. Furthermore, it is recommended that any VHSV and IHNV isolates be genotyped.
As part of the evaluation of the proficiency results it was decided this year to look into the quality and similarity of the sequence results for selected viruses.
Ampoule III in the proficiency test 2013 contained an EHNV isolate. The EURL received 43 sequences from 41 laboratories. All but one sequence mapped to the MCP gene while the last sequence mapped to the Neurofilament gene. Approx. half of the sequences contained no errors while the rest differed with 88-99 percent similarity with most having 99% similarity. One sequence, when BLASTed, showed most similarity to European Sheatfish and not EHNV. Generally, mistakes occurred at the ends of the sequences. This can be due to several factors. One is that the sequence
has not been trimmed of the sequence primer sites. Another is the lack of quality control of the chromatogram. Finally, sequencing in just one direction can result in unclear determination of nucleotides at places with a bad quality score. This talk will present some of the problems that can occur with sequencing as well as discuss potential pitfalls.

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Organisations: National Veterinary Institute, Section for Virology
Authors: Mikkelsen, S. S. (Intern)
Publication date: 2014
Event: Abstract from 18th Annual Workshop of the National Reference Laboratories for Fish Diseases, Frederiksberg C, Denmark.
Main Research Area: Technical/natural sciences
Electronic versions:
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Source: PublicationPreSubmission
Source-ID: 103605952
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2014

Comparative pathogenicity study of ten different betanodavirus strains in experimentally infected European sea bass, *Dicentrarchus labrax* (L.)
Viral encephalopathy and retinopathy (VER), otherwise known as viral nervous necrosis (VNN), is a severe pathological condition caused by RNA viruses belonging to the Nodaviridae family, genus Betanodavirus. The disease, described in more than 50 fish species worldwide, is considered as the most serious viral threat affecting marine farmed species in the Mediterranean region, thus representing one of the bottlenecks for further development of the aquaculture industry. To date, four different genotypes have been identified, namely red-spotted grouper nervous necrosis virus (RGNNV), striped jack nervous necrosis virus (SJNNV), tiger puffer nervous necrosis virus and barfin flounder nervous necrosis virus, with the RGNNV genotype appearing as the most widespread in the Mediterranean region, although SJNNV-type strains and reassortant viruses have also been reported. The existence of these genetically different strains could be the reason for the differences in mortality observed in the field. However, very little experimental data are available on the pathogenicity of these viruses in farmed fish. Therefore, in this study, the pathogenicity of 10 isolates has been assessed with an in vivo trial. The investigation was conducted using the European sea bass, the first target fish species for the disease in the Mediterranean basin. Naive fish were challenged by immersion and clinical signs and mortality were recorded for 68 days; furthermore, samples collected at selected time points were analysed to evaluate the development of the infection. Finally, survivors were weighed to estimate the growth reduction. The statistically supported results obtained in this study demonstrated different pathogenicity patterns, underlined the potential risk represented by different strains in the transmission of the infection to highly susceptible species and highlighted the indirect damage caused by a clinical outbreak of VER/VNN.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Instituto Zooprofilattico Sperimentale delle Venezie
Authors: Vendramin, N. (Intern), Toffan, A. (Ekstern), Mancin, M. (Ekstern), Cappellozza, E. (Ekstern), Panzarin, V. (Ekstern), Cattoli, G. (Ekstern), Capua, I. (Ekstern), Terregino, C. (Ekstern)
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Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.12
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 1.71
Web of Science (2015): Indexed yes
Complete Genome Sequence of Border Disease Virus Genotype 3 Strain Gifhorn
The complete genome sequence of the genotype 3 border disease virus strain Gifhorn has been determined; this strain was originally isolated from pigs. This represents the consensus sequence for the virus used to produce the bacterial artificial chromosome (BAC) cDNA clone pBeloGif3, which yields a virus that is severely attenuated in cell culture.

General information
State: Published
Organisations: Molecular Evolution, National Veterinary Institute, Section for Virology, Friedrich Loeffler Institute
Authors: Fahnøe, U. (Intern), Höper, D. (Ekstern), Beer, M. (Ekstern), Rasmussen, T. B. (Intern)
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BFI (2017): BFI-level 1
The complete genome sequence of the genotype 2.2 classical swine fever virus strain Bergen has been determined; this strain was originally isolated from persistently infected domestic pigs in the Netherlands and is characterized to be of low virulence.
Coupled adaptations affecting cleavage of the VP1/2A junction by 3C protease in foot-and-mouth disease virus infected cells

The foot-and-mouth disease virus (FMDV) capsid protein precursor P1-2A is cleaved by the 3C protease to produce VP0, VP3, VP1 and 2A. It was shown previously that modification of a single amino acid residue (K210) within the VP1 protein, close to the VP1/2A cleavage site, inhibited cleavage of this junction and resulted in the production of "self-tagged" virus particles containing the 2A peptide. A second site substitution (E83K) within VP1 was also observed within the rescued virus (Gullberg et al., 2013). It is now shown that introduction of this E83K change alone into a serotype O virus resulted in the rapid accumulation of a second site substitution within the 2A sequence (L2P) that also blocked VP1/2A cleavage suggesting a linkage between the E83K change in VP1 and cleavage of the VP1/2A junction. In a serotype A background, the K210E substitution in VP1 rapidly reverted to wild type. However, introduction of the 2A L2P substitution alone, or with the VP1 K210E change, into this virus resulted in the production of viable viruses. Cells infected with viruses containing the VP1 K210E and/or the 2A L2P substitutions contained the uncleaved VP1-2A protein; the 2A L2P substitution rendered the VP1/2A junction totally resistant to cleavage by 3C protease. The basis for the linkage between amino acid substitutions that are well separated on the surface of the virus particle will be discussed.

General information
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Organisations: National Veterinary Institute, Section for Virology
Authors: Gullberg, M. (Intern), Polacek, C. (Intern), Belsham, G. (Intern)
Number of pages: 1
Publication date: 2014
Event: Abstract from 18th International Picornavirus Meeting (Europic 2014), Blankenberge, Belgium.
Main Research Area: Technical/natural sciences
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Detection of European bat lyssavirus type 2 in Danish Daubenton's bats

European bat lyssavirus (EBLV) is considered to be endemic in the Danish bat populations, but limited information exists about the types of EBLV strains currently in circulation. EBLV type 1 (EBLV-1) is seen as the predominant type in the Serotine bats (Eptesicus serotinus) with the latest case identified in 2009.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, University of Copenhagen, Central Veterinary Institute
Authors: Rasmussen, T. B. (Intern), Chriél, M. (Intern), Baagøe, H. J. (Ekstern), Fjederholt, E. (Ekstern), Kooi, E. A. (Ekstern), Belsham, G. (Intern), Batnér, A. (Intern)
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Event: Abstract from 8th Annual Meeting of Epizone, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
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Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2014

Detection of virus level in tissues of rainbow trout, Oncorhinchus mykiss in clinical stage of viral hemorrhagic septicemia

In order to detecting VHS virus titer in various tissues in clinical stage of VHS disease, rainbow trout, Oncorhynchus mykiss, were exposed to virus by bath. The experiments were carried out with 140 fish obtained from rainbow trout farm. The fish were divided into two equal groups in 120 Liter tanks containing 70 fish. Group one was considered as control and group two infected by bath challenge with 103 TCID50 ml-1 of a VHS virus strain serologically similar to reference strain F1 with high pathogenicity in rainbow trout. At days 12, 13 and 14 post infection the organs including kidney, spleen, heart, skin, liver, pyloric caeca and brain were sampled from dead fish with appropriate clinical signs of VHS separately. Each sample was placed in vials adding 1 ml transport medium to assess virus titer in various tissues. Results of the study, showed that significant difference between virus loads in various organs (ps 0.05). The highest virus titer belongs to the heart while it is in minimum amount in the skin. According to the virus quantity the experimental tissues can be divided in three categories, respectively. Heart and kidney performed the highest amount of virus quantities while liver, gill, pyloric caeca and skin showed the lowest with brain and spleen lying in between. These results point out that the significant levels of VHS virus found in rainbow trout tissues are relevant for the biosecurity in VHS-free areas mainly when fish are displayed and retained as whole fish.

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Organisations: National Veterinary Institute, Section for Virology
Authors: Rasmussen, T. B. (Intern), Chriél, M. (Intern), Baagøe, H. J. (Ekstern), Fjederholt, E. (Ekstern), Kooi, E. A. (Ekstern), Belsham, G. (Intern), Bøtner, A. (Intern)
Publication date: 2014
Event: Abstract from 8th Annual Meeting of Epizone, Copenhagen, Denmark.
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Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2014
Development of tailored real-time RT-PCR assays for the detection and differentiation of serotype O, A and Asia-1 foot-and-mouth disease virus lineages circulating in the Middle East

Rapid and accurate diagnosis is essential for effective control of foot-and-mouth disease (FMD). In countries where FMD is endemic, identification of the serotypes of the causative virus strains is important for vaccine selection and tracing the source of outbreaks. In this study, real-time reverse transcription polymerase chain reaction (rRT-PCR) assays using primer/probe sets designed from the VP1 coding region of the virus genomes were developed for the specific detection of serotype O, A and Asia-1 FMD viruses (FMDVs) circulating in the Middle East. These assays were evaluated using representative field samples of serotype O strains belonging exclusively to the PanAsia-2 lineage, serotype A strains of the Iran-05 lineage and serotype Asia-1 viruses from three relevant sub-groups. When RNA extracted from archival and contemporary field strains was tested using one- or two-step rRT-PCR assays, all three primer/probe sets detected the RNA from homotypic viruses and no cross-reactivity was observed with heterotypic viruses. Similar results were obtained using both single- and multiplex assay formats. Using plasmid standards, the minimum detection level of these tests was found to be lower than two copies. The results illustrate the potential of tailored rRT-PCR tools for the detection and categorization of viruses circulating in the Middle East belonging to distinct subgroups of serotypes O, A and Asia-1. These assays can also overcome the problem of serotyping samples which are found positive by the generic rRT-PCR diagnostic assays but negative by virus isolation and antigen-detection ELISA which would otherwise have to be serotyped by nucleotide sequencing. A similar approach could be used to develop serotyping assays for FMDV strains circulating in other regions of the world.
Foot-and-mouth disease virus, FMDV serotyping, FMDV real-time serotyping RT-PCR assay, FMDV multiplex real-time serotyping RT-PCR assay
DIVA vaccine properties of the live chimeric pestivirus strain CP7_E2gif

Live modified vaccines to protect against classical swine fever virus (CSFV), based on chimeric pestiviruses, have been developed to enable serological Differentiation of Infected from Vaccinated Animals (DIVA). In this context, the chimeric virus CP7_E2gif vaccine candidate is unique as it does not include any CSFV components. In the present study, the DIVA vaccine properties of CP7_E2gif were evaluated in comparison to the conventional live attenuated Riemser C-strain vaccine. Sera and tonsil samples obtained from pigs immunised with these two vaccines were analysed. No viral RNA was found in serum after vaccination with CP7_E2gif, whereas some serum samples from C-strain vaccinated animals were positive. In both vaccinated groups, individual viral RNA-positive tonsil samples were detected in animals euthanised between 7 and 21 days post vaccination. Furthermore, serum samples from these animals, together with archival samples from pigs vaccinated with CP7_E2gif and subsequently CSFV challenged, were analysed for specific antibodies using ELISAs and for homologous neutralising antibodies. In animals vaccinated with CP7_E2gif, neutralising antibodies were detected from day 10. However, the sera remained negative for anti-CSFV E2-specific antibodies whereas pigs vaccinated with C-strain seroconverted against CSFV by 14 days after vaccination, as determined by a CSFVE2 specific blocking ELISA. One week after subsequent CSFV challenge, a strong anti-CSFV E2 reaction was detected in CP7_E2gif vaccinated pigs and anti-Erns antibodies were detected from 10 days after infection. In conclusion, CP7_E2gif has the potential to be used as a DIVA vaccine in combination with detection of anti-CSFV E2-specific antibodies.

General information
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Organisations: Section for Virology, National Veterinary Institute
Authors: von Rosen, T. (Intern), Rangelova, D. Y. (Intern), Nielsen, J. (Intern), Rasmussen, T. B. (Intern), Uttenhal, Å. (Intern)
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Web of Science (2017): Indexed yes
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Scopus rating (2016): CiteScore 2.65 SJR 1.326 SNIP 1.208
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.393 SNIP 1.21 CiteScore 2.56
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.281 SNIP 1.262 CiteScore 2.54
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.438 SNIP 1.484 CiteScore 3
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.437 SNIP 1.579 CiteScore 3.18
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.562 SNIP 1.738 CiteScore 3.27
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.
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.

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Scopus rating (2016): CiteScore 3.11 SJR 1.201 SNIP 1.092
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.414 SNIP 1.131 CiteScore 3.32
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.545 SNIP 1.141 CiteScore 3.54
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.74 SNIP 1.147 CiteScore 3.94
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.945 SNIP 1.142 CiteScore 4.15
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 2.369 SNIP 1.23 CiteScore 4.58
ISI indexed (2011): ISI indexed no
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.631 SNIP 1.161
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 2.473 SNIP 0.985
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 2.323 SNIP 0.96
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.289 SNIP 0.525
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Evolutionary dynamics and genetic diversity from three genes of *Anguillid rhabdovirus*

Wild freshwater eel populations have dramatically declined in recent past decades in Europe and America, partially through the impact of several factors including the wide spread of infectious diseases. The anguillid rhabdoviruses eel virus European X (EVEX) and eel virus American (EVA) potentially play a role in this decline, even if their real contribution is still unclear. In this study, we investigate the evolutionary dynamics and genetic diversity of anguillid rhabdoviruses by analysing sequences from the glycoprotein, nucleoprotein and phosphoprotein (P) genes of 57 viral strains collected from seven countries over 40 years using maximum-likelihood and Bayesian approaches. Phylogenetic trees from the three genes are congruent and allow two monophyletic groups, European and American, to be clearly distinguished. Results of nucleotide substitution rates per site per year indicate that the P gene is expected to evolve most rapidly. The nucleotide diversity observed is low (2-3 %) for the three genes, with a significantly higher variability within the P gene, which encodes multiple proteins from a single genomic RNA sequence, particularly a small C protein. This putative C protein is a potential molecular marker suitable for characterization of distinct genotypes within anguillid rhabdoviruses. This study provides, to our knowledge, the first molecular characterization of EVA, brings new insights to the evolutionary dynamics of two genotypes of *Anguillid rhabdovirus*, and is a baseline for further investigations on the tracking of its spread.

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Authors: Bellec, L. (Ekstern), Cabon, J. (Ekstern), Bergmann, S. (Ekstern), de Boisséson, C. (Ekstern), Engelsma, M. (Ekstern), Haenen, O. (Ekstern), Morin, T. (Ekstern), Olesen, N. J. (Intern), Schuetze, H. (Ekstern), Toffan, A. (Ekstern), Way, K. (Ekstern), Bigarré, L. (Ekstern)
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BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.93 SJR 1.499 SNIP 0.886
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.729 SNIP 1.007 CiteScore 3.26
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.683 SNIP 1.059 CiteScore 3.25
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.749 SNIP 1.161 CiteScore 3.64
ISI indexed (2013): ISI indexed yes
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African swine fever virus (ASFV) causes a severe hemorrhagic fever in domestic pigs. The disease was introduced from the African continent to Georgia in 2007 and has since spread throughout the Caucasus and the Russian Federation. ASF is now established in Eastern Europe and outbreaks have occurred in domestic pigs and wild boar in Poland and the Baltic countries in 2014. Therefore, there is an increased risk of further transmission across Europe. The present study investigates the properties and the effect of the circulating ASF virus strain in Danish pregnant sows.

General information
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Organisations: National Veterinary Institute, Section for Virology
Authors: Lohse, L. (Intern), Strandbygaard, B. (Intern), Nielsen, J. (Intern), Uttenenthal, Å. (Intern), Rasmussen, T. B. (Intern), Belsham, G. J. (Intern), Bøtner, A. (Intern)
Number of pages: 1
Publication date: 2014
First isolation of hirame rhabdovirus from freshwater fish in Europe.

A rhabdovirus was isolated in cell culture inoculated with tissue material from diseased grayling, Thymallus thymallus (L.), originating from a fish farm affected by a mortality episode in Poland. Diagnostics tests showed that the virus was not related to novirhabdoviruses known in Europe, nor to vesiculovirus-like species, except perch rhabdovirus (PRhV) with which it shared moderate serological relations. However, RT-PCR with PRhV probes gave negative results. To identify the virus, a random-priming sequence-independent single primer amplification was adopted. Surprisingly, two of the obtained sequences exhibited a high identity (>99%) with hirame rhabdovirus (HIRRV), a novirhabdovirus usually found in fish in marine Asian countries, for instance Japan, China and Korea. The full-length sequence of the phosphoprotein gene (P) demonstrated a higher identity of the present isolate with HIRRV from China compared with the Korean isolate. An identical viral sequence was also found in brown trout, Salmo trutta trutta L., affected by mortalities in a second farm in the same region, after a likely contamination from the grayling farm. To our knowledge, this is the first report of HIRRV in Europe, and in two hosts from fresh water that have not been described before as susceptible species.
Fish surgery – A dirty business? Comments to a letter submitted by D. Mulcahy and C.A. Harms

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Organisations: National Institute of Aquatic Resources, Section for Freshwater Fisheries Ecology, National Veterinary Institute, Section for Virology, Institute Management, Carleton University
Authors: Jepsen, N. (Intern), Boutrup, T. S. (Intern), Midwood, J. D. (Ekstern), Koed, A. (Intern)
Pages: 6-8
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Main Research Area: Technical/natural sciences

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BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.21 SJR 1.12 SNIP 1.136
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.067 SNIP 1.133 CiteScore 2.01
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.105 SNIP 1.312 CiteScore 2.17
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.037 SNIP 1.173 CiteScore 1.85
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Brown trout, Grayling, Molecular tracing, Outbreak, Rhabdovirus, Sequence-independent single primer amplification

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Publication: Research - peer-review › Journal article – Annual report year: 2014
FMDV-induced stress granules are disrupted by the viral L-protease

Eukaryotic cells respond to environmental stress by entering a state of reduced protein synthesis, redirecting resources to damage control and defense. This reduced translation is closely linked to the formation of cytoplasmic stress granules (SGs). SGs are multicomponent foci, which contain stalled translation preinitiation complexes, including polyadenylated mRNAs, and several aggregation-prone RNA binding factors, such as the Ras-GAP SH3 domain-binding protein (G3BP) that enable their formation. Once the stress is lifted, the stalled complexes from the SGs are believed to re-engage in translation, facilitating cellular recovery.

A growing body of evidence shows that various viruses can trigger SG formation. However, the presence of SGs may not be beneficial to the virus and many viruses have found ways to circumvent, disrupt or even utilize these granules, suggesting a role for SGs as a general cellular defense mechanism. For picornaviruses, poliovirus have been shown to disrupt SGs by the 3C-protease dependent cleavage of G3BP (3) and for cardioviruses (Theiler’s murine encephomyelitis virus and mengovirus), SG formation is inhibited by the presence of the viral L-protein (1, 2).

We have found that foot-and-mouth disease virus (FMDV) triggers SG formation early during infection in IBRS-2 cells. These SGs contain G3BP and TIA-1, but not dsRNA. However, the presence of the FMDV-induced SGs is transient due to the cleavage of G3BP by the viral L-protease (Lpro), which results in subsequent SG dispersal. Cells infected with an Lpro-deficient mutant FMDV are not subjected to G3BP cleavage and the SGs formed upon infection with this mutant
maintain throughout the infection. In vitro studies using different variants of the Lpro show different G3BP cleavage efficiencies, suggesting a superior function of the full length Lpro for this substrate. Furthermore, the Lpro-directed G3BP cleavage is not dependent on virus replication, as investigated by transfecting FMDV RNAs lacking a functional 3D-polymerase. Finally, FMDV RNAs that contain Lpro, but lack the FMDV 3C-protease, also induce cleavage of G3BP, showing that both FMDV and poliovirus target the same SG component but with different proteases.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Karolinska Institutet
Authors: Polacek, C. (Intern), Belsham, G. (Intern), McInerney, G. (Ekstern)
Number of pages: 1
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Main Research Area: Technical/natural sciences
Conference: 18th International Picornavirus Meeting (Europic 2014), Blankenberge, Belgium, 09/03/2014 - 09/03/2014

Bibliographical note
Oral presentation.
Source: dtu
Source-ID: u::10942
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2014

Full-length genomic analysis of korean porcine sapelovirus strains.
Porcine sapelovirus (PSV), a species of the genus Sapelovirus within the family Picornaviridae, is associated with diarrhea, pneumonia, severe neurological disorders, and reproductive failure in pigs. However, the structural features of the complete PSV genome remain largely unknown. To analyze the structural features of PSV genomes, the full-length nucleotide sequences of three Korean PSV strains were determined and analyzed using bioinformatic techniques in comparison with other known PSV strains. The Korean PSV genomes ranged from 7,542 to 7,566 nucleotides excluding the 3' poly(A) tail, and showed the typical picornavirus genome organization; 5'untranslated region (UTR)-L-VP4-VP2-VP3-VP1-2A-2B-2C-3A-3B-3C-3D-3'UTR. Three distinct cis-active RNA elements, the internal ribosome entry site (IRES) in the 5'UTR, a cis-replication element (CRE) in the 2C coding region and 3'UTR were identified and their structures were predicted. Interestingly, the structural features of the CRE and 3'UTR were different between PSV strains. The availability of these first complete genome sequences for PSV strains will facilitate future investigations of the molecular pathogenesis and evolutionary characteristics of PSV.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Chonnam National University, Korea Basic Science Institute
Authors: Son, K. (Ekstern), Kim, D. (Ekstern), Kwon, J. (Ekstern), Choi, J. (Ekstern), Kang, M. (Ekstern), Belsham, G. (Intern), Cho, K. (Ekstern)
Publication date: 2014
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Journal: P L o S One
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Scopus rating (2016): CiteScore 3.11 SJR 1.201 SNIP 1.092
Web of Science (2016): 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
Authors: Pedersen, K. S. (Ekstern), Guedes, R. M. C. (Ekstern), Angen, Ø. (Intern), Ståhl, M. (Intern), Hjulsager, C. K. (Intern), Larsen, L. E. (Intern), Nielsen, J. P. (Ekstern), Baekbo, P. (Ekstern), Jensen, T. K. (Intern)
Publication date: 2014
Event: Abstract from 6th European Symposium of Porcine Health Management (ESPHM 2014), Italy.
Main Research Area: Technical/natural sciences
Publication: Research - peer-review » Journal article – 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
Authors: Kvisgaard, L. K. (Intern), Hjulsager, C. K. (Intern), Larsen, L. E. (Intern)
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XIIIth international nidovirus symposium, Salamanca, Spain, 1-6 June 2014<br/>Poster
Source: PublicationPreSubmission
Source-ID: 103484984
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2014

Genetic diversity of serotype A foot-and-mouth disease viruses in Kenya from 1964 to 2013; implications for control strategies in eastern Africa
Serotype A is the most genetically and antigenically diverse of the foot-and-mouth disease virus (FMDV) serotypes. Records of its occurrence in Kenya date back to 1952 and the antigenic diversity of the outbreak viruses in this region is reflected by the current use of two different vaccine strains (K5/1980 and K35/1980) and previous use of two other strains (K18/66 and K179/71). This study aimed at enhancing the understanding of the patterns of genetic variation of serotype A FMDV in Kenya. The complete VP1 coding region sequences of 38 field isolates, identified as serotype A FMDV, collected between 1964 and 2013 were determined. Coalescent-based methods were used to infer times of divergence of the virus strains and the evolutionary rates alongside 27 other serotype A FMDV sequences from Genbank and the World Reference Laboratory (WRL). This study represents the first comprehensive genetic analysis of serotype A FMDVs from Kenya. The study detected four previously defined genotypes/clusters (termed G-I, G-III, G-VII and G-VIII), within the Africa topotype, together with a fifth lineage that has apparently emerged from within G-I; these different lineages have each had a nationwide distribution. Genotypes G-III and G-VIII that were first isolated in 1964 are now apparently extinct; G-VII was last recorded in 2005, while G-I (including the new lineage) is currently in widespread circulation. High genetic diversity, widespread distribution and transboundary spread of serotype A FMDVs across the region of eastern Africa was apparent. Continuous surveillance for the virus, coupled to genetic and antigenic characterization is recommended for improved regional control strategies.

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State: Published
Organisations: National Veterinary Institute, Section for Virology, Foot-and-Mouth Disease Laboratory, Makerere University, Instituto Gulbenkian de Ciência, University of Copenhagen
Authors: Wekesa, S. N. (Ekstern), Sangula, A. K. (Ekstern), Belsham, G. (Intern), Muwanika, V. B. (Ekstern), Heller, R. (Forskerdatabase), Balinda, S. N. (Ekstern), Masembe, C. (Ekstern), Siegismund, H. R. (Forskerdatabase)
Pages: 408-417
Publication date: 2014
Main Research Area: Technical/natural sciences

Publication information
Journal: Infection, Genetics and Evolution
Volume: 21
Issue number: 92
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.
Identification of rhabdoviral sequences in oropharyngeal swabs from German and Danish bats

Background: In the frame of active lyssavirus surveillance in bats, oropharyngeal swabs from German (N = 2297) and Danish (N = 134) insectivorous bats were investigated using a newly developed generic pan-lyssavirus real-time reverse transcriptase PCR (RT-qPCR).

Findings: In total, 15 RT-qPCR positive swabs were detected. Remarkably, sequencing of positive samples did not confirm the presence of bat associated lyssaviruses but revealed nine distinct novel rhabdovirus-related sequences.

Conclusions: Several novel rhabdovirus-related sequences were detected both in German and Danish insectivorous bats. The results also prove that the novel generic pan-lyssavirus RT-qPCR offers a very broad detection range that allows the collection of further valuable data concerning the broad and complex diversity within the family Rhabdoviridae.

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.
Immunohistochemical detection of interleukin-8 in inflamed porcine tissues

The objective of this study was to identify the specific localization of interleukin-8 (IL-8) in cells in situ in a variety of inflammatory processes in different tissues from pigs. Our hypothesis was that IL-8 primarily is a neutrophil related cytokine present in all extravascular neutrophils while expression also occurs in other cell types in response to an inflammatory stimulus. Using IL-8 immunohistochemistry we discovered that neutrophils were the predominant IL-8 positive cell population while epithelial cell types and endothelium of postcapillary venules could be positive when situated in close vicinity of an inflammatory lesion. Furthermore, endothelial cells of newly formed vessels in granulation tissue were positive in some specimens. Some sub-populations of inflammatory neutrophils were, however, IL-8 negative which could reflect some phase of neutrophil swarming.
General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, University of Copenhagen
Authors: Laursen, H. (Ekstern), Jensen, H. E. (Ekstern), Leifsson, P. S. (Ekstern), Jensen, L. K. (Ekstern), Christiansen, J. G. (Ekstern), Trebbien, R. (Intern), Nielsen, O. L. (Ekstern)
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BFI (2018): BFI-level 2
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Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 1.63 SJR 0.73 SNIP 0.704
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 0.856 SNIP 0.752 CiteScore 1.67
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 0.768 SNIP 0.719 CiteScore 1.6
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 0.808 SNIP 0.805 CiteScore 1.89
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 0.837 SNIP 0.922 CiteScore 2.15
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 0.849 SNIP 0.996 CiteScore 2.16
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 0.77 SNIP 0.945
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 0.768 SNIP 0.852
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 0.69 SNIP 0.866
Scopus rating (2007): SJR 0.77 SNIP 0.925
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.784 SNIP 0.993
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.676 SNIP 0.937
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.742 SNIP 0.984
Web of Science (2004): Indexed yes
Koi herpesvirus disease (khvd) surveillance and diagnosis

According to the European Council Directive 2006/88/EC, additional legislation should be implemented describing sampling and diagnostic procedures for the diseases listed in Annex IV Part 2 of the Directive. The sampling plans and the diagnostic methods for the detection and confirmation of VHS and IHN diseases and for ISA disease are described in commission decisions from 2001 and 2003, respectively. However, KHV was only included as a non-exotic disease at the implementation of the Council Directive and no descriptions of procedures were available for this disease. A preliminary version, describing sampling and diagnostic procedures, was later provided on the EURL Fish web page. This version was based on recommendations from the report of a KHV expert working group under the EPIZONE network “KHV PCR diagnosis and surveillance” convened at the Central Veterinary Institute, Lelystad, The Netherlands, in 2009. However, significant new knowledge based on new research on KHV has appeared in recent years. So, the EURL asked the Commission for permission to organize an expert meeting in order to discuss and agree common new recommendations for sampling and diagnosis of KHV for implementation in a new Commission Decision. The two day meeting was held at the premises of the EURL at Frederiksberg, Denmark and three of the top experts in the field of KHV from Germany, Netherlands and UK, respectively, were invited to participate. The meeting was very successful and produced final drafts of two documents:

1) The Commission decision Part 2 on surveillance and diagnostic methods for KHV
2) Diagnostic procedures for the surveillance and confirmation of KHV disease

Significant changes from the former versions were accepted and recommended for inclusion in the commission decision. Among the changes are:
- The splitting of sampling and diagnostic tests for diagnostic and surveillance purposes respectively.
- Inclusion of real-time PCR as the method of choice for surveillance.
- Specification on how to define a CyHV-3 strain.

The participants agreed that the meeting had been fruitful and brought together skills and experience on this fish disease from different parts of Europe. In the report of the meeting sent to the commission important issues concerning serology and cyprinid herpesvirus variants were raised. We hope that our recommendations to resolve these issues will be considered by the Standing Committee On the Food Chain and Animal Health (SCOFCAH). This presentation will provide more details of these issues as well as providing detail from the final documents described above.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Aquatic Health and Hygiene Division, Friedrich Loeffler Institute, Central Veterinary Institute
Authors: Way, K. (Ekstern), Bergmann, S. M. (Ekstern), Engelsma, M. (Ekstern), Mikkelsen, S. S. (Intern), Vendramin, N. (Intern), Olesen, N. J. (Intern)
Publication date: 2014
Event: Abstract from 18th Annual Workshop of the National Reference Laboratories for Fish Diseases, Frederiksberg C, Denmark.
Main Research Area: Technical/natural sciences
Electronic versions:
Pages_from_Report_18th_AW_2014_1_1.pdf
Source: PublicationPreSubmission
Source-ID: 103605890
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2014
Limited interlaboratory comparison of Schmallenberg virus antibody detection in serum samples

Eight veterinary institutes in seven different countries in Europe participated in a limited interlaboratory comparison trial to evaluate laboratory performances of Schmallenberg virus (SBV) antibody detection in serum. Seven different sheep sera and three different cattle sera were circulated, and all participating institutes were asked to test these sera using SBV antibody detection assay(s) in place in their laboratories. All laboratories within the trial performed a virus neutralisation test (VNT) as well as one or two ELISAs on all samples, and swiftly detected SBV antibodies using these assays. VNT was more sensitive in detecting SBV antibodies than several of the used ELISA assays. Based on the test results, one cattle and one sheep SBV antibody-positive serum were selected to serve as reference sera, which now can be supplied to other laboratories on request.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Central Veterinary Institute, Centrum voor Onderzoek in Diergeneeskunde en Agrochemie, ANSES - French Agency for Food, Environmental and Occupational Health & Safety, Animal Health and Veterinary Laboratories Agency, National Veterinary Institute, Animal Health Service, Friedrich Loeffler Institute
Authors: van der Poel, W. H. M. (Ekstern), Cay, B. (Ekstern), Zientara, S. (Ekstern), Steinbach, F. (Ekstern), Valarcher, J. F. (Ekstern), Bøtner, A. (Intern), Mars, M. H. (Ekstern), Hakze-van der Honing, R. (Ekstern), Schirrmeier, H. (Ekstern), Beer, M. (Ekstern)
Publication date: 2014
Main Research Area: Technical/natural sciences

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Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.442 SNIP 0.692 CiteScore 0.3
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.509 SNIP 0.794 CiteScore 0.39
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.469 SNIP 0.839 CiteScore 0.41
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.474 SNIP 0.821 CiteScore 0.5
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.491 SNIP 0.883 CiteScore 0.52
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.563 SNIP 0.9 CiteScore 0.62
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.574 SNIP 0.835
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.642 SNIP 0.996
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
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.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Section for Bacteriology, Pathology and Parasitology
Authors: Jensen, T. H. (Intern), Krog, J. S. (Intern), Hjulsager, C. K. (Intern), Larsen, L. E. (Intern), Chriél, M. (Intern), Holm, E. (Intern), Pedersen, K. (Intern), Hansen, M. S. (Intern)
Number of pages: 1
Publication date: 2014
Main Research Area: Technical/natural sciences

Publication information
Journal: Wildlife Disease Association Newsletter
Issue number: October
Original language: English
Source: PublicationPreSubmission
Modification of FMDV anti-host defense mechanism

Foot-and-mouth disease virus (FMDV) is the etiologic agent of FMD, an infectious and sometimes fatal viral disease that affects cloven-hoofed animals. The FMDV genome encodes a large polyprotein, the first component of which is the Leader protein. Unusually, within the picornavirus family, the FMDV Leader protein (LPRO) is a protease. This protease induces a very rapid inhibition of host cell cap-dependent protein synthesis within infected cells. This results from cleavage of the cellular translation initiation factor eIF4G. Translation of the viral RNA is unaffected since it is dependent on an internal ribosome entry site (IRES) that directs cap-independent translation initiation. LPRO also releases itself from the virus capsid precursor (at the L/P1 junction). The aim of this project is to identify amino acids that are essential for eIF4G cleavage but not for the self-processing. This study may allow design of mutant viruses that are deficient in blocking host cell responses to infection (e.g. interferon induction) and assist in the rational design of antiviral agents targeting this process.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Guan, S. (Intern), Belsham, G. (Intern)
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Event: Poster session presented at 8th Annual Meeting of Epizone, Copenhagen, Denmark.
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Suhua_Poster.pdf
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Publication: Research - peer-review › Poster – Annual report year: 2014

Molecular double-check strategy for the identification and characterization of European Lyssaviruses

The “gold standard” for post-mortem rabies diagnosis is the direct fluorescent antibody test (FAT). However, in the case of ante-mortem non-neural sample material or decomposed tissues, the FAT reaches its limit, and the use of molecular techniques can be advantageous. In this study, we developed and validated a reverse transcription PCR cascade protocol feasible for the classification of samples, even those for which there is no epidemiological background knowledge. This study emphasises on the most relevant European lyssaviruses.

In a first step, two independent N- and L-gene based pan-lyssavirus intercalating dye assays are performed in a double-check application to increase the method's diagnostic safety. For the second step, characterization of the lyssavirus positive samples via two independent multiplex PCR-systems was performed. Both assays were probe-based, species-specific multiplex PCR-systems for Rabies virus, European bat lyssavirus type 1 and 2 as well as Bokeloh bat lyssavirus. All assays were validated successfully with a comprehensive panel of lyssavirus positive samples, as well as negative material from various host species.

This double-check strategy allows for both safe and sensitive screening, detection and characterization of all lyssavirus species of humans and animals, as well as the rapid identification of currently unknown lyssaviruses in bats in Europe.

General information
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Organisations: National Veterinary Institute, Section for Virology, Friedrich Loeffler Institute, Central Veterinary Institute
Authors: Fischer, M. (Ekstern), Freuling, C. M. (Ekstern), Müller, T. (Ekstern), Wegelt, A. (Ekstern), Kooi, E. A. (Ekstern), Rasmussen, T. B. (Intern), Voller, K. (Ekstern), Marston, D. A. (Ekstern), Fooks, A. R. (Ekstern), Beer, M. (Ekstern), Hoffmann, B. (Ekstern)
Pages: 23-32
Publication date: 2014
Main Research Area: Technical/natural sciences

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Molecular tracing of aquatic viruses - MOLTRAQ

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Friedrich Loeffler Institute, Danish Veterinary and Food Administration, National Veterinary Institute
Authors: Mikkelsen, S. S. (Intern), Schuetze, H. (Ekstern), Korsholm, H. (Ekstern), Jensen, B. B. (Ekstern), Olesen, N. J. (Intern)
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Main Research Area: Technical/natural sciences
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Relations
Activities:
Molecular tracing of aquatic viruses - MOLTRAQ
Source: PublicationPreSubmission
Source-ID: 103605720
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2014

Molecular Tracing of Aquatic Viruses - MOLTRAQ

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Friedrich Loeffler Institute, Danish Veterinary and Food Administration, National Veterinary Institute
Authors: Mikkelsen, S. S. (Intern), Schuetze, H. (Ekstern), Korsholm, H. (Ekstern), Jensen, B. B. (Ekstern), Bruun, M. S. (Intern), Olesen, N. J. (Intern)
Number of pages: 2
Publication date: 2014
Event:
Main Research Area: Technical/natural sciences
Electronic versions:
orbit.dtu.dk_admin_files_103604906_9th_isvlv_abstract_book.pdf

Relations
Activities:
9th International Symposium on Viruses of Lower Vertebrates
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2014

Molecular tracing of VHS in Denmark
MOLTRAQ is a pan-European project that aims to increase knowledge on a wide array of economically important viral diseases in fish and molluscs on both the epidemiological and the genetic level. It centers on the use of spatio-temporal and phylogenetic information to create phylogeographic and scenario-simulation models to identify important factors for the spread of disease and to develop and evaluate new control strategies.

Viral haemorrhagic septicaemia Virus (VHSV) is one of the most important viral fish diseases and is widely spread all over Europe and creates significant losses every year for European fish farmers. VHSV has been endemic in Denmark since the 1950’s but after an effective control and eradication programme that spanned more than 45 years the virus was finally eradicated from Denmark in 2009.

As part of MOLTRAQ more than 200 Danish isolates, including isolates from both marine and freshwater outbreaks, spanning from 1978-2003 were selected for analysis. The full-length G-gene was sequenced for all isolates and together with epidemiological information these data are being used to create phylogenetic and phylogeographic models to help infer the relationship between VHS outbreaks in Denmark and to look into the spread of the disease over a historical period as well as the effectiveness of containment and eradication programmes.

Molecular tracing shows that the numerous VHS outbreaks in marine fish farms were due to stocking these with VHS infected rainbow trout in the incubation phase and not to infection with VHSV from the marine environment. From evaluating more than 400 VHSV isolates from Denmark it appears that evolution of low virulent VHSV from marine fish species is a very rare event and is most likely related to feeding with fresh fish which is now prohibited in rainbow trout farming.
**General information**

State: Published

Organisations: National Veterinary Institute, Section for Virology, Friedrich Loeffler Institute, Danish Veterinary and Food Administration, National Veterinary Institute

Authors: Mikkelsen, S. S. (Intern), Schuetze, H. (Ekstern), Korsholm, H. (Ekstern), Jensen, B. B. (Ekstern), Bruun, M. S. (Intern), Olesen, N. J. (Intern)

Number of pages: 1

Publication date: 2014

Event: Abstract from 18th Annual Workshop of the National Reference Laboratories for Fish Diseases, Copenhagen, Denmark.

Main Research Area: Technical/natural sciences

Electronic versions:

1_Susie_VHS_in_Denmark_1.pdf

Source: PublicationPreSubmission

Source-ID: 118581048

Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2015

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**Overvågning af flagermuserabies i Danmark**

**General information**

State: Published

Organisations: National Veterinary Institute, Section for Virology

Authors: Rasmussen, T. B. (Intern), Chriél, M. (Intern), Bøtner, A. (Intern)

Publication date: 2014

Main Research Area: Technical/natural sciences

**Publication information**

Journal: Dansk Veterinaertidsskrift

Volume: 2

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Ratings:

BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
BFI (2016): BFI-level 1
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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: PublicationPreSubmission

Source-ID: 103605959

Publication: Communication › Journal article – Annual report year: 2014

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**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.

**General information**

State: Published

Organisations: National Veterinary Institute, Section for Virology

Authors: Krog, J. S. (Intern), Hjulsager, C. K. (Intern), Larsen, L. E. (Intern)
PMCV and PRV occurrence in wild and farmed fish in Denmark

Every year salmon are restocked in the 7 rivers Storå, Skjern Å, Varde Å, Sneum Å, Kongeå, Ribe Å and Gudenåen. Six-month-old and 1-year-old salmon for about 2 mio. Kr (€268000) are restocked every year. The salmon are restocked in both the main rivers as well as the larger inlets. 6-month-old salmon are restocked in smaller rivers where the spawning and growth is ideal. They are released from a boat drifting downstream between September and October. 1-year-old smolt are restocked in a few places in the main rivers in April. They are restocked in large numbers to provide better protection against birds and other predators.

In 2007 more than 200000 6-month-old and 1-year-old salmon were restocked in the west-facing rivers. At first Irish, Scottish and Swedish wild salmon were used for restocking, but in 2001 it was discovered that there were still original populations in the rivers and since then all the broodstock have been genetically tested and now only broodstock from the original populations in western Denmark are being used.

The broodstock are caught by electrofishing in a collaboration between local sports fisheries organizations and the Danish Center for Wild Salmon, DCV and used for breeding at the premises of DCV close to the towns of Skjern and Randers, respectively. Before being selected for breeding the broodstock are tested for an array of pathogens, including ISA, VHSV, IHNV, IPNV and BKD.

Piscine Reovirus (PRV) is a double-stranded non-enveloped RNA-virus in the family of Reoviridae, while Piscine myocarditis virus (PMCV) is a double-stranded RNA virus of the Totiviridae family. Wild and farmed salmon and trout have not been tested for PRV or PMCV in Denmark before, but both viruses are found in Norway, where they are suspected of causing Heart and Skeletal Muscle Inflammation (HSMI) and Cardiomyopathy Syndrome (CMS), respectively.

In 2013, broodstock from four different rivers in Denmark were received for surveillance. These rivers are Ribe, Varde, Skjern and Store Å, which are all west-facing rivers. Of these fish 8 were Sea Trout and the rest Salmon. 184 fish were tested by real-time RT-PCR for PRV and 30 fish from each river were tested by real-time RT-PCR for PMCV. This is the first time wild and farmed fish have been tested for either virus in Denmark.
Rapid Spread of Schmallenberg Virus-infected Biting Midges (Culicoides spp.) across Denmark in 2012
Detection of Schmallenberg virus RNA, using real-time RT-PCR, in biting midges (Culicoides spp.) caught at 48 locations in 2011 and four well-separated farms during 2012 in Denmark, revealed a remarkably rapid spread of virus-infected midges across the country. During 2012, some 213 pools of obsoletus group midges (10 specimens per pool) were examined, and of these, 35 of the 174 parous pools were Schmallenberg virus RNA positive and 11 of them were positive in the heads. Culicoides species-specific PCRs identified both C. obsoletus and C. dewulfi as vectors of Schmallenberg virus.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Section for Epidemiology
Authors: Rasmussen, L. D. (Intern), Kirkeby, C. (Intern), Bødker, R. (Intern), Kristensen, B. (Intern), Rasmussen, T. B. (Intern), Belsham, G. (Intern), Bøtner, A. (Intern)
Pages: 12-16
Publication date: 2014
Main Research Area: Technical/natural sciences

Publication information
Journal: Transboundary and Emerging Diseases
Volume: 61
Issue number: 1
ISSN (Print): 1865-1674
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.16 SJR 0.994 SNIP 1.096
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.258 SNIP 1.262 CiteScore 2.29
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.038 SNIP 1.19 CiteScore 2.23
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.953 SNIP 1.123 CiteScore 2.33
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.917 SNIP 1.149 CiteScore 2.04
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.941 SNIP 1.146 CiteScore 2.05
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.747 SNIP 0.986
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.597 SNIP 0.899
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.356 SNIP 0.7
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
Authors: Jorsal, S. E. L. (Intern), Hjulsager, C. K. (Intern), Kokotovic, B. (Intern), Larsen, L. E. (Intern)
Publication date: 2014
Event: Abstract from 6th European Symposium of Porcine Health Management (ESPHM 2014), Italy.
Main Research Area: Technical/natural sciences
Source: PublicationPreSubmission
Source-ID: 103450835
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2014

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
Authors: Jorsal, S. E. L. (Intern), Hjulsager, C. K. (Intern), Kokotovic, B. (Intern), Larsen, L. E. (Intern)
Publication date: 2014
Event: Poster session presented at 6th European Symposium of Porcine Health Management (ESPHM 2014), Italy.
Main Research Area: Technical/natural sciences
Electronic versions:
Publication: Research - peer-review › Poster – Annual report year: 2014

Report on EURL training course 2014
The training courses took place in Copenhagen at DTU National Veterinary Institute, Bülowsvej 27, 2700 Frederiksberg C Denmark, from September the 8th to the 17th, 2014. Two courses were prepared, the first one, with 10 trainees, was entitled "Methods for implementation of surveillance procedures for listed fish diseases" and took place from 8th to 12th September 2014. The second course was entitled “Real-time PCR for diagnostics and surveillance of Fish Diseases” and took place in Copenhagen 15th to 17th September 2014 with 13 participants. 3 persons participated in both training courses. The overall purpose of the training course was to provide an opportunity for the NRLs to send employees for training in techniques relevant when working with fish diseases. Staff of the EURL provided this training, together with teachers from the Danish Veterinary and Food Administration and CVI, The Netherlands. Also, knowledge-sharing and discussions between participants and teachers were important parts of the courses.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Olesen, N. J. (Intern), Vendramin, N. (Intern), Bruun, M. S. (Intern), Mikkelsen, S. S. (Intern)
Number of pages: 17
Publication date: 2014

Publication information
Original language: English
Rescue of the highly virulent classical swine fever virus strain "Koslov" from cloned cDNA and first insights into genome variations relevant for virulence

Classical swine fever virus (CSFV) strain "Koslov" is highly virulent with a mortality rate of up to 100% in pigs. In this study, we modified non-functional cDNAs generated from the blood of Koslov virus infected pigs by site-directed mutagenesis, removing non-synonymous mutations step-by-step, thereby producing genomes encoding the consensus amino acid sequence. Viruses rescued from the construct corresponding to the inferred parental form were highly virulent, when tested in pigs, with infected animals displaying pronounced clinical symptoms leading to high mortality. The reconstruction therefore gave rise to a functional cDNA corresponding to the highly virulent Koslov strain of CSFV. It could be demonstrated that two single amino acid changes (S763L and P968H) in the surface structural protein E2 resulted in attenuation in the porcine infection system while another single amino acid change within the nonstructural protein NS3 (D2183G) reduced virus growth within cells in vitro.

Rescue of the CSFV Koslov strain from a cloned cDNA

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Friedrich Loeffler Institute
Authors: Fahnøe, U. (Intern), Belsham, G. (Intern), Höper, D. (Ekstern), Beer, M. (Ekstern), Rasmussen, T. B. (Intern)
Publication date: 2014
Event: Abstract from Workshop on Laboratory Diagnosis of African and Classical Swine Fever (ASF and CSF), Madrid, Spain.
Main Research Area: Technical/natural sciences
Electronic versions:
Abstract_Fahn_e_et_al_2014.pdf
Source: PublicationPreSubmission
Source-ID: 103605933
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2014
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
Authors: Jakobsen, S. (Ekstern), Hjulsager, C. K. (Intern), Christensen, C. (Ekstern), Lind, P. (Intern), Bak, H. (Ekstern), Larsen, L. E. (Intern)
Publication date: 2014

Host publication information
Title of host publication: Proceedings of the 23rd IPVS Congress
Main Research Area: Technical/natural sciences
Conference: 23rd IPVS Congress, Cancun, Mexico, 08/06/2014 - 08/06/2014
Electronic versions:
PRDC_Sine_abstract_IPVS2014.pdf
Results of the proficiency test, PT1 and PT2, 2014

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, EU Reference Laboratory for Fish Diseases
Authors: Verdramin, N. (Ekstern), Ojala, A. (Intern), Mikkelsen, S. S. (Intern), Olesen, N. J. (Intern)
Number of pages: 1
Publication date: 2014
Event: Abstract from 18th Annual Workshop of the National Reference Laboratories for Fish Diseases, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Electronic versions:
Session5.pdf

Screening for Viral Hemorrhagic Septicemia Virus in Marine Fish along the Norwegian Coastal Line

Viral hemorrhagic septicemia virus (VHSV) infects a wide range of marine fish species. To study the occurrence of VHSV in wild marine fish populations in Norwegian coastal waters and fjord systems a total of 1927 fish from 39 different species were sampled through 5 research cruises conducted in 2009 to 2011. In total, VHSV was detected by rRT-PCR in twelve samples originating from Atlantic herring (Clupea harengus), haddock (Melanogrammus aeglefinus), whiting (Merlangius merlangus) and silvery pout (Gadilculus argenteus). All fish tested positive in gills while four herring and one silvery pout also tested positive in internal organs. Successful virus isolation in cell culture was only obtained from one pooled Atlantic herring sample which shows that today's PCR methodology have a much higher sensitivity than cell culture for detection of VHSV. Sequencing revealed that the positive samples belonged to VHSV genotype Ib and phylogenetic analysis shows that the isolate from Atlantic herring and silvery pout are closely related. All positive fish were sampled in the same area in the northern county of Finnmark. This is the first detection of VHSV in Atlantic herring this far north, and to our knowledge the first detection of VHSV in silvery pout. However, low prevalence of VHSV genotype Ib in Atlantic herring and other wild marine fish are well known in other parts of Europe. Earlier there have been a few reports of disease outbreaks in farmed rainbow trout with VHSV of genotype Ib, and our results show that there is a possibility of transfer of VHSV from wild to farmed fish along the Norwegian coast line. The impact of VHSV on wild fish is not well documented.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Institute of Marine Research, National Veterinary Institute
Authors: Sandlund, N. (Ekstern), Gjerset, B. (Ekstern), Bergh, Ø. (Ekstern), Modahl, I. (Ekstern), Olesen, N. J. (Intern), Johansen, R. (Intern)
Number of pages: 12
Publication date: 2014
Main Research Area: Technical/natural sciences

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Journal: PLOS ONE
Volume: 9
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BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.11 SJR 1.201 SNIP 1.092
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.414 SNIP 1.131 CiteScore 3.32
Multidisciplinary, herring Clupea harengus, prince-william-sound, flounder Paralichthys olivaceus, turbot Scophthalmus maximus, trout Onchorhynchus mykiss, cod Gadus morhua, rainbow-trout, Atlantic salmon, great-lakes, north-sea, Finnmark Norway, Europe Palearctic region, Norwegian Sea Arctic Ocean, GenBank sequence data, Negative Sense ssRNA Viruses Viruses Microorganisms (Microorganisms, Negative Sense Single-Stranded RNA Viruses, Viruses) - Rhabdoviridae [03504] Viral hemorrhagic septicemia virus species pathogen, Pisces Vertebrata Chordata Animalia (Animals, Chordates, Fish, Nonhuman Vertebrates, Vertebrates) - Osteichthyes [85206] rainbow trout common host commercial species Clupea harengus species Atlantic herring common host commercial species Melanogrammus aeglefinus species haddock common host commercial species Merlangius merlangus species whiting common host commercial species Gadiculus argenteus species silvery pout common host commercial species, 07516, Ecology: environmental biology - Wildlife management: aquatic, 16004, Respiratory system - Physiology and biochemistry, 32500, Tissue culture, apparatus, methods and media, 33502, Virology - General and methods, Gill respiratory system, cell culture laboratory techniques, culturing techniques, phylogenetic analysis mathematical and computer techniques, rRT-PCR laboratory techniques, genetic techniques, sequencing laboratory techniques, genetic techniques, Aquaculture, Infection

Electronic versions:

pone.0108529.pdf
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Bibliographical note

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Source: FindIt
Source-ID: 271921102
Publication: Research - peer-review › Journal article – Annual report year: 2014

Sequence Adaptation during Growth of Modified Classical Swine Fever Viruses in Cell Culture

General information

State: Published
Sequence adaptations affecting cleavage of the VP1/2A junction by the 3C protease in foot-and-mouth disease virus-infected cells.

The foot-and-mouth disease virus (FMDV) capsid protein precursor P1-2A is cleaved by the virus-encoded 3C protease to VP0, VP3, VP1 and 2A. It was shown previously that modification of a single amino acid residue (K210E) within the VP1 protein and close to the VP1/2A cleavage site, inhibited cleavage of this junction and produced 'self-tagged' virus particles. A second site substitution (E83K) within VP1 was also observed within the rescued virus [Gullberg et al. (2013). J Virol 87, 11591-11603]. It was shown here that introduction of this E83K change alone into a serotype O virus resulted in the rapid accumulation of a second site substitution within the 2A sequence (L2P), which also blocked VP1/2A cleavage. This suggests a linkage between the E83K change in VP1 and cleavage of the VP1/2A junction. Cells infected with viruses containing the VP1 K210E or the 2A L2P substitutions contained the uncleaved VP1-2A protein. The 2A L2P substitution resulted in the VP1/2A junction being highly resistant to cleavage by the 3C protease, hence it may be a preferred route for 'tagging' virus particles.
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.675 SNIP 1.149 CiteScore 3.6
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.657 SNIP 1.058
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.644 SNIP 1.13
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.636 SNIP 1.068
Web of Science (2008): Indexed yes
Web of Science (2007): SJR 1.688 SNIP 1.127
Web of Science (2006): Indexed yes
Web of Science (2005): Indexed yes
Web of Science (2004): Indexed yes
Web of Science (2003): Indexed yes
Web of Science (2002): Indexed yes
Web of Science (2001): Indexed yes
Web of Science (2000): Indexed yes
Web of Science (1999): Indexed yes

Spatio-temporal risk factors for viral haemorrhagic septicaemia (VHS) in Danish aquaculture

Viral haemorrhagic septicaemia (VHS) is an economically very important fish disease in the northern hemisphere. When the VHS virus was first isolated in Denmark 50 yr ago, more than 80% of the 800 Danish fish farms were considered to be infected, but vigilant surveillance and eradication programmes led to a drastic reduction in prevalence, and finally, to complete eradication of VHS. Denmark thus obtained official status as an approved VHS-free member state within the European Union in November 2013. Data on outbreaks within the country have been collected since 1970, and here we combined these data with the geographical coordinates of fish farms to identify clusters of high disease prevalence and other risk factors. Our analyses revealed a statistically significant cluster in the southwestern part of the country, which persisted throughout the study period. Being situated within such a cluster was a significant risk factor for VHS. For freshwater rainbow trout farms situated inland, the number of upstream farms was a determining risk factor for VHS, as was distance to the nearest VHS-infected farm and year. Whether the farm used fresh or marine water in production did not have any influence on the risk of VHS, when accounting for whether the farm was situated inside a cluster of high risk. This information can be used when implementing risk-based surveillance programmes.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Technical University of Denmark, University of Southern Denmark, Danish Veterinary and Food Administration
Authors: Jensen, A. B. B. (Intern), Ersbøll, A. K. (Ekstern), Korsholm, H. (Ekstern), Skall, H. F. (Intern), Olesen, N. J. (Intern)
Studies on genetic diversity of bovine viral diarrhea viruses in Danish cattle herds

Scandinavian countries have successfully pursued bovine viral diarrhea virus (BVDV) eradication without the use of vaccines. In Denmark, control and eradication of BVDV were achieved during the last two decades, but occasionally new BVDV infections are detected in some Danish cattle herds. The aim of this study was to determine recent BVDV subtypes isolated from 4 Danish herds (A, B, C, and D) isolated in 2009–2012 and to analyze the genetic variation of these isolates within the same herd and its relation with those of other herds. The results showed that three herds (B, C, D) were BVDV 1-b and only one herd (herd A) was BVDV 1-d, no other subtypes were detected. The deduced E2 amino acids result showed a high identity percent (99–100 %) between isolates originating from the same herd, but with higher variation compared to isolates of the other herds. Some of these new Danish strains have closer relationship to BVDVs from outside Denmark than to older Danish strains indicating that these are new introductions to Denmark. In conclusion, BVDV-1 subtypes recently detected in Denmark were only subtypes 1b and 1d, and BVDV infections established in a herd is genetically stable over a long time period.
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
Authors: Larsen, L. E. (Intern), Hjulsager, C. K. (Intern), Trebbien, R. (Intern), Krog, J. S. (Intern), Breum, S. Ø. (Intern)
Publication date: 2014

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Title of host publication: Proceedings of the 23rd IPVS Congress
Main Research Area: Technical/natural sciences
Conference: 23rd IPVS Congress, Cancun, Mexico, 08/06/2014 - 08/06/2014
Electronic versions:
SIV_abstract_IPVS2014.pdf
Source: PublicationPreSubmission
Source-ID: 103450987
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2014

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 næsesvabprøver af alle grise ved fravænning være en hjælp. Resultatet fra et enkelt fravænningshold kan dog ikke stå alene, når det skal afgøres om en tømning af smågrisestalden er tilstrækkeligt for at der fremadrettet kan produceres PRRSV-negative grise ved 30 kg. Det vil ofte være nødvendigt at tage næsesvabprøver af alle grise i flere fravænningshold.

General information
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 analyzes 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.
**Targeted modifications of foot-and-mouth disease virus; towards improved vaccine candidates**

Foot-and-mouth disease virus (FMDV) is responsible for one of the most economically important diseases of farm animals (estimated annual costs are about US$10 billion globally). The virus is the prototypic Aphthovirus within the family Picornaviridae and has a positive sense RNA genome (ca. 8.3kb) encoding a single large polyprotein that is processed to generate about 15 mature proteins plus precursors. The virus particle comprises 60 copies of 4 separate capsid proteins (VP1-VP4) plus a single copy of the genome. By modifying full length cDNAs, producing RNA transcripts in vitro, and introducing these into susceptible cells it is possible to rescue specifically altered FMDVs. We have used this approach to generate modified viruses that have particular properties; these studies can assist in the development of improved and safer vaccines to protect against FMDV. For example, we have made changes to the leader (L) protein coding sequence. The L protein is the first component of the viral polyprotein and is produced in two forms, termed Lab and Lb as the result of use of alternative initiation codons, 84 nt apart. Both forms have protease activity (which separates the L protein from the capsid precursor) and induce the shut-off of host cell protein synthesis. When the shorter form, Lb, is precisely deleted then FMD viruses that grow well in cell culture are produced (Belsham, 2013). However such viruses are attenuated within cattle. In contrast, when the entire Lab coding sequence is deleted then no viable viruses are generated. In an alternative approach, we have modified a processing site within the viral polyprotein so that incomplete processing occurs. It has been shown that a single amino acid substitution that blocks cleavage of the VP1/2A junction within the capsid precursor results in the production of modified “self-tagged” virus particles that contain the VP1-2A precursor (Gullberg et al., 2013). This approach works for two of the most common FMDV serotypes (O and A) and offers the possibility of a single approach to purifying virus particles from different serotypes using reagents targeted to the conserved 2A peptide.

**Targeting the genetic complexity within adapting RNA virus populations**

**General information**
State: Published
Organisations: Molecular Evolution, National Veterinary Institute, Section for Virology, Department of Systems Biology, Center for Biological Sequence Analysis
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The diagnostic utility of stabilized blood for detection of foot-and-mouth disease virus RNA by RT-qPCR

In Europe, clinical signs indicative of foot-and-mouth disease (FMD), would immediately lead to collection of blood and relevant organ material for further laboratory examination for this vesicular disease virus. Today, the first line system for detection of virus in the sample material is real time RT-PCR (RT-qPCR). The aim of this study was to investigate the diagnostic utility of stabilized blood for detection of FMDV RNA in this system.

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Organisations: National Veterinary Institute, Section for Virology, Technical University of Denmark
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Uncovering of Classical Swine Fever Virus adaptive response to vaccination by Next Generation Sequencing

Next Generation Sequencing (NGS) has rapidly become the preferred technology in nucleotide sequencing, and can be applied to unravel molecular adaptation of RNA viruses such as Classical Swine Fever Virus (CSFV). However, the detection of low frequency variants within viral populations by NGS is affected by errors introduced during sample preparation and sequencing, and so far no definitive solution to this problem has been presented.

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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.

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Mælken sladrer om koens fortid

**General information**

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Overvågning af aviær influenza i vilde fugle 2012 i Danmark

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Organisations: National Veterinary Institute, Section for Public sector service and commercial diagnostics, Section for Virology, Natural History Museum of Denmark
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Overvågning af influenza i svin 2012

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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.
A multiplex Real Time RT-PCR for genotyping of VHSV

General information
State: Published
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Authors: Vázquez, D. (Ekstern), López-Vázquez, C. (Ekstern), Skall, H. F. (Intern), Mikkelsen, S. S. (Intern), Olesen, N. J. (Intern), Dopazo, C. P. (Ekstern)
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Analysis of classical swine fever virus RNA replication determinants using replicons
Self-replicating RNAs (replicons), with or without reporter gene sequences, derived from the genome of the Paderborn strain of classical swine fever virus (CSFV) have been produced. The full-length viral cDNA, propagated within a bacterial artificial chromosome (BAC), was modified by targeted recombination within E. coli. RNA transcripts were produced in vitro and introduced into cells by electroporation. The translation and replication of the replicon RNAs could be followed by the accumulation of luciferase (from Renilla reniformis or Gaussia princeps) protein expression (where appropriate), as well as by detection of the CSFV NS3 protein production within the cells. Inclusion of the viral E2 coding region within the replicon was advantageous for the replication efficiency. Production of chimeric RNAs, substituting the NS2 and NS3 coding regions (as a unit) from the Paderborn strain with the equivalent sequences from the highly virulent Koslov strain or
the vaccine strain Riems, blocked replication. However, replacing the Paderborn NS5B coding sequence with the RNA polymerase coding sequence from the Koslov strain greatly enhanced expression of the reporter protein from the replicon. In contrast, replacement with the Riems NS5B sequence significantly impaired replication efficiency. Thus these replicons provide a system for determining specific regions of the CSFV genome required for genome replication without the constraints of maintaining infectivity.

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Scopus rating (2010): SJR 1.657 SNIP 1.058
Web of Science (2010): Indexed yes
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Scopus rating (2009): SJR 1.644 SNIP 1.13
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Web of Science (2008): Indexed yes
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Antiviral immunity in fish – functional analysis using DNA vaccination as a tool

In fish, DNA vaccines encoding the glycoproteins (G proteins) of the salmonid rhabdoviruses VHSV and IHNV have proved very efficient under experimental conditions. Nano-gram amounts of plasmid DNA can induce long-lasting protective immunity when delivered by intramuscular injection in rainbow trout fingerlings. Vaccination of fish at an early stage appears advantageous, since larger fish require higher doses of vaccine to be protected. Even in fish with an average size of 0.5 g at the time of vaccination, good protection can be obtained. Interestingly, immunity is established already a few days after vaccination and cross-challenge experiments have revealed that protection in the early phase is non-specific. Later on, protection becomes very specific in terms of virus species. The protection in the early non-specific phase is related to interferon induced defence mechanisms whereas specific antibodies and cellular components both play a role in the long lasting protection. The similarity of the functional immune response profile to that induced by a natural virus infection is striking and is most likely one of the major reasons for the efficacy of the rhabdovirus DNA vaccines. Although other elements like CpG motifs in the plasmid backbone sequence might play a role, the viral G protein appears to have an inherent ability to stimulate innate immune mechanisms by receptors and pathways that still remain to be characterized in detail. Immunity to VHS in rainbow trout can be induced by DNA vaccination across a temperature range of at least 5-15°C. Interestingly, the initial non-specific phase is significantly prolonged at lower temperatures, thereby ensuring protection despite a slow activation of adaptive mechanisms. Expression of the rhabdovirus G protein on the surface of transfected muscle cells induces a histologically visible local inflammatory reaction with higher doses of VHSV G DNA vaccine. Cell surface expression may be important for a proper activation of the fish immune system, since blocking of the intracellular trafficking of the expressed glycoprotein G-gene interferes with protection. It may be anticipated that the viral G protein acts like a PAMP (pathogen associated molecular pattern), but it remains to be determined which PRRs (pattern recognition receptors) that may be involved in the recognition of the G protein. Recent data from DNA vaccination trials with variant forms of the G protein gene suggest that the structural requirements for antigenicity are different from the requirements for immunogenicity.

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A polyvalent influenza A DNA vaccine induces heterologous immunity and protects pigs against pandemic A(H1N1)pdm09 virus infection

The composition of current influenza protein vaccines has to be reconsidered every season to match the circulating influenza viruses, continuously changing antigenicity. Thus, influenza vaccines inducing a broad cross-reactive immune response would be a great advantage for protection against both seasonal and emerging influenza viruses. We have developed an alternative influenza vaccine based on DNA expressing selected influenza proteins of pandemic and seasonal origin. In the current study, we investigated the protection of a polyvalent influenza DNA vaccine approach in pigs. We immunised pigs intradermally with a combination of influenza DNA vaccine components based on the pandemic 1918 H1N1 (M and NP genes), pandemic 2009 H1N1pdm09 (HA and NA genes) and seasonal 2005 H3N2 genes (HA and NA genes) and investigated the protection against infection with virus both homologous and heterologous to the DNA vaccine components. We found that pigs challenged with a virus homologous to the HA and NA DNA vaccine components were well protected from infection. In addition, heterologous challenge virus was cleared rapidly compared to the unvaccinated control pigs. Immunisation by electroporation induced HI antibodies >40 HAU/ml seven days after second vaccination. Heterologous virus challenge as long as ten weeks after last immunisation was able to trigger a vaccine antibody HI response 26 times higher than in the control pigs. The H3N2 DNA vaccine HA and NA genes also triggered an effective vaccine response with protective antibody titres towards heterologous H3N2 virus. The described influenza DNA vaccine is able to induce broadly protective immune responses even in a larger animal, like the pig, against both heterologous and homologous virus challenges despite relatively low HI titres after vaccination. The ability of this DNA vaccine to limit virus shedding may have an impact on virus spread among pigs which could possibly extend to humans as well, thereby diminishing the risk for epidemics and pandemics to evolve.

General information
State: Published
Organisations: National Veterinary Institute, Section for Bacteriology, Pathology and Parasitology, Section for Virology, Statens Serum Institut
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ASFV in Tanzania: Asymptomatic pigs harbor virus of molecular similarity to Georgia 2007

In 2011 African swine fever virus (ASFV) genome was detected in asymptomatic pigs in field samples in Mbeya, Tanzania. The aim of this paper is to partly characterize the virus that was harboured in these pigs and furthermore to confirm, by a second sampling, the latest occurrence of ASFV in the study area. ASFV genome was detected in serum from 10 out of 127 healthy European/crossbreed pigs. ASFV DNA was polymerase chain reaction (PCR) amplified and sequenced from sera with high viral loads using primers targeting p54 or p72. Both p54 and p72 had total identity to ASFV Genotype II (Georgia 2007/1). The ASFV epidemiology in Mbeya was studied in a new collection of 804 pig sera obtained in 2012. The antibody prevalence in four age groups (3-6 mo.; 7-12 mo; 13-18 mo or 19-36 mo) was 3-5%; all antibody positive sera were analysed by PCR with negative results. The presence of antibodies in 3-month-old pigs confirms the circulation of ASFV in Mbeya several months after our detection of ASFV in asymptomatic pigs. The initial blood samples were obtained on Whatman FTA filter papers as dried blood samples. The samples were stored under field conditions and ASFV could be sequenced in DNA eluted 10 months later, showing the use of FTA samples. Studies on the genetic breed of the pigs are needed as well as sequence studies including the variable region of ASFV to elucidate why asymptomatic pigs with high viral loads were detected.

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Organisations: National Veterinary Institute, Section for Virology, Sokoine University of Agriculture, University of Copenhagen
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Assembly and characterization of foot-and-mouth disease virus empty capsid particles expressed within mammalian cells

The foot-and-mouth disease virus (FMDV) structural protein precursor, P1-2A, is cleaved by the virus-encoded 3C protease (3Cpro) into the capsid proteins VP0, VP1 and VP3 (and 2A). In some systems, it is difficult to produce large amounts of these processed capsid proteins since 3Cpro can be toxic for cells. The expression level of 3Cpro activity has now been reduced relative to the P1-2A, and the effect on the yield of processed capsid proteins and their assembly into empty capsid particles within mammalian cells has been determined. Using a vaccinia-virus-based transient expression system, P1-2A (from serotypes O and A) and 3Cpro were expressed from monocistronic cDNA cassettes as P1-2A-3C, or from dicistronic cassettes with the 3Cpro expression dependent on a mutant FMDV internal ribosome entry site (IRES) (designated P1-2A-mIRES-3C). The effects of using a mutant 3Cpro with reduced catalytic activity or using two different mutant IRES elements (the wt GNRA tetraloop sequence GCAGA converted, in the cDNA, to GAGA or GTTA) were analysed. For both serotypes, the P1-2A-mIRES-3C construct containing the inefficient GTTA mutant IRES produced the highest amount of processed capsid proteins. These products self-assembled to form FMDV empty capsid particles, which have a related, but distinct, morphology (as determined by electron microscopy and reconstruction) from that determined previously by X-ray crystallography. The assembled empty capsids bind, in a divalent cation-dependent manner, to the RGD-dependent integrin αvβ6, a cellular receptor for FMDV, and are recognized appropriately in serotype-specific antigen ELISAs.

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Organisations: National Veterinary Institute, Section for Virology, Pennsylvania State University
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A Step Forward in Molecular Diagnostics of Lyssaviruses – Results of a Ring Trial among European Laboratories

Rabies is a lethal and notifiable zoonotic disease for which diagnostics have to meet the highest standards. In recent years, an evolution was especially seen in molecular diagnostics with a wide variety of different detection methods published. Therefore, a first international ring trial specifically designed on the use of reverse transcription polymerase chain reaction (RT-PCR) for detection of lyssavirus genomic RNA was organized. The trial focussed on assessment and comparison of the performance of conventional and real-time assays. In total, 16 European laboratories participated. All participants were asked to investigate a panel of defined lyssavirus RNAs, consisting of Rabies virus (RABV) and European bat lyssavirus 1 and 2 (EBLV-1 and -2) RNA samples, with systems available in their laboratory. The ring trial allowed the important conclusion that conventional RT-PCR assays were really robust assays tested with a high concordance between different laboratories and assays. The real-time RT-PCR system by Wakeley et al. (2005) in combination with an intercalating dye, and the combined version by Hoffmann and co-workers (2010) showed good sensitivity for the detection of all RABV samples included in this test panel. Furthermore, all used EBLV-specific assays, real-time RT-PCRs as well as conventional RT-PCR systems, were shown to be suitable for a reliable detection of EBLVs. It has to be mentioned that differences were seen in the performance between both the individual RT-PCR systems and
the laboratories. Laboratories which used more than one molecular assay for testing the sample panel always concluded a correct sample result. Due to the markedly high genetic diversity of lyssaviruses, the application of different assays in diagnostics is needed to achieve a maximum of diagnostic accuracy. To improve the knowledge about the diagnostic performance proficiency testing at an international level is recommended before using lyssavirus molecular diagnostics e.g. for confirmatory testing.

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Organisations: National Veterinary Institute, Section for Virology, Friedrich Loeffler Institute, Ettlik Central Veterinary Control and Research Institute, Scientific Institute of Public Health, ANSES - French Agency for Food, Environmental and Occupational Health & Safety, Instituto de Salud Carlos III, National Veterinary Institute, Finnish Food Safety Authority, Central Veterinary Institute, Central Veterinary Research Laboratory, Institute for Diagnosis and Animal Health, Austrian Agency for Health and Food Safety, National Veterinary Research Institute, Animal Health and Veterinary Laboratories Agency
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BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.11 SJR 1.201 SNIP 1.092
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.414 SNIP 1.131 CiteScore 3.32
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.545 SNIP 1.141 CiteScore 3.54
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.74 SNIP 1.147 CiteScore 3.94
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.945 SNIP 1.142 CiteScore 4.15
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 2.369 SNIP 1.23 CiteScore 4.58
ISI indexed (2011): ISI indexed no
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.631 SNIP 1.161
Web of Science (2010): Indexed yes
Atlantic herring shows high mortality rate in bath challenge with viral haemorrhagic septicaemia virus (VHSV)

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, National Veterinary Institute, Institute of Marine Research
Authors: Johansen, R. (Ekstern), Boutrup, T. S. (Intern), Skall, H. F. (Intern), Sandlund, N. (Ekstern), Gjerset, B. (Ekstern), Modahl, I. (Ekstern), Bergh, Ø. (Ekstern), Olesen, N. J. (Intern)
Number of pages: 1
Publication date: 2013
Event: Abstract from 17th Annual Workshop of the National Reference Laboratories for Fish Diseases, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2013

Bat Rabies Surveillance in Europe

Rabies is the oldest known zoonotic disease and was also the first recognized bat associated infection in humans. To date, four different lyssavirus species are the causative agents of rabies in European bats: the European Bat Lyssaviruses type 1 and 2 (EBLV-1, EBLV-2), the recently discovered putative new lyssavirus species Bokeloh Bat Lyssavirus (BBLV) and the West Caucasian Bat Virus (WCBV). Unlike in the new world, bat rabies cases in Europe are comparatively less frequent, possibly as a result of varying intensity of surveillance. Thus, the objective was to provide an assessment of the bat rabies surveillance data in Europe, taking both reported data to the WHO Rabies Bulletin Europe and published results into account. In Europe, 959 bat rabies cases were reported to the RBE in the time period 1977–2010 with the vast majority characterized as EBLV-1, frequently isolated in the Netherlands, North Germany, Denmark, Poland and also in parts of France and Spain. Most EBLV-2 isolates originated from the United Kingdom (UK) and the Netherlands, and EBLV-2 was also detected in Germany, Finland and Switzerland. Thus far, only one isolate of BBLV was found in Germany. Published passive bat rabies surveillance comprised testing of 28 of the 52 different European bat species for rabies. EBLV-1 was isolated exclusively from Serotine bats (Eptesicus serotinus and Eptesicus isabellinus), while EBLV-2 was detected in 14 Daubenton’s bats (Myotis daubentonii) and 5 Pond bats (Myotis dasycneme). A virus from a single Natterer’s bat (Myotis nattereri) was characterized as BBLV. During active surveillance, only oral swabs from 2 Daubenton’s bats (EBLV-2) and from several Eptesicus bats (EBLV-1) yielded virus positive RNA. Virus neutralizing antibodies against lyssaviruses were detected in various European bat species from different countries, and its value and implications are discussed.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Friedrich Loeffler Institute, Animal Health and Veterinary Laboratories Agency, Instituto de Salud Carlos III, Central Veterinary Institute
Authors: Schatz, J. (Ekstern), Fooks, A. R. (Ekstern), McElhinney, L. (Ekstern), Horton, D. (Ekstern), Echevarria, J. (Ekstern), Vázquez-Moron, S. (Ekstern), Kooi, E. A. (Ekstern), Rasmussen, T. B. (Intern), Müller, T. (Ekstern), Freuling, C. M. (Ekstern)
Pages: 22-34
Publication information
Journal: Zoonoses and Public Health
Volume: 60
Issue number: 1
ISSN (Print): 1863-1959
Ratings:
- BFI (2018): BFI-level 2
- Web of Science (2018): Indexed yes
- BFI (2017): BFI-level 2
- Web of Science (2017): Indexed Yes
- BFI (2016): BFI-level 2
- Scopus rating (2016): CiteScore 2.3 SJR 1.068 SNIP 0.979
- Web of Science (2016): Indexed yes
- BFI (2015): BFI-level 2
- Scopus rating (2015): SJR 1.256 SNIP 1.103 CiteScore 2.27
- Web of Science (2015): Indexed yes
- BFI (2014): BFI-level 2
- Scopus rating (2014): SJR 1.026 SNIP 0.951 CiteScore 1.97
- BFI (2013): BFI-level 2
- Scopus rating (2013): SJR 0.905 SNIP 1.039 CiteScore 2.24
- ISI indexed (2013): ISI indexed yes
- Web of Science (2013): Indexed yes
- BFI (2012): BFI-level 2
- Scopus rating (2012): SJR 1.049 SNIP 1.226 CiteScore 2.35
- ISI indexed (2012): ISI indexed yes
- Web of Science (2012): Indexed yes
- BFI (2011): BFI-level 2
- Scopus rating (2011): SJR 0.928 SNIP 1.129 CiteScore 2.05
- ISI indexed (2011): ISI indexed yes
- Web of Science (2011): Indexed yes
- BFI (2010): BFI-level 2
- Scopus rating (2010): SJR 0.863 SNIP 1.147
- Web of Science (2010): Indexed yes
- BFI (2009): BFI-level 2
- Scopus rating (2009): SJR 0.773 SNIP 1.165
- Web of Science (2009): Indexed yes
- BFI (2008): BFI-level 2
- Scopus rating (2008): SJR 0.606 SNIP 0.883
- Scopus rating (2007): SJR 0.71 SNIP 1.083
- Web of Science (2007): Indexed yes
- Scopus rating (2006): SJR 0.64 SNIP 0.911
- Scopus rating (2005): SJR 0.682 SNIP 0.906
- Web of Science (2005): Indexed yes
- Scopus rating (2004): SJR 0.554 SNIP 0.957
- Scopus rating (2003): SJR 0.332 SNIP 0.588
- Scopus rating (2002): SJR 0.388 SNIP 0.685
- Scopus rating (2001): SJR 0.377 SNIP 0.682
- Scopus rating (2000): SJR 0.36 SNIP 0.702
- Scopus rating (1999): SJR 0.333 SNIP 0.633

Original language: English
Rabies, Bats, Lyssavirus, Surveillance
DOIs: 10.1111/zph.12002
Classical swine fever virus infection modulates serum levels of INF-α, IL-8 and TNF-α in 6-month-old pigs

Several studies have highlighted the important role of cytokines in disease development of classical swine fever virus (CSFV) infection. In the present study, we examined the kinetics of 7 porcine cytokines in serum from pigs infected with 3 different CSFV strains. Based on the clinical picture in 6-month-old Danish pigs, the strains used for inoculation were classified as being of low (Bergen), low to moderate (Eystrup) and moderate to high (Lithuania) virulence. The cytokines interferon-alpha (INF-α), interleukin-8 (IL-8) and tumor necrosis factor-alpha (TNF-α) showed increased levels after CSFV infection with more or less comparable course in the 3 groups. However, the cytokine level peaked with a 2–3 days delay in pigs infected with the low virulent strain compared to those infected with a moderately or highly virulent strain. These findings may indicate that INF-α, IL-8 and TNF-α are involved in the immune response during CSFV infection with strains of different virulence.
Comparative assay of fluorescent antibody test results among twelve European National Reference Laboratories using various anti-rabies conjugates

Twelve National Reference Laboratories (NRLs) for rabies have undertaken a comparative assay to assess the comparison of fluorescent antibody test (FAT) results using five coded commercial anti-rabies conjugates (Biorad, Bioveta, Fujirebio, Millipore, and SIFIN conjugates). Homogenized positive brain tissues infected with various lyssavirus species as well as negative samples were analyzed blindly using a standardized FAT procedure. Conjugates B, C, D, and E were found to be significantly more effective than conjugate A for GS7 (French RABV) diluted samples (1/8 and 1/100) while the frequency of concordant results of conjugates C and D differ significantly from conjugates A, B and E for CVS 27. For detection of EBLV-1 strains, conjugates C and D also presented a significantly lower frequency of discordant results compared to conjugates A, B and E. Conjugates B, C and D were found to be significantly more effective than conjugates E and A for EBLV-2 and ABLV samples. In view of these results, conjugates C and D set themselves apart from the others and appeared as the most effective of this 5-panel conjugates. This study clearly demonstrates that the variability of conjugates used by National Reference Laboratories can potentially lead to discordant results and influence assay sensitivity. In case of false negative results this could have a dramatic impact if the animal under investigation is responsible for human exposure. To avoid such situations, confirmatory tests should be implemented.

General information

State: Published
Organisations: National Veterinary Institute, Section for Virology, ANSES - French Agency for Food, Environmental and Occupational Health & Safety, Institute of Food Safety, Animal Health and Environment, Animal Health and Veterinary Laboratories Agency, National Veterinary Institute, National Food and Veterinary Risk Assessment Institute, Central Veterinary Institute, Friedrich Loeffler Institute, Instituto Zooprofilattico Sperimentale delle Venezie, Austrian Agency for Health and Food Safety
Authors: Robardet, E. (Ekstern), Andrieu, S. (Ekstern), Rasmussen, T. B. (Intern), Dobrostanova, M. (Ekstern), Horton, D. L. (Ekstern), Hostnik, P. (Ekstern), Jaceviciene, I. (Ekstern), Juhasz, T. (Ekstern), Müller, T. (Ekstern), F. Mutinelli (Ekstern), Servat, A. (Ekstern), M. Smreczak (Ekstern), Vanek, E. (Ekstern), S. Vázquez-Morón (Ekstern), Cliquet, F. (Ekstern)
Pages: 88-94
Publication date: 2013
Main Research Area: Technical/natural sciences

Publication information

Journal: Journal of Virological Methods
Volume: 191
ISSN (Print): 0166-0934
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
Comparison of the performance of five different immunoassays to detect specific antibodies against emerging atypical bovine pestivirus
Bovine pestiviruses represent a considerably variable group. In addition to the two accepted species BVDV-1 and BVDV-2, a number of atypical bovine pestiviruses have been detected both in foetal calf sera and in field samples. The sera collected during the initial six weeks of experimental infection of calves with atypical pestivirus, BVDV-1 and a combination of both viruses have been examined by routine and new diagnostic tests to validate their robustness and sensitivity. As expected, virus neutralization tests using homologous virus were able to differentiate the two groups infected by BVDV-1 or atypical pestivirus, whereas the animals inoculated with a mixture of these two viruses had a reaction pattern very similar to the homologous virus alone. It was found that immunoassays using whole virus and polyclonal antibodies are the most robust, but all tests examined were able to detect antibodies also from cattle infected with atypical pestivirus a few weeks after infection. The detection, however, was at a lower level and slightly delayed. Statistical validation of the threshold suggested by the manufacturer showed that in some cases the reduction of the cut-off values would improve the test sensitivity.

**General information**

State: Published  
Organisations: National Veterinary Institute, Division of Virology, Sektion for Eksotiske Virussygdomme, Lund University, National Veterinary Research Institute, National Veterinary Institute  
Authors: Larska, M. (Ekstern), Polak, M. P. (Ekstern), Liu, L. (Ekstern), Alenius, S. (Ekstern), Uttenthal, Å. (Intern)  
Pages: 103-109  
Publication date: 2013  
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Journal of Virological Methods  
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ISSN (Print): 0166-0934  
Ratings:  
BFI (2018): BFI-level 1  
Web of Science (2018): Indexed yes  
BFI (2017): BFI-level 1  
Web of Science (2017): Indexed Yes  
BFI (2016): BFI-level 1  
Scopus rating (2016): SJR 0.87 SNIP 0.736 CiteScore 1.78  
Web of Science (2016): Indexed yes  
BFI (2015): BFI-level 1  
Scopus rating (2015): SJR 0.868 SNIP 0.799 CiteScore 1.68  
BFI (2014): BFI-level 1  
Scopus rating (2014): SJR 0.893 SNIP 0.952 CiteScore 1.87  
Web of Science (2014): Indexed yes  
BFI (2013): BFI-level 1  
Scopus rating (2013): SJR 0.861 SNIP 0.91 CiteScore 1.99  
ISI indexed (2013): ISI indexed yes  
Web of Science (2013): Indexed yes  
BFI (2012): BFI-level 1  
Scopus rating (2012): SJR 0.869 SNIP 0.935 CiteScore 2.08  
ISI indexed (2012): ISI indexed yes  
Web of Science (2012): Indexed yes  
BFI (2011): BFI-level 1  
Scopus rating (2011): SJR 0.907 SNIP 0.994 CiteScore 2.23  
ISI indexed (2011): ISI indexed yes  
Web of Science (2011): Indexed yes  
BFI (2010): BFI-level 1  
Scopus rating (2010): SJR 0.892 SNIP 0.998  
Web of Science (2010): Indexed yes  
BFI (2009): BFI-level 1  
Scopus rating (2009): SJR 0.964 SNIP 1.061  
Web of Science (2009): Indexed yes  
BFI (2008): BFI-level 1
Comparison of two Next Generation sequencing platforms for full genome sequencing of Classical Swine Fever Virus

Next Generation Sequencing (NGS) is becoming more adopted into viral research and will be the preferred technology in the years to come. We have recently sequenced several strains of Classical Swine Fever Virus (CSFV) by NGS on both Genome Sequencer FLX (GS FLX) and Ion torrent PGM platforms. In this study, we analyzed NGS data of virus rescued from a CSFV C-strain vaccine strain cDNA clone. The virus analyzed was obtained from a 4th and a 12th passage of rescued virus in SFT cell culture, which had shown a difference in growth kinetics between the passages, and NGS analysis was chosen in order to look for molecular differences. Identical RT-PCR products were run on both GS FLX and an Ion torrent PGM platform for comparison. The NGS data was compared by quality and the percentage mapped reads. Results showed good quality of reads for both platforms and a close to 100% of the reads mapped to the consensus sequence. Additionally, we got an average sequence depth for the genome of 4000 for the Ion torrent PGM and 400 for the FLX platform making the mapping suitable for single nucleotide variant (SNV) detection. The analysis revealed a single non-silent SNV A10665G leading to the amino acid change D3431G in the RNA dependent RNA polymerase NS5B. This SNV was present at 100% frequency in the 12th passage and only at 55% in the 4th passage, which could explain the difference in growth kinetics between the passages.

General information
State: Published
Organisations: Molecular Evolution, National Veterinary Institute, Section for Virology, Department of Systems Biology, Center for Biological Sequence Analysis, Behavioral Phenomics, Friedrich Loeffler Institute
Authors: Fahnøe, U. (Intern), Pedersen, A. G. (Intern), Höper, D. (Ekstern), Beer, M. (Ekstern), Rasmussen, T. B. (Intern)
Number of pages: 1
Pages: 124
Publication date: 2013

Host publication information
Title of host publication: ABSTRACTS : 7th Annual Meeting EPIZONE
Article number: D 2
Main Research Area: Technical/natural sciences
Conference: 7th Annual Meeting EPIZONE, Brussels, Belgium, 01/10/2013 - 01/10/2013
Electronic versions:
AbstractEpizoneFahn_etal2013.pdf

Bibliographical note
Poster presentation.
Source: dtu
Concentrating antibodies towards BVDV from milk

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Section for Epidemiology, Knowledge Centre for Agriculture
Authors: Uttenthal, Å. (Intern), Foddai, A. (Intern), Krogh, K. (Ekstern), Hansen, F. (Intern), Rattenborg, E. (Ekstern), Enøe, C. (Intern)
Number of pages: 1
Pages: 36
Publication date: 2013

Host publication information
Title of host publication: 16th International Symposium of the World Association of Veterinary Laboratory Diagnosticians: Abstract book
Main Research Area: Technical/natural sciences
Conference: 16th International Symposium of the World Association of Veterinary Laboratory Diagnosticians (WAVLD 2013), Berlin, Germany, 05/06/2013 - 05/06/2013
Electronic versions:
Uttenthal WAVLD 2013.pdf

Bibliographical note
Oral presentation.
Source: dtu
Source-ID: u::7676
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2013

Detection of Cyprinid herpesvirus 2 in association with an Aeromonas sobria infection of Carassius carassius (L.), in Italy
Sixteen specimens of female crucian carp, Carassius carassius (L.), during the breeding season, were investigated for post-mortem and full diagnostic examination during a mortality outbreak in a tributary stream of the Arno River in Tuscany in 2011. Necropsy highlighted the presence of a swollen anus and widespread haemorrhages in the body, fins, gills and eyes. Haemorrhages in internal organs and spleen granulomas were also observed. Bacteria isolated from the brain, kidney and spleen of affected fish were identified as A. sobria. Microscopic lesions observed in gills were characterized by necrosis of the secondary lamellae, congestion and multifocal lamellar fusion. The kidney showed necrosis, oedema, fibrin exudation and areas of haemorrhages, while in the spleen the main lesions were by multifocal necrosis of the lymphoid tissue. In the gills, transmission electron microscopy revealed herpesvirus-like particles, subsequently identified as Cyprinid herpesvirus-2 (CyHV-2) with a nested PCR protocol. Although it was not possible to attribute a pathogenic role to CyHV-2 in this mortality event, the identification of this herpesvirus in crucian carp increases the concern about its potential role in this species.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Istituto Zooprofilattico Sperimentale delle Regioni Lazio e Toscana, Instituto Zooprofilattico Sperimentale delle Venezie, Polizia Provinciale Provincia di Arezzo
Authors: Fichi, G. (Ekstern), Cardeti, G. (Ekstern), Cocumelli, C. (Ekstern), Vendramin, N. (Intern), Toffan, A. (Ekstern), Eleni, C. (Ekstern), Siemoni, N. (Ekstern), Fischetti, R. (Ekstern), Susini, F. (Ekstern)
Pages: 823-830
Publication date: 2013
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Fish Diseases
Volume: 36
Issue number: 10
ISSN (Print): 0140-7775
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
Detection of novel strains of cyprinid herpesvirus closely related to koi herpesvirus

Cyprinid herpesvirus 3 (CyHV-3) or koi herpesvirus (KHV) is a devastating virus of carp. Using generic primers for the DNA polymerase and the major capsid protein genes of cyprinid herpesviruses, nucleotide sequences divergent from previously described CyHV-3 were obtained. At least 3 novel groups of putative CyHV-3-like viruses were identified, sharing 95 to 98% nucleotide identity with CyHV-3 strains. Carp carrying the CyHV-3 variants did not show clinical signs consistent with CyHV-3 infection and originated from locations with no actual CyHV-3 outbreaks. These strains might represent low-or non-pathogenic variants of CyHV-3.
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, Universidad Autonoma de Barcelona, Centre de Recerca en Sanitat Animal, University of Copenhagen
Authors: Hansen, M. S. (Intern), Segalés, J. (Ekstern), Fernandes, L. (Forskerdatabase), Grau-Roma, L. (Ekstern), Bille-Hansen, V. (Intern), Larsen, L. E. (Intern), Nielsen, O. L. (Ekstern)
Pages: 20980-988
Publication date: 2013
Main Research Area: Technical/natural sciences

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
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.923 SNIP 1.111 CiteScore 1.68
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.082 SNIP 1.329 CiteScore 2.05
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.914 SNIP 1.163 CiteScore 1.74
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.101 SNIP 1.278 CiteScore 2
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.809 SNIP 1.07 CiteScore 1.64
ISI indexed (2012): ISI indexed yes
Development and validation of a novel Taqman-based real-time RT-PCR assay suitable for demonstrating freedom from viral haemorrhagic septicaemia virus

Viral haemorrhagic septicaemia (VHS) is a serious disease in several fish species. VHS is caused by the rhabdovirus viral haemorrhagic septicaemia virus (VHSV). To prevent spreading of the pathogen, it is important to use a fast, robust, sensitive and specific diagnostic tool to identify the infected fish. Traditional diagnosis based on isolation in cell culture followed by identification using, for example, ELISA is sensitive and specific but slow. By switching to RT-PCR for surveillance and diagnosis of VHS the time needed before a correct diagnosis can be given will be considerably shortened and the need for maintaining expensive cell culture facilities reduced. Here we present the validation, according to OIE guidelines, of a sensitive and specific Taqman-based real-time RT-PCR. The assay detects all isolates in a panel of 79 VHSV isolates covering all known genotypes and subtypes, with amplification efficiencies of approximately 100%. The analytical and diagnostic specificity of the real-time RT-PCR is close to 1, and the analytical and diagnostic sensitivity is comparable with traditional cell-based methods. In conclusion, the presented real-time RT-PCR assay has the necessary qualities to be used as a VHSV surveillance tool on par with cell culture assays.

General information
State: Published
Organisations: National Veterinary Institute, Division of Poultry, Fish and Fur Animals, Section of Fish Diseases, Section for Virology
Authors: Jonstrup, S. P. (Intern), Kahns, S. (Intern), Skall, H. F. (Intern), Boutrup, T. S. (Intern), Olesen, N. J. (Intern)
Pages: 9-23
Publication date: 2013
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Fish Diseases
Volume: 36
Issue number: 1
ISSN (Print): 0140-7775
Ratings:
Development of a primer–probe energy transfer based real-time PCR for the detection of Swine influenza virus

Swine influenza virus (SIV) causes a contagious and requiring official notification disease of pigs and humans. In this study, a real-time reverse transcription-polymerase chain reaction (RT-PCR) assay based on primer–probe energy transfer (PriProET) for the detection of SIV RNA was developed. The assay uses matrix gene-specific primers and an Oregon Green-labeled fluorescent probe and was employed for the detection of SIV in clinical samples to identify outbreaks and to monitor the prevalence of disease. The PriProET technology was used to obtain a probe melting profile for confirmation of the specific product amplification. The assay is specific for influenza virus with a sensitivity of detection limit of approximately 10 copies of RNA by PCR. Based on serial dilutions of SIV, the detection limit of the assay was approximately 0.003 TCID50/ml for H1N1 A/Swine/Poland/KPR9/2004 virus. The PriProET RT-PCR was suitable for the detection of SIV RNA isolated directly from clinical samples. The assay detected SIV RNA in pre-clinical swab samples as early as 2 days post-infection (dpi). The PriProET RT-PCR assay is an alternative to the existing diagnostic assays and could have enhanced applicability for clinical diagnosis.
General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, National Veterinary Research Institute
Authors: Kowalczyk, A. (Ekstern), Markowska-Daniel, I. (Ekstern), Rasmussen, T. B. (Intern)
Pages: 228-233
Publication date: 2013
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Virological Methods
Volume: 187
Issue number: 2
ISSN (Print): 0166-0934
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.87 SNIP 0.736 CiteScore 1.78
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.868 SNIP 0.799 CiteScore 1.68
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.893 SNIP 0.952 CiteScore 1.87
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.861 SNIP 0.91 CiteScore 1.99
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.869 SNIP 0.935 CiteScore 2.08
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.907 SNIP 0.994 CiteScore 2.23
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.892 SNIP 0.998
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.964 SNIP 1.061
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.918 SNIP 1.082
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 0.955 SNIP 1.029
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.879 SNIP 1.073
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.859 SNIP 1.005
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.715 SNIP 1.028
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.753 SNIP 1.008
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**

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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

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Does the level of asepsis impact the success of surgically implanting tags in Atlantic salmon?

It is generally recommended that a high level of asepsis be maintained during surgical implantation of electronic tags into fish. However, documentation of a positive effect of asepsis in fish surgery is lacking. To compare the effects of surgical implantation performed under different sanitary conditions, 100 hatchery salmon smolts (Salmo salar) were surgically implanted with tags with and without trailing antenna and were kept in a hatchery facility. After 34 days, the surviving smolts were euthanized and survival, growth and healing were compared between fish tagged under aseptic conditions and fish tagged without regard to aseptic technique. The results demonstrated that there was no detectable difference in survival, growth and healing between the treatments. Thus, this study could not provide evidence supporting the general recommendation of achieving a high level of asepsis during fish surgery.

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Organisations: National Institute of Aquatic Resources, Section for Freshwater Fisheries Ecology, National Veterinary Institute, Section for Virology, Carleton University
Efficient generation of recombinant RNA viruses using targeted recombination-mediated mutagenesis of bacterial artificial chromosomes containing full-length cDNA

**Background**

Infectious cDNA clones are a prerequisite for directed genetic manipulation of RNA viruses. Here, a strategy to facilitate manipulation and rescue of classical swine fever viruses (CSFVs) from full-length cDNAs present within bacterial artificial chromosomes (BACs) is described. This strategy allows manipulation of viral cDNA by targeted recombination-mediated mutagenesis within bacteria.

**Results**

A new CSFV-BAC (pBeloR26) derived from the Riems vaccine strain has been constructed and subsequently modified in the E2 coding sequence, using the targeted recombination strategy to enable rescue of chimeric pestiviruses (vR26_E2gif and vR26_TAV) with potential as new marker vaccine candidates. Sequencing of the BACs revealed a high genetic stability during passages within bacteria. The complete genome sequences of rescued viruses, after extensive passages in mammalian cells showed that modifications in the E2 protein coding sequence were stably maintained. A single amino acid substitution (D3431G) in the RNA dependent RNA polymerase was observed in the rescued viruses vR26_E2gif and vR26, which was reversion to the parental Riems sequence.

**Conclusions**

These results show that targeted recombination-mediated mutagenesis provides a powerful tool for expediting the construction of novel RNA genomes and should be applicable to the manipulation of other RNA viruses.
RNA, Genome, Targeted recombination, Bacterial artificial chromosome, Genetic stability, RNA virus, Pestivirus, Classical swine fever virus
Efficient production of foot-and-mouth disease virus empty capsids in insect cells following down regulation of 3C protease activity

Foot-and-mouth disease virus (FMDV) is a significant economically and distributed globally pathogen of Artiodactyla. Current vaccines are chemically inactivated whole virus particles that require large-scale virus growth in strict biocontainment with the associated risks of accidental release or incomplete inactivation. Non-infectious empty capsids are structural mimics of authentic particles with no associated risk and constitute an alternate vaccine candidate. Capsids self-assemble from the processed virus structural proteins, VP0, VP3 and VP1, which are released from the structural protein precursor P1-2A by the action of the virus-encoded 3C protease. To date recombinant empty capsid assembly has been limited by poor expression levels, restricting the development of empty capsids as a viable vaccine. Here expression of the FMDV structural protein precursor P1-2A in insect cells is shown to be efficient but linkage of the cognate 3C protease to the C-terminus reduces expression significantly. Inactivation of the 3C enzyme in a P1-2A-3C cassette allows expression and intermediate levels of 3C activity resulted in efficient processing of the P1-2A precursor into the structural proteins which assembled into empty capsids. Expression was independent of the insect host cell background and leads to capsids that are recognised as authentic by a range of anti-FMDV bovine sera suggesting their feasibility as an alternate vaccine.
Eradication of viral haemorrhagic septicaemia in Danish aquaculture

Viral haemorrhagic septicaemia (VHS) virus was first isolated in Denmark in 1962, when more than half of the approximately 800 Danish fish farms were considered to be infected. Today, 50 years later, the country obtained status as EU approved VHS free zone. In the years in between very significant resources have been used to control and eradicate the disease. The control program included strict biosecurity and preventative measures, trade regulations, zoning and intensive inspections and laboratory testing. During the first decades of control and eradication programs the number of infected farms was significantly reduced while the curve flattened the last 20 years. It was only after a large and costly coordinated action in 2009-2013 including all affected areas that the country managed to free itself totally from VHS. Molecular tracing of the origin of VHSV isolates revealed that despite strict trade regulations and ban on introduction of live salmonids into the country VHSV seemed to have crossed the boarders into Denmark in a couple of cases. It is the first time that VHS has been eradicated from an endemically infected country. Among the causes of the success are a close collaboration between industry, stakeholders, veterinary authorities and scientists. Also the reduction of the number of farms and novel farming strategies account for the success. Furthermore, in Denmark rainbow trout farming would not survive in the international competition being endemically infected with this serious disease providing a strong incitement for
the fish farmers. Vaccination was not included in the control in Denmark but if licensed, vaccines would have been useful in order to reduce virus load before stamping-out. Similar control strategies will hopefully be implemented in other VHS infected countries in order to improve fish health and efficiently combat the disease.

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Organisations: Section for Virology, National Veterinary Institute, Technical University of Denmark, National Veterinary Institute, Danish Aquaculture Association, Danish Veterinary and Food Administration
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Organisations: National Veterinary Institute, Section for Virology
Authors: Olesen, N. J. (Intern), Vendramin, N. (Intern), Nicolajsen, N. (Intern)
Number of pages: 1
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European herring shows high mortality rate in bath challenge with viral haemorrhagic septicaemia virus (VHSV)

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Organisations: National Veterinary Institute, Section for Virology, National Veterinary Institute, Institute of Marine Research
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Evaluation of the potential anti-viral activity of microRNAs in rainbow trout (Oncorhynchus mykiss)
Micro ribonucleic acids (miRNAs) are small (18-22 nucleotides) endogenous RNAs that potently mediate post-transcriptional silencing of a wide range of genes. They are emerging as critical regulators of cellular processes and some miRNAs have been demonstrated to possess direct antiviral effects. We have previously observed and validated that the fishspecific miRNAs, miR-462 and miR-731, were among the most highly expressed miRNAs in rainbow trout liver following Viral hemorrhagic septicemia virus (VHSV) infection. These miRNAs were also upregulated in the liver and muscle (vaccination site) of fish vaccinated with a DNA vaccine encoding the glycoprotein gene of VHSV. Recent studies further suggest that the expression of these miRNAs is induced by interferons. In order to analyze if miRNA-462 and miRNA-731 have any antiviral effects, we designed inhibitory synthetic oligonucleotides called antagomiRs or anti-miRNAs. These antagomiRs were injected intraperitoneally into rainbow trout fingerlings followed by exposure of the fish to VHSV. Development of disease and levels of infection will be analysed and compared to data from fish treated with control miRNAs.

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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.
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 at 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.
Expression of innate immune genes, proteins and microRNAs in lung tissue and leukocytes of pigs infected with influenza virus

This study aimed at providing a better understanding of the involvement of innate immune factors, including miRNA, in the local and systemic host response to influenza virus infection. Twenty pigs were challenged by influenza A virus subtype H1N2. Expression of miRNA, mRNA and proteins were quantified at different time points after challenge (24h, 72h, and 14 days post infection (p.i.)). Gene expression was quantified using 48.48 Dynamic Arrays (Fluidigm Corporation, CA, USA) combining 48 samples with 48 primer sets for 2304 individual and simultaneous qPCR reactions. Several groups of genes were significantly regulated according to time point and infection status: Pattern recognition receptors (TLR2, TLR3, TLR7, RIG1, MDA5), IFN and IFN induced genes (IFNB, IFNG, IRF7, STAT1, ISG15 and OASL), cytokines (IL1B, IL1RN, IL6, IL7, IL10, IL12A, TNF, CCL2, CCL3 and CXCL10), and several acute phase proteins. Likewise, the following miRNAs were differentially expressed in one or more time groups compared to the control pigs: miR-15a, miR-21, miR-146, miR-206, miR-223 and miR-451. At day one p.i lung tissue protein levels of IL-6, IL-12 and IFN-α were significantly increased compared to the control group, and haptoglobin and C-reactive protein were at significantly increased at day three p.i. MiRNA are small non coding RNA molecules, that regulate gene expression in a wide range of organisms. Cellular miRNAs might be involved in influenza infection, both by targeting immune related host transcripts but also by targeting viral gene products. Our results suggest that in addition to a wide range of immune factors, miRNAs are involved in fine tuning of an efficient innate immune response to influenza infection.

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Expression of innate immune genes, proteins and microRNAs in lung tissue of pigs infected experimentally with influenza virus (H1N2)

This study aimed at providing a better understanding of the involvement of innate immune factors, including miRNA, in the local host response to influenza virus infection. Twenty pigs were challenged by influenza A virus subtype H1N2. Expression of miRNA (miRNA), mRNA and proteins were quantified in lung tissue at different time points after challenge (24 h, 72 h and 14 d post-infection (p.i.)). Several groups of genes were significantly regulated according to time point and infection status including pattern recognition receptors (TLR2, TLR3, TLR7, retinoic acid-inducible gene I, melanoma differentiation associated protein-5), IFN and IFN-induced genes (IFN-β, IFN-γ, IRF7, STAT1, ISG15 and OASL), cytokines (IL-1β, IL-1RN, IL-6, IL-7, IL-10, IL-12A, TNF-α, CCL2, CCL3 and CXCL10) and several acute phase proteins. Likewise, the following miRNAs were differentially expressed in one or more time groups compared with the control pigs: miR-15a, miR-21, miR-146, miR-206, miR-223 and miR-451. At d 1 p.i. lung tissue protein levels of IL-6, IL-12 and IFN-α were significantly increased compared with the control group, and haptoglobin and C-reactive protein were significantly increased at d 3 p.i. Our results suggest that, in addition to a wide range of innate immune factors, miRNAs may also be involved in controlling acute influenza infection in pigs.
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.

Fishpathogens.EU/NODA: A free and handy online platform for betanodavirus targeted research and data sharing

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Foot-and-mouth disease: past, present and future

ABSTRACT: Foot-and-mouth disease (FMD) is a highly contagious disease of cloven-hoofed animals including cattle, pigs, sheep and many wildlife species. It can cause enormous economic losses when incursions occur into countries which are normally disease free. In addition, it has long-term effects within countries where the disease is endemic due to reduced animal productivity and the restrictions on international trade in animal products. The disease is caused by infection with foot-and-mouth disease virus (FMDV), a picornavirus. Seven different serotypes (and numerous variants) of FMDV have been identified. Some serotypes have a restricted geographical distribution, e.g. Asia-1, whereas others, notably serotype O, occur in many different regions. There is no cross-protection between serotypes and sometimes protection conferred by vaccines even of the same serotype can be limited. Thus it is important to characterize the viruses that are circulating if vaccination is being used for disease control. This review describes current methods for the detection and characterization of FMDVs. Sequence information is increasingly being used for identifying the source of outbreaks. In addition such information can be used to understand antigenic change within virus strains. The challenges and opportunities for improving the control of the disease within endemic settings, with a focus on Eurasia, are discussed, including the role of the FAO/EuFMD/OIE Progressive Control Pathway. Better control of the disease in endemic areas reduces the risk of incursions into disease-free regions.
Foot-and-Mouth Disease Virus Serotype O Phylodynamics: Genetic Variability Associated with Epidemiological Factors in Pakistan

One of the most challenging aspects of foot-and-mouth disease (FMD) control is the high genetic variability of the FMD virus (FMDV). In endemic settings such as the Indian subcontinent, this variability has resulted in the emergence of pandemic strains that have spread widely and caused devastating outbreaks in disease-free areas. In countries trying to control and eradicate FMD using vaccination strategies, the constantly evolving and wide diversity of field FMDV strains is an obstacle for identifying vaccine strains that are successful in conferring protection against infection with field viruses. Consequently, quantitative knowledge on the factors that are associated with variability of the FMDV is prerequisite for preventing and controlling FMD in the Indian subcontinent. A hierarchical linear model was used to assess the association between time, space, host species and the genetic variability of serotype O FMDV using viruses collected in Pakistan from 2005 to 2011. Significant (P < 0.05) amino acid and nucleotide variations were associated with spatial distance, but not with differences in host species, which is consistent with the frequent multi-species infection of this serotype O FMDV. Results from this study will contribute to the understanding of FMDV variability and to the design of FMD control strategies in Pakistan. Viruses sequenced here also provide the earliest reported isolate from the Pan Asia IANT-10 sublineage, which has caused several outbreaks in the Middle East and spread into Europe (Bulgaria) and Africa (Libya).
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 protogentype 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.

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General information

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Genetic and biological characterisation of an avian-like H1N2 swine influenza virus generated by reassortment of circulating avian-like H1N1 and H3N2 subtypes in Denmark

BACKGROUND: The influenza A virus subtypes H1N1, H1N2 and H3N2 are the most prevalent subtypes in swine. In 2003, a reassorted H1N2 swine influenza virus (SIV) subtype appeared and became prevalent in Denmark. In the present study, the reassortant H1N2 subtype was characterised genetically and the infection dynamics compared to an “avian-like” H1N1 virus by an experimental infection study.

METHODS: Sequence analyses were performed of the H1N2 virus. Two groups of pigs were inoculated with the reassortant H1N2 virus and an “avian-like” H1N1 virus, respectively, followed by inoculation with the opposite subtype four weeks later. Measurements of HI antibodies and acute phase proteins were performed. Nasal virus excretion and virus load in lungs were determined by real-time RT-PCR.

RESULTS: The phylogenetic analysis revealed that the reassorted H1N2 virus contained a European “avian-like” H1-gene and a European “swine-like” N2-gene, thus being genetically distinct from most H1N2 viruses circulating in Europe, but similar to viruses reported in 2009/2010 in Sweden and Italy. Sequence analyses of the internal genes revealed that the reassortment probably arose between circulating Danish “avian-like” H1N1 and H3N2 SIVs. Infected pigs developed cross-reactive antibodies, and increased levels of acute phase proteins after inoculations. Pigs inoculated with H1N2 exhibited nasal virus excretion for seven days, peaking day 1 after inoculation two days earlier than H1N1 infected pigs and at a six times higher level. The difference, however, was not statistically significant. Pigs euthanized on day 4 after inoculation, had a high virus load in all lung lobes. After the second inoculation, the nasal virus excretion was minimal. There were no clinical sign except elevated body temperature under the experimental conditions.

CONCLUSIONS: The “avian-like” H1N2 subtype, which has been established in the Danish pig population at least since 2003, is a reassortant between circulating swine “avian-like” H1N1 and H3N2. The Danish H1N2 has an “avian-like” H1 and differs from most other reported H1N2 viruses in Europe and North America/Asia, which have H1-genes of human or “classical-swine” origin, respectively. The variant seems, however, also to be circulating in countries like Sweden and Italy. The infection dynamics of the reassorted “avian-like” H1N2 is similar to the older “avian-like” H1N1 subtype.

General information
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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
Authors: Trebbien, R. (Intern), Bragstad, K. (Forskerdatabase), Larsen, L. E. (Intern), Nielsen, J. (Intern), Bøtner, A. (Intern), Heegaard, P. M. H. (Intern), Fomsgaard, A. (Forskerdatabase), Viuff, B. M. (Forskerdatabase), Hjulsager, C. K. (Intern)
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Publication information
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BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
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Scopus rating (2016): CiteScore 2.43 SJR 1.097 SNIP 0.894
Scopus rating (2015): SJR 1.185 SNIP 0.947 CiteScore 2.47
Scopus rating (2014): SJR 1.044 SNIP 0.911 CiteScore 2.27
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.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Section for Public sector service and commercial diagnostics, University of Hong Kong
Authors: Kvisgaard, L. K. (Intern), Hjulsager, C. K. (Intern), Brar, M. S. (Ekstern), Leung, F. C. C. (Ekstern), Larsen, L. E. (Intern)
Pages: 334-344
Publication date: 2013
Main Research Area: Technical/natural sciences

Publication information
Journal: Veterinary Microbiology
Volume: 167
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
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.326 SNIP 1.208
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.393 SNIP 1.21 CiteScore 2.56
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.281 SNIP 1.262 CiteScore 2.54
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.438 SNIP 1.484 CiteScore 3
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.437 SNIP 1.579 CiteScore 3.18
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.562 SNIP 1.738 CiteScore 3.27
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.371 SNIP 1.476
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.29 SNIP 1.472
Hepatitis E virus: En overset zoonose, der smitter fra svin

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Statens Serum Institut
Authors: Krog, J. S. (Intern), Midgley, S. (Ekstern), Breum, S. Ø. (Intern), Larsen, L. E. (Intern)
Pages: 28-32
Publication date: 2013
Main Research Area: Technical/natural sciences

Publication information
Journal: Dansk Veterinaertidsskrift
Volume: 15
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
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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
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
Authors: Krog, J. S. (Intern), Breum, S. Ø. (Intern), Jensen, T. H. (Intern), Larsen, L. E. (Intern)
Pages: 2028-2030
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Main Research Area: Technical/natural sciences

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
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 4.92 SJR 3.305 SNIP 2.206
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 3.026 SNIP 2.033 CiteScore 4.23
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 3.437 SNIP 2.437 CiteScore 4.59
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 3.19 SNIP 2.293 CiteScore 4.68
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 2.809 SNIP 2.133 CiteScore 4.25
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 2.764 SNIP 2.193 CiteScore 4.46
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 2.95 SNIP 2.307
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Human cytomegalovirus chemokine receptor US28 induces migration of cells on a CX3CL1-presenting surface.

Human cytomegalovirus (HCMV)-encoded G protein-coupled-receptor US28 is believed to participate in virus dissemination through modulation of cell migration and immune evasion. US28 binds different CC chemokines and the CX3C chemokine CX3CL1. Membrane-anchored CX3CL1 is expressed by immune-activated endothelial cells, causing redirection of CX3CR1-expressing leukocytes in the blood to sites of infection. Here, we used stable transfected cell lines to examine how US28 expression affects cell migration on immobilized full-length CX3CL1, to model how HCMV-infected leukocytes interact with inflamed endothelium. We observed that US28-expressing cells migrated more than CX3CR1-expressing cells when adhering to immobilized CX3CL1. US28-induced migration was G protein-signalling dependent and was blocked by the phospholipase Cβ inhibitor U73122 and the intracellular calcium chelator BAPTA-AM. In addition, migration was inhibited in a dose-dependent manner by competition from CCL2 and CCL5, whereas CCL3 had little effect. Instead of migrating, CX3CR1-expressing cells performed ‘dancing-on-the-spot’ movements, demonstrating that anchored CX3CL1 acts as a strong tether for these cells. At low receptor expression levels, however, no significant difference in migration potential was observed when comparing the migration of CX3CR1- and US28-expressing cells. Thus, these data showed that, in contrast to CX3CR1, which promotes efficient cell capture upon binding to anchored CX3CL1, US28 acts to increase the migration of cells upon binding to the same ligand. Overall, this indicates that infected cells probably move more than uninfected cells in inflamed tissues with high CX3CL1 expression, with soluble chemokines affecting the final migration.

**General information**

State: Published

Organisations: Department of Micro- and Nanotechnology, Polymer Microsystems for Cell Processing, Polymer Microsystems for Medical Diagnostics, National Veterinary Institute, Section for Virology

Authors: Hjortø, G. M. (Intern), Kiilerich-Pedersen, K. (Intern), Selmeczi, D. (Intern), Kledal, T. N. (Intern), Larsen, N. B. (Intern)

Pages: 1111-1120

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Journal: Journal of General Virology

Volume: 94
Hvad målken gemmer

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Section for Epidemiology, Landbrug og Fødevarer
Authors: Uttenthal, Å. (Intern), Hansen, F. (Intern), Foddai, A. (Intern), Enøe, C. (Intern), Krogh, K. (Ekstern), Rattenborg, E. (Ekstern)
Pages: 28-29
Publication date: 2013
Main Research Area: Technical/natural sciences

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Journal: Dyrlægen
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Artikel i Dyrlægen 2013, 6. årgang, vol 1 pg 1-2. Frank Hansen er laborant på DTU-Vet, Lindholm. Mvh Åse
Source: dtu
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Hvordan ser afrikansk svinepest ud i danske grise?

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Organisations: National Veterinary Institute, Section for Virology
Authors: Nielsen, J. (Intern), Uttenthal, Å. (Intern)
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BFI (2016): BFI-level 1
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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
Identification of the determinants of efficient Pestivirus replication
The key for the survival of a virus is to copy its own genome into progeny genomes that allows continued reproduction. The mechanism behind this "copy function" or "replication" is a wellorganized process that involves the formation of a replication complex in the cell and interactions between the viral proteins. The replication process in single-stranded RNA viruses of positive polarity requires a particular enzyme, an RNA dependent RNA polymerase, that has no direct counterpart elsewhere in nature. The variable nature of rapidly evolving viral genomes, pose a constant challenge to the host, and in depth knowledge of the traits that determine the fitness of the virus in this regard are highly valuable. Recent advances in the field of molecular virology with methods to manipulate viral genomes have significantly helped to uncover these core mechanisms responsible for exploitation of the host. This includes aspects of the infection, evasion from host antiviral defense, genome replication and viral assembly. With special reference to a particular RNA virus, Classical swine fever virus (CSFV), this thesis deals with the elucidation of traits involved in replication of the viral genome. This is accomplished via the application of precisely bioengineered viral constructs and through the use of state-of-the-art virological methods. The presence of full-length cDNA sequences of RNA viruses within stable vectors has been the "holy grail" for the reverse genetics approaches, and for the rescue of bioengineered mutants. The availability, in our lab, of bacterial artificial chromosomes (BACs) containing full-length cDNA sequences which can be used to rescue three different CSFV strains with a spectrum of virulence, have been a central resource for this work. The thesis is composed of four parts: Part 1, gives a general introduction to RNA viruses, with the focus on viruses classified within the Flaviviridae. Next, pestiviruses are described with special attention to classical swine fever virus and the disease it is responsible for. A brief history of types of viral vaccines is provided, finishing with a description of the molecular methods used for viral cDNA manipulation, bio-engineering approaches, description of viral reporters and so forth. Part 2, "Pestiviruses: Infection and requirements for viral RNA replication" is meant as a walk through the literature describing Pestivirus/Classical swine fever virus replication determinants, including a thorough presentation of the viral proteins, and the involvement of these in the infection progress. Part 3, "The manuscripts", includes the papers published and submitted on this work. These describe the outcome of experiments performed during the three years. Manuscript I is a coauthored paper that describes a summary of the work I have been doing in my thesis dealing with the application of the Red/ET mediated homologous recombination method to modify viral cDNA. For proof of this method, CSFV/BDV chimeric clones were produced and characterized (Submitted paper, BMC genomics). Manuscript II describes the generation of replicons that express two different types of luciferases (RLuc and Gluc), and their application as a tool for easy monitoring of replication competence (published paper, Journal of General Virology (94), 1739-1748). Manuscript III describes the properties of chimeric replicons and infectious clones that include a RNA dependent RNA polymerase (NS5B) from one of three different CSFV strains with distinct virulence properties. The entire NS5B proved to influence replication competence and key residues for replication competence was identified as judged by reporter protein expression kinetics and from using infectious clones. Furthermore, evidence is provided that these specific single amino acid substitutions in the NS5B fingertip region, can influence the rate of viral RNA replication and virus spread. Part 4, is a summary and discussion of the general and overall conclusions and a walk through the milestones that have been achieved. Future perspectives and work that should be carried out are addressed as well.

Influence of the Leader protein coding region of foot-and-mouth disease virus on virus replication
The foot-and-mouth disease virus (FMDV) Leader (L) protein is produced in two forms, Lab and Lb, differing only at their amino-termini, due to the use of separate initiation codons, usually 84 nt apart. It has been shown previously, and confirmed here, that precise deletion of the Lab coding sequence is lethal for the virus, whereas loss of the Lb coding
sequence results in a virus that is viable in BHK cells. In addition, it is now shown that deletion of the ‘spacer’ region between these two initiation codons can be tolerated. Growth of the virus precisely lacking just the Lb coding sequence resulted in a previously undetected accumulation of frameshift mutations within the ‘spacer’ region. These mutations block the inappropriate fusion of amino acid sequences to the amino-terminus of the capsid protein precursor. Modification, by site-directed mutagenesis, of the Lab initiation codon, in the context of the virus lacking the Lb coding region, was also tolerated by the virus within BHK cells. However, precise loss of the Lb coding sequence alone blocked FMDV replication in primary bovine thyroid cells. Thus, the requirement for the Leader protein coding sequences is highly dependent on the nature and extent of the residual Leader protein sequences and on the host cell system used. FMDVs precisely lacking Lb and with the Lab initiation codon modified may represent safer seed viruses for vaccine production.

**General information**
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Organisations: National Veterinary Institute, Section for Virology
Authors: Belsham, G. (Intern)
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BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.93 SJR 1.499 SNIP 0.886
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.729 SNIP 1.007 CiteScore 3.26
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.683 SNIP 1.059 CiteScore 3.25
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.749 SNIP 1.161 CiteScore 3.64
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.518 SNIP 1.038 CiteScore 3.28
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.675 SNIP 1.149 CiteScore 3.6
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.657 SNIP 1.058
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.644 SNIP 1.13
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.636 SNIP 1.068
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.581 SNIP 1.135
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.

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Organisations: National Veterinary Institute, Section for Virology, Section for Public sector service and commercial diagnostics
Authors: Breum, S. Ø. (Intern), Hjulsager, C. K. (Intern), Trebbien, R. (Intern), Larsen, L. E. (Intern)
Number of pages: 1
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Main Research Area: Technical/natural sciences

Publication information
Journal: Genome Announcements
Volume: 1
Issue number: 5
Article number: e00712-13
ISSN (Print): 2169-8287
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BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
Scopus rating (2016): CiteScore 0.41 SJR 0.217 SNIP 0.233
Web of Science (2016): Indexed yes
Scopus rating (2015): SJR 0.199 SNIP 0.077
Scopus rating (2014): SJR 0.218 SNIP 0.089
ISI indexed (2013): ISI indexed no
Original language: English
Electronic versions:
Genome_Announc._2013_Breum_.pdf
DOIs:
10.1099/vir.0.052126-0
Source: dtu
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Publication: Research - peer-review › Journal article – Annual report year: 2013

Bibliographical note
Copyright © 2013 Breum et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 3.0 Unported license.
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 procline 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
Authors: Johansen, M. (Ekstern), Nielsen, M. (Ekstern), Dahl, J. (Ekstern), Svensmark, B. (Ekstern), Bækbo, P. (Ekstern), Kristensen, C. S. (Ekstern), Hjulsager, C. K. (Intern), Jensen, T. K. (Intern), Ståhl, M. (Intern), Larsen, L. E. (Intern), Angen, Ø. (Intern)
Pages: 63-72
Publication date: 2013
Main Research Area: Technical/natural sciences

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
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.2 SJR 1.185 SNIP 1.329
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.26 SNIP 1.23 CiteScore 2.1
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.267 SNIP 1.421 CiteScore 2.37
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.247 SNIP 1.552 CiteScore 2.49
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.274 SNIP 1.452 CiteScore 2.45
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Low levels of foot-and-mouth disease virus 3C protease expression are required to achieve optimal capsid protein expression and processing in mammalian cells

The foot-and-mouth disease virus (FMDV) capsid protein precursor (P1-2A) is processed by the virus-encoded 3C protease (3Cpro) to produce VP0, VP3, VP1 and 2A. Within the virus-encoded polyprotein, the P1-2A and 3Cpro can be expected to be produced at equivalent concentrations. However, using transient-expression assays, within mammalian cells, it is possible to modify the relative amounts of the substrate and protease. It has now been shown that optimal production of the processed capsid proteins from P1-2A is achieved with reduced levels of 3Cpro expression, relative to the P1-2A, compared with that achieved with a single P1-2A-3C polyprotein. Expression of the FMDV 3Cpro is poorly tolerated by mammalian cells and higher levels of the 3Cpro greatly inhibit protein expression. In addition, it is demonstrated that both the intact P1-2A precursor and the processed capsid proteins can be efficiently detected by FMDV antigen detection assays. Furthermore, the P1-2A and the processed forms each bind to the integrin αvβ6, the major FMDV receptor. These results contribute to the development of systems which efficiently express the components of empty capsid particles and may represent the basis for safer production of diagnostic reagents and improved vaccines against foot-and-mouth disease.
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.

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Article number: 206
ISSN (Print): 1746-6148
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BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.83 SJR 0.847 SNIP 0.983
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Microfluidic Sensing Platforms for Medicine and Diagnostics

New and emerging infectious diseases pose a growing global challenge for patient diagnosis and treatment, and for public health responses. Biosensors are one of the fastest growing technologies for in vitro diagnostics, and the sophisticated microsystems offer exciting opportunities for decentralized clinical applications in medicine and diagnostics. In this PhD project, low cost electrochemical plastic sensors for basic research, diagnosis of viral infections or drug discovery were developed and evaluated.

In the developed biosensor chip, early signs of virus infection in cell culture could be detected electrically using a cell based biosensing platform. The system responded for the infection of human cells within a few hours. This is a highly competitive time frame compared to viral culture, which is still the golden standard for laboratory diagnosis of viral infections.

The biosensing platform was adapted to selectively fish out virions from body fluid by aptamer functionalization. The intact virus particles were captured by immobilized aptamer probes on conductive polymer electrodes, allowing fast and easy electrical detection. The sensor responded rapidly, and showed high sensitivity and specificity. Influenza virus in saliva specimen was detectable within fifteen minutes at a clinically relevant concentration. The device has potential for miniaturization into a cost effective field ready point of care diagnostic system, where the majority of established techniques fail to function outside the specialized laboratory.

Microfluidic cell migration devices, imitating in vivo conditions were developed with success, improving the in vitro experimental setup for basic research and drug discovery.

Polymer biosensors have reached a new level of maturity, and pathogen detection could benefit from the integration of electrical sensors into low cost plastic microdevices pioneering point of care testing. The presented biosensing platforms have potential for scaling up towards high throughput screening, and are adaptable to other applications in medicine and
Molecular double check strategy for the identification and characterization of European Lyssaviruses

Lyssaviruses (order Mononegavirales, family Rhabdoviridae), the causative agents of rabies, represent a remarkable public health threat in developing countries. Among human exposures RABV is transmitted predominantly by dog bite; however bat lyssaviruses have also caused human cases. The "gold standard" for post-mortem rabies diagnosis is the fluorescence antibody test (FAT). However, in the case of ante-mortem non-neural sample material (e.g. saliva, cerebral spinal fluid, skin biopsies) or badly decomposed tissues the FAT reaches its limit and the use of molecular methods like reverse transcription PCR (RT-PCR) can be advantageous. In this study we developed a reverse transcription PCR cascade protocol feasible for screening and classification of samples even without any epidemiologic background with emphasis on the most relevant European lyssaviruses. As a first step two independent pan-lyssavirus assays based on the detection of an intercalating dye are performed in a double check application to increase diagnostic safety. Additionally, two independent internal control systems (endogenous and heterologous) were established. For the second line characterization of the lyssavirus positive samples two independent probe based (TaqMan) species-specific multiplex systems for RABV, EBLV-1, EBLV-2 and BBLV were developed. All assays were successfully validated with a comprehensive panel of 52 lyssavirus positive samples (including RABV, LBV, MOKV, DUVV, EBLV-1 & -2, ABLV, BBLV) as well as negative material from various host species. Furthermore, a synthetic positive control for all assays (intercalating dye and TaqMan assays) was established which enables a quantification of the viral load. In conclusion the developed pan-lyssavirus real-time RT-PCR assays and the two independent species-specific multiplex real-time RT-PCR systems allow the safe and sensitive screening and detection of all known lyssaviruses in humans and different animals as well as the characterization of the lyssavirus species circulating in the main land of Europe. The presented workflow combines all known advantages of the real-time PCR technology like speed and reduced risk of cross-contamination with improved safety of molecular testing based on double check strategy for the screening as well as the confirmation assays.
Molecular tracing of viral pathogens in aquaculture - A multidisciplinary trans-European research project

General information
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Organisations: National Veterinary Institute, Section for Virology, National Veterinary Institute, Agence nationale de la sécurité sanitaire, alimentation, environnement et travail, Friedrich Loeffler Institute, IFREMER, IRD, Norwegian Computing Center
Authors: Jensen, B. B. (Ekstern), Jansen, P. A. (Ekstern), Olesen, N. J. (Intern), Mikkelsen, S. S. (Intern), Bigarré, L. (Ekstern), Schuetze, H. (Ekstern), Bergmann, S. M. (Ekstern), Renault, T. (Ekstern), Avarre, J. (Ekstern), Aldrin, M. (Ekstern), Brun, E. (Ekstern)
Number of pages: 1
Publication date: 2013
Event: Poster session presented at 16th International Conference on Diseases of Fish and Shellfish, Tampere, Finland.
Main Research Area: Technical/natural sciences
Electronic versions: MOLTRAQ poster.pdf

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.

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Organisations: National Veterinary Institute, Section for Virology, Section for Public sector service and commercial diagnostics
Occurrence of Schmallenberg virus in Danish biting midges (Culicoides spp.)

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Section for Epidemiology
Authors: Rasmussen, L. D. (Intern), Kirkeby, C. (Intern), Kristensen, B. (Intern), Rasmussen, T. B. (Intern), Belsham, G. (Intern), Bødker, R. (Intern), Bøtner, A. (Intern)
Number of pages: 1
Publication date: 2013
Event: Poster session presented at EDENext Annual Meeting, Barcelona, Spain.
Main Research Area: Technical/natural sciences
Electronic versions:
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Source: dtu
Source-ID: u::7276
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Omfattende udbrud af hvalpesyge i danske mink (Neovison vison) og vilde rovdyr

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Kopenhagen Fur
Authors: Trebbien, R. (Intern), Chriél, M. (Intern), Struve, T. (Ekstern), Hjulsager, C. K. (Intern), Larsen, G. (Intern), Larsen, L. E. (Intern)
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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
Authors: Breum, S. Ø. (Intern), Hjulsager, C. K. (Intern), Trebbien, R. (Intern), Fobian, K. (Intern), Larsen, L. E. (Intern)
Pages: 26
Publication date: 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
Porcine Reproductive and Respiratory Syndrome Virus (PRRSV)

This PhD thesis presents the diversity of Porcine Reproductive and Respiratory Syndrome viruses (PRRSV) circulating in the Danish pig population. PRRS is a disease in pigs caused by the PRRS virus resulting in reproductive failures in sows and gilts and respiratory diseases in pigs. Due to genetic heterogeneity, PRRSV is divided into two genotypes, Type 1 and Type 2. Type 1 PRRS viruses are further divided into at least 3 subtypes. The virus evolves rapidly and reports of high pathogenic variants of both Type 1 and Type 2 appearing in Europe, North America, and Asia have been reported within recent years. This abrupt occurrence of highly pathogenic PRRSV strains emphasizes the significance of monitoring the diversity of circulating strains around the world both in respect to the sensitivity and specificity of diagnostic tests as well as efficacy of available vaccines.

The aims and objectives of the PhD project will be introduced in the objectives section together with a short introduction to the situation of PRRSV in Denmark at the start of this study. The background chapter will provide a review on PRRSV with the emphasis on genetic diversity.

The results of the work performed during the PhD are presented in the four manuscripts included in the PhD thesis and a short summary of each manuscript is depicted below:

Manuscript I is focusing on the development of methods for complete genome sequencing of PRRSV. The sequencing strategy was based on the production of long range PCR fragments covering the PRRSV genome in two or four fragments with full-length cDNA as template. The sequencing of the PCR fragments was performed using Next Generation Sequencing (NGS) technologies and three different platforms were used. A total of 18 complete PRRSV genomes were obtained using this new method.

Manuscript II is focusing on the diversity of Type 1 PRRSV in Denmark. For the first time genetic and antigenic examinations of complete genomes of Danish isolated Type 1 PRRSV was conducted. Furthermore, extensive studies of ORF5 and ORF7 sequences were performed from 44 viruses collected from 2003 to February 2013. The diversity study confirmed that only Type 1 subtype 1 PRRSV is circulating in the Danish pig population. The examination of the Danish PRRS field viruses confirmed that there is a high overall diversity among Type 1 viruses in Europe. The phylogenetic study also indicated the presence of two Danish virus clusters, one dominating vaccine/LV like and one resembling an early introduced strain.

Manuscript III is focusing on the diversity of Type 2 PRRSV in Denmark. For the first time examinations of complete genomes of European isolated Type 2 PRRSV were performed. Furthermore, ORF5 and ORF7 sequences obtained from 57 viruses collected in the years 2003-2012 were examined. The diversity study confirmed that Danish Type 2 PRRS viruses share high genetic similarity to the vaccine strain and there was no obviously reason to believe that new Type 2 PRRSV strains have been introduced. However, a few viruses showed both a higher diversity to the other Danish viruses and to the vaccine strain and one virus harbored the largest deletion in NSP2 reported in Danish Type 2 PRRSV. Manuscript IV is focusing on an experimental infection study in pigs with a Type 2 PRRS virus causing significant clinical disease in the field. Genetic and antigenic examination of ORF5 and partial NSP2 sequences obtained from the case virus revealed several variations compared to the vaccine strain. However, complete genome comparison of the case virus to the vaccine strain showed high genetic similarity and no obvious virulence maker was found. The results of the experimental infection study revealed that the strain induced only sparse clinical symptoms and the magnitude and duration of viraemia was comparable to an older Danish Type 2 strain. The results emphasized that infections in the field is often more severe than in experimental studies due to the multifactorial nature of PRRSV. Furthermore, the study underlined the need for more research on virulence markers of PRRSV.
Processing of the VP1/2A Junction Is Not Necessary for Production of Foot-and-Mouth Disease Virus Empty Capsids and Infectious Viruses: Characterization of "Self-Tagged" Particles

The foot-and-mouth disease virus (FMDV) capsid protein precursor, P1-2A, is cleaved by 3Cpro to generate VP0, VP3, VP1, and the peptide 2A. The capsid proteins self-assemble into empty capsid particles or viruses which do not contain 2A. In a cell culture-adapted strain of FMDV (O1 Manisa [Lindholm]), three different amino acid substitutions (E83K, S134C, and K210E) were identified within the VP1 region of the P1-2A precursor compared to the field strain (wild type [wt]). Expression of the O1 Manisa P1-2A (wt or with the S134C substitution in VP1) plus 3Cpro, using a transient expression system, resulted in efficient capsid protein production and self-assembly of empty capsid particles. Removal of the 2A peptide from the capsid protein precursor had no effect on capsid protein processing or particle assembly. However, modification of E83K alone abrogated particle assembly with no apparent effect on protein processing. Interestingly, the K210E substitution, close to the VP1/2A junction, completely blocked processing by 3Cpro at this cleavage site, but efficient assembly of "self-tagged" empty capsid particles, containing the uncleaved VP1-2A, was observed. These self-tagged particles behaved like the unmodified empty capsids in antigen enzyme-linked immunosorbent assays and integrin receptor binding assays. Furthermore, mutant viruses with uncleaved VP1-2A could be rescued in cells from full-length FMDV RNA transcripts encoding the K210E substitution in VP1. Thus, cleavage of the VP1/2A junction is not essential for virus viability. The production of such engineered self-tagged empty capsid particles may facilitate their purification for use as diagnostic reagents and vaccines.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Gullberg, M. (Intern), Polacek, C. (Intern), Bøtner, A. (Intern), Belsham, G. (Intern)
Pages: 11591-11603
Publication date: 2013
Main Research Area: Technical/natural sciences

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BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): SJR 3.052 SNIP 1.131 CiteScore 4.42
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 3.286 SNIP 1.138 CiteScore 4.42
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 3.168 SNIP 1.219 CiteScore 4.4
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 3.468 SNIP 1.26 CiteScore 4.92
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 3.154 SNIP 1.227 CiteScore 5.2
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Reconstructing the highly virulent Classical Swine Fever Virus strain Koslov

Classical swine fever virus (CSFV) may be highly virulent in pigs with a mortality rate close to 100%. The CSFV “Koslov strain” is known to be one of the most virulent CSFV, but so far a functional cloned cDNA of this strain has not been described. We suggest that this may be due to the error-prone nature of the RNA-dependent RNA polymerase resulting in the majority of circulating forms being non-functional. However, since any infectious virus particle should necessarily be the offspring of a functional virus, we hypothesized that it should be possible to synthesize a highly virulent form by reconstructing ancestral sequences. To test this hypothesis, we inferred sequences that correspond to ancestral nodes in a phylogenetic tree built from full-length nucleotide sequences of non-functional Koslov cDNAs and then proceeded to test the reconstructions. Specifically, we altered a non-functional cDNA by site directed mutagenesis, removing non-synonymous mutations step by step. In vitro testing of modified constructs did indeed lead to fully functional viruses with similar growth kinetics as the wild-type strain. Moreover, viruses rescued from the construct had the ancestral amino acid sequence and, when tested in pigs, were at least as virulent as the Koslov strain. The ancestral reconstruction therefore proved to give rise to a functional cDNA of the highly virulent Koslov strain. In vivo studies confirmed our methods and enabled us to identify nucleotide positions within the viral genome important for virulence.

General information
State: Published
Organisations: Molecular Evolution, National Veterinary Institute, Section for Virology, Department of Systems Biology, Center for Biological Sequence Analysis, Behavioral Phonemics, Friedrich Loeffler Institute
Authors: Fahnøe, U. (Intern), Pedersen, A. G. (Intern), Nielsen, J. (Intern), Höper, D. (Ekstern), Beer, M. (Ekstern), Rasmussen, T. B. (Intern)
Report on EURL training course 2013

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Olesen, N. J. (Intern), Vendramin, N. (Intern), Mikkelsen, S. S. (Intern)
Number of pages: 22
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Main Research Area: Technical/natural sciences
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training_course_report2013.pdf

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Activities:
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EURL training course 2013
Publication: Research › Report – Annual report year: 2013

Rescue of infectious Foot-and-Mouth Disease viruses from preserved viral RNA

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Belsham, G. (Intern), Bøtner, A. (Intern)
Pages: 2-4
Publication date: 2013
Main Research Area: Technical/natural sciences

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Journal: EAVLD Newsletter
Issue number: 7
Original language: English
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Links:
http://www.eavld.org/
Source: dtu
Source-ID: u::7179
Publication: Research - peer-review › Journal article – Annual report year: 2013

Results of the Proficiency Test, PT1 and PT2, 2012
A comparative test of diagnostic procedures was provided by the European Union Reference Laboratory (EURL) for Fish Diseases. The test was divided into proficiency test 1 (PT1) and proficiency test 2 (PT2).

The number of National Reference Laboratories (NRLs) participating in PT1 and PT2 was 43.

The tests were sent from the EURL in the beginning of September 2012. Both PT1 and PT2 are accredited by DANAK under registration number 515 for proficiency testing according to the quality assurance standard DS/EN ISO/IEC 17043.
Schmallenberg virus experimental infection of sheep

Since late 2011, a novel orthobunyavirus, named Schmallenberg virus (SBV), has been implicated in many cases of severely malformed bovine and ovine offspring in Europe. In adult cattle, SBV is known to cause a mild transient disease; clinical signs include short febrile episodes, decreased milk production and diarrhoea for a few days. However, the knowledge about clinical signs and pathogenesis in adult sheep is limited. In the present study, adult sheep of European domestic breeds were inoculated with SBV either as cell culture grown virus or as virus with no history of passage in cell cultures. Various experimental set-ups were used. Sampling included blood collection at different time points during the experimental period and selected organ material at autopsy. Data from this study showed, that the RNAemic period in
sheep was as short as reported for cattle; viral genome was detectable for about 3–5 days by real-time RT-PCR. In total, 13 out of 30 inoculated sheep became RNAemic, with the highest viral load in animals inoculated with virus from low cell culture passaged or the animal passaged material. Contact animals remained negative throughout the study. One RNAemic sheep showed diarrhoea for several days, but fever was not recorded in any of the animals. Antibodies were first detectable 10–14 days post inoculation. Viral RNA was detectable in spleen and lymph nodes up to day 44 post inoculation.

In conclusion, as described for cattle, SBV-infection in adult sheep predominantly results in subclinical infection, transient RNAemia and a specific antibody response. Maintenance of viral RNA in the lymphoreticular system is observed for an extended period.

**General information**

State: Published
Organisations: National Veterinary Institute, Section for Virology, Friedrich Loeffler Institute, Agence nationale de la sécurité sanitaire, alimentation, environnement et travail, National Laboratory for Sanitary Controls in Breeding Animals, INRA Institut National de La Recherche Agronomique


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Main Research Area: Technical/natural sciences
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.169 SNIP 1.3
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.043 SNIP 1.322
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.022 SNIP 1.401
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.078 SNIP 1.262
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.869 SNIP 1.259
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.913 SNIP 1.186
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.84 SNIP 1.112
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.833 SNIP 1.058
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 0.82 SNIP 1.088
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 0.703 SNIP 1.078
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Publication: Research - peer-review › Journal article – 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
Authors: Krog, J. S. (Intern), Forslund, A. (Ekstern), Breum, S. Ø. (Intern), Larsen, L. E. (Intern), Dalsgaard, A. (Ekstern), Schultz, A. C. (Intern)
Pages: 25
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Place of publication: Lyngby
Main Research Area: Technical/natural sciences
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Susceptibility of various Japanese freshwater fish species to an isolate of viral haemorrhagic septicaemia virus (VHSV) genotype Ivb
Genotype Ivb of viral haemorrhagic septicaemia virus (VHSV) was isolated for the first time in the Great Lakes basin in 2003, where it spread and caused mass mortalities in several wild fish species throughout the basin. In order to prevent further spreading of the disease and to assess risks of new genotypes invading new watersheds, basic microbiological information such as pathogenicity studies are essential. In this study, experimental infections were conducted on 7
indigenous freshwater fish species from Japan by immersion with a VHSV genotype IVb isolate. In Expt 1, cumulative mortalities in bluegill Lepomis macrochirus used as positive controls, Japanese fluvial sculpin Cottus pollux, and iwana Salvelinus leucomaenis pluvius were 50, 80 and 0%, respectively. In Expt 2, cumulative mortalities of 100, 100 and 10% were observed in Japanese fluvial sculpin C. pollux, Japanese rice fish Oryzias latipes and yoshinobori Rhinogobius sp., respectively. No mortality was observed in honmoroko Gnathopogon caerulescens, akaza Liobagrus reini or Japanese striped loach Cobitis biwae. VHSV was detected by RT-PCR from samples of kidney, spleen, and brain from all dead fish, and virus re-isolation by cell culture was successful from all dead fish. We detected the virus in the brain from a few surviving bluegill 50 d post exposure by both cell culture and RT-PCR. These results revealed that VHSV IVb could become a serious threat to wild freshwater fish species in Japan, and that some surviving fish might become healthy carriers of the virus.

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Organisations: National Veterinary Institute, Section for Virology
Authors: Ito, T. (Intern), Olesen, N. J. (Intern)
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Web of Science (2017): Indexed Yes
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Scopus rating (2016): CiteScore 1.95 SJR 0.858 SNIP 0.929
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.949 SNIP 0.935 CiteScore 1.96
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.889 SNIP 0.881 CiteScore 1.86
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.812 SNIP 0.918 CiteScore 1.77
ISI indexed (2013): ISI indexed yes
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BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.912 SNIP 1.092 CiteScore 2.04
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.11 SNIP 1.165 CiteScore 2.29
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.91 SNIP 0.951
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.889 SNIP 0.99
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.859 SNIP 0.998
Scopus rating (2007): SJR 0.949 SNIP 1.054
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
Authors: Hedegaard, C. J. (Intern), Ballegaard, A. (Ekstern), Røjel, N. (Ekstern), Bendix Hansen, M. (Ekstern), Kjær Lindved, B. (Ekstern), Bisgaard Frantzen, K. (Ekstern), Larsen, L. E. (Intern), Lihme, A. (Ekstern), Heegaard, P. M. H. (Intern)
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Swine Plasma Immunoglobulins for Prevention and Treatment of Post-Weaning Diarrhoea: Optimizing Stability Towards Gut Conditions

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Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Section for Virology, Technical University of Denmark, Upfront Chromatography A/S, KiBif ApS, Multimerics ApS
Authors: Hedegaard, C. J. (Intern), Ballegaard, A. (Ekstern), Røjel, N. (Ekstern), Bendix Hansen, M. (Ekstern), Kjær Lindved, B. (Ekstern), Bisgaard Frantzen, K. (Ekstern), Larsen, L. E. (Intern), Lihme, A. (Ekstern), Heegaard, P. M. H. (Intern)
Number of pages: 1
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Event: Poster session presented at 10th Workshop in Protein.DTU, Kgs. Lyngby, Denmark.
Main Research Area: Technical/natural sciences
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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.

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State: Published
Organisations: National Veterinary Institute, Section for Immunology and Vaccinology, Section for Virology, Technical University of Denmark, Upfront Chromatography A/S, KiBif ApS, Multimers ApS
Authors: Hedegaard, C. J. (Intern), Ballegaard, A. (Ekstern), Røjel, N. (Ekstern), Hansen, M. B. (Ekstern), Lindved, B. K. (Ekstern), Frantzen, K. B. (Ekstern), Larsen, L. E. (Intern), Lihme, A. (Ekstern), Heegaard, P. M. H. (Intern)
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Publication date: 2013
Event: Abstract from 10th International Veterinary Immunology Symposium, Milano, Italy.
Main Research Area: Technical/natural sciences
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Swine plasma immunoglobulins for prevention and treatment of post-weaning diarrhoea: Optimizing stability towards gut conditions

Brief description of research area:
A common problem in swine production is diarrhoea in newly weaned piglets, and huge quantities of antibiotics go to treat post-weaning diarrhoeas in piglets. The use of antibiotics can lead to the development of multi- and fully resistant bacteria, 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 challenged 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, Ufront Chromatography A/S, KiBif ApS, Multimerics ApS

Authors: Hedegaard, C. J. (Intern), Ballegaard, A. (Ekstern), Rejel, N. (Ekstern), Hansen, M. B. (Ekstern), Lindved, B. K. (Ekstern), Frantzen, K. B. (Ekstern), Larsen, L. E. (Intern), Lihme, A. (Ekstern), Heegaard, P. M. H. (Intern)

Number of pages: 1

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Main Research Area: Technical/natural sciences

Electronic versions:

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Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2013

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**The comparative utility of oral swabs and probang samples for detection of foot-and-mouth disease virus infection in cattle and pigs**

Foot-and-mouth disease virus (FMDV) RNA was measured using quantitative reverse transcription-PCR (qRT-PCR) assays in oral swab and probang samples collected from cattle and pigs during experimental infections with serotype O FMDV. During acute infection, FMDV RNA was measurable in oral swabs as well as in probang samples from both species. FMDV RNA could be detected in oral swabs and probang samples from a time point corresponding to the onset of viremia in directly inoculated animals, whereas animals which were infected through contact exposure had low levels of FMDV RNA in oral swabs before viral RNA could be measured in serum. Analysis of samples collected from cattle persistently infected with FMDV showed that it was not possible to detect FMDV RNA in oral swabs harvested beyond 10 days post infection (dpi), despite the presence of FMDV RNA in probang samples that had been collected as late as 35 dpi. An interesting feature of the persistent infection in the cattle was the apparent decline in the level of FMDV RNA in probang samples after the acute phase of infection, which was followed by a marked rise again (in all the carrier animals) by 28 dpi.

Results from this study indicate that qRT-PCR analysis of oral swabs is a useful approach in order to achieve a time efficient and reliable initial diagnosis of acute FMD in cattle and pigs, whereas probang sampling is essential for the detection of cattle that are persistently infected “carriers” of FMDV.

**General information**

State: Published

Organisations: National Veterinary Institute, Section for Virology

Authors: Stenfeldt, A. C. (Intern), Lohse, L. (Intern), Belsham, G. (Intern)

Pages: 330-337

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**Publication Information**

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Scopus rating (2015): SJR 1.393 SNIP 1.21 CiteScore 2.56
The diversity of Porcine Reproductive and Respiratory Syndrome Virus Type 1 and 2 in Denmark

Both Type 1 and Type 2 PRRSV 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 stains 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
Authors: Kvisgaard, L. K. (Intern), Hjulsager, C. K. (Intern), Kristensen, C. S. (Forskerdatabase), Brar, M. S. (Ekstern), Leung, F. C. (Ekstern), Larsen, L. E. (Intern)
Number of pages: 1
Publication date: 2013
Event: Abstract from International Porcine Reproductive and Respiratory Syndrome Symposium (PRRS 2013), Beijing, China.
Main Research Area: Technical/natural sciences

Third generation DIVA vaccine towards classical swine fever virus. Efficacy in face of maternal immunity
General purpose and objectives
Classical swine fever (CSF) is a highly contagious disease that causes huge economical losses and animal welfare concerns worldwide. Generally, vaccination is an effective and safe method to control the disease. Following vaccination the pig’s immune system develops antibodies that are significant part of the protection. However, vaccination with the only live attenuated vaccines existing on the market that contain a whole CSF virus (CSFV) with reduced infectivity, leads to production of an antibody response that does not differ from the antibody response developed after infection. Thus, implementation of these vaccines in case of outbreak will not give the possibility to differentiate infection in vaccinated animals (DIVA). For countries like Denmark, which are heavily dependent upon export of pigs and pig products the use of these traditional vaccines, will hamper the ability to proof a disease free status by serosurveillance, as all vaccinated piglets will be seropositive.

This PhD-project is a part of an EU project (CSFV_goDIVA grant no 227003) that has been funded by the European Commission with a main goal to develop and test to a level of registration a new DIVA vaccine candidate. The vaccine candidate “CP7E2alf” is intended for either intramuscular vaccination of domestic pig or for bait vaccination of wild boar. In this thesis as part of the clinical testing of the injection vaccine the efficacy of “CP7E2alf” was evaluated in young piglets that were positive for maternally derived antibodies (MDA). These antibodies were obtained with colostrum from their mothers vaccinated with traditional live attenuated vaccine C-strain (Riems). The promising results concerning the safety and the efficacy of the candidate DIVA vaccine showed new opportunities for control of a possible CSF outbreak that will have reduced impact on the export.

General information
State: Published
Organisations: Section for Virology, National Veterinary Institute
Authors: Rangelova, D. Y. (Intern), Uttenthal, Á. (Intern)
Number of pages: 94
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Publisher: Technical University of Denmark (DTU)
Original language: English
Main Research Area: Technical/natural sciences
Electronic versions:
Trade practices are main factors involved in the transmission of viral haemorrhagic septicaemia

Viral haemorrhagic septicaemia (VHS), caused by the novirhabdovirus viral haemorrhagic septicaemia virus (VHSV), causes significant economic problems to European rainbow trout, Oncorhynchus mykiss (Walbaum), production. The virus isolates can be divided into four distinct genotypes with additional subgroups. The main source of outbreaks in European rainbow trout farming is sublineage Ia isolates. Recently, this group of isolates has been further subdivided in to two subclades of which the Ia-2 consists of isolates occurring mainly in Continental Europe outside of Denmark. In this study, we sequenced the full-length G-gene sequences of 24 VHSV isolates that caused VHS outbreaks in Polish trout farms between 2005 and 2009. All these isolates were identified as genotype Ia-2; they divided however into two genetically distinct subgroups, that we name Pol I and Pol II. The Pol I isolates mainly caused outbreaks in the southern part of Poland, while Pol II isolates predominantly were sampled in the north of Poland, although it seems that they have been transmitted to other parts of the country. Molecular epidemiology was used for characterization of transmission pathways. This study shows that a main cause of virus transmission appears to be movement of fish. At least in Polish circumstances trading practices appear to have significant impact on spreading of VHSV infection.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, National Veterinary Research Institute
Authors: Reichert, M. (Ekstern), Matras, M. (Ekstern), Skall, H. F. (Intern), Olesen, N. J. (Intern), Kahns, S. (Intern)
Pages: 103-114
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Web of Science (2014): Indexed yes
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Scopus rating (2013): CiteScore 1.74
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Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 1.7
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Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.09
ISI indexed (2011): ISI indexed yes
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BFI (2010): BFI-level 1
Transplacental transmission of field and rescued strains of BTV-2 and BTV-8 in experimentally infected sheep

Transplacental transmission of bluetongue virus has been shown previously for the North European strain of serotype 8 (BTV-8) and for tissue culture or chicken egg-adapted vaccine strains but not for field strains of other serotypes. In this study, pregnant ewes (6 per group) were inoculated with either field or rescued strains of BTV-2 and BTV-8 in order to determine the ability of these viruses to cross the placental barrier. The field BTV-2 and BTV-8 strains was passaged once in Culicoides KC cells and once in mammalian cells. All virus inoculated sheep became infected and seroconverted against the different BTV strains used in this study. BTV RNA was detectable in the blood of all but two ewes for over 28 days but infectious virus could only be detected in the blood for a much shorter period. Interestingly, transplacental transmission of BTV-2 (both field and rescued strains) was demonstrated at high efficiency (6 out of 13 lambs born to BTV-2 infected ewes) while only 1 lamb of 12 born to BTV-8 infected ewes showed evidence of in utero infection. In addition, evidence for horizontal transmission of BTV-2 between ewes was observed. As expected, the parental BTV-2 and BTV-8 viruses and the viruses rescued by reverse genetics showed very similar properties to each other. This study showed, for the first time, that transplacental transmission of BTV-2, which had been minimally passaged in cell culture, can occur; hence such transmission might be more frequent than previously thought.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, University of Glasgow, Istituto Zooprofilattico Sperimentale dell’Abruzzo e del Molise “G. Caporale”
Authors: Rasmussen, L. D. (Intern), Savini, G. (Ekstern), Lorusso, A. (Ekstern), Bellacicco, A. (Ekstern), Palmarini, M. (Ekstern), Caporale, M. (Ekstern), Rasmussen, T. B. (Intern), Belsham, G. (Intern), Bøtner, A. (Intern)
Number of pages: 15
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Main Research Area: Technical/natural sciences

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Scopus rating (2014): SJR 1.189 SNIP 1.197 CiteScore 2.46
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ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.254 SNIP 1.279 CiteScore 2.97
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Scopus rating (2011): SJR 1.593 SNIP 1.645 CiteScore 3.85
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BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.472 SNIP 1.702
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.557 SNIP 2.009
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.745 SNIP 2.184
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.348 SNIP 1.946
Scopus rating (2005): SJR 0.879 SNIP 1.593
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.782 SNIP 1.302
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.729 SNIP 1.076
Scopus rating (2002): SJR 0.8 SNIP 1.191
Scopus rating (2001): SJR 0.629 SNIP 1.081
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 0.575 SNIP 0.994
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 0.388 SNIP 0.75
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Source-ID: n:oai:DTIC-ART:bmc/392607821::32322
Publication: Research - peer-review › Journal article – Annual report year: 2013

**Update on Fish Disease Situation in the Mediterranean Basin**

**General information**
State: Published
Organisations: National Veterinary Institute, Section for Virology
Use of DNA vaccination for determination of onset of adaptive immunity in rainbow trout fry

Vaccine producers often recommend a minimum size of 5g for vaccination of rainbow trout, but implementation of prophylactic vaccination in smaller sized fish would be an advantage for several infectious diseases. To implement a cost efficient vaccination strategy, it is important to know the duration and nature of the protective immunity induced by the vaccines in the fish. The present work aimed at determination of the smallest size at which specific immunity could be induced in rainbow trout fry by DNA vaccination against viral haemorrhagic septicaemia (VHS). Earlier experiments revealed that intramuscular injection of the DNA vaccine encoding the viral glycoprotein G induced protective immunity to VHS in rainbow trout fry of 0.5g. However, the vaccine is known to induce both innate and adaptive protection. The present work therefore aimed at determination of which type of protection the DNA vaccine induced in such early life stages of rainbow trout. Vaccination trials were performed with fry at average sizes of 0.25 g and 0.5 g respectively and included both the homologous VHSV G-gene vaccine and a heterologous DNA vaccine encoding the G-protein of infectious haematopoietic necrosis virus (IHNV). The fish were challenged by immersion at different times post vaccination. Protective immunity was induced in both sizes of fish, but whereas clear-cut specific protection was evident in the fish vaccinated at 0.5g, the results suggested that the protection in the fish vaccinated at 0.25 g was mainly due to innate cross-reactive antiviral mechanisms of shorter duration. The critical size for induction of an adaptive immune response in rainbow trout to this type of vaccination thus appears to be between 0.25 and 0.5g. This work was supported by the “DAFINET” grant from the Danish Council for Strategic Research.
Viral Haemorrhagic Septicaemia Virus
This chapter covers the genetics (genotypes and serotypes), clinical signs, host species, transmission, prevalence, diagnosis, control and prevention of viral haemorrhagic septicaemia virus.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology
Authors: Olesen, N. J. (Intern), Skall, H. F. (Intern)
Number of pages: 14
Pages: 323-336
Publication date: 2013
Whole inactivated virus vaccine prototype protects against viral encephalopathy and retinopathy in European sea bass (D. labrax)

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Section for Immunology and Vaccinology
Authors: Borghesan, F. (Ekstern), Vendramin, N. (Intern), Bovo, G. (Ekstern), Quartesan, R. (Ekstern), Cappellozza, E. (Ekstern), Lorenzen, N. (Intern), Terregino, C. (Ekstern), Toffan, A. (Ekstern)
Pages: 124
Publication date: 2013

Zoonotic Aspects of Hepatitis E Virus in Denmark
In this thesis the epidemiology of hepatitis E virus (HEV) in Denmark was explored. Globally, four genotypes of HEV are recognized along with several species specific variants. Non-zoonotic genotypes of the virus are found in the developing world, where they cause epidemics due to faecal contaminated water resources. Zoonotic genotypes have a primary reservoir in pigs worldwide. Humans infected with HEV are often asymptomatic, but can experience an acute self-limiting hepatitis. Pigs are asymptomatic and only mild lesions have been observed in the liver of infected animals. In the developed world, sporadic cases of HEV induced disease have been more frequently reported as awareness of the disease increases, including human cases in Denmark where HEV is also prevalent in pigs.

The thesis consists of an introduction into HEV where the literature on specific subjects is reviewed. The results obtained during the work of this PhD are presented in the form of four manuscripts. Finally, the four manuscripts are discussed in a broader context.

In Manuscript I, the work performed to investigate if HEV was found in other animal reservoirs than pigs in Denmark is presented. The research focused on mink (Nevison vison), an economically important livestock in Denmark. The main finding was the discovery of a novel variant of HEV. The virus was found in four different locations in samples collected in 2008 and in samples collected in 2011 indicating that the virus is widespread and has been circulating in minks for years. The virus did not seem to cause clinical disease in mink, however, this should be investigated further.

Manuscript II describes the leaching of HEV along with rotavirus (RV), porcine circovirus type 2 (PCV2), somatic coliphages, E. coli and Enterococcus spp. through field soil into tile drains under natural conditions of field fertilization. The microorganisms were naturally present in the pig slurry applied to the field. The results showed that HEV along with the other five microorganisms were found in water drained from the field, indicating potential contamination of water reservoirs in connection with the untreated drainage runoff. Rotavirus was detected in deeper groundwater screen indicating the possibility of groundwater contamination of viruses originating from manure, posing a risk for the contamination of important drinking water reservoirs in Denmark.

Manuscript III focuses on the viral contamination of mussels farmed in Denmark. The mussels was assayed for HEV and Rotavirus, known to occur in shellfish and cause disease. Furthermore, PCV2 was also assayed as an indicator of porcine waste contamination. All samples analyzed were negative for HEV and RV, however, a large proportion of the samples tested positive for the PCV2. This is the first report that shows the potential of PCV2 as an indicator organism. The lack of HEV in the mussels is in accordance with previous studies, although shellfish has been reported as the source of multiple sporadic cases of HEV infection.

Manuscript IV report the results of a longitudinal study performed in a multi-site farm, where HEV development in 104 pigs were followed from farrowing to 17 weeks of age. The pigs were divided into three groups according to the level of antibody titers of their sows. During the study, successful transfers of maternal antibodies were observed only for the pigs
born to sows with the highest antibody level. Furthermore, a significant reduction of the number of pigs shedding HEV from approx. 70% to 50% was observed in the group that received maternal antibodies. Ten of the pigs that were shedding HEV at week 17 were necropsied at week 20 and three of these were still shedding HEV. Correspondingly, HEV was found in different tissues, e.g. liver, tonsils and lungs, of these three pigs. HEV was, however, not found in muscles. In addition, high level of HEV was found in 1 out of 73 Danish livers purchased at grocery stores in the larger Copenhagen area.

Based on these studies it could be concluded that HEV belongs to a diverse family of viruses with variants in multiple species, and there is a possibility that many more of these will be identified during the coming years. However, clinical illness have so far only been described in humans and birds. HEV is known to be present in the water environment of poorly sanitized regions of the world, however, our study also emphasized the need for better understanding of viral leaching as well as the need for diagnostic tools enabling survey of water to maintain high drinking water quality also in the developed part of the world. We did not find HEV or RV in shellfish although indications of porcine waste contamination of shellfish occurring were observed in though the detection of the porcine specific virus PCV2. This is an interesting finding and suggest that PCV2 may be utilized to monitor viral contamination of shellfish, which is completely lacking today. Lastly, high levels of maternal antibodies can diminish the number of pigs shedding or carrying infectious HEV when entering the food supply chain. This could be utilized by vaccinating sows prior to farrowing, ensuring transfer of maternal antibodies and thereby reducing human exposure to HEV.

General information

State: Published
Organisations: National Veterinary Institute, Section for Virology, National Food Institute, Division of Food Microbiology
Authors: Krog, J. S. (Intern), Breum, S. Ø. (Intern), Larsen, L. E. (Intern), Schultz, A. C. (Intern)
Number of pages: 159
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Original language: English
Main Research Area: Technical/natural sciences
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Publication: Research › Ph.D. thesis – Annual report year: 2013

Analysis of viremia and transplacental transmission of field and rescued strains of BTV-2 and BTV-8 following inoculation of pregnant sheep

Objectives

Live bluetongue virus (BTV) vaccine-strains and also, surprisingly, the European strain of BTV-8 can cross the placental-barrier and thus pass from one generation of animals to another without involvement of the insect vector. A better understanding of the genetic basis for the transmission characteristics of the virus would help to identify the risks posed by further BTV incursions and facilitate the design of better control strategies. The development of reverse genetics for BTV enables investigation of the genetic traits conferred by individual genome segments within rescued viruses by making defined reassortants. To date, only a few experiments have investigated whether field and rescued virus strains behave similarly in vivo.

Methods

Twenty-four sheep (in 4 groups of 6) were inoculated (s.c.) with 4 strains of BTV in late pregnancy (approx. 1 month before lambing). The viruses used were: BTV-2 wt (Italian field strain), BTV-2 (rescued), BTV-8 wt (field strain from the Netherlands) and BTV-8 (rescued). Four sheep were non-inoculated controls. Blood samples from the sheep were tested frequently for viremia and anti-BTV antibodies (by ELISA) in the period until lambing. Pre-colostral blood samples were collected from all newborn lambs, except for one born dead, to determine if transplacental transmission had occurred. Milk from ewes was collected daily for 7 days after lambing and blood samples from the lambs were collected on days 0, 3 and 7 after birth. All samples have being tested for the presence of anti-BTV antibodies and for virus (RT-qPCR).

Results

All inoculated animals developed viremia. The viremia was significantly higher at all sampling points following inoculation (p<0.01 or p< 0.05, Mann-Whitney's U Test) in animals inoculated with BTV-2 wt compared to animals inoculated with BTV-2 rescued, whereas no significant difference was detected between BTV-8 wt and BTV-8 rescued. Wild type virus infected animals had a longer lag phase before antibodies were detected but the response increased at a faster rate. Some of the animals displayed clinical signs of infection, e.g. fever and panting. All the ewes delivered one lamb each, a few lambs born early did not thrive and were euthanized but most appeared healthy. Seven of the 28 lambs had been infected transplacentally; 2 from ewes inoculated with BTV-2 wt, 3 from ewes inoculated with BTV-2 rescued and 1 from a ewe inoculated with BTV-8 wt. The last infected lamb was from a non-inoculated control sheep, in the same stable but physically separated from, the BTV-2 wt inoculated ewes and became viremic with BTV-2 10 days after the others were inoculated.
Conclusion
Both wild-type and rescued BTVs induced viremia. Surprisingly, transplacental transmission occurred more frequently in ewes inoculated with BTV-2, both wt and rescued, than in ewes inoculated with BTV-8. The BTV-2 wt was passaged once in Kc and once in CPT-Tert cells. These very few passages may be enough to introduce changes enabling the virus to cross the placental barrier. This experiment indicates it will be difficult to identify a single BTV segment responsible for transplacental transmission in sheep using rescued BTV-2 and BTV-8 strains.

General information
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Organisations: National Veterinary Institute, Division of Virology, Sektion for Eksotiske Virussygdomme, Instituto G. Caporale, University of Glasgow
Authors: Rasmussen, L. D. (Intern), Savini, G. (Ekstern), Palmarini, M. (Ekstern), Rasmussen, T. B. (Intern), Belsham, G. (Intern), Botner, A. (Intern)
Number of pages: 1
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Electronic versions:
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Application of the Ceditest FMDV type O and FMDV-NS enzyme-linked immunosorbent assays for detection of antibodies against Foot-and-mouth disease virus in selected livestock and wildlife species in Uganda
Diagnosis and control of Foot-and-mouth disease virus (FMDV) requires rapid and sensitive diagnostic tests. Two antibody enzyme-linked immunosorbent assay (ELISA) kits, Ceditest FMDV-NS for the detection of antibodies against the nonstructural proteins of all FMDV serotypes and Ceditest FMDV type O for the detection of antibodies against serotype O, were evaluated under African endemic conditions where the presence of multiple serotypes and the use of nonpurified vaccines complicate serological diagnosis. Serum samples from 218 African buffalo, 758 cattle, 304 goats, and 88 sheep were tested using both kits, and selected samples were tested not only in serotype-specific ELISAs for antibodies against primarily FMDV serotype O, but also against other serotypes. The FMDV-NS assay detected far more positive samples (93%) than the FMDV type O assay (30%) in buffalo (P <0.05), with predominant antibodies against the South African Territories (SAT) serotypes, while the seroprevalence was generally comparable in cattle with antibodies against serotype O elicited by infection and/or vaccination. However, some districts had higher seroprevalence using the FMDV type O assay indicating vaccination without infection, while 1 cattle herd with antibodies against the SAT serotypes had far more positive samples (85%) using the FMDV-NS versus the FMDV type O (10%), consistent with the latter test's lower sensitivity for antibodies against SAT serotypes. Based on the current investigation, the FMDV type O ELISA may be limited by the presence of SAT serotypes. The FMD NS assay worked well as a screening test for antibodies against all FMDV serotypes present in Uganda; however, as long as nonpurified vaccines are applied in the region, this test cannot be used to differentiate between vaccinated and infected animals.

General information
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Organisations: National Veterinary Institute, Division of Virology, Sektion for Eksotiske Virussygdomme, Section of Vesicular virus diseases, Ministry of Agriculture, Animal Industry and Fisheries, Makerere University
Authors: Ayebazibwe, C. (Ekstern), Mwiine, F. N. (Ekstern), Balinda, S. N. (Ekstern), Tjørnehøj, K. (Intern), Alexandersen, S. (Intern)
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Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.708 SNIP 0.959 CiteScore 1.41
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.745 SNIP 1.028 CiteScore 1.37
ISI indexed (2012): ISI indexed yes
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Scopus rating (2011): SJR 0.708 SNIP 0.93 CiteScore 1.34
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BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.728 SNIP 1.023
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Scopus rating (2008): SJR 0.794 SNIP 0.972
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Scopus rating (2007): SJR 0.605 SNIP 0.773
Web of Science (2007): Indexed yes
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Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.589 SNIP 0.77
Scopus rating (2004): SJR 0.619 SNIP 0.815
Web of Science (2004): Indexed yes
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Scopus rating (2002): SJR 0.867 SNIP 1.043
Scopus rating (2001): SJR 0.809 SNIP 1.079
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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.
Atypical Pestivirus and Severe Respiratory Disease in Calves, Europe

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Organisations: National Veterinary Institute, Division of Virology, Sektion for Eksotiske Virussygdomme, National Veterinary Institute, National Veterinary Research Institute, Lund University, Qingdao Agricultural University, Lanzhou Veterinary Research Institute
Authors: Liu, L. (Ekstern), Larska, M. (Ekstern), Xia, H. (Ekstern), Uttenthal, Å. (Intern), Polak, M. P. (Ekstern), Ståhl, K. (Ekstern), Alenius, S. (Ekstern), Shan, H. (Ekstern), Yin, H. (Ekstern), Belák, S. (Ekstern)
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BFI (2017): BFI-level 2
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ISI indexed (2012): ISI indexed yes
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BFI (2011): BFI-level 2
Scopus rating (2011): SJR 2.764 SNIP 2.193 CiteScore 4.46
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
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Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 2.664 SNIP 2.316
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 2.847 SNIP 2.33
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 2.771 SNIP 2.283
Web of Science (2005): Indexed yes
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Scopus rating (2001): SJR 2.347 SNIP 2.893
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Capsid coding sequences of foot-and-mouth disease viruses are determinants of pathogenicity in pigs

The surface exposed capsid proteins, VP1, VP2 and VP3, of foot-and-mouth disease virus (FMDV) determine its antigenicity and the ability of the virus to interact with host-cell receptors. Hence, modification of these structural proteins may alter the properties of the virus. In the present study we compared the pathogenicity of different FMDVs in young pigs. In total 32 pigs, 7-weeks-old, were exposed to virus, either by direct inoculation or through contact with inoculated pigs, using cell culture adapted (O1K B64), chimeric (O1K/A-TUR and O1K/O-UKG) or field strain (O-UKG/34/2001) viruses. The O1K B64 virus and the two chimeric viruses are identical to each other except for the capsid coding region. Animals exposed to O1K B64 did not exhibit signs of disease, while pigs exposed to each of the other viruses showed typical clinical signs of foot-and-mouth disease (FMD). All pigs infected with the O1K/O-UKG chimera or the field strain (O-UKG/34/2001) developed fulminant disease. Furthermore, 3 of 4 in-contact pigs exposed to the O1K/O-UKG virus died in the acute phase of infection, likely from myocardial infection. However, in the group exposed to the O1K/A-TUR chimeric virus, only 1 pig showed symptoms of disease within the time frame of the experiment (10 days). All pigs that developed clinical disease showed a high level of viral RNA in serum and infected pigs that survived the acute phase of infection developed a serotype specific antibody response. It is concluded that the capsid coding sequences are determinants of FMDV pathogenicity in pigs.
Chemical modification of RNA-based medicine can be used to reduce its induction of the innate immune response
Small interfering RNAs (siRNAs) are regarded as promising new active compounds in gene medicine. They are small 21-22bp long double stranded RNAs which act by targeting and inhibiting expression of specific mRNAs through base complementarity to one of their strands. But one serious problem with siRNA based treatment is the non-specific activities of double stranded RNAs when formulated in some effective delivery reagents. Cellular reactions upon double stranded RNAs include those of the 2’-5’ oligoadenylate synthetase system, the protein kinase R, RIG-I and Toll-like receptor activated pathways all resulting in innate antiviral defence mechanisms. Following injection of formulated siRNAs we have shown that we are able to detect the effect of such defence mechanisms as lowered mortality of rainbow trout infected with the fish pathogenic virus Viral Haemorrhagic Septicaemia Virus (VHSV).
We used the trout and VHSV to screen siRNAs containing various chemical modifications of the RNA backbone and found that was possible to modify the backbone so as to reduce the antiviral effect of the RNA. Antiviral protection was also dependent upon localisation of the modified nucleotide residues in the RNA strands and we found some evidence of an effect of both base composition and thermal stability of the double strands.
We conclude that our model is a potent tool for gaining insight into the triggering of antiviral cellular reactions towards RNAs in living fish. The overall perspective is to learn how to avoid nonspecific antiviral responses of RNA-based gene medicine, but the knowledge gained also has a potential for use in the design of adjuvants (although adjuvance effect has not been tested for any of our siRNAs yet). The model can also be used for screening various commercial and noncommercial delivery reagents with the same perspective.
Comparison of the pathogenicity of two serotype O foot-and-mouth disease viruses (chimeric and field strain viruses) in pigs

General information
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Organisations: National Veterinary Institute, Section for Virology, Institute for Animal Health
Authors: Lohse, L. (Intern), Jackson, T. (Ekstern), Bøtner, A. (Intern), Belsham, G. (Intern)
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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.

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Culicoids as Vectors of Schmallenberg Virus

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Detection and genetic characterization of foot-and-mouth disease viruses in samples from clinically healthy animals in endemic settings

A total of 1501 oral swab samples from Pakistan, Afghanistan and Tajikistan were collected from clinically healthy animals between July 2008 and August 2009 and assayed for the presence of foot-and-mouth disease virus (FMDV) RNA. The oral swab samples from two (of four) live animal markets in Pakistan (n = 245), one (of three) live animal market in Afghanistan (n = 61) and both the live animal markets in Tajikistan (n = 120) all tested negative. However, 2 of 129 (∼2%) samples from Gondal and 11 of 123 (9%) from Chichawatni markets in Pakistan were positive for FMDV RNA. Similarly, 12 of 81 (15%) samples from Kabul and 10 of 20 (50%) from Badakhshan in Afghanistan were found to be positive. Serotypes A and O of FMDV were identified within these samples. Oral swab samples were also collected from dairy colonies in Harbanspura, Lahore (n = 232) and Nagori, Karachi (n = 136), but all tested negative for FMDV. In the Landhi dairy colony, Pakistan, a cohort of 179 apparently healthy animals was studied. On their arrival within the colony, thirty-nine (22%) of these animals were found positive for FMDV RNA (serotype A was identified), while 130 (72.6%) had antibodies to FMDV non-structural proteins. Thus, newly introduced animals may be a significant source of the disease in the colony. Only two animals from the cohort were detected as becoming positive for FMDV RNA during a follow-up period of 4 months; however, only 10 animals remained negative for anti-NSP antibodies during this period.

General information

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Organisations: Division of Virology, Sektion for Eksotiske Virussygdomme, National Veterinary Institute, Food and Agriculture Organization of the United Nations, FAO Project, National Veterinary Laboratory, Quaid-I-Azam University
Authors: Jamal, S. M. (Intern), Ferrari, G. (Ekstern), Hussain, M. (Forskerdatabase), Nawroz, A. H. (Ekstern), Aslami, A. A. (Ekstern), Khan, E. (Ekstern), Murvatulloev, S. (Ekstern), Ahmed, S. (Ekstern), Belsham, G. (Intern)
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Detection of African swine fever virus in asymptomatic pigs using FTA cards in Mbeya region, Tanzania

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Organisations: National Veterinary Institute, Division of Virology, Sektion for Eksotiske Virussygdomme, Sokoine University of Agriculture, University of Copenhagen
Authors: Uttenthal, Å. (Intern), Braae, U. C. (Forskerdatabase), Ngowi, H. A. (Ekstern), Rasmussen, T. B. (Intern), Nielsen, J. (Intern), Johansen, M. V. (Forskerdatabase)
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Bibliographical note
Oral presentation.
Detection of foot-and-mouth disease virus RNA in pharyngeal epithelium biopsy samples obtained from infected cattle: Investigation of possible sites of virus replication and persistence

Foot-and-mouth disease (FMD) is a highly contagious viral infection of significant financial importance to the export and trade of agricultural products. The occurrence of persistently infected “carriers” of FMD-virus (FMDV) in ruminant species adds further complications to disease control. There have been significant discrepancies in reports regarding the pathogenesis of FMDV infection in cattle with specific emphasis on the anatomical sites involved in early and persistent virus replication. In this study, collection of small biopsy samples from the dorsal soft palate (DSP) of live animals was used to investigate the level of FMDV RNA present at this site at sequential time points during the infection. Results were compared to measurements of virus excretion in samples of oropharyngeal fluid collected at corresponding time points. Possible sites of virus persistence were investigated through measurements of the levels of FMDV RNA in the DSP as well as mandibular and retropharyngeal lymph nodes beyond 28 days after infection. Results indicated only low levels of FMDV RNA present in samples of pharyngeal epithelia during both early and persistent phases of infection with significantly higher levels of virus detected in pharyngeal excretions. It is concluded that the targeted area for sampling within the DSP does not harbour significant levels of virus replication during acute or persistent FMDV infection in cattle. Furthermore, the DSP and the mandibular and retropharyngeal lymph nodes cannot be concluded to be principal sites for persistence of FMDV.
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 producers.

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) Continuously follow the genetic evaluation of especially Type I PRRSV subtype viruses and regularly update their primer sequences.
Detection of subgenomic mRNA of feline coronavirus by real-time polymerase chain reaction based on primer-probe energy transfer (P-sg-QPCR)

Feline infectious peritonitis is one of the most severe devastating diseases of the Felidae. Upon the appearance of clinical signs, a cure for the infected animal is impossible. Therefore rapid and proper diagnosis for both the presence of the causative agent, feline coronavirus (FCoV) and the manifestation of feline infectious peritonitis is of paramount importance. In the present work, a novel real-time RT-PCR method is described which is able to detect FCoV and to determine simultaneously the quantity of the viral RNA. The new assay combines the M gene subgenomic messenger RNA (sg-mRNA) detection and the quantitation of the genome copies of FCoV. In order to detect the broadest spectrum of potential FCoV variants and to achieve the most accurate results in the detection ability the new assay is applying the primer-probe energy transfer (PriProET) principle. This technology was chosen since PriProET is very robust to tolerate the nucleotide substitutions in the target area. Therefore, this technology provides a very broad-range system, which is able to detect simultaneously many variants of the virus(es) even if the target genomic regions show large scale of variations. The detection specificity of the new assay was proven by positive amplification from a set of nine different FCoV strains and negative from the tested non-coronaviral targets. Examination of faecal samples of healthy young cats, organ samples of perished animals, which suffered from feline infectious peritonitis, and cat leukocytes from uncertain clinical cases were also subjected to the assay. The sensitivity of the P-sg-QPCR method was high, since as few as 10 genome copies of FCoV were detected. The quantitative sg-mRNA detection method revealed more than 10–50,000 times increase of the M gene sg-mRNA in organ materials of feline infectious peritonitis cases, compared to those of the enteric FCoV variants present in the faeces of normal, healthy cats. These results indicate the applicability of the new P-sg-QPCR test as a powerful novel tool for the better detection and quantitation of FCoV and for the improved diagnosis of feline infectious peritonitis, this important disease of the Felidae, causing serious losses in the cat populations at a global scale.

General information
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Organisations: National Veterinary Institute, Division of Virology, Sektion for Eksotiske Virusygdomme, Lund University, Central Agricultural Office, Szent Istvan University, Uppsala University
Authors: Hornyák, Á. (Ekstern), Bálint, Á. (Ekstern), Farsang, A. (Ekstern), Balka, G. (Ekstern), Hakhverdyan, M. (Ekstern), Rasmussen, T. (Intern), Blomberg, J. (Ekstern), Belák, S. (Ekstern)
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BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.893 SNIP 0.952 CiteScore 1.87
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Scopus rating (2013): SJR 0.861 SNIP 0.91 CiteScore 1.99
ISI indexed (2013): ISI indexed yes
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Scopus rating (2012): SJR 0.869 SNIP 0.935 CiteScore 2.08
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Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
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ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.892 SNIP 0.998
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.964 SNIP 1.061
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.918 SNIP 1.082
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 0.955 SNIP 1.029
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.879 SNIP 1.073
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.859 SNIP 1.006
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.715 SNIP 1.028
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.753 SNIP 1.008
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.736 SNIP 1.059
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.758 SNIP 0.949
Scopus rating (2000): SJR 0.684 SNIP 0.883
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Publication: Research - peer-review › Journal article – Annual report year: 2012
Diagnostic capacity for viral haemorrhagic septicaemia virus (VHSV) infection in rainbow trout (Oncorhynchus mykiss) is greatly increased by combining viral isolation with specific antibody detection

Detection of disease specific antibodies in farmed rainbow trout (Oncorhynchus mykiss) has been proposed as an alternative or supplement to the currently approved procedures for diagnosis and surveillance in this species. In samples from natural outbreaks of the disease viral haemorrhagic septicaemia (VHS) at two freshwater farms in southern Denmark serologic testing was used to broaden the diagnostic window from outbreak to diagnosis in the laboratory as compared to traditional procedures of isolation and identification of the virus. The serologic assay clearly increased the chance of detecting present or previous infections where the pathogen could not be isolated by standard methods (indicating older infections where the virus had been cleared). Our data allowed us to monitor the levels of neutralising antibodies in relation to the presence of the virus in fish experiencing two different types of outbreaks at two different farms. By sequence analysis of the viral glycoprotein from selected isolates we found no evidence for escape mutants having developed in the fish showing high titres of neutralising antibodies.

General information
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Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Danish Veterinary and Food Administration
Authors: Schyth, B. D. (Intern), Ariel, E. (Intern), Korsholm, H. (Ekstern), Olesen, N. J. (Intern)
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  Web of Science (2016): Indexed yes
  BFI (2015): BFI-level 1
  Scopus rating (2015): SJR 1.268 SNIP 1.171 CiteScore 3.19
  Web of Science (2015): Indexed yes
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  Web of Science (2014): Indexed yes
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  ISI indexed (2012): ISI indexed yes
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  ISI indexed (2011): ISI indexed yes
  Web of Science (2011): Indexed yes
  BFI (2010): BFI-level 1
  Scopus rating (2010): SJR 1.131 SNIP 1.056
  Web of Science (2010): Indexed yes
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Differences in detection of foot-and-mouth disease virus RNA in oral swabs and probang samples during experimental infection of cattle and pigs

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Organisations: Division of Virology, Sektion for Eksotiske Virussygdomme, National Veterinary Institute, Section for Virology
Authors: Stenfeldt, A. C. (Intern), Lohse, L. (Intern), Belsham, G. (Intern)
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Event: Poster session presented at EuFMD meeting 2012, Jerez de la Frontera, Spain.
Main Research Area: Technical/natural sciences
Electronic versions:
Stenfeldt_et_al_poster_EuFMD_2012.pdf
Publication: Research › Poster – 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 PORRSCON 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, Centre de Recerca en Sanitat Animal, Agence nationale de la sécurité sanitaire, alimentation, environnement et travail, Ghent University
Number of pages: 1
Publication date: 2012
Event: Abstract from 22nd International Pig Veterinary Society Congress, Jeju, Korea, Republic of.
Main Research Area: Technical/natural sciences
Electronic versions:
prod21357332892212. Diversity_of_LE_Larsen.pdf

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

DNA vaccination of small rainbow trout fry against VHSV
Small rainbow trout fry were DNA vaccinated by intramuscular injection at 0.25g and other fish later at 0.5g. Vaccine groups included pcDNA3-vhsG, heterologous vaccine (pcDNA3-ihnG), empty vector (pcDNA3) and unhandled fish. Fry vaccinated at 0.25g were challenged with VHSV by immersion at 3wpv, 11wpv and 21wpv. The challenge at 3wpv was started 1wpv, however as no mortality was observed, the fish were re-challenged 3wpv using a modified setup. Fry vaccinated at 0.5g were challenged with VHSV by immersion at 11wpv. By early challenge (3wpv) of fish vaccinated at 0.25g both homologous and heterologous vaccines induced unspecific protection (10 % mortality for both). Challenge 11wpv showed waning unspecific protection (60 % mortality) but also a poor specific protection (30 % mortality). By challenge 21wpv, hardly no specific (75 % mortality) or unspecific (81 % mortality) protection was observed. In contrast, fish vaccinated at 0.5g and challenged at 11wpv showed good specific protection.
The results indicate that DNA vaccination of very small fry (0.25g) can induce an early innate response. However a late adaptive immune response is apparently not established. Vaccination of fry at 0.5g induces an adaptive response like in larger fish.
The experiment was repeated with same vaccination groups. Rainbow trout fry were vaccinated at 0.25g followed by challenge with homologous or heterologous virus at 13 dpv, 11 wpv and 21 wpv. At 13 dpv unspecific protection was induced with both homologous and heterologous challenge (5% mortality). At 11 wpv an unspecific protection with 30 %
Mortality was observed. At 21 wpv protection against VHSV had dropped further (50% mortality). Protection against IHNV was better (10% mortality) but equal for both homologous and heterologous vaccines confirming previous results, that vaccination of fry at 0.25g induces unspecific protection but no adaptive response.

**General information**

State: Published

Organisations: National Veterinary Institute, Division of Poultry, Fish and Fur Animals, Section of Fish Diseases

Authors: Rasmussen, J. S. (Intern), Lorenzen, E. (Intern), Kjær, T. E. (Intern), Einer-Jensen, K. (Intern), Lorenzen, N. (Intern)

Number of pages: 1

Publication date: 2012

**Host publication information**

Title of host publication: DAFINET Workshop: Book of abstracts

Publisher: Danish Fish Immunology Research Centre and Network

Main Research Area: Technical/natural sciences

Conference: DAFINET Workshop, Copenhagen, Denmark, 24/04/2012 - 24/04/2012

Links:

http://www.dafinet.dk/DAFINET/Abstract_books_files/DAFINET%20April%202012%20Abstracts.pdf

Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2012

**Early pathogenesis of classical swine fever virus (CSFV) strains in Danish pigs**

Host–virus interactions play an important role for the clinical outcome of classical swine fever virus (CSFV) infections in pigs. Strain virulence, host characteristics and environment are all factors that markedly influence disease severity. We tested CSFV strains of varying virulence in an experimental set-up, reducing the influence of host and environmental factors. Thus, weaner pigs were inoculated with one of 4 CSFV strains in order to compare the pathogenesis for a 3-week-period after infection. CSFV strains selected were 2 new and 2 previously characterized. None of these strains had been tested in Danish outbred pigs before.

Clinical observations grouped the infected pigs into two different categories reflecting either non-specific, mainly gastrointestinal, problems, or severe disease including high fever within the first week after inoculation. Gross-pathological findings varied between strains, however, lymphoid atrophy and growth retardation represented a consistent finding for all 4 strains. Virus distribution, viral load and in particular virus persistence differed, but supported present practice that recommends lymphoid tissue, most optimal tonsil and lymph nodes, as target material to be applied for early laboratory diagnosis.

The present study demonstrated constraints associated with early detection of infections with CSFV strains of low virulence. Since neither clinical symptoms nor pathological lesions observed with these strains constituted characteristic signs of CSF, the risk of neglecting a CSF suspicion is immediate. Therefore, topical information on new outbreaks and continuous enhancement of an efficient surveillance system is of great importance to prevent further spread of CSF within the pig population.

**General information**

State: Published

Organisations: National Veterinary Institute, Division of Virology, Sektion for Eksotiske Virussygdomme

Authors: Lohse, L. (Intern), Nielsen, J. (Intern), Uttenthal, Å. (Intern)

Pages: 327–336

Publication date: 2012

Main Research Area: Technical/natural sciences

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Journal: Veterinary Microbiology

Volume: 159

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Web of Science (2018): Indexed yes

BFI (2017): BFI-level 2

Web of Science (2017): Indexed yes

BFI (2016): BFI-level 2

Scopus rating (2016): CiteScore 2.65 SJR 1.326 SNIP 1.208

Web of Science (2016): Indexed yes
Efficacy of a glycoprotein DNA vaccine against viral haemorrhagic septicaemia (VHS) in Pacific herring, Clupea pallasii Valenciennes
Efficacy of marker vaccine candidate CP7 E2alf in piglets with maternally derived C-strain antibodies

Marker vaccines offer the possibility to differentiate classical swine fever (CSF) infected from CSF vaccinated animals based on serology and their implementation will ensure free trade with pigs. Therefore, new generations of promising marker vaccines have been developed, among them the chimeric vaccine CP7_E2alf. However, in populations previously vaccinated with live attenuated vaccines like the C-strain, passive immunity through maternal antibodies can interfere with efficacy of CP7_E2alf vaccination. Therefore, the efficacy of CP7_E2alf was examined in piglets from sows vaccinated once intramuscularly with C-strain vaccine 4 weeks before farrowing. Thus, these piglets were vaccinated intramuscularly with CP7_E2alf at the age of 5 or 8 weeks. Subsequently, the piglets and their mock-vaccinated littermate controls were challenged 2 weeks post vaccination with highly virulent Classical swine fever virus (CSFV) strain “Koslov”.
CP7_E2alf provided clinical protection upon challenge as no severe clinical signs or mortality was observed in the vaccinated piglets. Post mortem examination revealed pathological changes associated to CSFV only in the mock-vaccinated piglets. No infectious CSFV could be isolated from the tonsils of the vaccinated piglets. Two weeks after vaccination at the time of challenge, the vaccinated piglets only, had an increase in the ELISA antibody titer.

Interestingly, the maternally derived immunity in the mock-vaccinated control piglets seems to neutralize the challenge virus. Thus, the previously observed 100% mortality in naive (negative for antibodies to CSFV) piglets infected with CSFV Koslov was reduced in the control piglets of this study to 30% for challenge at the age of 7 weeks and 50% at the age of 10 weeks, respectively.

In conclusion, CP7_E2alf proved to be effective in preventing mortality, severe clinical signs and pathological lesions in 5 or 8 weeks old piglets positive for maternal antibodies derived from sows vaccinated intramuscularly 4 weeks before farrowing with one dose of C-strain vaccine.

General information
State: Published
Organisations: National Veterinary Institute, Division of Virology, Sektion for Eksotiske Virussygdomme, Centrum voor Onderzoek in Diergeneeskunde en Agrochemie, Friedrich Loeffler Institute
Authors: Rangelova, D. Y. (Intern), Nielsen, J. (Intern), Strandbygaard, B. (Intern), Koenen, F. (Ekstern), Blome, S. (Ekstern), Uttenthal, Å. (Intern)
Pages: 6376–6381
Publication date: 2012
Main Research Area: Technical/natural sciences

Publication information
Journal: Vaccine
Volume: 30
Issue number: 45
ISSN (Print): 0264-410X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.33 SJR 1.956 SNIP 1.155
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.068 SNIP 1.259 CiteScore 3.45
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.05 SNIP 1.231 CiteScore 3.57
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.73 SNIP 1.126 CiteScore 3.43
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.634 SNIP 1.159 CiteScore 3.56
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.74 SNIP 1.274 CiteScore 3.86
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.636 SNIP 1.207
Web of Science (2010): Indexed yes
EFSA Panel on Animal Health and Welfare (AHAW); Scientific Opinion on foot-and-mouth disease in Thrace: EFSA-Q-2010-01238

Following a request from the Commission, the Panel on Animal Health and Welfare was asked to deliver a Scientific Opinion on: 1) the expected prevalence (design prevalence) under different circumstances, and, 2) an updated scientific assessment of the size of the relevant geographical area for the purpose of monitoring and surveillance programmes for bluetongue. A systematic literature review and a review of monitoring and surveillance data from European Union Member States was performed in order to estimate the prevalences observed in the Member States. The prevalences observed in areas that have been infected for several years were slightly lower than the design prevalence of 2% currently used for monthly testing of sentinel animals, but much lower than the design prevalences of 20% and 10% for annual surveys in populations of unvaccinated and vaccinated ruminants, respectively. Currently there is no scientific evidence that suggests an optimal size of the relevant geographic unit for BTV monitoring and surveillance, since it depends on many factors, including the goal of the surveillance programmes. Early warning based on passive surveillance will take place irrespective of the size of the geographical unit but, when based on active surveillance, it is best targeted at regions considered at risk for introduction, using small geographical units, a high sampling frequency and sample size. For estimating the impact of interventions on the prevalence of infected animals, smaller areas result in more precise estimates of the prevalence and also take better account of local differences. For establishing freedom from infection, smaller areas result in lower design prevalence for a region as a whole and take better account of local differences in infection dynamics.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, European Food Safety Authority
Number of pages: 91
Publication date: 2012

Publication information
Publisher: European Food Safety Authority
Original language: English
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, Multimerics ApS, Upfront Chromatography A/S
Authors: Heegaard, P. M. H. (Intern), Hald, B. (Intern), Madsen, M. (Ekstern), Hoorfar, J. (Intern), Larsen, L. E. (Intern), Breum, S. Ø. (Intern), Bisgaard-Frantzen, K. (Ekstern), Bendix Hansen, M. (Ekstern), Lihme, A. (Ekstern)
Number of pages: 1
Publication date: 2012
Event: Poster session presented at International Symposium: Alternatives to antibiotics (ATA), Paris, France.
Main Research Area: Technical/natural sciences
Electronic versions:
IABS Poster2-29[1].pdf
Source: dtu
Source-ID: u::6569
Publication: 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
Authors: Larsen, G. (Intern), Holm, E. (Intern), Hjulsager, C. K. (Intern), Larsen, L. E. (Intern), Jensen, T. K. (Intern), Hansen, M. S. (Intern), Chriél, M. (Intern)
Pages: 41
Publication date: 2012
Main Research Area: Technical/natural sciences

Publication information
Journal: Dansk Veterinaertidsskrift
Volume: 2012
EURL activities in 2011

The duties of the EURL are described in Council Directive 2006/88/EC (Annex VI). The duties mainly concern fish diseases listed as exotic diseases: EHN and EUS; and fish diseases listed as non-exotic diseases: ISA, VHS, IHN, and KHV disease.

General information

State: Published
Organisations: National Veterinary Institute, Division of Poultry, Fish and Fur Animals, Section of Fish Diseases
Authors: Olesen, N. J. (Intern), Skall, H. F. (Intern), Nicolajsen, N. (Intern), Jonstrup, S. P. (Intern), Kahns, S. (Intern)
Number of pages: 1
Publication date: 2012

Host publication information
Title of host publication: 16th Annual Meeting of the National Reference Laboratories for Fish Diseases
Main Research Area: Technical/natural sciences
Conference: 16th Annual Meeting of the National Reference Laboratories for Fish Diseases, Aarhus, Denmark, 30/05/2012 - 30/05/2012
Electronic versions: 1_EURL_activities_2011.pdf
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2012

EURL Training Course 2012 and Request for Ideas for 2013

From late January to early February 17 participants from mainly European NRLs for Fish Diseases participated in an EURL training course in Aarhus, Denmark. Two modules were offered lasting from four to five days. The first module focused on “Molecular techniques for identification of listed fish diseases”, and the second module focused on “General Virology and immunochemical methods”. The content of the modules are presented as well as responses from the participants given on the evaluation scheme handed out.

As the course is set up to help you improve your laboratory skills and to harmonize the methods used we will ask you for ideas for next year’s course. So please have your ideas ready.

General information

State: Published
Organisations: National Veterinary Institute, Division of Poultry, Fish and Fur Animals, Section of Fish Diseases
Authors: Skall, H. F. (Intern)
Number of pages: 1
Publication date: 2012

Host publication information
Title of host publication: 16th Annual Meeting of the National Reference Laboratories for Fish Diseases
European freshwater VHSV genotype Ia isolates divide into two distinct subpopulations

Viral haemorrhagic septicemia (VHS), caused by the bornavirus VHSV, often leads to significant economic losses to European rainbow trout production. The virus isolates are divided into 4 distinct genotypes with additional subgroups including sublineage Ia, isolates of which are the main source of outbreaks in European rainbow trout farming. A significant portion of Danish rainbow trout farms have been considered endemically infected with VHSV since the first disease outbreak was observed in the 1950s. However, following a series of sanitary programs starting in 1965, VHSV has not been detected in Denmark since January 2009. Full-length G-genes of all Danish VHSV isolates that were submitted for diagnostic analyses in the period 2004−2009 were sequenced and analysed. All 58 Danish isolates from rainbow trout grouped with sublineage Ia isolates. Furthermore, VHSV isolates from infected Danish freshwater catchments appear to have evolved into a distinct clade within sublineage Ia, herein designated clade Ia-1, whereas trout isolates originating from other continental European countries cluster in another distinct clade, designated clade Ia-2. In addition, phylogenetic analyses indicate that VHSV Ia-1 strains have caused a few outbreaks in Germany and the UK. It is likely that viruses have been transmitted from infected site(s) out of the Danish environment, although a direct transmission pathway has not been identified. Furthermore, VHSV Ia-2 isolates seem to have been transmitted to Denmark at least once. Interestingly, one viral isolate possibly persisted in a Danish watershed for nearly 4 yr without detection whereas other subclades of VHSV isolates appear to have been eliminated, probably because of implemented eradication procedures.
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.95 SJR 0.856 SNIP 0.929
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.949 SNIP 0.935 CiteScore 1.96
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.889 SNIP 0.881 CiteScore 1.86
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.812 SNIP 0.918 CiteScore 1.77
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.912 SNIP 1.092 CiteScore 2.04
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.11 SNIP 1.165 CiteScore 2.29
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.91 SNIP 0.951
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.889 SNIP 0.99
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.859 SNIP 0.998
Scopus rating (2007): SJR 0.949 SNIP 1.054
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.868 SNIP 0.964
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.898 SNIP 1.046
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.972 SNIP 1.105
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.931 SNIP 1.187
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 1.083 SNIP 1.187
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 1.347 SNIP 1.197
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.091 SNIP 1.221
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 1.192 SNIP 1.136

Original language: English
Viral haemorrhagic septicaemia, Geographic subgroups, Molecular tracing, Genotype Ia-1, Genotype Ia-2, Epidemiology

DOIs:
10.3354/dao02444
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 Laboratories for Swine Influenza, Wellcome Trust Sanger Institute, Ghent University
Authors: Reid, S. M. (Ekstern), Simon, G. (Ekstern), Larsen, L. E. (Intern), Kellam, P. (Ekstern), Loeffen, W. (Ekstern), van Reeth, K. (Ekstern), Brown, I. H. (Ekstern)
Number of pages: 1
Publication date: 2012
Event: Abstract from 4th European Symposium of Porcine Health Management, Bruges, Belgium.
Main Research Area: Technical/natural sciences
Electronic versions:
Reid et al ESNIP 3 Abstract for European.pdf
Source: dtu
Source-ID: u::6608
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2012
Evaluation of classical swine fever virus antibody detection assays with an emphasis on the differentiation of infected from vaccinated animals

The aim of this study was to evaluate the general characteristics of commercially available enzyme-linked immunosorbent assays (ELISAs) to detect antibody against classical swine fever (CSF), as well as to assess their potential use as accompanying marker tests able to differentiate infected from vaccinated animals (DIVA). The Chekit® CSF-Sero and the HerdChek® CSFV Ab, both of which detect antibodies against the E2 protein of classical swine fever virus (CSFV), had the highest sensitivity. Both tests were practicable and showed good reproducibility. Comparable sensitivity was shown by the Chekit® CSF-Marker, an Erns ELISA. However, this test does not allow differentiation between antibodies directed against ruminant pestiviruses and those against CSFV. Therefore, it is not suitable for use with the chimeric marker vaccines tested. The PrioCHECK® CSFV Erns was the only ELISA suitable for use in DIVA with marker vaccines containing Erns proteins from ruminant pestiviruses. However, this test was less sensitive and selective than the E2-ELISAs and cannot be recommended.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, University of Veterinary Medicine, Friedrich Loeffler Institute, Central Veterinary Institute, Centrum voor Onderzoek in Diergeneeskunde en Agrochemie
Authors: Schroeder, S. (Ekstern), von Rosen, T. (Intern), Blome, S. (Ekstern), Loeffen, W. (Ekstern), Haegeman, A. (Ekstern), Koenen, F. (Ekstern), Uttenthal, Å. (Intern)
Pages: 997-1010
Publication date: 2012
Main Research Area: Technical/natural sciences

Publication information
Journal: OIE Scientific and Technical Review
Volume: 31
Issue number: 3
ISSN (Print): 0253-1933
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BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.24 SJR 0.575 SNIP 0.758
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.554 SNIP 0.759 CiteScore 1.11
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.543 SNIP 0.738 CiteScore 1.12
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.432 SNIP 0.56 CiteScore 0.99
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.521 SNIP 0.516 CiteScore 1.03
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.609 SNIP 0.617 CiteScore 1.39
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.624 SNIP 0.627
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.436 SNIP 0.629
BFI (2008): BFI-level 1
Evidence for Culicoides obsoletus group as vector for Schmallenberg virus in Denmark

Schmallenberg virus (SBV) was first identified in Germany in late 2011 by the Friedrich Loeffler Institute and has now been found in several European countries including Holland, France, Belgium, U.K. and Spain. The disease, which affects sheep, cattle and goats, was first recognized due to transient clinical symptoms including fever, diarrhea and loss of milk production. However, a more significant consequence of infection in pregnant animals is the production of severe congenital malformations in newborn animals, especially lambs. The virus is a member of the Orthobunyavirus genus within the Bunyaviridae family and is closely related to Shamonda and Akabane viruses. These viruses are transmitted by insect vectors (including biting midges (Culicoides sp.) and mosquitoes). To determine whether these insects may act as vectors for SBV, biting midges (Culicoides spp.) caught in October 2011, in the south-west of Denmark (close to the German border), were sorted into pools and tested for the presence of Schmallenberg virus RNA by RT-qPCR. From 18 pools of 5 midges from the C. obsoletus group, 2 pools were both found positive in two separate assays, targeting the L- and S- segments of the SBV RNA. However, 4 pools of C. punctatus s.str were negative. The sequence of 80bp (excluding the primer sequences) from the amplicons (ca. 145bp) was identical to that published for the expected region of the SBV L-segment. The levels of SBV RNA detected in the biting midges were much higher than could be accounted for due to the residue of a blood meal and no ruminant actin mRNA could be detected either. These results strongly suggest that SBV has replicated within specimens of the C. obsoletus group and indicates that these biting midges can act as vectors for this virus. To date (end of March), no cases of disease due to SBV have been detected in sheep, cattle or goats in Denmark.

General information
State: Published
Organisations: National Veterinary Institute, Division of Virology, Sektion for Eksotiske Virussygdomme, Division of Veterinary Diagnostics and Research, Section for Veterinary Epidemiology and public sector consultancy
Authors: Rasmussen, L. D. (Intern), Kristensen, B. (Intern), Kirkeby, C. (Intern), Rasmussen, T. B. (Intern), Belsham, G. (Intern), Bodker, R. (Intern), Bøtner, A. (Intern)
Number of pages: 1
Publication date: 2012
Event: Abstract from 6th Annual Meeting EPIZONE, Brighton, United Kingdom.
Main Research Area: Technical/natural sciences
Electronic versions:
SchmallenbergEpizone_3_.pdf
Links:
http://www.epizone-eu.net/6th-annual-meeting.aspx

Bibliographical note
Abstract accepted for an oral presentation at the "Schmallenberg virus Satellite Symposium".

Relations
Activities:
Epizone Satellite Symposium: Schmallenberg virus
Expert groups in Denmark with special reference to Classical and African swine fever

The Danish (National Veterinary) Expert group for Classical and African swine fever has been active during the last 10 years. The group is composed of experts in EU-legislation, in Danish pig production, in pig diseases and in virology. The group has participated in a national workshop on CSFV surveillance, in Contingency planning exercises and many efforts is done to keep the group updated on the current international situation for swine fevers.

The group has been very stabile and especially our participation in a Taiteix workshop in 2005 in Romania was a very good basis for our fruitful collaboration. In many later discussions our experiences then when we observed the problems in vivo.

The obligations of the expert group are both to follow the progress of eradication but definitely also to take care of some of the more time consuming discussions that could otherwise burden the Veterinary Authorities. Questions like "Could we be allowed to vaccinate the pigs in Zoo if there is an outbreak", or other things that may have a high interest in the press but which do not matter that much in the gross picture of the eradication could be handed over to the expert group.

My presentation will give examples of what we have done and how we have kept the group alive. It is my impression that the "good chemistry" of the group is very important for the success in peacetime. Should there ever be a war-time, I feel confident that "my" Expert group will be of use.

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Expression of Matrix Metalloproteinase-9 and -12 In Porcine Lung Infections

Matrix metalloproteinases (MMPs) play a variety of roles during organogenesis, in the immune response and during acute and chronic diseases as well as in tissue remodelling. During the last decade, the pig has become used increasingly as a model for human diseases; however, studies on the expression of porcine MMPs are limited. In the present study species-specific antibodies were produced to investigate the expression of MMP-9 and MMP-12 immunohistochemically in lungs from pigs infected with Actinobacillus pleuropneumoniae, Pasteurella multocida and Staphylococcus aureus. The immunolabelling of lung tissues (one infected and one control pig representing each infection) was evaluated for cellular distribution and intensity, which was scored semiquantitatively. When compared with healthy, non-infected controls, the expression of both MMP-9 and MMP-12 was higher in infected lungs. The highest expressions were seen in the alveolar epithelium (MMP-9) and alveolar macrophages (MMP-12). These results are in accordance with studies of human lungs.

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Expression of micro-RNAs and immune-relevant genes in rainbow trout (Oncorhynchus mykiss Walbaum) upon vaccination with a Viral Haemorrhagic Septicemia Virus

Development of strategies to alleviate potential disease outbreaks in sea-farmed rainbow trout (Oncorhynchus mykiss Walbaum) due to wildlife marine reservoir of Viral hemorrhagic septicemia virus (VHSV) remains imperative. A DNA vaccine expressing VHSV glycoprotein (G) gene has been developed and shown to protect fish in VHSV challenge
Expression of microRNAs and innate immune factor genes in lung tissue of pigs infected with influenza virus (H1N2)

Swine influenza is a highly infectious respiratory disease in pigs caused by influenza A virus. Activation of a frontline of pattern-recognition receptors (PRRs) expressed by epithelial cells as well as immune cells of the upper respiratory tract, leads to a potent type 1 interferon (IFN) release and simultaneous proinflammatory cytokine expression. A transient induction of cytokines is required for an efficient antiviral defence; however, an over-reactive and prolonged inflammatory response may lead to excessive infiltration of immune cells, contributing to immunopathology of the infected lung. Thus, this response must be tightly regulated. Recently, microRNA (miRNA) has been proposed to play an important role in modulating and fine tuning the innate immune response in order to avoid such harmful overreactions. Little is known about the significance of miRNA regulation in the lung during acute influenza A infection. The present work aimed of providing a better understanding of the involvement of innate immune factors including miRNA in the host response to establishment and progression of influenza virus infection. Twenty pigs were challenged by aerosol containing H1N2 (A/swine/Denmark/12687/03) influenza virus. Expression of mRNA coding for cytokines, chemokines, pattern recognition receptors and other antiviral effector molecules were quantified in lung tissue at different time points after challenge (24 h PI, 72 h PI, and 14 days PI). Likewise, microRNA in the lung tissue was quantified at the same time points. Our results demonstrate a significant regulation of several microRNAs and their targeted mRNA in the lungs of pigs during acute influenza.

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Expression of microRNAs and innate immune factor genes in lung tissue of pigs infected with influenza virus (H1N2)
First Detection of Hirame Rhabdovirus (HIRRV) in Europe

Introduction

Hirame rhabdovirus (HIRRV) is one of the four recognized species within the Novirhabdovirus genus, represented by the type species Infectious Haematopoietic Necrosis (IHNV). HIRRV was first isolated during an outbreak on cultured flounder (Paralichthys olivaceus) and ayu (Plecoglossus altivelis) in Japan (1). It was also found on other marine fish in Asia, such as stone flounder (Kareius bicoloratus) in China (2). Furthermore, it was shown to be pathogenic for a range of salmonids species, including rainbow trout, experimentally challenged in freshwater. The major clinical signs of HIRRV infection were congestion of the gonads, focal hemorrhages of the skeletal muscle and fins and ascitic fluid collection (3).

We report the first description of HIRRV in Europe, isolated from grayling and brown trout in a farm in Poland.

Materials & methods

Thirty adult graylings (Thymallus thymallus) with clinical signs and thirty asymptomatic adult brown trouts (Salmo trutta m. fario) from the same farm in Poland were tested for the presence of novirhabdoviruses by cell culture. Pools of kidney and spleen from a maximum of 10 fish were homogenized. For virus propagation, epithelioma papulosum cyprini (EPC), fathead minnow (FHM), rainbow trout gonad (RTG) and bluegill fry (BF-2) cell lines were inoculated and incubated at 15°C. Cell cultures were collected for virus identification when cytopathic effect (CPE) appeared, usually 4 to 7 d later. Starting from RNA extracted from cell culture supernatant, a random-priming sequence-independent single primer amplification (SISPA) was adopted to search for viral sequences (4). PCR products were cloned and sequenced according to the Sanger method.

Transmission studies were carried out on rainbow trout (Oncorhynchus mykiss) fry and grayling fry. Virus was propagated in EPC cells and a harvested at maximum CPE, about 4-5 days post inoculation (dpi). Experimental fish were kept in 10 l aquaria supplied with freshwater, the temperature was maintained at 10 or 12°C.

Results

After inoculation on various cell lines, the homogenates from graylings induced a strong cytopathic effect (CPE) after 72 hours, suggesting the presence of a virus.

The virus isolated in cell culture induced mortalities on experimentally infected graylings, reaching 10-25% after 21 days. In moribund graylings, light petechiae and congestions in rump muscles and also in internal organs were observed. Although some antigenic similarities with perch rhabdovirus (PRhV) were observed, RT-PCR with several sets of generic primers amplifying all fish vesiculoi-like viruses, gave consistently negative results. Therefore, we used a sequence independent single primer amplification (SISPA) strategy to obtain and identify viral genomic fragments with similarities to other viruses in GenBank. Surprisingly, of the 60 clones sequenced, two of them showed high sequence similarities (>99%) with either the L gene or the N gene of HIRRV, a viral species that had been reported only in Japan, China and Korea till now. By amplifying specifically the P gene, we observed that the virus exhibited a higher identity with the Chinese strain compared to the Korean, suggesting that the virus was imported from China, maybe in frozen food. A specific qPCR was developed and used to demonstrate that the same virus was also present in cell culture inoculated with brown trouts extracts from the same farm.

Discussion & conclusions

This study identified for the first time the presence of HIRRV in grayling and brown trouts in a farm in fresh water in Europe. The European isolate was highly similar to two other Asiatic strains, from Korean and China. Meanwhile, the sequence of the P gene revealed a stronger similarity with the Chinese strain, which would be consistent with the hypothesis of the introduction of the virus via frozen food imported from China and used in the farm. This finding raises concerns about the spread of this virus out of Asiatic countries and its potential emergence in freshwater conditions. Any symptom was visible on the graylings and brown trouts from the affected farm, suggesting a latent infection. However, the virus, once produced in cell culture, provoked mortalities during an infectious challenge on graylings and rainbow trouts. The conditions of virulence should be further investigated to estimate the epizootic risks in Europe on grayling and other freshwater fish. It must be mentioned that at the same period of viral isolation, a massive mortality occurred on wild grayling in a river in the same region. Although no samples could be analyzed at that time, the possibility of an HIRRV outbreak is hypothesized. We now have the specific diagnostic tools for routine surveillance and investigation of any other mortality event.
Fish Farm Inspections and Sampling Procedures: The Mediterranean Point of View

Marine Mediterranean aquaculture meant as intensive rearing system for zootechnical production has known a recent development extremely fast. The development of efficacious breeding protocols, the availability of artificial feeding more and more efficient and some principles adopted in facing diseases have lead the growth of an industrial rearing system.

If we consider the health management approach within the context of this complex productive scenario there is the need to discriminate between, at least, two main different groups of farms that are extremely different and characterised by peculiar health/disease management issues.

First of all there are to be considered the hatcheries, this kind of farm are characterised by having an extremely high level of technology and control of the water that; in these system biosecurity measures are generally high and the water quality parameters are kept monitored constantly.

Secondly there are to be considered all the farms that undergo to the category of "ongrowing". These kind of rearing activities, once obtained the seed / juveniles provide them feeding till the juveniles have reached the market size. Within this group sea cages have affirmed as the best ones both for economical and technological/environmental aspects.

Sanitary issues to be managed, their evolution, related control strategies and analytical tools are, in this complex, quite different but all are linked to a common data: they are part of a framework that need to be considered firstly.

In this presentation, mainly based on pictures, different aspects of clinical inspection/sampling protocols are described.

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.
Health Categorisation of Fish Farms in Europe In 2011
The Questionnaire on Surveillance and Diagnosis (S&D) included questions on how fish farms are health categorised according to Council Directive 2006/88/EC in the respective countries. More than half of the authorised farms in Europe are in category III for VHS and IHN and the remaining in category I or II. According to these official data almost no farms are infected with either of these diseases. This might be more due to a significant underreporting than of the de facto situation. For KHV most carp farms are in category III, unknown status. Many farms in Europe are not categorised yet, and unfortunately the situation have not improved much from 2010. In the questionnaire we ask for the number of APBs in these areas. There are several different views on how categorisation shall be performed, e.g. should VHS free marine rainbow trout farms be placed in Category III or I? If Isavirus HPR0 is found in or in proximity of a farm can it remain its Category I status? Some Member states do not include registered APBs in the categorisation but according to 2006/88/EC Annex III health categorisation comprise Member states, zone and compartments NOT single APBs. A new Animal Health Law is under preparation and revision and will now include aquatic animals; in this connection the categorisation system might be simplified and be made more transparent.

Humane End Points – Danish considerations

Inactivation of VHSV by Percolation and Salt Under Experimental Conditions
At the moment the only legal method in Denmark to sanitize wastewater from fish cutting plants is by percolation. To evaluate the inactivation effect of percolation on VHSV an experimental examination was initiated. A column packed with...
gravel as top- and bottom layer (total of 22 cm) and a mid layer consisting of dug sand (76 cm) was used for the trial. Over a period of 18 h 3.9 x 10^10 TCID50 VHSV was supplied to the column, where after normal tap water was supplied for the rest of the trial period, in total 7 days. During the 7 days samples for virological examination was taken. The sampling was most intensive in the period where the risk of VHSV breaking through the column was highest. The sensitivity of the virological examination was 13.9 TCID50/ml and no virus was isolated. A reduction of VHSV > 4 log in the outlet water was seen. This experiment suggests that percolation can be a valuable method to sanitize VHSV infected water. Changes in temperature, pH, earth types in the area used for percolation etc. may change the virus reduction, though.

As some of the fish cutting plants are also smoking rainbow trout fillets, the question arose whether a brine solution will inactivate VHSV. In order to answer this question a small trial was set up. VHSV and NaCl was added to cell culture medium with 10% foetal bovine serum, in order to mimic a “dirty” environment, to obtain from 1.9% to 20.9% NaCl and kept in the dark at 4°C. Samples were titrated after 5 min, 1 h and 20 h. No reduction in titer was observed in any of the samples.

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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.

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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 immunohistochemistry (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. EuroPRRS2012 Budapest, Hungary ISH showed better sensitivity than IHC while there was an obvious discrepancy between sensitivity among the probes.

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Inter-Species Transmission of Viral Haemorrhagic Septicaemia Virus Between Turbot (Scophthalmus Maximus) and Rainbow Trout (Onchorhynchus Mykiss)
Viral haemorrhagic septicaemia is a serious viral disease of teleost fish with high economic impact on the aquaculture industry. The disease is caused by the viral haemorrhagic septicaemia virus (VHSV), an RNA virus belonging to the family Rhabdoviridae. Compared to other rhabdoviruses infecting fish, VHSV has an exceptional wide host range of more than 70 species across marine and aquatic environments. To establish such a wide host range host-specific adaptation would be disadvantageous, nevertheless, host-specific differences in pathogenicity have been observed for VHSV. The divergence in pathogenicity, however, is not fully resembled in the phylogeny, which indicates a correlation between geographic regions rather than host species. The objective of this study was to identify whether VHSV has the ability to transmit between different host species or whether viral transmission is restricted to one host species through host-specific adaptation. To investigate the existence of inter-species transmission and host-specificity a cohabitation challenge between turbot and rainbow trout was conducted with turbot as donor- and rainbow trout as recipient host species. Turbot were ip challenged with a turbot- or a rainbow trout adapted VHSV isolate and subsequently grouped with naïve rainbow trout. Mortality and viral shed was monitored daily. Both virus isolates showed signs of host-specific adaptation based on differences in replication dynamics, viral production, and virulence. Host-specific adaptation, however, did not result in total restriction of inter-species transmission. Despite of host-specific adaptation, the rainbow trout adapted VHSV isolate was able to cause disease in turbot resulting in subsequent infection of cohabiting rainbow trout, thus indicating the existence of inter-species transmission of VHSV between turbot and rainbow trout.

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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.
In vivo screening of modified siRNAs for non-specific antiviral effect in a small fish model: number and localization in the strands are important

Small interfering RNAs (siRNAs) are promising new active compounds in gene medicine but the induction of non-specific immune responses following their delivery continues to be a serious problem. With the purpose of avoiding such effects chemically modified siRNAs are tested in screening assay but often only examining the expression of specific immunologically relevant genes in selected cell populations typically blood cells from treated animals or humans. Assays using a relevant physiological state in biological models as read-out are not common. Here we use a fish model where the innate antiviral effect of siRNAs is functionally monitored as reduced mortality in challenge studies involving an interferon sensitive virus. Modifications with locked nucleic acid (LNA), altritol nucleic acid (ANA) and hexitol nucleic acid (HNA) reduced the antiviral protection in this model indicative of altered immunogenicity. For LNA modified siRNAs, the number and localization of modifications in the single strands was found to be important and a correlation between antiviral protection and the thermal stability of siRNAs was found. The previously published sisiRNA will in some sequences, but not all, increase the antiviral effect of siRNAs. The applied fish model represents a potent tool for conducting fast but statistically and scientifically relevant evaluations of chemically optimized siRNAs with respect to non-specific antiviral effects in vivo.
Kinetics of single and dual infection of calves with an Asian atypical bovine pestivirus and a highly virulent strain of bovine viral diarrhoea virus 1

Atypical bovine pestiviruses related to bovine viral diarrhoea virus (BVDV) have recently been detected in cattle from South America, Asia and Europe. The purpose of this study was to compare the clinical and virological aspects of dual infection with BVDV-1 (Horton 916) and an Asian atypical bovine pestivirus (Th/04_KhonKaen) in naïve calves, in comparison to single infections. Milder clinical signs were observed in the animals infected with single Th/04_KhonKaen strain. Leukocytopenia and lymphocytopenia were observed in all infected groups at a similar level which correlated with the onset of viraemia. Co-infection with both viruses led to prolonged fever in comparison to singlestrain inoculated groups and simultaneous replication of concurrent viruses in blood and in the upper respiratory tract. Following the infections all the calves seroconverted against homologous strains. Atypical pestiviruses pose a serious threat to livestock health and BVDV eradication, since they may have the potential to be widely spread in cattle populations without being detected and differentiated from other BVDV infections.
Modulation of Cytokine mRNA Expression in Pharyngeal Epithelial Samples obtained from Cattle Infected with Foot-and-Mouth Disease Virus

A novel technique of endoscopical collection of small tissue samples was used to obtain sequential tissue samples from the dorsal soft palate (DSP) of individual cattle infected with foot-and-mouth disease virus (FMDV) at different phases of the infection. Levels of mRNA encoding interferon (IFN)-a and IFN-b as well as tumour necrosis factor (TNF)-a were measured in these samples by quantitative reverse transcriptase polymerase chain reaction. Expression of IFN-b mRNA was significantly down-regulated in the biopsy samples harvested during the acute phase of infection, while there was no statistically significant effect on the expression of IFN-a mRNA compared with baseline levels. In contrast, the mRNA encoding TNF-a was significantly up-regulated in samples collected during both acute and late (>28 days post infection) phases of infection. There were also significantly higher levels of TNF-a mRNA expressed in samples derived from animals that were identified subsequently as persistently infected FMDV-carriers. It was concluded that there was a significant difference in the host-response in the DSP of calves that were identified as persistently infected, subclinical carriers of FMDV.

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Modulation of Translation Initiation Efficiency in Classical Swine Fever Virus

Modulation of translation initiation efficiency on classical swine fever virus (CSFV) RNA can be achieved by targeted mutations within the internal ribosome entry site (IRES). In this study, cDNAs corresponding to the wild type (wt) or mutant forms of the IRES of CSFV strain Paderborn were amplified and inserted into dicistronic reporter plasmids encoding Fluc and Rluc under the control of a T7 promoter. The mutations were within domains II, IIId1 and IIIf of the IRES. The plasmids were transfected into BHK cells infected with the recombinant vaccinia virus, vTF7-3, which expresses the T7 RNA polymerase. IRES mutants with different levels of IRES activity were identified and then introduced by homologous recombination into bacterial artificial chromosomes (BACs), containing CSFV Paderborn cDNA downstream of a T7 promoter. From the wt and mutant BACs, full-length CSFV RNA transcripts were produced in vitro and electroporated into porcine PK15 cells. Rescued mutant viruses were obtained from RNAs that contained mutations within domain IIIf which retained more than 75% of wt translation efficiency. Sequencing of cDNA generated from these rescued viruses verified the maintenance of the introduced changes within the IRES. The growth characteristics of each rescued mutant virus were compared to that of the wt virus. It was shown that viable mutant viruses with reduced translation initiation efficiency can be designed and generated and that viruses containing mutations within domain IIIf of the IRES have reduced growth in cell culture compared to the wt virus.

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Scopus rating (2011): SJR 3.399 SNIP 1.288 CiteScore 5.37
ISI indexed (2011): ISI indexed yes
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Scopus rating (2010): SJR 3.532 SNIP 1.278
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Scopus rating (2009): SJR 3.595 SNIP 1.307
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Scopus rating (2008): SJR 3.803 SNIP 1.264
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Web of Science (2000): Indexed yes
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Molecular Tracing of Viral Pathogen in Aquaculture (MOLTRAQ): a new EMIDA project

Here we present a new research-project funded under the EMIDA-ERA Net under the EU 7th Framework program (For more details about EMIDA: www.emida-era.net).

The purpose of the project is to increase knowledge on transmission, prevention and control of viral diseases in aquaculture and develop a generic approach to viral disease control by using information on epidemiological and phylogenetic attributes from several important aquatic animal viruses.

The project will i) generate and use spatio-temporal epidemiological data, phylogeographic data and gene expression data for important host-viral pathogen systems to identify important factors affecting the spread of diseases in aquaculture, and ii) integrate these in scenario simulation models to assess effects of various control strategies for selected host-pathogen systems.


Partners into the project are: Norwegian Veterinary Institute (NO, Coordinator), Technical University of Denmark-National Veterinary Institute (DK), Agence Nationale de Sécurité Sanitaire (FR), Friedrich-Loeffler Institut (DE), Institut Francais de Recherche pour l’Exploitation de la Mer (FR), Institut de Recherche pour le Développement (FR) and Norwegian Computing Center (NO).

The project began on April 1st, 2012, and will run until March 31st, 2015. The total budget is 1.9€, of which 1.4€ is funded via the EMIDA-ERA Net.

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Organisations: National Veterinary Institute, Division of Poultry, Fish and Fur Animals, Section of Fish Diseases, National Veterinary Institute, Norwegian Computing Center, IRD, Friedrich Loeffler Institute, Agence nationale de la sécurité sanitaire, alimentation, environnement et travail, IFREMER
Authors: Jensen, B. B. (Ekstern), Aldrin, M. (Ekstern), Avarre, M. C. (Ekstern), Bergmann, S. M. (Ekstern), Bigarre, L. (Ekstern), Brun, E. (Ekstern), Jansen, P. A. (Ekstern), Olesen, N. J. (Intern), Renault, T. (Ekstern), Schuetze, H. (Ekstern)
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Monitoring the determinants of efficient viral replication using Classical Swine Fever Virus-reporter replicons

Classical swine fever virus (CSFV) is the etiological agent of the severe porcine disease, classical swine fever. Unraveling the molecular determinants of efficient replication is crucial for gaining improved knowledge of the pathogenic features of this virus. Monitoring the replication competence of the CSFV genome within cells can be achieved using autonomously replicating constructs (replicons) containing a reporter gene that expresses a readily quantifiable enzyme.

Here, a newly implemented cloning technique was applied to genome modification of the fulllength CSFV cDNA previously inserted into a single-copy bacterial artificial chromosome (BAC). This technique, the Red/ET counter-selection method, is based upon homologous recombination, thus obviating the need for internal restriction sites or complex cloning strategies. Several CSFV replicons with deletions in regions encoding virus structural proteins considered non-essential for RNA replication were constructed and these deletions were replaced with an in-frame insertion of the Renilla luciferase (Rluc) sequence. RNA transcripts from these replicons should be translated as a single functional open reading frame. Full-genome cDNAs (~10-12,3 kb) were amplified from the BACS using a stable long-PCR method and in vitro transcripts were assayed in permissive cells. The CSFV-Rluc replicons were evaluated for their ability to replicate using immunofluorescence staining (-NS3 and -E2), and the Renilla luciferase assay.

We conclude that Rluc expression is an efficient way of monitoring replication of these constructs.

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Organisations: National Veterinary Institute, Division of Virology, Sektion for Eksotiske Virussygdomme, Animal Health and Veterinary Laboratories Agency
Authors: Risager, P. C. (Intern), Everett, H. (Ekstern), Crooke, H. (Ekstern), Belsham, G. (Intern), Rasmussen, T. B. (Intern)
Number of pages: 1
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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.
Next Generation Sequencing of Classical Swine Fever Virus and Border Disease virus cloned in Bacterial Artificial Chromosomes

Next generation sequencing is a powerful tool for complete sequencing of large amounts of DNA. We have recently cloned full genome cDNA copies (obtained by long-range RT-PCR) of entire genomes of classical swine fever virus (CSFV) strain Koslov and Border disease virus strain Gifhorn into bacterial artificial chromosomes (BACs). From these BACs, RNA copies of the viral genomes can be transcribed in vitro and upon transfection of these RNAs into mammalian cells, autonomous replication of the viral genome occurs and infectious progeny can be rescued. However, we have observed that virus progeny can be rescued only from some of our BAC constructs whereas others are not replication competent. To further analyze this discrepancy we have completely sequenced selected pestivirus BAC DNAs using a 454 Genome Sequencer FLX to evaluate the number/kind of deviations in the cloned genome sequences. In addition, we have sequenced the full genome cDNA fragments used for the BACs by the same approach. This enables us to evaluate in more detail the nature of nucleotide changes in the pestivirus BACs that lead to lack of replicationcompetence and/or virus rescue. Additionally, detailed knowledge of the genomic sequence can aid the attempts to create new infectious BAC clones. The quality and the depth of the sequence data will be carefully analyzed, compared and presented.

Oral transmission as a route of infection for viral haemorrhagic septicaemia virus in rainbow trout, Oncorhynchus mykiss (Walbaum)

Surveys among wild marine fish have revealed occurrence of viral haemorrhagic septicaemia virus (VHSV) infections in a high number of diverse fish species. In marine aquaculture of rainbow trout, preying on invading wild fish might thus be a risk factor for introduction and adaptation of VHSV and subsequent disease outbreaks. Our objective was to determine whether an oral transmission route for VHSV in rainbow trout exists. Juvenile trout were infected through oral, waterborne and cohabitation transmission routes, using a recombinant virus strain harbouring Renilla luciferase as reporter gene. Viral replication in stomach and kidney tissue was detected through bioluminescence activity of luciferase and qRT-PCR.

Replication was detected in both tissues, irrespective of transmission route. Replication patterns, however, differed among transmission routes. In trout infected through oral transmission, replication was detected in the stomach prior to kidney tissue. In trout infected through waterborne or cohabitation transmission, replication was detected in kidney prior to stomach or in both tissues simultaneously. We demonstrate the existence of an oral transmission route for VHSV in rainbow trout. This implies that preying on invading infected wild fish is a risk factor for introduction of VHSV into marine cultures of rainbow trout.
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.

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Source: dtu
Source-ID: u::6611
Publication: 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.

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Outcome of EPIZONE Extension ON VER/VNN: Pathogenicity study of 10 betanodavirus strains with an in vivo challenge in European sea bass (Dicentrarchus labrax)

Viral encephalopathy and retinopathy (VER) otherwise known as viral nervous necrosis (VNN) is a severe pathological condition, caused by small RNA viruses belonging to the Nodaviridae family, genus Betanodavirus. The disease, which has been described in more than 45 fish species worldwide, is considered the most serious viral threat affecting marine farmed species in the Mediterranean region, thus representing one of the bottlenecks for further development of aquaculture industry.

Epidemiological investigations carried out in different geographical areas demonstrated that Betanodavirus can be detected in wild fish as well as other aquatic organisms (artemia, rotifers, molluscs and crustaceans) in addition to farmed fish.

The RGNNV genotype is the most widespread in the Mediterranean region, nevertheless some strains, characterized by containing genetic material belonging to both the RGNNV and the SJNNV genotypes in their genome, have been identified too. The existence and the spread of these genetically different viral agents that share inter-genotype genetic material could be one of the major causes that characterize the differences in mortality observed in the field.

In order to contribute to a better understanding of the pathogenicity of circulating viruses, ten selected VER/VNN strains differing for origin and/or genotype were tested “in vivo” by challenging sea bass juveniles in infection trials. The infection was performed under controlled conditions and all the infected groups were monitored for 68 days after infection. The results clearly confirmed the pathogenicity, to different degrees, of all the selected strains, including one strain belonging to SJNNV genotype and four reassortant strains from SJNNV and RGNNV genotypes and underlined the potential risk represented by sea bream and other apparently resistant species in the transmission of the disease to other highly susceptible species.

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Organisations: National Veterinary Institute, Division of Poultry, Fish and Fur Animals, Section of Fish Diseases, Instituto Zooprofilattico Sperimentale delle Venezie
Authors: Vendramin, N. (Intern), Toffan, A. (Ekstern), Cappellozza, E. (Ekstern), Mancin, M. (Ekstern), Bovo, G. (Ekstern)
Number of pages: 1
Publication date: 2012
disadvantages depending on the method and the viral isolates.

Conclusions

Both sets of the nodavirus probes proved to be useful for detection of betanodaviruses in each lab's usual conditions. Ideally, both RNA should be targeted for samples exhibiting high Ct values (for instance in healthy carriers) to confirm the presence of low loads of virus.
Overview of the Disease Situation and Surveillance in Europe In 2011

The Questionnaire on Surveillance and Diagnosis (S&D) which is collated annually is the only comprehensive overview of the disease situation in aquaculture in Europe. The information has been made available on the EURL web site (www.eurl-fish.eu), where all raw data can be obtained. The S&D have evolved over the years, for 2011 it comprise 4 parts:

2. Epidemiological data on the disease situation in each Member State with focus on the listed diseases but also including other diseases of interest.
3. Laboratory data from the NRLs and other laboratories, including number of samples examined, diagnoses of fish diseases made.
4. Status on implementation of the new fish health surveillance legislation.

A new part was included for 2011 as a deliverable for the EFSA project CFP/EFSA/AHAW/2011/03: Risk categorisation for Aquatic Animal Health Surveillance:

The data on the European aquaculture production were obtained from the FIGIS database. Unfortunately this database does not include information on the number and size of fish farms, which are epidemiologically important data. The production in 2010 is almost the same as in 2009 and has for the sixth time in row raised from the previous year and has now passed 2 million ton (Figur 1) Data from 2011 is not yet available. The farm sizes vary a lot between countries, e.g. the majority of farms in Germany produced < 5 tonnes, and for Spain the number of farms producing < 5 tonnes, 5-100 tonnes and > 100 tonnes is nearly equal.

The Atlantic salmon production has increased significantly while the rainbow trout production slightly decreased in Europe in 2010. The carp production is still mainly in the Eastern part of Continental Europe and at the same level as the year before. The production of sea bream decreased while the sea bass production increased in the Mediterranean countries. Among other fish species of interest are pike-perch (472t), eel (6845t), sturgeon (3545t), cod (22558t), turbot (8348t), and halibut (1821t). Unfortunately none of these species have observed the foreseen significant increase in production.

Data on the health categorisation of fish farms will be given in a later presentation.

Concerning the epidemiological data, obviously, there is still a severe underreporting of VHS and IHN in many countries. For VHS the infection status in only known for 33% of the farms, for IHN the situation is known in 37% of the farms. While for KHV the disease situation is unknown on 954% of the farms! For farms producing Atlantic salmon and categorised for ISA, the infection status for ISA is known for 49% of the farms. The findings of Isavirus HPR0 pose some problems regarding the health categorisation of salmon farms.

Many countries have surveillance programmes for SVC (16 of 35 countries), BKD (14 of 35 countries), IPN (18 of 35 countries) and Gyrodactylus salaries (8 of 35 countries), for which they are seeking “additional guaranties” according to §42 in CD 2006/88/EC. The number of farms in the programmes varies from very few farms to many farms.

There are very large differences between countries on how many samples are tested on cell cultures, ranging from < 100 to several thousands. PCR is coming up in many countries, and the large number of PCR-tests conducted in some countries mostly reflects the KHV and ISA testing.

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Organisations: National Veterinary Institute, Division of Poultry, Fish and Fur Animals, Section of Fish Diseases
Authors: Olesen, N. J. (Intern), Nicolajsen, N. (Intern)
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Påvisning af afrikansk svinepest på tørrede blodprøver

General information
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Organisations: National Veterinary Institute, Section for Virology
Authors: Uttenthal, Å. (Intern)
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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 herds. In Denmark oral fluid has been used for detection of PCV2 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 assay.

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.
Picornaviruses
Diseases of Swine, Tenth Edition is a fully revised and updated version of this indispensable reference for detailed and comprehensive information on diseases in the pig. Now published in association with the American Association of Swine Veterinarians, this new edition adds new knowledge throughout in a more consistent, reorganized format for more intuitive access to information, with new chapters on the cardiovascular system, food safety and zoonotic diseases, and performing clinical trials. Diseases of Swine remains an essential resource on swine production, health, and management for swine practitioners at all levels, including students, swine veterinarians, and researchers.

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 Circovirus 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.
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.

Reconstruction of the Transmission History of RNA Virus Outbreaks Using Full Genome Sequences: Foot-and-Mouth Disease Virus in Bulgaria in 2011

Improvements to sequencing protocols and the development of computational phylogenetics have opened up opportunities to study the rapid evolution of RNA viruses in real time. In practical terms, these results can be combined with field data in order to reconstruct spatiotemporal scenarios that describe the origin and transmission pathways of viruses during an epidemic. In the case of notifiable diseases, such as foot-and-mouth disease (FMD), these analyses provide important insights into the epidemiology of field outbreaks that can support disease control programmes. This study reconstructs the origin and transmission history of the FMD outbreaks which occurred during 2011 in Burgas Province, Bulgaria, a country that had been previously FMD-free-without-vaccination since 1996. Nineteen full genome sequences (FGS) of FMD virus (FMDV) were generated and analysed, including eight representative viruses from all of the virus-positive outbreaks of the disease in the country and 11 closely-related contemporary viruses from countries in the region where FMD is endemic (Turkey and Israel). All Bulgarian sequences shared a single putative common ancestor which was closely related to the index case identified in wild boar. The closest relative from outside of Bulgaria was a FMDV collected during 2010 in Bursa (Anatolia, Turkey). Within Bulgaria, two discrete genetic clusters were detected that corresponded to two episodes of outbreaks that occurred during January and March-April 2011. The number of nucleotide substitutions that were present between, and within, these separate clusters provided evidence that undetected FMDV infection had occurred. These conclusions are supported by laboratory data that subsequently identified three additional FMDV-infected livestock premises by serosurveillance, as well as a number of antibody positive wild boar on both sides of the border with Turkish Thrace. This study highlights how FGS analysis can be used as an effective on-the-spot tool to...
support and help direct epidemiological investigations of field outbreaks.

**General information**

*State:* Published

*Organisations:* National Veterinary Institute, Section for Virology, The Pirbright Institute, National Diagnostic and Research Veterinary Medical Institute, Bulgarian Food Safety Agency, Foot and Mouth Disease Institute, Food and Agriculture Organization of the United Nations

*Authors:* Valdazo-González, B. (Ekstern), Polihronova, L. (Ekstern), Alexandrov, T. (Ekstern), Normann, P. (Intern), Knowles, N. J. (Ekstern), Hammond, J. M. (Ekstern), Georgiev, G. K. (Ekstern), Ozyörük, F. (Ekstern), Sumption, K. J. (Ekstern), Belsham, G. (Intern), King, D. P. (Ekstern)

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- Web of Science (2014): Indexed yes
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- BFI (2009): BFI-level 1
- Scopus rating (2009): SJR 2.473 SNIP 0.985
- Web of Science (2009): Indexed yes
- BFI (2008): BFI-level 1
- Scopus rating (2008): SJR 2.323 SNIP 0.96
- Web of Science (2008): Indexed yes
- Scopus rating (2007): SJR 1.289 SNIP 0.525
- Web of Science (2006): Indexed yes

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Results of the Proficiency Test, PT1 and PT2, 2011
A comparative test of diagnostic procedures was provided by the EU Reference Laboratory (EURL) for Fish Diseases to 41 National Reference Laboratories (NRLs) in the start of middle of October 2011. The test was prepared and tested according to protocols accredited by DANAK under registration number 515 to proficiency testing according to the quality assurance standard DS/EN ISO/IEC 17043. The test consisted of 2 tests: PT1 and PT2.

Scheffersomyces stipitis: a comparative systems biology study with the Crabtree positive yeast Saccharomyces cerevisiae
Background: Scheffersomyces stipitis is a Crabtree negative yeast, commonly known for its capacity to ferment pentose sugars. Differently from Crabtree positive yeasts such as Saccharomyces cerevisiae, the onset of fermentation in S. stipitis is not dependent on the sugar concentration, but is regulated by a decrease in oxygen levels. Even though S. stipitis has been extensively studied due to its potential application in pentoses fermentation, a limited amount of information is available about its metabolism during aerobic growth on glucose. Here, we provide a systems biology based comparison between the two yeasts, uncovering the metabolism of S. stipitis during aerobic growth on glucose under batch and chemostat cultivations. Results: Starting from the analysis of physiological data, we confirmed through C-13-based flux analysis the fully respiratory metabolism of S. stipitis when growing both under glucose limited or glucose excess conditions. The patterns observed showed similarity to the fully respiratory metabolism observed for S. cerevisiae under chemostat cultivations however, intracellular metabolome analysis uncovered the presence of several differences in metabolite patterns. To describe gene expression levels under the two conditions, we performed RNA sequencing and the results were used to quantify transcript abundances of genes from the central carbon metabolism and compared with those obtained with S. cerevisiae. Interestingly, genes involved in central pathways showed different patterns of expression, suggesting different regulatory networks between the two yeasts. Efforts were focused on identifying shared and unique families of transcription factors between the two yeasts through in silico transcription factors analysis, suggesting a different regulation of glycolytic and glucoenogenic pathways. Conclusions: The work presented addresses the impact of high-throughput methods in describing and comparing the physiology of Crabtree positive and Crabtree negative yeasts. Based on physiological data and flux analysis we identified the presence of one metabolic condition for S. stipitis under aerobic batch and chemostat cultivations. Through metabolome analysis and genome-wide transcriptomic analysis several differences were identified. Interestingly, in silico analysis of transcription factors was useful to address a different regulation of mRNAs of genes involved in the central carbon metabolism. To our knowledge, this is the first time that the metabolism of S. stipitis is investigated in details and is compared to S. cerevisiae. Our study provides useful results and allows for the possibility to incorporate these data into recently developed genome-scaled metabolic, thus contributing to improve future industrial applications of S. stipitis as cell factory.
BIOTECHNOLOGY, PICHIA-STIPITIS, RNA-SEQ, FERMENTATIVE GROWTH, METABOLIC FLUXES, GENE-EXPRESSION, STATE ANALYSIS, IDENTIFICATION, TRANSCRIPTION, RESPIRATION, GLUCOSE
"Schmallenberg" virus: Analysis of the Epidemiological Data and Assessment of Impact: EFSA-Q-2012-00305

This scientific report provides an overall assessment of the impact of the infection on animal health, animal production and animal welfare of the provisionally named "Schmallenberg" virus (SBV) first detected in Germany. In Europe, 3745 holdings have been reported with SBV cases confirmed by laboratory testing across several Member States, mid May 2012. EFSA reviewed the epidemiological reports noting that SBV has been detected in cattle, sheep, goats and a bison. SBV antibodies have been detected in deer and no other species are known to be affected. EFSA also confirms that new studies support the initial assessment undertaken by the European Center for Disease Control and Prevention, that it is very unlikely that SBV poses a risk to humans. In terms of transmission routes, recent entomological investigations have identified SBV in field samples of biting midges of the Culicoides obsoletus group. Currently there is no evidence of any other route of transmission other than transplacental or vector borne routes. EFSA coordinated the collation of SBV epidemiological data during 2011-2012 in order to obtain comparable data for Europe. The maximum proportion of reported sheep holdings with SBV confirmed was 4% per country and 7.6% per region while for cattle less than 1.3 % of holdings were reported as SBV confirmed at both country and regional level. In order to assess the impact of SBV(spatial and temporal spread, proportion of affected holding and potential projection of arthrogryposis hydranencephaly syndrome cases) three models were used. In regions with SBV confirmed holdings, assuming a high prevalence of infection and post infection immunity, impact in the 2012-2013 calving and lambing season should be low. However, assuming SBV survived the winter of 2011, the models suggest that in unaffected regions with suitable temperatures for within herd transmission by vectors and high density of susceptible species (cattle and sheep) SBV infection is likely to spread. EFSA puts forward a number of recommendations to fill the knowledge gaps, these include but are not limited to: continuing serological investigations in affected regions and regions neighbouring affected areas, within herd and animal level impact investigation, monitoring putative vector population, setting SBV host vector transmission parameters, investigating other routes of transmission, host susceptibility, virulence and vulnerable period during gestation. Furthermore, the possible origins of the virus should be investigated as more information becomes available on the virus characteristics and infection epidemiology.

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Schmallenberg virus – et nyt virus hos drøvtyggere: Forekomst, spredning, klinik og diagnostik

General information
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Serotype identification and VP1 coding sequence analysis of foot-and-mouth disease virus from outbreaks in Eastern and Northern Uganda in 2008/9

In April 2008, foot-and-mouth disease (FMD) outbreaks were reported in Kamuli district of the eastern region of Uganda. Soon after lifting the quarantines in this area, further FMD outbreaks were reported in northern Uganda, which spread to more than 10 districts. The aim of this study was to identify the serotype and compare the variable protein (VP)1 coding sequences of the viruses responsible for FMD outbreaks during 2008 and 2009, to trace the transmission pathways of the disease in Uganda. Probang and epithelial swab samples were collected from cattle with clinical signs of FMD in the two regions, and the presence of FMDV RNA in these samples was determined using a standard diagnostic RT-PCR assay. From the total of 27 positive samples, the VP1 coding region was amplified and sequenced. Each of these sequences showed >99% identity to each other, and just five distinct sequences were identified. BLAST searches and phylogenetic
analysis of the complete variable protein (VP)1 coding sequences revealed that they belonged to serotype O, topotype EA-2. The close similarity between the virus sequences suggested introduction from a single source. We therefore conclude that FMD in the northern region of Uganda was most likely introduced from the outbreak in the eastern region across Lake Kyoga through movement of live animals. This has significant implications for the effectiveness of the current FMD control measures.
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.
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.

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.

**General information**

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Suspected zoonotic transmission of rotavirus group A in Danish adults

Group A rotviruses 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 diarrheoa, 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.
The efficacy of CP7_E2alf: an animal study involving piglets from C-strain vaccinated sows

Outbreaks of Classical Swine Fever (CSF) in the European Union have caused enormous economical losses. To facilitate the possibility of free trade with pigs and their products, a chimeric live DIVA vaccine CP7_E2alf was developed. Most likely, passive immunity against CSF virus in populations previously vaccinated with C-strain interferes with the efficacy of...
CP7_E2alf vaccination. To study the interaction with maternal antibodies, the efficacy of CP7_E2alf in piglets from C-strain vaccinated sows was examined. At 5 or at 8 weeks of age, piglets were vaccinated with CP7_E2alf. The vaccinated piglets together with mock-vaccinated littermate controls were challenged 2 weeks post vaccination with highly virulent CSFV Kozlov. The results showed that CP7_E2alf is effective in preventing mortality, severe clinical signs and pathological lesions in piglets vaccinated at 5 or at 8 weeks of age. Interestingly, the antibodies in the mock-vaccinated control piglets partly neutralized the challenge virus. In earlier studies CSFV Kozlov has resulted in 100% mortality in naïve piglets, in this study mortality was reduced to 30% in the piglets infected at 7 weeks of age and to 50% in the piglets infected at 10 weeks of age. In the present study optimal time point for vaccination of piglets with passive immunity was found to be 5 weeks of age.

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Typing of viral hemorrhagic septicemia virus by monoclonal antibodies
Seven mAbs with specific reaction patterns against each of the four genotypes and eight subtypes of viral hemorrhagic septicemia virus (VHSV) were produced, aiming to establish an immunoassay for typing VHSV isolates according to their genotype. Among the mAbs, VHS-1.24 reacted with all genotypes except genotype Ie, whilst mAb VHS-9.23 reacted with all genotypes except genotype III. mAb VHS-3.80 reacted with genotypes Ib, Ic, Id and II, mAb VHS-7.57 reacted with genotypes II and IVa, and mAb VHS-5.18 with genotype Ib only. Interestingly, mAb VHS-3.75 reacted with all of the genotype III isolates except a rainbow trout-pathogenic isolate from the west coast of Norway, and reacted in addition with the IVb isolate, CA-NB00-01, from the east coast of the USA. Finally, mAb VHS-1.88 reacted with all genotype IVb isolates from the Great Lakes, but not with CA-NB00-01. In conclusion, we can distinguish between all four genotypes and between five of eight subtypes of VHSV by testing isolates in immunoassay using a panel of nine mAbs. By Western blotting and transfection of cell cultures, it was shown that mAb VHS-1.24 recognized an epitope on the viral phosphoprotein (P), whilst all others recognized antigenic determinants on the nucleoprotein (N). From amino acid alignments of the various genotypes and subtypes of VHSV isolates, it was possible to determine the epitope specificity of mAb VHS-1.24 to be aa 32–34 in the P-protein; the specificities of mAbs VHS-3.80, VHS-7.57 and VHS-3.75 were found to be aa 43 and 45–48, aa 117 and 121, and aa 103, 118 and 121 of the N-protein, respectively.

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

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Update on Eus Diagnostics, Infection Trials and Online Slide Collection
Following the presentation with an update on growth and sporulation of Aphanomyces invadans, by Christian Fry at last year’s annual meeting, we have conducted a series of infection trials. These infection trials have had several functions, both to establish an infection model in our laboratory and getting experiences in this context, but also to use the fish for performing diagnostic procedures from clinical cases, and to collect positive tissue material from infected fish.

We performed a pre-trial with three different species of gourami’s: three spot gourami, pearl gourami and dwarf gourami. Each fish was intramuscularly injected with 1600 spores in 10 μl of miliQ water. We observed that 3 out of 9 three spotted gouramis got clinical diseased, none of 4 pearl gouramis got diseased and all of 5 dwarf gouramis got diseased. From this we chose to use the three spotted gouramis as the fish of choice, to include as positive control of the pathogenicity of injected spores.

Secondly we set up a confirmatory trial in three spotted gouramis, here it was also seen that around a third of the fish got clinically diseased. From these and later trials it is our experience that using A. invadans grown on agar, around a third of the threspotted gouramis will show clinical disease ranging from 2-5 fish, some of these might resolve the lesion within a couple of weeks. Further, using an A. invadans reisolated from a three spot gourami we have seen 100% morbidity. In contrast, using an A. invadans reisolated from a rainbow trout, with clinically disease, resulted in no mortality in 10 three spotted guramis, with only one fish showing a slight reddening.

We have performed intra muscular injection trials in rainbow trout at temperatures at 10, 15, 18 and 22 degrees Celsius respectively. Here we have seen variable morbidity; at 10 degrees Celsius we have not observed any symptoms, at 15 degrees Celsius we have seen a few fish with clinical disease, at 18 degrees Celsius up to 70 % have been clinically affected and at 22 degrees Celsius almost 100% morbidity was seen. This shows that rainbow trout can support fungal growth and develop lesions at temperatures present in European rearing conditions, however, at the predominant temperatures, for rearing salmonids in Europe, disease and lesion development most likely will be to a limited degree.

Moreover, our preliminary results indicates that Oomycal growth in rainbow trout don’t support a normal pathogenic potential of the organism, but an attenuated strain with lower virulence.

Following the above described trials we have collected material for histology, Oomycete reisolation and PCR. From this material, pictures will be uploaded to the EURL website. The pictures will show different types of lesions using standard H&E stain and special stains, explanatory text will follow each picture. First we will upload tissue from infected Gouramis, following this; pictures of lesions in rainbow trout.

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Update on Fish Disease Situation in Italy

In this presentation we provide a general overview of the aquatic animal health issues related to the aquaculture sector and wild environment in Italy in 2011. Considering saltwater species European sea bass (Dicentrarchus labrax) and Gilthead sea bream (Sparus aurata) are still the most widely farmed species, nevertheless some “new” candidates are employed often. The first two species represents more than 95% of the total production while the remaining is obtained by different promising candidates species, including sole (Solea solea), meagre (Argyrosomus regius), northern blue fin tuna (Thunnus thynnus) and amberjack (Seriola dumerili) for which some breeding/reproduction plans have been attempted by some hatcheries.

The farming of sea bass and sea bream is affected by the presence of several important diseases. Firstly considering Bacterial diseases, Marine Flexibacteriosis, caused by Tenacibaculum maritimum; Vibriosis, caused by Listonella anguillarum and Pasteurellosis caused by Photobacterium Damselia subsp. piscicida are considered the major bacterial diseases even though for these pathogens exists chemicals and for some of them efficacious vaccines. Considering viral diseases Viral encephalopathy and retinopathy (VER) still plays a key role in some areas where, mortalities ranging from 30-40% can be observed in sea bass rearing unit. Nevertheless in recent years, serious epizootics affecting sea bream larvae, previously considered a resistant species, have been reported. Finally the appearance of the clinical disease has been recorded also in the wild.

Lymphocystis disease (LCD) represents an important disease not for its pathogenicity but for the interferences with strict production plans of farm.

Finally, considering parasites, over than “old” protozoans (Cryptocarion irritans and Amyloodinium ocellatum) and gill flukes (Diplectanum aequans and Sparicotyle chrysophrii) mainly present in inland farms (earth ponds and concrete tanks based); isopods crustacea (Ceratotoa, Anylocra) and Enteromyxidiosis (Enteromyxum leei) represent a treat for offshore cages.

Among the dissectabolic unknown aetiology disease Winter Syndrome, affects mainly 1-year-old sea bream causing mortalities ranging from 5-15%. The therapeutic treatment addresses great attention to the diet, especially at the end of Summer and the approaching winter season.

Considering trout farming which is a well developed industry two main pathological scenarios are present. Farms with low water temperature (mainly located in the mountains) can be more affected and damaged by viral diseases (i.e. viral haemorrhagic septicemia VHS) which is one of the most important problem. Rainbow trout fry syndrome (RTFS) is responsible for significant mortalities in salmonids, during juvenile stages, particularly if not treated promptly.

Another bacterial problem that seems to be re-emerging is Enteric Red mouth (Yersinia ruckerii).

Finally considering freshwater wild environment a mortality outbreak in eels is presented.

Virulence in pigs of vPader10 rescued from an Infectious cDNA clone of the CSFV strain Paderborn

The BAC clone, pBeloPader10, contains a complete cDNA of the CSFV strain Paderborn. Virus, named vPader10, was rescued from this construct by electroporation of RNA transcripts into porcine PK15 cells. To further study the characteristics of vPader10, we evaluated the virulence of this virus in vivo in pigs. An animal experiment was performed where three pigs were inoculated with vPader10 and housed in-contact with two non-inoculated pigs for 5 weeks.
Following inoculation with vPader10, two out of three pigs displayed severe clinical signs of CSF from PID 14 that progressed until death of the pigs at PID 21 and PID 22, respectively. High fever (>41°C) was observed in these pigs from PID 14 and remained at a high level until day of death. One of two contact pigs developed similar clinical disease that initiated at PID 21 and progressed until it was euthanised at PID 32 due to severe clinical signs. One inoculated and one in-contact pig showed little or no clinical symptoms. Virus was detected in blood by RT-qPCR from PID 3-4 in all inoculated pigs and from PID 14 in both contact pigs. In the severely diseased pigs the viral loads reached high levels (Ct ≈ 20) whereas the two pigs without clinical symptoms displayed transient viral loads that peaked at Ct ≈ 30. The results from this experiment demonstrate that vPader10 rescued from pBeloPader10 is virulent and transmissible in pigs.

Virus kan påvises i spyt fra grise

Virus survival in slurry: Analysis of the stability of foot-and-mouth disease, classical swine fever, bovine viral diarrhoea and swine influenza viruses

Farm slurry can be highly contaminated with viral pathogens. The survival of these pathogens within slurry is important since this material is often distributed onto farm land either directly or after heat treatment. There is clearly some risk of spreading pathogens in the early stages of an outbreak of disease before it has been recognized. The survival of foot-and-mouth disease virus, classical swine fever virus, bovine viral diarrhoea virus and swine influenza virus, which belong to three different RNA virus families plus porcine parvovirus (a DNA virus) was examined under controlled conditions. For each RNA virus, the virus survival in farm slurry under anaerobic conditions was short (generally ≤1h) when heated (to 55°C) but each of these viruses could retain infectivity at cool temperatures (5°C) for many weeks. The porcine parvovirus survived considerably longer than each of the RNA viruses under all conditions tested. The implications for disease spread are discussed.
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.

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Organisations: Adaptive Immunology & Parasitology, National Veterinary Institute, Division of Veterinary Diagnostics and Research, Bacteriology & Pathology, Section for Veterinary Diagnostics, Virology, University of Copenhagen
Authors: Pedersen, K. S. (Intern), Pedersen, K. H. (Forskerdatabase), Hjulsager, C. K. (Intern), Larsen, L. E. (Intern), Ståhl, M. (Intern), Stege, H. (Forskerdatabase), Angen, Ø. (Intern), Nielsen, J. P. (Ekstern)
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Scopus rating (2014): SJR 0.781 SNIP 0.902 CiteScore 1.36
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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.
Host-response to foot-and-mouth disease in cattle; possible implications for the development of persistently infected “carriers”

General purpose and objectives Foot-and-mouth disease (FMD) is a viral infection of implicit financial importance for countries, such as Denmark, which rely on a significant trade in agricultural products. The disease is highly contagious with rapid spread amongst susceptible animals, causing substantial economical implications for farmers and live-stock industries of affected countries. The occurrence of persistently infected, so called “carriers” of FMD-virus (FMDV) which may shed infectious virus for prolonged periods of time following exposure to the virus, causes significant complications for effective disease control. The main purpose of this PhD-project has been to investigate the host response to FMD infection in cattle, with further objectives of elucidating any detectable differences in the measured immune response between animals that developed into FMDV carriers and those that did not. Experimental studies The thesis is based on results obtained from seven separate animal experiments with FMDV serotype O, which have been performed at DTU-Vet, Lindholm. In five out of the six experiments that were performed in cattle, animals were infected with FMDV O UKG 34/2001, representing the virus isolate responsible for the FMD outbreak in the UK and northern Europe in 2001. One cattle experiment was performed with an FMDV serotype O isolated from samples collected from a cattle farm in Uganda during an outbreak in 2006, whilst one additional experiment was designed to investigate the clinical course of infection with FMDV O UKG 34/2001 in sheep. An experimental study design involving endoscopic collection of small biopsies of pharyngeal mucosa from live cattle was developed. This technique enables collection of sequential tissue samples from infected animals, allowing investigation of the local tissue response to infection within this specific anatomical region of individual animals, at different time points following infection. This sampling system was used to investigate the pathogenesis of FMD infection in cattle through quantification of the levels of FMDV RNA present within the pharyngeal epithelia during early infection. Similar analyses were performed on samples of pharyngeal epithelia and associated lymph nodes collected during post mortem examinations performed at around 32-35 days post infection in order to investigate possible sites of virus persistence. The early host response to FMDV O in cattle was investigated through measurements of systemic parameters consisting of the acute phase proteins, serum amyloid A (SAA) and haptoglobin (HP), as well as type 1 interferon (IFN). The local tissue response within the pharyngeal epithelia was investigated through measurements of mRNA levels of inflammatory cytokines in sequential biopsy samples. Structure of Thesis The first chapter contains general background information on the host response to virus infections, as well as characteristics of FMDV and the pathogenesis of the infection. Detailed aims and objectives of the project are stated at the end of chapter 1. Chapter 2 contains overall descriptions of the animal experiments included in the project. The general concepts of the experimental procedures are described, as well as the clinical characteristics of infection caused by the two different FMDV O isolates in cattle. The clinical description of the experiment performed with FMDV O UKG 34/2001 in sheep includes results of measurements of viremia and the development of specific anti-FMDV O antibodies, as these results are not presented in the included manuscripts. The third chapter of the thesis contains three manuscripts of research articles for publication in peer-reviewed scientific journals. The first manuscript is based on serological measurements of the acute phase proteins SAA and HP, together with the bioactivity of type 1 IFN, in three out of the performed cattle experiments. Measurements of the systemic response to early infection with FMDV is related to the observed development of clinical signs of infection as well as the occurrence of viremia and development of anti-FMDV antibodies. Observed variations in the acute phase response of HP between carriers and non-carriers are discussed. The second manuscript contains results from measurements of mRNA levels of inflammatory cytokines IFNα- and –β, as well as tumor necrosis factor –α (TNF-α), in collected biopsy samples. The type 1 interferon response in the analyzed tissue samples is discussed in relation to the previously reported systemic interferon response. The measured cytokine responses, as well as an observed variation in the TNF-α response between carriers and non-carriers, are discussed in relation to previous publications within the subject area. The third manuscript deals with investigations of possible sites of virus replication during early and persistent phases of infection. Levels of FMDV RNA was quantified in sequential biopsy samples of pharyngeal mucosa harvested during early infection, as well as in corresponding tissue samples collected post mortem. The final chapter of the thesis contains a general discussion of the obtained results, together with overall conclusions and future perspectives for continued research within the specific area.
A Bayesian Clinical Decision Support for Early Detection of Classical Swine Fever in Individual Pigs - Evaluation of the Sensitivity and Specificity of the Model

A Comparative Study of CSFV Antibody Levels in Pigs Vaccinated with the Chimeric Vaccine CP7_E2GIF or a C-Strain Vaccine
A global taqman based real time RT-PCR assay suitable for surveillance and diagnosis of viral haemorrhagic septicaemia virus

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Jonstrup, S. P. (Intern), Kahns, S. (Intern), Skall, H. F. (Intern), Boutrup, T. S. (Intern), Olesen, N. J. (Intern)
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Event: Abstract from 15th International Conference on Diseases of Fish and Shellfish, Split, Croatia.
Main Research Area: Technical/natural sciences

Analysis of the acute phase responses of Serum Amyloid A, Haptoglobin and Type 1 Interferon in cattle experimentally infected with foot-and-mouth disease virus serotype O

A series of challenge experiments were performed in order to investigate the acute phase responses to foot-and-mouth disease virus (FMDV) infection in cattle and possible implications for the development of persistently infected "carriers". The host response to infection was investigated through measurements of the concentrations of the acute phase proteins (APPs) serum amyloid A (SAA) and haptoglobin (HP), as well as the bioactivity of type 1 interferon (IFN) in serum of infected animals. Results were based on measurements from a total of 36 infected animals of which 24 were kept for observational periods exceeding 28 days in order to determine the carrier-status of individual animals. The systemic host response to FMDV in infected animals was evaluated in comparison to similar measurements in sera from 6 mock-inoculated control animals. There was a significant increase in serum concentrations of both APPs and type 1 IFN in infected animals coinciding with the onset of viremia and clinical disease. The measured parameters declined to baseline levels within 21 days after inoculation, indicating that there was no systemically measurable inflammatory reaction related to the carrier state of FMD. There was a statistically significant difference in the HP response between carriers and non-carriers with a lower response in the animals that subsequently developed into FMDV carriers. It was concluded that the induction of SAA, HP and type 1 IFN in serum can be used as markers of acute infection by FMDV in cattle.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Innate Immunology, Division of Veterinary Diagnostics and Research
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Scopus rating (2014): SJR 1.189 SNIP 1.197 CiteScore 2.46
An E2-Substituted Chimeric Pestivirus With DIVA Vaccine Properties.

An advantage of the use of chimeric pestiviruses as modified live vaccines against classical swine fever (CSF) resides in their capacity to be manipulated to achieve the characteristics desired for safe and efficacious DIVA vaccines. We have recently generated a new chimeric virus, Riems26_E2gif engineered specifically for this purpose. The E2-substituted Riems26_E2gif was derived by homologues recombination of the complete E2 protein encoding genome region from Border disease strain Gifhorn into a bacterial artificial chromosome (BAC) harbouring the genome of the CSFV vaccine strain C-Riems. The virulence, immunogenicity and vaccine properties of Riems26_E2gif were tested in a vaccine-challenge experiment in pigs. Riems26_E2gif vaccinated pigs could be differentiated from infected pigs using a CSFV-E2 specific ELISA. Following challenge infection with highly virulent CSFV strain Koslov, all vaccinated pigs were protected. This new chimeric pestivirus represents a C-strain based DIVA vaccine candidate that can be differentiated based on CSFV E2 specific antibodies.
**Application of a Real-time Reverse Transcription Loop Mediated Amplification Method to the Detection of Rabies Virus in Arctic Foxes in Greenland.**

Reverse transcription loop mediated amplification (RT-LAMP) offers a rapid, isothermal method for amplification of virus RNA. In this study a panel of positive rabies virus samples originally prepared from arctic fox brain tissue was assessed for the presence of rabies viral RNA using a real time RT-LAMP. The method had previously been shown to work with samples from Ghana which clustered with cosmopolitan lineage rabies viruses but the assay had not been assessed using samples from animals infected with rabies from the arctic region. The assay is designed to amplify both cosmopolitan strains and arctic-like strains of classical rabies virus due to the primer design and is therefore expected to be universally applicable independent of region of the world where the virus is isolated. Of the samples tested all were found to be positive after incubation for 25 to 30 minutes. The method made use of novel enzymology from OptiGene but fluorescence reads were performed in a Stratagene MX instrument. The identity of the product was confirmed using melt analysis with all products melting at temperatures between 87.1 and 88.2°C, similar to a rabies virus positive control. This demonstrates that rabies virus of arctic origin virus can be detected using RT-LAMP and the method reported is more rapid than the real-time RT-PCR. Further arctic fox samples are under analysis in order to confirm these findings.

**Assessment of the Epitope Specificity of Monoclonal Antibodies that can Discriminate between the Various Genotypes of VHSV**

**Betydning af Lawsonia og gødningsscore for daglig tilvækst i slagtesvin**
Capsid proteins from field strains of foot-and-mouth disease virus confer a pathogenic phenotype in cattle on an attenuated, cell-culture-adapted virus

Chimeric foot-and-mouth disease viruses (FMDVs) have been generated from plasmids containing full-length FMDV cDNAs and characterized. The parental virus cDNA was derived from the cell-culture-adapted O1Kaufbeuren B64 (O1K B64) strain. Chimeric viruses, containing capsid coding sequences derived from the O/UKG/34/2001 or A/Turkey 2/2006 field viruses, were constructed using the backbone from the O1K B64 cDNA, and viable viruses (O1K/O-UKG and O1K/A-Tur, respectively) were successfully rescued in each case. These viruses grew well in primary bovine thyroid cells but grew less efficiently in BHK cells than the rescued parental O1K B64 virus. The two chimeric viruses displayed the expected antigenicity in serotype-specific antigen ELISAs. Following inoculation of each virus into cattle, the rescued O1K B64 strain proved to be attenuated whereas, with each chimeric virus, typical clinical signs of foot-and-mouth disease were observed, which then spread to in-contact animals. Thus, the surface-exposed capsid proteins of the O1K B64 strain are responsible for its attenuation in cattle. Consequently, there is no evidence for any adaptation, acquired during cell culture, outside the capsid coding region within the O1K B64 strain that inhibits replication in cattle. These chimeric infectious cDNA plasmids provide a basis for the analysis of FMDV pathogenicity and characterization of receptor utilization in vivo.
Characterization of an E2-Substituted C strain Vaccine Candidate with Potential Diva Vaccine Properties

General information
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Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Friedrich Loeffler Institute
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Classical swine fever virus detection: results of a real-time reverse transcription polymerase chain reaction ring trial conducted in the framework of the European network of excellence for epizootic disease diagnosis and control

The current study reports on a real-time reverse transcription polymerase chain reaction (real-time RT-PCR) ring trial for the detection of Classical swine fever virus (CSFV) genomic RNA undertaken by 10 European laboratories. All laboratories were asked to use their routine in-house real-time RT-PCR protocols and a standardized protocol commonly used by the Friedrich-Loeffler-Institute (FLI) on a panel of well-characterized samples. In general, all participants produced results within the acceptable range. The FLI assay, several in-house assays, and the commercial kits had high analytical sensitivity and specificity values. Nevertheless, some in-house systems had unspecific reactions or suboptimal sensitivity with only a single CSFV genotype. Follow-up actions involved either improvement of suboptimal assays or replacement of specific laboratory assays with the FLI protocol, with or without modifications. In conclusion, the ring trial showed reliability of classical swine fever diagnosis on an international level and helped to optimize CSFV-specific RT-PCR diagnostics.

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Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Friedrich Loeffler Institute, Lombardy and Emilia Romagna Experimental Zootechnic Institute, Animal Health Research Center, University of Veterinary Medicine, Centrum voor Onderzoek in Diergeneeskunde en Agrochemie, National Veterinary Institute, Institute of Virology and Immunoprophylaxis, ANSES - French Agency for Food, Environmental and Occupational Health & Safety, Central Veterinary Institute, National Veterinary Research Institute
Authors: Hoffmann, B. (Ekstern), Blome, S. (Ekstern), Bonilauri, P. (Ekstern), Fernández-Piñero, J. (Ekstern), Greiser-Wilke, I. (Ekstern), Haegeman, A. (Ekstern), Isaaksson, M. (Ekstern), Koenen, F. (Ekstern), LeBlanc, N. (Ekstern), Leifer, I. (Ekstern), Le Potier, M. (Ekstern), Loeffen, W. (Ekstern), Rasmussen, T. B. (Intern), Stadejek, T. (Ekstern), Ståhl, K. (Ekstern), Tignon, M. (Ekstern), Uttenthal, Å. (Intern), van der Poel, W. (Ekstern), Beer, M. (Ekstern)
Classical Swine Fever Virus-Rluc Replicons: A Tool for Monitoring the Determinants of Efficient Viral Replication

Classical swine fever virus (CSFV) is the etiologic agent of the severe porcine disease, classical swine fever. Unraveling the molecular determinants of efficient replication is crucial for gaining proper knowledge of the pathogenic traits of this virus. Monitoring the replication competence within cells can be achieved using autonomously replicating genome constructs (replicons) containing a reporter gene that expresses a readily quantifiable enzyme. Here, a newly implemented cloning technique was applied to genome modification of the full-length CSFV cDNA previously inserted into a single-copy bacterial artificial chromosome (BAC). This technique, the Red/ET counter-selection method, is based upon homologous recombination, thus obviating the need for internal restriction sites. Several CSFV replicons with deletions in regions encoding structural viral proteins considered non-essential for RNA replication were constructed and these deletions were swapped with an in-frame insertion of the Renilla luciferase (Rluc) sequence. RNA transcripts from these replicons should be translated as a single functional open reading frame. Full-genome cDNA’s (~10-12,3 kb) were amplified from the BACs using a stable long-PCR method and in vitro transcripts were assayed in permissive cells. The CSFV-Rluc replicons were evaluated for their replication competence using antibody staining (against NS3), qRT-PCR and the Renilla luciferase assay. A CSFV-Rluc replicon with similar replication kinetics compared to the wild type CSFV-Paderborn strain, as judged by qRT-PCR, was picked as the candidate and could potentially be useful as a tool for further downstream applications including investigation of CSFV non-structural proteins involvement in viral replication.

Clinical, Pathological and Immunological Aspects of Transplacental PRRS Virus Infection: Results from Danish Experiments

The present paper describes Danish research activities on porcine reproductive and respiratory syndrome (PRRS) with emphasis on experimental infections in pregnant swine. The first case of PRRS was diagnosed in Denmark in 1992 and subsequently the disease spread to most other parts of the country. The first animal experiments elucidated the pathogenicity of Danish PRRS virus (PRRSV) isolates in pregnant sows together with the effects of infection at various stages of gestation. In 1996, the introduction of a vaccination program using an attenuated live PRRS vaccine led to an epidemic of American type PRRSV in the previously unaffected Danish pig population. Acute PRRS like disease was observed in non-vaccinated as well as in vaccinated herds, and it was demonstrated that the vaccine strain had reverted to virulence. By experimental infection of late term pregnant sows, we demonstrated that a field isolate of PRRS vaccine-derived virus (VDV) could cause disease in swine consistent with PRRS, thus confirming the etiological role of VDV. Since the complex pathology following in utero infection with PRRSV indicates impairment of the immune system of congenitally infected pigs, we studied various aspect of the host defence in piglets surviving transplacental infection with PRRSV. Leukocyte subpopulations in peripheral blood and bronchoalveolar fluid (BALF) were modulated, viability of lung macrophages was reduced, phagocytosis against Salmonella in blood monocytes as well as oxidative burst capacity of alveolar macrophages was inhibited, there was an over-expression of cytokine IL-10 in BALF cells, and ciliary disruption in the airways was observed. Altogether, our findings supported the hypothesis of the existence of immunosuppression in piglets congenitally infected with PRRSV.
Complete Genomes of Classical Swine Fever Virus Cloned into Bacterial Artificial Chromosomes

Complete genome amplification of viral RNA provides a new tool for the generation of modified pestiviruses. We have used our full-genome amplification strategy for generation of amplicons representing complete genomes of classical swine fever virus. The amplicons were cloned directly into a stable single-copy bacterial artificial chromosome (BAC) generating full-length pestivirus DNAs from which infectious RNA transcripts could be also derived. Our strategy allows construction of stable infectious BAC DNAs from a single full-length PCR product.

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Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Friedrich Loeffler Institute
Authors: Rasmussen, T. B. (Intern), Reimann, I. (Ekster), Uttenthal, Å. (Intern), Beer, M. (Ekster)
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Event: Abstract from ASF/CSF workshop, Lipica, Slovenia,
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Correlation of mRNA Profiles, miRNA Profiles, and Functional Immune Response in Rainbow Trout (Oncorhynchus Mykiss) During Infection With Viral Hemorrhagic Septicemia Virus (VHSV) and in Fish Vaccinated With an Anti-VHSV DNA Vaccine

This project seeks to characterize molecular genetic and immunological mechanisms involved in rainbow trout (Oncorhynchus mykiss) immunity towards Viral hemorrhagic septicemia virus (VHSV). To do so, we consider both relevant genes and the newly discovered small double-stranded RNAs called microRNAs (miRNAs), which are 18- to 22-nucleotide
long RNAs that regulate gene expression. By targeting mRNAs, miRNAs could be involved in controlling the expression of fish immune response genes. As immune regulators, miRNA expression analysis may thus help explain differential immunocompetence in fish. MRNA and miRNA levels in organs of fish coming from families showing high and low mortality in previous VHSV infection trials will be analyzed using quantitative real-time PCR and cDNA microarray. Highly expressed and down-regulated genes and miRNAs during infection can be identified in the fish and expression profiles will be measured relative to highly susceptible fish, allowing the identification of mRNA and miRNA signatures of immunological competence. These markers of immunity will be correlated with phenotype and genotype, as well as to correlates of protective immune (innate, humoral, and cell-mediated) responses. MRNA and miRNA profiles will be correlated and combined with in vitro work in cell culture to describe target relationships between miRNAs and mRNAs and the effect of this targeting in fish. Vaccinated fish will also be used for mRNA/miRNA profiling and in challenge studies alongside non-vaccinated fish. Linking mRNA and miRNA profiles with phenotypic, genotypic, and immunological data will provide an integrated view of the mechanisms of resistance and the strong protective immune responses provided by vaccination. This information is important in designing effective strategies to mitigate the danger of potential VHS disease outbreaks.

General information
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Organisations: National Veterinary Institute, Section of Fish Diseases, Division of Poultry, Fish and Fur Animals
Authors: Bela-Ong, D. (Intern), Schyth, B. D. (Intern), Lorenzen, N. (Intern)
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Event: Abstract from 15th International Conference on Diseases of Fish and Shellfish, Split, Croatia.
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Correlation of mRNA Profiles, miRNA Profiles, and Functional Immune Response in Rainbow Trout (Oncorhynchus Mykiss) Infected With Viral Hemorrhagic Septicemia Virus (VHSV) and in Fish Vaccinated With a DNA Vaccine Against VHSV

Micro ribonucleic acids (miRNAs) are a diverse class of small (18-22 nucleotides) endogenous RNAs that potently mediate post-transcriptional silencing of a wide range of genes and are emerging as critical regulators of cellular processes. They are transcribed and processed from larger precursors and are incorporated into the RNA-Induced Silencing Complex (RISC), which target specific mRNA sequences, causing either mRNA degradation or translation repression. This results in altered mRNA and protein profiles characteristic of a particular cellular phenotype or physiological state. By targeting immune relevant mRNAs, miRNAs could be involved in controlling the expression of fish immune response genes. This project aims to analyze mRNA and miRNA expression in organs of vaccinated and non-vaccinated rainbow trout (Oncorhynchus mykiss) families showing differential mortality in previous infection trials with the highly pathogenic fish rhabdovirus viral hemorrhagic septicemia virus (VHSV). This talk will discuss our overall strategy and present preliminary data on the expression of miRNAs and the type I interferon-inducible Mx gene in the liver and the skeletal muscle tissue of fish injected with a DNA vaccine encoding the VHSV glycoprotein gene. We will link mRNA and miRNA profiles with phenotypic, genotypic, and immunological data, which will provide an integrated view of the mechanisms of resistance and the strong protective immune responses provided by vaccination. This information is important in designing effective strategies to mitigate the danger of potential VHS disease outbreaks.

General information
State: Published
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Detection and quantification of porcine circovirus type 2 (PCV2) and PCV2-antibodies in oral fluid from finisher pigs.

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Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Virology, Danish Agriculture and Food Council, University of Copenhagen
Authors: Leth, S. C. (Ekstern), Pedersen, K. S. (Ekstern), Hjulsager, C. K. (Intern), Stege, H. (Ekstern), Kristensen, C. S. (Ekstern), Breum, S. Ø. (Intern), Larsen, L. E. (Intern)
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Detection of HPR0 in Denmark and Criteria for diagnosis of ISA

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Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Skall, H. F. (Intern)
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Development of immune response and decay of maternal immunity after vaccination with C-strain

General information
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Organisations: National Veterinary Institute, Sektion for Eksotiske Virussygdomme, Division of Virology
Authors: Rangelova, D. Y. (Intern), Nielsen, J. (Intern), Uttenthal, Å. (Intern)
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Event: Abstract from The International Pestivirus Symposium of the European Society for Veterinary Virology, Hanover, Germany,
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DRangelova.pdf
Links:
http://www.pestivirus2011.de/

Bibliographical note
Diagnosis of porcine respiratory disease with a real-time PCR diagnostic package

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Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Virology, Bacteriology & Pathology
Authors: Hjulsager, C. K. (Intern), Breum, S. Ø. (Intern), Jorsal, S. E. L. (Intern), Kokotovic, B. (Intern), Larsen, L. E. (Intern)
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Event: Abstract from 1st Congress of the European Association of Veterinary Laboratory Diagnosticians, Lelystad, Netherlands.
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http://www.eavld2010.org/UK/

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Diagnostic tools: Development and validation of tests for detection of viral diseases

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Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Olesen, N. J. (Intern), Kahns, S. (Intern), Jonstrup, S. P. (Intern), Skall, H. F. (Intern)
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Diagnostic value of meat juice in early detection of classical swine fever infection

To evaluate the diagnostic potential of meat juice for early detection of Classical swine fever virus (CSFV), meat juice and serum samples from pigs experimentally infected with different strains of CSFV were compared for virus load. From all samples, viral RNA was extracted by automated procedure before real-time reverse transcription polymerase chain reaction analysis was performed. Viral RNA was detected in meat juice, but at a lower level than in corresponding serum. Sensitivity was calculated to 91% and specificity to 97%. Disagreements between meat juice and serum results were found when samples originated from pigs infected with low virulence CSFV strains and/or when samples were collected within the first days after infection. In conclusion, while not the first choice for sample material for CSFV diagnosis, meat juice may constitute a useful alternative for herd-based studies or when blood and/or target organ material is not available. Strain virulence and time points for sample collection after infection are factors of importance for diagnostic success.

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Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Lohse, L. (Intern), Uttenthal, Å. (Intern), Rasmussen, T. B. (Intern), Nielsen, J. (Intern)
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Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Virology, Technical University of Denmark, Videncenter for Svineproduktion, Landbrug & Fedevarer, University of Copenhagen
Authors: Christensen, S. (Ekstern), Hjulsager, C. K. (Intern), Larsen, L. E. (Intern), Pedersen, K. S. (Ekstern), Stege, H. (Ekstern), Kristensen, C. S. (. (Ekstern)
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Differentiating infection in vaccinated animals: Work Package 4.3 DIVA diagnostics

General information
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Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Uttenthal, Å. (Intern)
Publication date: 2011
Event: Poster session presented at 5th Annual Meeting EPIZONE, Arnhem, Netherlands.
Main Research Area: Technical/natural sciences
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http://www.epizone-eu.net/annualmeeting/default.aspx
Source: orbit
Source-ID: 276410
Publication: Research - peer-review › Poster – Annual report year: 2011

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

Source: orbit
Source-ID: 282204
Publication: Research - peer-review › Journal article – 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 (SAalpha-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 bronchiolar 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.
DNA vaccine based on genes from pandemic influenza A viruses induces broadly protective immunity in swine

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Bacteriology & Pathology, Division of Veterinary Diagnostics and Research, Statens Serum Institut
Authors: Bragstad, K. (Ekstern), Vinner, L. (Ekstern), Nielsen, J. (Intern), Hansen, M. S. (Intern), Fomsgaard, A. (Ekstern)
Publication date: 2011
Event: Poster session presented at ESWI influenza conference, Malta, .
Main Research Area: Technical/natural sciences
Electronic versions:
Influenza DNA Malta.pdf
Links:
http://www.eswiconference.org/
Publication: Research - peer-review › Journal article – Annual report year: 2011

Does PCV2 reduce the impact of subsequent infection with Lawsonia 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
Authors: Hansen, M. S. (Intern), Jensen, T. K. (Intern), Hjulsager, C. K. (Intern), Angen, Ø. (Intern), Riber, U. (Intern), Nielsen, J. (Intern), Larsen, L. E. (Intern)
EFSA Panel on Animal Health and Welfare (AHAW); Scientific Opinion on bluetongue monitoring and surveillance: EFSA-Q-2010-01238

Following a request from the Commission, the Panel on Animal Health and Welfare was asked to deliver a Scientific Opinion on: 1) the expected prevalence (design prevalence) under different circumstances, and, 2) an updated scientific assessment of the size of the relevant geographical area for the purpose of monitoring and surveillance programmes for bluetongue. A systematic literature review and a review of monitoring and surveillance data from European Union Member States was performed in order to estimate the prevalences observed in the Member States. The prevalences observed in areas that have been infected for several years were slightly lower than the design prevalence of 2 % currently used for monthly testing of sentinel animals, but much lower than the design prevalences of 20 % and 10 % for annual surveys in populations of unvaccinated and vaccinated ruminants, respectively. Currently there is no scientific evidence that suggests an optimal size of the relevant geographic unit for BTV monitoring and surveillance, since it depends on many factors, including the goal of the surveillance programmes. Early warning based on passive surveillance will take place irrespective of the size of the geographical unit but, when based on active surveillance, it is best targeted at regions considered at risk for introduction, using small geographical units, a high sampling frequency and sample size. For estimating the impact of interventions on the prevalence of infected animals, smaller areas result in more precise estimates of the prevalence and also take better account of local differences. For establishing freedom from infection, smaller areas result in lower design prevalence for a region as a whole and take better account of local differences in infection dynamics.

EFSA Panel on Animal Health and Welfare (AHAW); Scientific Opinion on bluetongue serotype 8: EFSA-Q-2010-01237

To answer a question from the European Commission on the potential special characteristics of bluetongue virus (BTV) serotype 8 (BTV-8) compared to other serotypes and their possible impact on the epidemiology of the disease, a systematic literature review was carried out by a working group established by the Animal Health and Welfare Panel. Currently, three special features can be assigned to BTV-8, which are the ability to cause serious disease in cattle and
goats, the ability to be transmitted transplacentally, and the ability to contaminate semen. The transplacental transmission and the contamination of semen are also observed for several serotypes of modified live virus (MLV) vaccines and for some cell culture/egg passaged strains. These two features may have an impact on the epidemiology of the disease, since they may increase the ability of BTV-8 to survive the winter period, for example, when pregnant cows are infected in late autumn and give birth to viraemic offspring in the next vector season, or, through infecting the recipient dam via artificial insemination (AI) with frozen contaminated semen. Furthermore, the chance of BTV-8 spread may be increased either through movement of seropositive but virus negative pregnant animals, which may give birth to viraemic calves, or through natural mating or AI using BTV-8 contaminated semen by transmission from semen to receiving dam. The current legislation provides effective measures to ensure that all dams are immune to BTV before insemination or mating, so there is no subsequent risk of transplacental infection of their offspring. Furthermore, pregnant animals are effectively restricted in their movement. More research is needed to determine whether oral transmission and/or transmission through embryo transfer are more likely to occur for BTV-8 than for other BTV serotypes.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, European Food Safety Authority
Authors: Bøtner, A. (Intern), Oura, C. (Ekstern), Saegerman, C. (Ekstern), MacLachlan, J. (Ekstern), Van Rijn, P. (Ekstern), Sharp, J. M. (Ekstern), Stegeman, J. A. (Ekstern), Dhollander, S. (Ekstern), Gervelmeyer, A. (Ekstern), Lefebvre, D. (Ekstern)
Number of pages: 51
Publication date: 2011

Publication information
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Original language: English
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Source-ID: 282944
Publication: Research - peer-review › Report – Annual report year: 2011

Following the emergence in 2009 of the new pandemic H1N1 influenza virus, which contained gene segments from pig, bird and human influenza viruses, it was apparent that a better scientific understanding is required of influenza viruses to protect public and animal health. The latest scientific data on biological properties of the virus, transmissibility, host susceptibility and epidemiology has been evaluated in order to identify factors that could be monitored in animals and that would suggest a risk of emergence of a new pandemic influenza strains. Virological studies and animal models have highlighted the importance of individual virus proteins but virulence and transmissibility are polygenic effects and no single genetic marker can be reliably associated with increased pathogenicity or transmissibility. It was concluded that current monitoring of the influenza gene pool in humans has been able to provide an alert for the emergence of new human influenza strains of public health significance. In contrast, there is an incomplete view of the influenza virus strains circulating among pigs and birds at the global level. Interpretation of the origins and pandemic potential of influenza viruses do require knowledge of the influenza gene pools in both pigs and birds, as well as other animal species. It is recommended that there should be long term support for a passive monitoring network in pigs and birds in order to promote greater understanding of the evolution of influenza viruses at the global level. Maximum benefit can only be obtained by applying an integrated approach involving the medical and veterinary networks including development of harmonised tools and approaches, exchange of virus strains and sequence data and enhancing the coordination and dissemination of the findings from the human, swine and avian networks.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, European Food Safety Authority
Authors: Bøtner, A. (Intern), Capua, I. (Ekstern), Gatherer, D. (Ekstern), Katz, J. (Ekstern), Lemey, P. (Ekstern), Lopez, V. (Ekstern), Monne, I. (Ekstern), Mumford, E. (Ekstern), Nicoll, A. (Ekstern), Salman, M. (Ekstern), Sharp, M. (Ekstern), Stegeman, J. A. (Ekstern), Have, P. (Ekstern), Correia, S. (Ekstern)
Number of pages: 36
Epizone: Interlaboratory Ring Trial to Compare DNA Transfection Efficiencies

Chemical-based transfection of DNA into cultured cells is routinely used to study for example viral or cellular gene functions involved in virus replication, to analyse cellular defence mechanisms or develop specific strategies to interfere with virus replication. Other applications include rescue of viruses by reverse genetics and/or generation of mutated viruses. A large number of transfection chemicals like calcium phosphate, branched organic compounds, liposomes, cationic polymers etc. are available on the market which are used by different laboratories for different cell lines. To obtain an overview on the efficiencies of varying transfection procedures, an interlaboratory ring trial was initiated within EPIZONE theme 5. A total of 15 participating laboratories from 7 member institutions received RK13 cells, plasmid DNA encoding firefly luciferase under the transcriptional control of the human cytomegalovirus major immediate early promoter, a specially developed lysis buffer and a detailed protocol. Transfected cells were harvested in the laboratories of the participants, frozen and sent to the FLI where both the luciferase activity and protein content of the individual samples were determined to compare transfection efficiency between laboratories with the same protocol and equipment. In addition some laboratories sent samples from cells they are routinely using, transfected with the provided firefly luciferase plasmid, to allow comparison of transfection efficiency between different cell types. About 50 different samples were analysed and the luciferase activity per nanogram total protein (RLU/ng) was determined. The results revealed for RK13 cells a large range of specific luciferase activities between laboratories and, in comparison to RK13 cells, also varying transfection efficacies for other the cell lines. Details will be presented.

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State: Published
Organisations: National Veterinary Institute, Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, Sektion for Ekstotiske Vierussygdomme, Division of Virology, Agence nationale de la sécurité sanitaire, alimentation, environnement et travail, Centre de cooperation Internationale en Recherche Agronomique pour le Développement, Friedrich Loeffler Institute, Institute for Animal Health, INIA, Veterinary Laboratories Agency
Authors: Dory, D. (Ekstern), Albina, E. (Ekstern), Kwiatek, O. (Ekstern), Keil, G. (Ekstern), Finke, S. (Ekstern), Fuchs, W. (Ekstern), Kluup, B. (Ekstern), König, P. (Ekstern), Dixon, L. (Ekstern), Goatley, L. (Ekstern), Takamatsu, H. (Ekstern), Borrego, B. (Ekstern), Brun, A. (Ekstern), Ortego, J. (Ekstern), Friis, M. B. (Intern), Lorenzen, N. (Intern), Rasmussen, T. B. (Intern), Schyth, B. D. (Intern), Crooke, H. (Ekstern), Sosan, O. (Ekstern)
Publication date: 2011
Main Research Area: Technical/natural sciences
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Publication: Research › peer-review › Conference abstract for conference – Annual report year: 2011

Epizootic ulcerative syndrome (EUS): development and implementation of diagnostic methods

General information
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Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Section of Poultiy Diseases, NRL, NRL for fish diseases, Cefas
Publication date: 2011
Evaluation of commercial ELISA kits for detection of antibodies against bovine atypical pestivirus

A group of emerging bovine pestiviruses becomes a possible threat to Bovine Viral diarrhea virus (BVDV) control and eradication programs in the countries of their origin and in the new continents due to the lack of validated detection methods. The use of ELISA kits may be a cheaper, time saving and less laborious option allowing screening for antibodies in large populations. Since test specific for emerging and new BVDV strains are still under preparation, the purpose of this work was to evaluate available BVDV antibody ELISA assays for their ability to detect antibodies against Hobi-like viruses. Analysis of a panel of sera obtained from calves experimentally inoculated with Hobi-like virus (isolated from a calf from Thailand) and BVDV type 1 strain using five different ELISA kits in comparison to neutralization test was performed. The specificity and sensitivity of the tests depended greatly on the level of antibodies with some tests enabling detection of specific antibodies against atypical pestivirus a week earlier than with other assays. Despite significant antigenic differences between atypical pestivirus and BVDV-1, the use of some tests may be recommended while no specific methods are available.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, National Veterinary Research Institute, Lund University, National Veterinary Institute
Authors: Larska, M. (Ekstern), Polak, M. P. (Ekstern), Uttenhal, Å. (Intern), Alenius, S. (Ekstern), Ståhl, K. (Ekstern), Zmudzinski, J. F. (Ekstern), Liu, L. (Ekstern)
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Event: Abstract from The International Pestivirus Symposium of the European Society for Veterinary Virology, Hanover, Germany
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Foot-and-mouth disease (FMD) is endemic in Pakistan and Afghanistan. Three different serotypes of the virus, namely O, A and Asia-1, are responsible for the outbreaks of this disease in these countries. In the present study, the nucleotide-coding sequences for the VP1 capsid protein (69 samples) or for all four capsid proteins (P1, seven representative samples) of the serotype A FMD viruses circulating in Pakistan and Afghanistan were determined. Phylogenetic analysis of the foot-and-mouth disease virus (FMDV) VP1-coding sequences from these countries collected between 2002 and 2009 revealed the presence of at least four lineages within two distinct genotypes, all belonging to the Asia type, within serotype A. The predominant lineage observed was A-Iran05 but three other lineages (a new one is named here A-Pak09) were also identified. The A-Iran05 lineage is still evolving as revealed by the presence of seven distinct variants, the dominant being the A-Iran05AFG-07 and A-Iran05BAR-08 sublineages. The rate of evolution of the A-Iran05 lineage was found to be about 1.2x10–2 substitutions per nucleotide per year. This high rate of change is consistent with the rapid appearance of new variants of FMDV serotype A in the region. The A22/Iraq FMDV vaccine is antigenically distinct from the A-Iran05BAR-08 viruses. Mapping of the amino acid changes between the capsid proteins of the A22/Iraq vaccine strain and the A-Iran05BAR-08 viruses onto the A22/Iraq capsid structure identified candidate amino acid substitutions, exposed on the virus surface, which may explain this antigenic difference.

General information
State: Published
Organisations: National Veterinary Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, Food and Agriculture Organization of the United Nations, Quaid-I-Azam University, Imperial College London
Authors: Jamal, S. M. (Intern), Ferrari, G. (Ekstern), Ahmed, S. (Ekstern), Normann, P. (Intern), Curry, S. (Ekstern), Belsham, G. (Intern)
Pages: 2849-2864
Experimental inoculation of calves with atypical Hobi-like pestivirus shows pattern similar to BVDV-1

Newly emerging pestiviruses, detected first as containment of cell culture fluids originated from Brazil and named Hobi-like are becoming a concern for diagnostic labs, vaccine producers and for BVDV control and eradication programs. The epidemiology of the virus is not known, however recent studies show that the viruses which were thought to be restricted to South America and Southeast Asia, may have reached other continents, including Europe. The pathogenesis of the infection with Hobi-like viruses has not yet been fully elucidated. The purpose of our study was to investigate the course of experimental inoculation of European cattle with atypical pestivirus. The experiment included 4 groups of 5 calves each inoculated with: BVDV-1 (Ho916), Hobi-like pestivirus (Th/04_KhonKaen), a mixture of both viruses or EaglesMEM (control animals). Th/04_KhonKaen induced milder clinical signs than observed in BVDV-1 inoculated calves including moderate pyrexia on day 7-9 post inoculation (PID) and slight depression, cough, conjunctivitis, mucous to mucopurulent ocular and nasal discharge PID 5 and 21. In the group inoculated with Hobi-like virus, similarly to BVDV-1, the decrease in the number of leucocytes, lymphocytes and granulocytes in blood on PID 2 correlated to the onset of viraemia. Animals started to seroconvert on PID 14, however the level of anti- Th/04_KhonKaen antibodies was significantly lower that the level of anti-BVDV-1 antibodies, probably due to the specificity of the test used. The experiment has shown that Hobi-like viruses share similar to BVDV-1 clinical pattern inducing rather subclinical disease with apparent immunosuppression of the host.

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Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, National Veterinary Research Institute, National Veterinary Institute, Lanzhou Veterinary Research Institute, Animal Health and Veterinary Laboratories Agency
Authors: Larska, M. (Ekstern), Polak, M. P. (Ekstern), Uttenthal, Å. (Intern), Alenius, S. (Ekstern), Ståhl, K. (Ekstern), Belák, S. (Ekstern), Yin, H. (Ekstern), Gao, S. (Ekstern), Strong, R. (Ekstern), Riitho, V. (Ekstern), Liu, L. (Ekstern)
Publication date: 2011
Event: Abstract from The International Pestivirus Symposium of the European Society for Veterinary Virology, Hanover, Germany.
Main Research Area: Technical/natural sciences
Electronic versions:
Pestivirus(1)Calf.pdf
Links:
http://www.pestivirus2011.de/

Bibliographical note
Presented as poster.

FishPathogens.eu a new database in the research of aquatic animal diseases
We live in a world where the amount of information available is enormous. In order to keep track of the available knowledge, databases are needed to collect, store, and sort it. www.fishpathogens.eu is a database developed and maintained by the European Union Reference Laboratory for Fish Diseases. The database was launched in June 2009 focusing on Viral Haemorrhagic Septicaemia Virus (VHSV), extended with Infectious Haemorrhagic Necrosis Virus (IHNV) in 2010, and is now being extended to include Spring Viraemia of Carp Virus (SVCV), Infectious Salmon Anemia Virus (ISAV), Betanodaviruses, and Koi Herpes Virus (KHV). The database design is based on freeware and could easily be implemented to include pathogens relevant for other species than fish. We present the database using the data on the different fish pathogens as example. However if some are interested in the platform we are happy to cooperate and share the database structure with other Epizone members.
General and family-specific gene expression responses to viral hemorrhagic septicaemia virus infection in rainbow trout (Oncorhynchus mykiss)

The ability of rainbow trout (Oncorhynchus mykiss) to respond successfully to infection by viral hemorrhagic septicaemia virus (VHSV) is expected to involve a large number of biochemical processes. We hypothesized that this would be reflected at the gene expression level in infected fish, and we tested it by examining gene expression levels in the head kidney of trout at a genome-wide scale with a 16K cDNA microarray for salmonids. Expression levels were recorded during 16 days following bath challenge. The challenge experiment included a relatively low susceptibility (32% survival following challenge) and a relatively high susceptibility (18% survival following challenge) trout family that were both split into a group exposed to virus and a non-exposed control group. In total, 939 genes were differentially expressed between infected and non-infected fish (FDR p = 0.05). Five groups of Gene Ontology categories were involved in immune-related processes and over-represented in infected fish: (i) stress and defense response, (ii) NFkappaB signal transduction, (iii) response to non-self, (iv) antigen processing and presentation, and (v) proteasome complexes. The first four categories were also over-represented among the 642 differentially expressed genes in the low-susceptibility trout family but not among the 556 differentially expressed genes in the high-susceptibility trout family. Expression profiles for most immune genes discussed showed increased transcription from day 3 post-challenge. The results suggest that the innate immune system may play an important role in the successful response to VHSV in rainbow trout. In addition, the results indicate that a superior regulation of the transcription of several key innate immune-related genes contribute to the increased survival in resistant fish. (C) 2011 Elsevier Ltd. All rights reserved.
Generation of Modified Pestiviruses by Targeted Recombination

Infectious cDNA clones are a prerequisite for directed genetic manipulation of pestivirus RNA genomes. We have developed a novel strategy to facilitate manipulation and rescue of modified pestiviruses from infectious cDNA clones based on bacterial artificial chromosomes (BACs). The strategy involves targeted modification of viral cDNA genomes, cloned within BACs, by Red/ET recombination-mediated mutagenesis in E.coli DH10B cells. Using recombination-mediated mutagenesis for the targeted design, the work can be expedited and focused in principle on any sequence within the viral genome and hence is not limited to the use of internal restriction sites. Rescue of modified pestiviruses can be obtained by electroporation of cell cultures with full-length RNA transcripts in vitro transcribed from the recombined BAC clones. We have used this approach to generate a series of new pestivirus BACs modified within different genomic

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http://www.sciencedirect.com/science?_ob=ArticleURL&_udi=B6T9R-527FRRR-1&_user=641802&_coverDate=04%2F30%2F2011&_rdoc=1&_fmt=high&_orig=gateway&_sort=d&_acct=C000034418&_version=1&_urlVersion=0&_userid=641802&md5=5877feab16efc1c57f03a8ca3bf

http://www.sciencedirect.com/globalproxy.cvt.dk/science?_ob=ArticleURL&_udi=B6T9R-527FRRR-1&_user=641802&_coverDate=04%2F30%2F2011&_rdoc=1&_fmt=high&_orig=gateway&_sort=d&_acct=C000034418&_version=1&_urlVersion=0&_userid=641802&md5=5877feab16efc1c57f03a8ca3bf

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Publication: Research - peer-review › Journal article – Annual report year: 2011
Gene regulatory mechanisms in infected fish

This talk will highlight the regulatory mechanisms of gene expression especially the programmed form of mRNA decay which is known as RNA interference (RNAi) and how this and other mechanisms contribute to the regulation of genes involved in immunity. In the RNAi mechanism, small double-stranded RNA molecules produced by the eukaryotic cell are used to program the RNA Induced Silencing Complex (RISC) for cleavage of specific mRNAs and/or translational repression in the cytoplasm or even chromatin methylation in the nucleus. All processes leading to silencing of the target gene. MicroRNAs (or miRNAs) are one class of such small RNAs which are expressed from the genome. The RISC system allows for non-perfect base pairing of miRNAs to their target genes, making it possible for one small RNA to silence large groups of genes at the same time. It is therefore anticipated that they are able to depress whole pathways for the fine-tuning of physiological states like immunological reaction. But miRNAs are themselves under control of regulatory sequences for their timed expression. We will give an example of the finding of two rainbow trout microRNAs, which are up-regulated in the liver during infection with viral hemorrhagic septicemia virus (VHSV), and a genomic upstream sequence which we believe contains their promoter. Particular transcription factor binding motifs inside this potential promoter area point to its use in dsRNA induced antiviral defence. Other sites point to a role in leukocyte differentiation. Thus the expression of these miRNAs might be steered by different mechanisms in different cell types and have different roles in terms of the genes they target in different cell types. Thus gene regulation and function is better looked upon as a web of interactions. Data from zebrafish studies seem to show that these microRNAs are only expressed above a certain stage in the development of the fish.
PanAsia-III. The rates of evolution of the O-PanAsia-II and III sublineages prevalent in the region were found to be 6.65×10⁻³ (95% CI=5.49–7.80×10⁻³) and 7.80×10⁻³ (95% CI=6.72–8.89×10⁻³) substitutions per nucleotide per year, respectively. The present study reveals the presence of multiple (sub-)lineages of FMDV serotype O co-circulating in the region and that significant new variants are frequently emerging.

**General information**

*State:* Published

*Organisations:* National Veterinary Institute, Sektion for Ekotiske Virusselsgdomme, Division of Virology, Food and Agriculture Organization of the United Nations, Quaid-I-Azam University

*Authors:* Jamal, S. M. (Intern), Ferrari, G. (Ekstern), Ahmed, S. (Ekstern), Normann, P. (Intern), Belsham, G. (Intern)

*Pages:* 1229-1238

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*Main Research Area:* Technical/natural sciences

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Scopus rating (2015): SJR 1.435 SNIP 1.083 CiteScore 2.85

BFI (2014): BFI-level 1

Scopus rating (2014): SJR 1.376 SNIP 1.141 CiteScore 2.99

Web of Science (2014): Indexed yes

BFI (2013): BFI-level 1

Scopus rating (2013): SJR 1.545 SNIP 1.174 CiteScore 3.26

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BFI (2012): BFI-level 1

Scopus rating (2012): SJR 1.216 SNIP 0.993 CiteScore 2.87

ISI indexed (2012): ISI indexed yes

BFI (2011): BFI-level 1

Scopus rating (2011): SJR 1.182 SNIP 1.194 CiteScore 3.11

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Web of Science (2011): Indexed yes

BFI (2010): BFI-level 1

Scopus rating (2010): SJR 1.313 SNIP 1.05

Web of Science (2010): Indexed yes

BFI (2009): BFI-level 1

Scopus rating (2009): SJR 1.263 SNIP 1.094

BFI (2008): BFI-level 1

Scopus rating (2008): SJR 1.092 SNIP 0.905

Web of Science (2008): Indexed yes

Scopus rating (2007): SJR 1.167 SNIP 1.096

Scopus rating (2006): SJR 1.219 SNIP 1.188

Scopus rating (2005): SJR 1.334 SNIP 1.235

Scopus rating (2004): SJR 1.026 SNIP 0.779

Scopus rating (2003): SJR 0.472 SNIP 0.806

Scopus rating (2002): SJR 0.235 SNIP 0.264

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*Picornavirus, RNA sequence, Genetic characterization, FMD, Evolution, Molecular epidemiology*

DOIs:
Identification of an antigenically different porcine parvovirus (PPV) isolate in Denmark

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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
Authors: Breum, S. Ø. (Intern), Hjulsager, C. K. (Intern), Shangjin, C. (Ekstern), Larsen, K. V. (Ekstern), Larsen, L. E. (Intern)
Number of pages: 52
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Source: orbit
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Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2011

Implementation and validation of a sensitive PCR detection method in the eradication campaign against Aleutian mink disease virus

Aleutian mink disease virus (AMDV) is a severe progressive disease causing multiple different clinical syndromes in mink. In Denmark, the disease is notifiable and under official control. The control programme, based on serological screening, has confined successfully AMDV to the northern part of Denmark. However, re-infections and new introductions of virus into farms require a confirmatory virological test to verify the positive test results of single animals and ultimately to investigate disease transmission. A one step PCR amplifying a 374-base fragment of the NS1 gene of AMDV was compared to the counter-current immune electrophoresis (CIE) routinely used in the serological screening programme. Mink organs (n = 299) obtained from 55 recently infected farms and 8 non-infected farms from 2008 to 2010 were tested by PCR, and the results were found to have a high correlation with the serological status of the mink. The relative diagnostic sensitivity of the PCR was 94.7%, and the relative diagnostic specificity was 97.9% when read in parallel with the CIE. PCR positive samples were sequenced and phylogenetic analysis revealed high similarity within the analysed AMDV strains and to AMDV strains described previously.

General information
State: Published
Organisations: Section of Fur Animal Diseases and Wildlife, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Division of Microbiology and Risk Assessment, National Food Institute, Sektion for Eksotiske Virussygdomme, Division of Virology
Authors: Jensen, T. H. (Intern), Christensen, L. S. (Intern), Chriél, M. (Intern), Utenthal, Å. (Intern), Hammer, A. S. (Intern)
Pages: 81-85
Publication date: 2011
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Virological Methods
Volume: 171
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ISSN (Print): 0166-0934
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BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
Infectious Pancreatic Necrosis (IPN), a New Threat of Cultured Rainbow Trout in Iran

Background: Infectious pancreatic necrosis virus (IPNV), a member of the virus family Birnaviridae, causes an acute, contagious disease with high mortality rate in a number of economically important fish species specially salmonids. During April 2009, one Rainbow trout farm, situated in Gilan province, north of Iran, reported unusually high losses of
Inhibition of Reporter Genes by Small Interfering RNAs in Cell Culture and Living Fish

RNA interference is a mechanism for silencing specific genes. It has been applied in cell culture to inhibit expression of genes involved in disease including viral genes as recently shown for the fish pathogenic rhabdovirus viral haemorrhagic septicaemia virus or VHSV (Bohle et al., 2011). But evidence of specific siRNA inhibition in living fish is still needed. Using genes involved in disease including viral genes as recently shown for the fish pathogenic rhabdovirus viral haemorrhagic septicaemia virus or VHSV (Bohle et al., 2011). But evidence of specific siRNA inhibition in living fish is still needed. Using the small interfering RNAs (siRNAs), messenger RNA (mRNA) can be targeted resulting in degradation of targeted transcript or translational repression. Reporter genes such as luciferase and green fluorescence protein (GFP) can be transfect and generally show high expression of transfected genes. Various types of fish including albino trouts and transparent fish were used as animal models to get better visualization of reporter gene expression. High variability of reporter gene expression was found between individual fish but it seems that in glass catfish, siRNAs are able to reduce the specific knock down effect of siRNAs in cell culture and in living fish and to establish easy-read out models for testing the effect especially in vivo. Cell culture from human embryonic kidney HEK293t cells was used because they are easy to transfect and generally show high expression of transfected genes. Various types of fish including albino trouts and transparent fish were used as animal models to get better visualization of reporter gene expression. High variability of reporter gene expression was found between individual fish but it seems that in glass catfish, siRNAs are able to reduce reporter gene expression in the muscle showing that it is possible to use siRNA as technology to target genes locally in living fish. In parallel experiments, which will not be reported here, we examine the delivery of siRNAs using pharmacological formulations in order to achieve systemic delivery and knock down effect.

General information
State: Published
Organisations: National Veterinary Institute, Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, Islamic Azad University, Iranian Fisheries Research Organization, University of Tehran
Authors: Larashati, S. (Intern), Schyth, B. D. (Intern), Lorenzen, N. (Intern)
Publication date: 2011
Event: Abstract from 15th International Conference on Diseases of Fish and Shellfish, Split, Croatia.
Main Research Area: Technical/natural sciences
Iran, Rainbow trout, Aquabirnavirus, IPN
Source: orbit
Source-ID: 316799
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2011
used to observe the knock down effect by siRNAs designed to target these reporters. One aim of this project is to verify the specific knock down effect of siRNAs in cell culture and in living fish and to establish easy-read out models for testing the effect especially in vivo. Cell culture from human embryonic kidney HEK293t cells was used because they are easy to transfect and generally show high expression of transfected genes. Two types of fish including albino trouts were used as animal models to get better visualization of reporter gene expression. The luciferase gene was used as reporter gene as it provides low background compared to other reporter genes such as green fluorescence protein (GFP). In cell culture, the luciferase can be used as reporter gene to see the effect of gene silencing. In the living fish, the bioluminescence signal detected is influenced by the melanin pigment. Timing between coinjection and the assay is important in order to detect knock down by siRNA. Our experiment reveal in vivo knock down at 72 hours post injection of reporter gene and siRNA, but further dose-response experiments are required to confirm specificity.
Microchip-based body temperature measurements in pigs
In the present study, we tested whether an electronic identification and body temperature monitoring technology presently applied in small experimental animals could be transferred for use in pigs.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Nielsen, J. (Intern), Lohse, L. (Intern)
Publication date: 2011
Event: Abstract from NADIR Telemetry Workshop, Israel, .
Main Research Area: Technical/natural sciences
Electronic versions:
NADIR.Microchip-based.pdf
Links:
http://www.nadir-project.eu/nadir_project
Source: orbit
Source-ID: 276905
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2011

MicroRNA regulation in rainbow trout infected with a fish pathogenic rhabdovirus
Rainbow trout is a major worldwide aquaculture species and viral disease has a high cost to fish farmers every year why effective treatment and a deeper understanding of immune components involved in the coexistence between fish and virus is of big concern to our field. We present here a study of microRNA regulation in rainbow trout during infection with the fish pathogenic rhabdovirus viral haemorrhagic septicaemia virus (VHSV). Infected fish as well as infected and immune stimulated cell cultures have been tested for microRNA regulation by microarray using a ‘all species’ approach followed by qPCR. Two regulated rainbow trout microRNAs have been cloned, sequenced and upstream promoter areas characterized and tested for functionality upon immune stimulation.

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Aarhus University
Authors: Schyth, B. D. (Intern), Hajiabadi, S. A. H. J. (Intern), Kristensen, L. B. J. (Intern), Pedersen, F. S. (Ekstern), Lorenzen, N. (Intern)
Publication date: 2011
Event: Abstract from Keystone Symposium on Mechanisms and Biology of Silencing, Monterey, California, USA, .
Main Research Area: Technical/natural sciences
Electronic versions:
C7_RNASilencing_Keystone_Schyth_etal_2011.pdf
Links:
http://www.keystonesymposia.org/meetings/viewMeetings.cfm?MeetingID=1119
Source: orbit
Source-ID: 277002
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2011
Minor epidemiological importance of CSFV in *porcine high fever syndrome*

The "porcine high fever syndrome (PHFS)" causing severe losses in China has been associated with several agents such as PCV-2, PRRS, APP and streptococcus. The aim of this study was to analyze the importance of CSFV in pigs in PHFS cases in China. Samples originating from 8 farms (733 Sera and 47 tissue samples) were analyzed for presence of CSFV by virus isolation on PK15 cells and by TaqMan RT-PCR. Sera and tissue samples were collected from large pig farms in Guangdong province, China between 2007 and 2009. Samples were obtained either caused by a suspicion of PHFS or for surveillance. As vaccination is compulsory in China, more than 95% of all pigs have antibodies and serosurveillance cannot be used. Therefore, the method for detection of CSFV in China was an IDEXX antigen ELISA analyzing full blood; based on this kit the majority of the farms were diagnosed with CSFV. Further CSFV analysis was performed in Denmark and CSFV was confirmed in samples from one herd only indicating a very low specificity of the previously used IDEXX antigen kit. The herd that was found CSFV positive did not use prophylactic vaccination against CSFV. In spite of the many similarities in the clinical picture of CSFV and PHFS the impact or importance of CSFV in the syndrome seem to be low.

Modulation of Translation Initiation Efficiency in Classical Swine Fever Virus

Modulation of translation initiation efficiency on classical swine fever virus (CSFV) RNA can be achieved by targeted mutations within the internal ribosome entry site (IRES). In this study, the nucleotides 47 to 427, including the IRES region of the wt CSFV strain Paderborn, were amplified and inserted, under T7 promoter control, into mono- and dicistronic plasmids containing the reporter genes rLuc and fLuc. Mutant fragments of the IRES sequence were generated by overlap PCR and inserted into the reporter plasmids. To evaluate IRES functionality, translation of the rLUC was placed under the control of the wt or mutant CSFV IRES and transfected into BHK cells infected with vTF7-3 which expresses the T7 RNA polymerase. rLuc activity was measured in cell lysates. A series of IRES mutants representing different levels of IRES activity (20% - 100%) were selected and inserted by homologous recombination into Bacterial Artificial Chromosomes (BAC) clones, containing the full-length Paderborn sequence under the transcriptional control of a T7 promoter and a selection marker in place of the IRES. RNA transcripts were produced in vitro and electroporated into porcine PK15 cells. Rescued mutant viruses were obtained after one cell culture passage from constructs with more than 75 % translation efficiency compared to the wildtype IRES. cDNA was generated from these clones and sequenced to verify the maintenance of the changes in the IRES. These results show that full-length viable mutant viruses of the CSFV strain Paderborn with modulated translation initiation efficiency can be designed and generated.
Molecular characterization of serotype Asia-1 foot-and-mouth disease viruses in Pakistan and Afghanistan; emergence of a new genetic Group and evidence for a novel recombinant virus

Foot-and-mouth disease (FMD) is endemic in Pakistan and Afghanistan. The FMD virus serotypes O, A and Asia-1 are responsible for the outbreaks in these countries. Diverse strains of FMDV, even within the same serotype, co-circulate. Characterization of the viruses in circulation can facilitate appropriate vaccine selection and tracing of outbreaks. The present study characterized foot-and-mouth disease serotype Asia-1 viruses circulating in Pakistan and Afghanistan during the period 1998–2009. Phylogenetic analysis of FMDV type Asia-1 revealed that three different genetic Groups of serotype Asia-1 have circulated in Pakistan during this time. These are Group-II, -VI and, recently, a novel Group (designated here as Group-VII). This new Group has not been detected in neighbouring Afghanistan during the study period but viruses from Groups I and -II are in circulation there. Using near complete genome sequences, from FMD viruses of serotypes Asia-1 and A that are currently circulating in Pakistan, we have identified an interserotypic recombinant virus, which has the VP2-VP3-VP1-2A coding sequences derived from a Group-VII Asia-1 virus and the remainder of the genome from a serotype A virus of the A-Iran05AFG-07 sub-lineage. The Asia-1 FMDVs currently circulating in Pakistan and Afghanistan are not efficiently neutralized by antisera raised against the Asia-1/Shamir vaccine strain. Thus, new Asia-1 vaccine strains may be required to block the spread of the current Asia-1 viruses.

General information
State: Published
Organisations: National Veterinary Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, Food and Agriculture Organization of the United Nations, Quaid-I-Azam University
Authors: Jamal, S. M. (Intern), Ferrari, G. (Ekstern), Ahmed, S. (Ekstern), Normann, P. (Intern), Belsham, G. (Intern)
Pages: 2049-2062
Publication date: 2011
Main Research Area: Technical/natural sciences

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BFI (2018): BFI-level 1
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Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.77 SJR 1.306 SNIP 1.04
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.435 SNIP 1.083 CiteScore 2.85
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.376 SNIP 1.141 CiteScore 2.99
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.545 SNIP 1.174 CiteScore 3.26
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.216 SNIP 0.993 CiteScore 2.87
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.182 SNIP 1.194 CiteScore 3.11
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.313 SNIP 1.05
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.263 SNIP 1.094
BFI (2008): BFI-level 1
Molecular Diagnosis of Classical Rabies Virus in Polar Foxes in Greeneland

Classical rabies virus continues to circulate in polar foxes in Greenland. Within the last 5 years more than 30 animals, mainly polar foxes have been tested positive for rabies. In this study, brain samples from this period were assessed for the presence of rabies viral RNA using molecular diagnostic methods.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Rasmussen, T. B. (Intern), Strandbygaard, B. (Intern)
Publication date: 2011
Event: Abstract from 4th Workshop for Rabies, Nancy, France
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 316468
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2011

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 pvH1N1 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, State Serum Institute
Authors: Larsen, L. E. (Intern), Nielsen, L. P. (Ekstern), Breum, S. Ø. (Intern), Trebbien, R. (Intern), Hjulsager, C. K. (Intern)
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. In Norway, pH1N1v infection was recorded in a swine herd on the 10th of October of 2009. Here, we report results from the investigation performed during the outbreak and the follow up surveillance performed in the Norwegian pig population. Nasal swabs were collected from herds i) where pigs had been exposed to persons with verified pH1N1-09v infection or with influenza-like illness (ILI); ii) where pigs showed clinical signs or iii) with a history of close contact with or close proximity to infected herds. In addition, blood samples were collected from nucleus and multiplier breeding herds. Detection of pH1N1-09v was initially performed using a real-time RT-PCR targeted to detect influenza A virus. Positive samples were tested by a pH1N1-09v specific real-time RT-PCR. Blood samples were tested for presence of antibodies against influenza A virus by ELISA (IDVET) and positive samples in the ELISA were tested by haemagglutinin inhibition test using A/California/07/09 as antigen. From the onset of the outbreak and until 31st of December 2009, the pH1N1-09v was detected in nasal swabs from 54 of 114 herds investigated tested, while 55 of 140 herds tested positive for antibodies against pH1N1-09v. No herd has been tested positive for pH1N1-09v since early January 2010, however, results of the Norwegian surveillance and control programme for specific swine herds for 2010 so far indicates that 40 % of the swine herds (154 herds) are positive for antibodies against pH1N1-09. Serological evaluation of swine herds and detailed back tracking of the outbreak indicated that the virus was introduced in September 2009. The Norwegian swine population has, until the outbreak of pH1N1-09v, been considered free from influenza A virus infection as documented through serological surveillance program running since 1997. Virus isolated from one of the herds positive for pH1N1-09v was fully identical across the full genome to virus isolated from a confirmed human case at the farm. The majority of the positive herds had a history of contact with humans that were diagnosed with pandemic influenza or with ILI. This suggests that infected humans are the most likely source for introduction of pH1N1-09v to the Norwegian pig herds, especially in the early phase of the outbreak.

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Virology, National Veterinary Institute, National Institute of Public Health
Authors: Germundsson, A. (Ekstern), Gjerset, B. (Ekstern), Hjulsager, C. K. (Intern), Larsen, L. E. (Intern), Er, C. (Ekstern), Hungnes, O. (Ekstern), Lium, B. (Ekstern)
Number of pages: 73
Publication date: 2011
Event: Abstract from Influenza 2010: Zoonotic Influenza and Human Health, Oxford, United Kingdom, .
Main Research Area: Technical/natural sciences
Electronic versions:
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Source-ID: 282127
Publication: Research - peer-review › Conference abstract for conference – 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
Authors: Hjulsager, C. K. (Intern), Breum, S. Ø. (Intern), Nielsen, L. P. (Ekstern), Trebbien, R. (Intern), Larsen, L. E. (Intern)
Number of pages: 73
Publication date: 2011
Event: Abstract from Influenza 2010: Zoonotic Influenza and Human Health, Oxford, United Kingdom, .
Main Research Area: Technical/natural sciences
Electronic versions:
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Source: orbit
Source-ID: 282127
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2011

Host publication information
Title of host publication: 6th International Symposium on Emerging and Re-emerging Pig Diseases : Proceedings
Persistent Classical Swine Fever infection in newborn piglets

Pestiviruses are unique in their ability to cause persistent infection (PI) in pigs infected in utero. In cattle, PI calves play an important role in maintenance of bovine viral diarrhoea virus infection in the herd. In pigs, the occurrence of classical swine fever virus (CSFV) PI piglets is anticipated to be epidemiologically important. To study the course of CSFV PI in pigs, four sows were infected with 2009-CSFV Lithuania between day 50-60 of gestation. The sows gave birth to 66 piglets of which 55% were live-born. Out of these, thirty % were considered to be PI pigs, while 40% were acutely infected and seroconverted rapidly. The status of the remaining 30% is unclear. Both PI and acutely infected piglets occurred in the same litters. All piglets were tested CSFV antibody-negative at birth if precolostral blood samples were available. PI piglets quickly lost the maternally derived antibodies as free antibodies were not detected in serum even though the sows had Virus neutralization titer (Vnt) titers of 100. Non-PI piglets were able to raise active immunity, since specific antibodies to CSFV stabilized at a mean Vnt titer of 200. While some PI piglets showed growth retardation as well as central nervous disturbances, several other developed normally without showing clinical symptoms. The correlations between clinical signs, virus isolation, antibody levels and detection of CSFV by quantitative RT-PCR will be compared for PI and acutely infected piglets.
Persistent Classical Swine Fever Virus Infection in Pigs

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Uttenthal, Å. (Intern), Lohse, L. (Intern), Bruun, T. (Intern), Nielsen, J. (Intern)
Publication date: 2011
Main Research Area: Technical/natural sciences
Diagnostics, Pig, CSFV, Virus, Persistent infection
Electronic versions:
Oral Uttenthal.pdf

Pig transgenesis by Sleeping Beauty DNA transposition
Modelling of human disease in genetically engineered pigs provides unique possibilities in biomedical research and in studies of disease intervention. Establishment of methodologies that allow efficient gene insertion by non-viral gene carriers is an important step towards development of new disease models. In this report, we present transgenic pigs created by Sleeping Beauty DNA transposition in primary porcine fibroblasts in combination with somatic cell nuclear transfer by handmade cloning. Göttingen minipigs expressing green fluorescent protein are produced by transgenesis with DNA transposon vectors carrying the transgene driven by the human ubiquitin C promoter. These animals carry multiple copies (from 8 to 13) of the transgene and show systemic transgene expression. Transgene-expressing pigs carry both transposase-catalyzed insertions and at least one copy of randomly inserted plasmid DNA. Our findings illustrate critical issues related to DNA transposon-directed transgenesis, including coincidental plasmid insertion and relatively low Sleeping Beauty transposition activity in porcine fibroblasts, but also provide a platform for future development of porcine disease models using the Sleeping Beauty gene insertion technology.

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Aarhus University, Danish Agriculture and Food Council, Randers Hospital, University of Copenhagen
Authors: Jakobsen, J. E. (Ekstern), Li, J. (Ekstern), Kragh, P. M. (Ekstern), Moldt, B. (Ekstern), Lin, L. (Ekstern), Liu, Y. (Ekstern), Schmidt, M. (Ekstern), Winther, K. D. (Ekstern), Schyth, B. D. (Intern), Holm, I. E. (Ekstern), Vajta, G. (Ekstern), Bolund, L. (Ekstern), Callesen, H. (Ekstern), Jørgensen, A. L. (Ekstern), Nielsen, A. L. (Ekstern), Mikkelsen, J. G. (Ekstern)
Pages: 533-545
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Main Research Area: Technical/natural sciences
Publication information
Journal: Transgenic Research
Volume: 20
Issue number: 3
ISSN (Print): 0962-8819
Ratings:
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Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.991 SNIP 0.784 CiteScore 2.43
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.946 SNIP 0.937 CiteScore 2.05
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.913 SNIP 0.94 CiteScore 2.22
BFI (2013): BFI-level 1
Primary infection protects pigs against re-infection with Lawsonia intracellularis in experimental challenge studies

In two separate trials previous termpigsnext term were experimentally infected with previous termLawsonia intracellularisnext term at 5–6 weeks of age followed by antibiotic treatment and resolution of the previous termprimary infection and then renext term-inoculated at 12–13 weeks of age. A treatment-control group of previous termprimary infectionnext term and antibiotic treatment only, and served as control for the antibiotic treatment of the previous termprimary infectionnext term A previous termchallengenext term-control group of previous termprimary infectionnext term received the second inoculation dose only at 12–13 weeks of age to control infectivity of the previous termchallengenext term-dose and susceptibility of previous termpigsnext term to L. previous termintracellularisnext term at this age. previous termpignext term were monitored for shedding of L. previous termintracellularisnext term in faeces by previous termPCRnext term, and for the development of antibodies and responses of acute phase proteins in serum. The presence of L. previous termantigen in the intestinal mucosa was examined in post mortem samples by immunohistochemistry. In both trials previous termpignext term infected previous termpigsnext term were protected from previous termprimary infectionnext term after previous termchallengenext term inoculation as evidenced by absence of faecal shedding of L. previous termtracellularisnext term, lack of changes in acute phase protein concentrations after previous termchallengenext term and with low levels of bacterial antigen in the intestinal mucosa of previous termtracellularisnext term-inoculated previous termpignext term comparable to that of the treatment-control previous termpignext term. In contrast, previous termchallengenext term-control previous termpignext term shed L. previous termtracellularisnext term in
faeces, had L. previous termintracellularis next term antigen extensively present within all layers of the intestinal mucosa and developed a significant acute phase protein response in serum after the previous term experimental infection. The acute phase protein response to L. previous termintracellularis infection next term was detected as an increased rise in the serum concentrations of C-reactive protein and haptoglobin from day-6 post previous terminfection next term and increased serum concentrations of haptoglobin were generally seen 2–3 weeks after inoculation both at 5–6 and 12–13 weeks of age. In conclusion substantial protection previous term against next term L. previous termintracellularis infection next term was found in the previous term inoculated previous term pigs next term in contrast to the development of previous terminfection next term in age-matched control previous term pigs next term The acute phase protein responses reflected both the observed protection previous term against next term L. previous termintracellularis infection next term upon secondary previous term infection next term and that increased resistance to the previous infection next term develops with age.

General information
State: Published
Organisations: Adaptive Immunology & Parasitology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, Section for Veterinary Diagnostics, Innate Immunology
Authors: Riber, U. (Intern), Hvass, H. C. (Intern), Boutrup, T. S. (Intern), Jensen, T. K. (Intern), Heegaard, P. M. H. (Intern), Jungersen, G. (Intern)
Pages: 406-414
Publication date: 2011
Main Research Area: Technical/natural sciences

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Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.326 SNIP 1.208
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.393 SNIP 1.21 CiteScore 2.56
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.281 SNIP 1.262 CiteScore 2.54
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.438 SNIP 1.484 CiteScore 3
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.437 SNIP 1.579 CiteScore 3.18
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.562 SNIP 1.738 CiteScore 3.27
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.371 SNIP 1.476
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.29 SNIP 1.472
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.
Rainbow trout surviving infections of viral haemorrhagic septicemia virus (VHSV) show lasting antibodies to recombinant G protein fragments

Rainbow trout antibodies (Abs) binding to recombinant fragments (frgs) derived from the protein G of the viral haemorrhagic septicemia virus (VHSV)-07.71 strain, could be detected by ELISA (frg-ELISA) in sera from trout surviving laboratory-controlled infections. Abs were detected not only by using sera from trout infected with the homologous VHSV isolate but also with the VHSV-DK-201433 heterologous isolate, which had 13 amino acid changes. Sera from healthy trout and/or from trout surviving infectious haematopoietic necrosis virus (IHNV) infection, were used to calculate cut-off absorbances to differentiate negative from positive sera. Specific anti-VHSV Abs could then be detected by using any of the following frgs: frg11 (56–110), frg15 (65–250), frg16 (252–450) or G21-465. While high correlations were found among the ELISA values obtained with the different frgs, no correlations between any frg-ELISA and complement-dependent 50% plaque neutralization test (PNT) titres could be demonstrated. Between 4 and 10 weeks after VHSV infection, more trout sera were detected as positives by using heterologous frg-ELISA rather than homologous PNT. Furthermore, the percentage of positive sera detected by frg11-ELISA increased with time after infection to reach 100%, while those detected by complement-dependent PNT decreased to 29.4%, thus confirming that the lack of neutralizing Abs does not mean the lack of any anti-VHSV Abs in survivor trout sera. Preliminary results with sera from field samples suggest that further refinements of the frg-ELISA could allow detection of anti-VHSV trout Abs in natural outbreaks caused by different heterologous VHSV isolates. The homologous frg-ELISA method could be useful to follow G immunization attempts during vaccine development and/or to best understand the fish Ab response during VHSV infections. The viral frgs approach might also be used with other fish species and/or viruses.

General information

State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, SGIT – Dept Biotecnologia Crt, INIA, Universidad Miguel Hernandez, SGIT e Dept Biotecnologia Crt, INIA, Universidad de Leon
Authors: Encinas, P. (Ekstern), Gomez-Casado, E. (Ekstern), Grandes, F. (Ekstern), Olesen, N. J. (Intern), Lorenzen, N. (Intern), Estepa, A. (Ekstern), Coll, J. M. (Ekstern)
Pages: 929-935
Publication date: 2011
Main Research Area: Technical/natural sciences

Publication information

Journal: Fish and Shellfish Immunology
Volume: 30
Issue number: 3
ISSN (Print): 1050-4648
Ratings:
- BFI (2018): BFI-level 1
- Web of Science (2018): Indexed yes
- BFI (2017): BFI-level 1
- Web of Science (2017): Indexed Yes
- BFI (2016): BFI-level 1
- Scopus rating (2016): CiteScore 3.36 SJR 1.114 SNIP 1.16
- Web of Science (2016): Indexed yes
- BFI (2015): BFI-level 1
- Scopus rating (2015): SJR 1.268 SNIP 1.171 CiteScore 3.19
- Web of Science (2015): Indexed yes
- BFI (2014): BFI-level 1
- Scopus rating (2014): SJR 1.138 SNIP 1.089 CiteScore 2.92
- Web of Science (2014): Indexed yes
- BFI (2013): BFI-level 1
- Scopus rating (2013): SJR 1.001 SNIP 1.149 CiteScore 3.11
- ISI indexed (2013): ISI indexed yes
- Web of Science (2013): Indexed yes
- BFI (2012): BFI-level 1
- Scopus rating (2012): SJR 1.151 SNIP 1.174 CiteScore 3.02
- ISI indexed (2012): ISI indexed yes
Rapid detection and identification of viral and bacterial fish pathogens using a DNA array-based multiplex assay

Fish diseases can be caused by a variety of diverse organisms, including bacteria, fungi, viruses and protozoa, and pose a universal threat to the ornamental fish industry and aquaculture. The lack of rapid, accurate and reliable means by which fish pathogens can be detected and identified has been one of the main limitations in fish pathogen diagnosis and fish disease management and has consequently stimulated the search for alternative diagnostic techniques. Here, we describe a method based on multiplex and broad-range PCR amplification combined with DNA array hybridization for the simultaneous detection and identification of all cyprinid herpesviruses (CyHV-1, CyHV-2 and CyHV-3) and some of the most important fish pathogenic Flavobacterium species, including F. branchiophilum, F. columnare and F. psychrophilum. For virus identification, the DNA polymerase and helicase genes were targeted. For bacterial identification, the ribosomal RNA gene was used. The developed methodology permitted 100% specificity for the identification of the target species. Detection sensitivity was equivalent to 10 viral genomes or less than a picogram of bacterial DNA. The utility and power of the array for sensitive pathogen detection and identification in complex samples such as infected tissue is demonstrated in this study.

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, KU Leuven, Fish Diseases Laboratory
Authors: Lievens, B. (Ekstern), Frans, I. (Ekstern), Heusdens, C. (Ekstern), Justé, A. (Ekstern), Jonstrup, S. P. (Intern), Lieffrig, F. (Ekstern), Willems, K. A. (Ekstern)
Pages: 861-875
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Journal: Journal of Fish Diseases
Volume: 34
Issue number: 11
ISSN (Print): 0140-7775
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BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.12
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 1.71
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 1.99
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 1.74
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 1.7
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.09
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Web of Science (2008): Indexed yes
Web of Science (2007): Indexed yes
Web of Science (2006): Indexed yes
Web of Science (2005): Indexed yes
Web of Science (2004): Indexed yes
Web of Science (2003): Indexed yes
Web of Science (2001): Indexed yes
Web of Science (2000): Indexed yes
Original language: English
Diagnosis, Herpesvirus, Flavobacterium, Multiplex, Koi herpesvirus (KHV)
DOIs:
10.1111/j.1365-2761.2011.01304.x
Source: orbit
Source-ID: 285371
Publication: Research - peer-review › Journal article – Annual report year: 2011
Recombinant hybrid infectious hematopoietic necrosis virus (IHNV) carrying viral haemorrhagic septicaemia virus (VHSV) G or NV genes show different virulence properties

Viral haemorrhagic septicaemia virus (VHSV) is the economically most important viral disease in European rainbow trout farming. The virus was introduced to fresh water farms in the 1950ies from a reservoir of VHSV in the marine environment. Isolates from wild marine fish and fresh water farms are difficult to distinguish serologically but they show different virulence profiles: marine isolates typically cause little or no mortality in rainbow trout fry following experimental waterborne challenge, while freshwater isolates often kill the majority of the fish. Genetic analysis reveal that the change in host range (to include rainbow trout) likely have occurred several times. Virus from the marine environment therefore continues to represent a threat to the expanding trout aquaculture industry in the marine environment. Identification of potential virulence markers are therefore of great importance. By a reverse genetics approach using the related novelrhabdovirus infectious hematopoietic necrosis virus (IHNV) as basis, four hybrid IHNV-VHSV variants were generated. These chimeric variants included substitution of the IHNV glyco(G) or nonstructural (Nv) protein with the corresponding G or Nv-protein from either a freshwater or a marine VHSV strain. Following rescue of the hybrid viruses, comparative challenge experiments in rainbow trout fingerlings have been performed. The pathogenicity of the recombinant IHNV-VHSV hybrid viruses were similar, regardless of whether the G or Nv originate from marine or fresh water VHSV. Recombinant IHNV gained higher virulence following substitution of the homologous G gene with the VHSV G gene, while the opposite was the case following substitution of the Nv gene. These findings suggest that higher virulence of VHSV compared to IHNV might be related to the G protein, while the VHSV Nv may not efficiently support in vivo propagation of IHNV.

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, National Institute for Agronomic Research
Authors: Einer-Jensen, K. (Intern), Biacchesi, S. (Ekstern), Stegmann, A. (Intern), Bremont, M. (Ekstern), Lorenzen, N. (Intern)
Publication date: 2011
Event: Abstract from 15th International Conference on Diseases of Fish and Shellfish, Split, Croatia.
Main Research Area: Technical/natural sciences
Electronic versions:
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Bibliographical note
Poster presentation.
Source: orbit
Source-ID: 282134
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2011

Rescue of foot-and-mouth disease viruses that are pathogenic for cattle from preserved viral RNA samples

Background: Foot and mouth disease is an economically important disease of cloven-hoofed animals including cattle, sheep and pigs. It is caused by a picornavirus, foot-and-mouth disease virus (FMDV), which has a positive sense RNA genome which, when introduced into cells, can initiate virus replication. Principal Findings: A system has been developed to rescue infectious FMDV from RNA preparations generated from clinical samples obtained under experimental conditions and then applied to samples collected in the “field”. Clinical samples from suspect cases of foot-and-mouth disease (FMD) were obtained from within Pakistan and Afghanistan. The samples were treated to preserve the RNA and then transported to National Veterinary Institute, Lindholm, Denmark. Following RNA extraction, FMDV RNA was quantified by real-time RT-PCR and samples containing significant levels of FMDV RNA were introduced into susceptible cells using electroporation. Progeny viruses were amplified in primary bovine thyroid cells and characterized using antigen ELISA and also by RT-PCR plus sequencing. FMD viruses of three different serotypes and multiple lineages have been successfully rescued from the RNA samples. Two of the rescued viruses (of serotype O and Asia 1) were inoculated into bull calves under high containment conditions. Acute clinical disease was observed in each case which spread rapidly from the inoculated calves to in-contact animals. Thus the rescued viruses were highly pathogenic. The availability of the rescued viruses enabled serotyping by antigen ELISA and facilitated genome sequencing. Conclusions: The procedure described here should improve the characterization of FMDVs circulating in countries where the disease is endemic and thus enhance disease control globally.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Belsham, G. (Intern), Jamal, S. M. (Intern), Tjørnehøj, K. (Intern), Bøtner, A. (Intern)
Pages: e14621
Publication date: 2011
Main Research Area: Technical/natural sciences

Publication information
Journal: P L o S One
Ring Trial on African Swine Fever Virus (ASFV) Real-Time PCR

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Centro de Investigación en Sanidad Animal, SVA, CVI, Friedrich Loeffler Institute, Institute for Animal Health, VLA, Agence
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
- **Authors:** Krog, J. S. (Intern), Breum, S. Ø. (Intern), Hjulsager, C. K. (Intern), Jensen, T. H. (Intern), Bøtner, A. (Intern), Larsen, L. E. (Intern)
- **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
- **Main Research Area:** Technical/natural sciences
- **Conference:** 6th International Symposium on Emerging and Re-emerging Pig Diseases, Barcelona, Spain, 12/06/2011 - 12/06/2011

**Electronic versions:**

- **Screening of reservoirs for hepatitis E virus.pdf**
- **Links:**

- **Source:** orbit
- **Source-ID:** 282018
- **Publication:** Research - peer-review › Conference abstract in proceedings – Annual report year: 2011

Search for genetic virulence markers in viral haemorrhagic septicaemia virus (VHSV) using a reverse genetics approach

VHSV is a negative strand RNA virus causing serious disease in farmed rainbow trout. Although VHSV has been eradicated by stamping out procedures in several fresh water bodies, recently including all streams in Denmark, the wildlife marine reservoir still represents a threat against rainbow trout farming. Particularly in Scandinavia, outbreaks of VHSV in sea reared rainbow trout have demonstrated that although marine variants of VHSV are considered to be avirulent to rainbow trout, the virus is potentially able to adapt to this host and cause disease. Limited knowledge about the genetic background for virulence to rainbow trout makes it difficult to differentiate between dangerous and harmless VHSV variants. With the aim of identification of genetic virulence markers, we have implemented reverse genetics technology for generation of hybrid virus variants. By substituting different regions in the genome of a virulent VHSV variant with the homologous regions from the genome of an avirulent variant, a set of chimeric viral genomes were generated. Following rescue of the hybrid viruses, the plan is to do comparative challenge experiments in rainbow trout fingerlings in order to assess which substitutions that affect the pathogenicity of the virus.

**General information**

- **State:** Published
- **Organisations:** Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, National Institute for Agronomic Research
- **Authors:** Stegmann, A. (Intern), Biacchesi, S. (Ekstern), Bremont, M. (Ekstern), Lorenzen, N. (Intern), Einer-Jensen, K. (Intern)
- **Publication date:** 2011
Small regulatory RNAs of the RNA interference (RNAi) pathway as a prophylactic treatment against fish pathogenic viruses

Small RNAs acting in the recently discovered gene regulatory mechanism called RNA interference has a potential as diagnostic signatures of disease and immunological state and when produced synthetically as prophylactic treatment of such diseases. In the RNAi mechanism the cell produces different small RNAs which inhibit gene expression through more or less specific interaction with messenger RNAs resulting in repression of translation to protein. In this way cells can turn off genes of specific pathways thereby leading to altered physiological stages of tissues and possibly of whole organisms. The mechanism can be programmed with several types of small double stranded RNAs - the type of which defines the destiny of the target. One such class of regulatory RNAs called microRNAs are upregulated due to various physiological responses of the cell and they suppress many genes simultaneously believed to be connected through common or related pathways. Another class of small RNAs, the so called small interfering RNAs (siRNAs) has received attention due their high degree of target specificity. Because synthetic siRNAs can be designed to target specific disease causing genes such as viral genes or oncogenes they hold promise in the treatment against cellular diseases in veterinary as well as human medicine. This presentation will give an overview of the RNAi mechanism, and examples from our studies of microRNA regulation in rainbow trout during infection with the fish pathogenic rhabdovirus viral hemorrhagic septicemia virus (VHSV) and examples of some of our results on delivery and effect of siRNAs designed to target viral genes of VHSV. The VHS disease causes high mortalities in salmonid fish aquacultures why intervention strategies are highly in demand.

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Schyth, B. D. (Intern), Hajiabadi, S. A. H. J. (Intern), Kristensen, L. B. J. (Intern), Lorenzen, N. (Intern)
Number of pages: 273
Publication date: 2011

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Title of host publication: Abstracts - 5th Annual Meeting EPIZONE
Main Research Area: Technical/natural sciences
Electronic versions:
CF7DEd01.pdf
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http://www.epizone-eu.net/annual-meetings/former-am%27s/5th-annual-meeting.aspx
Source: orbit
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Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2011

Små molekyler i veterinærmedicinens tjeneste

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Schyth, B. D. (Intern)
Pages: 43
Publication date: 2011
Main Research Area: Technical/natural sciences

Publication information
Journal: Dansk Veterinaertidsskrift
Volume: 4
ISSN (Print): 0106-6854
Species specific inhibition of viral replication using dicer substrate siRNAs (DsiRNAs) targeting the viral nucleoprotein of the fish pathogenic rhabdovirus viral hemorrhagic septicemia virus (VHSV)

Gene knock down by the use of small interfering RNAs (siRNAs) is widely used as a method for reducing the expression of specific genes in eukaryotic cells via the RNA interference pathway. But, the effectivity of siRNA induced gene knock down in cells from fish has in several studies been questioned and the specificity seems to be a general problem in cells originating from both lower and higher vertebrates. Here we show that we are able to reduce the level of viral gene expression and replication specifically in fish cells in vitro. We do so by using 27/25-mer DsiRNAs acting as substrates for dicer for the generation of siRNAs targeting the nucleoprotein N gene of viral hemorrhagic septicemia virus (VHSV). This rhabdovirus infects salmonid fish and is responsible for large yearly losses in aquaculture production. Specificity of the DsiRNA is assured in two ways: first, by using the conventional method of testing a control DsiRNA which should not target the gene of interest. Second, by assuring that replication of a heterologous virus of the same genus as the target virus was not inhibited by the DsiRNA. Target controls are, as we have previously highlighted, essential for verification of the specificity of siRNA-induced interference with virus multiplication, but they are still not in general use.

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Laboratorio de Diagnóstico y Biotechnología
Authors: Bohle, H. (Ekstern), Lorenzen, N. (Intern), Schyth, B. D. (Intern)
Pages: 187-194
Publication date: 2011
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Publication Information
Journal: Antiviral Research
Volume: 90
Issue number: 3
ISSN (Print): 0166-3542
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 2.026 SNIP 1.245 CiteScore 4.5
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.049 SNIP 1.28 CiteScore 4.52
Structural Features of the Seneca Valley Virus Internal Ribosome Entry Site (IRES) Element: a Picornavirus with a Pestivirus-Like IRES

The RNA genome of Seneca Valley virus (SVV), a recently identified picornavirus, contains an internal ribosome entry site (IRES) element which has structural and functional similarity to that from classical swine fever virus (CSFV) and hepatitis C virus, members of the FLAVIVIRIDAE: The SVV IRES has an absolute requirement for the presence of a short region of virus-coding sequence to allow it to function either in cells or in rabbit reticulocyte lysate. The IRES activity does not require the translation initiation factor elf4A or intact elf4G. The predicted secondary structure indicates that the SVV IRES is more closely related to the CSFV IRES, including the presence of a bipartite IIId domain. Mutagenesis of the SVV IRES, coupled to functional assays, support the core elements of the IRES structure model, but surprisingly, deletion of the conserved IIId2 domain had no effect on IRES activity, including 40S and elf3 binding. This is the first example of a picornavirus IRES that is most closely related to the CSFV IRES and suggests the possibility of multiple, independent recombination events between the genomes of the Picornaviridae and Flaviviridae to give rise to similar IRES elements.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, University of Surrey, Neotropix, Inc.
Temperature influences the expression profiling of immune response genes in rainbow trout following DNA vaccination and VHSV virus infection

A DNA vaccine encoding the glycoprotein (G) genes of the salmonid rhabdovirus viral haemorrhagic septicaemia virus (VHSV) has proven highly efficient against the disease caused by this virus in rainbow trout (Oncorhynchus mykiss). Several studies have demonstrated that this vaccine induces both an early unspecific antiviral response as well as a long-lasting specific protection. However, temperature appears to influence immune response with respect to the nature and duration of the protective mechanisms. In this study, groups of fish were temperature acclimated, vaccinated and challenged at three different temperatures (5, 10 and 15°C). Tissue and organ samples were collected at numerous time points post vaccination (pv) and post viral challenge (pch). Then, gene expression levels of a two immune genes (Vig-1 and Mx3) involved in unspecific antiviral response mechanisms were determined by Q-PCR. The expression profiles appeared similar for the two genes in terms of temperature dependency with a faster induction and shorter duration at the higher temperature. In order to analyze the temperature effect on the relative expression profiles across a larger set of immune genes time points displaying similar Mx3 expression levels post vaccination were identified: 4 days pv (15°C); 7 days pv (10°C); 23 days pv (5°C), respectively. A targeted trout immune gene array including probes for VHSV genes was used for analysis of vaccinated vs control fish per temperature (4-5 replicates). Temperature altered the transcriptome response to the viral challenge, and the number of responsive genes increased at higher temperature: 51 (5°C), 64 (10°C) and 72 (15°C), respectively, indicating that fish kept at higher temperature may have an enhanced immune response. Additional correlation analysis allowed identification of genes that were significantly up- or down regulated synchronous with expression of the vaccine G gene. These findings encompass that for example in fish kept at 5°C, putative CD3, CD4, CD9, CD28, CD53, CD63, CD83, CD84 were up regulated, while CD59, CD83 were down regulated, potentially indicating balancing mechanism of the immune system. An experimental VHSV challenge was performed 7 weeks pv. Similar protection levels of approximately 10% mortality were found for the vaccinated fish, regardless of temperature during immunisation and challenge, whereas the course and level of mortality among the controls were temperature dependent. At day 5 post infection, the number of differentially regulated genes in the livers of vaccinated versus control fish was highest in fish kept at 10°C and lowest in fish at 5°C. This difference presumably reflects the temperature dependent progression of the disease in the controls. Further analysis of the obtained data with respect to gene regulation pathways as a result of DNA vaccination and/or viral infection will be presented.

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Center for Biological Sequence Analysis, Department of Systems Biology, S.L.U. Bionostra Group, Bionostra Biotechnology Applications, University of Aberdeen, Norwegian School of Veterinary Science
Authors: Einer-Jensen, K. (Intern), Gautier, L. (Intern), Rasmussen, J. S. (Intern), Lorenzen, E. (Intern), Christensen, M. B. (Intern), Villanueva, S. A. (Ekstern), Martin, S. (Ekstern), Evensen, Ø. (Ekstern), Schyth, B. D. (Intern), Lorenzen, N. (Intern)
Publication date: 2011
Event: Abstract from Joint Western Fish Disease Workshop & AFS fish Health Section meeting, Nanaimo, British Columbia, Canada.
Main Research Area: Technical/natural sciences
Electronic versions:
Oral_Einer-Jensen_abstract_WFDM_june_2011_FINAL_18052011.pdf
Source: orbit
Source-ID: 282132
Publication: Research - peer-review » Conference abstract for conference – Annual report year: 2011
The Protective Mechanisms Induced by a DNA Vaccine in Fish Depend on Temperature

In veterinary vaccinology, DNA-vaccines encoding the viral glycoproteins of viral haemorrhagic septicaemia virus (VHSV) and infectious haematopoietic necrosis virus (IHNV) have proved highly efficient in fish under experimental conditions. In the early phase following vaccination, innate cross-protective mechanisms are dominating but the protection becomes highly specific within 3–4 weeks at 12–15°C. Temperature is known as an important external parameter affecting the immune response in fish and the present study aimed at characterizing temperature effects on the immune response to a VHS DNA vaccine. Rainbow trout fingerlings acclimated at 5, 10 or 15°C, were given an intramuscular injection of 1 lg purified plasmid DNA and challenged with virulent VHSV 9 or 36–40 days later. The vaccine protected the fish well at all three temperatures, however the non-specific mechanisms lasted for a longer period of time at lower temperatures, hereby apparently compensating for a delayed adaptive response. At 36 dpv fish kept at 5°C thus had no detectable response of neutralising antibodies while 67% of the fish kept at 15°C had seroconverted. Immunohistochemical time-course studies of the injection site of vaccinated fish also showed a clear effect of temperature: in fish maintained at 15°C the vhsG-protein...
occurred earlier on the surface of transfected myocytes than in fish kept at the lower temperatures and the inflammatory response clearing away these myocytes similarly arose earlier at high temperature. Long persistence of transfected myocytes expressing the vaccine antigen might explain the prolonged stimulation of innate protective mechanisms at low temperature. Quantitative gene expression profiles suggested interferon related mechanisms as the explanation for the early protection and also supported their temperature dependent kinetics.

**General information**

State: Published

Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute

Authors: Lorenzen, E. (Intern), Einer-Jensen, K. (Intern), Rasmussen, J. S. (Intern), Christensen, M. B. (Intern), Collet, B. (Ekstern), Secombes, C. J. (Ekstern), Lorenzen, N. (Intern)

Pages: 392-392

Publication date: 2011

Main Research Area: Technical/natural sciences

**Publication information**

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Volume: 73

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BFI (2017): BFI-level 1

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BFI (2016): BFI-level 1

Scopus rating (2016): CiteScore 2.03 SJR 0.951 SNIP 0.646

BFI (2015): BFI-level 1

Scopus rating (2015): SJR 0.93 SNIP 0.684 CiteScore 1.97

Web of Science (2015): Indexed yes

BFI (2014): BFI-level 1

Scopus rating (2014): SJR 0.898 SNIP 0.666 CiteScore 1.91

Web of Science (2014): Indexed yes

BFI (2013): BFI-level 1

Scopus rating (2013): SJR 0.86 SNIP 0.712 CiteScore 2.05

ISI indexed (2013): ISI indexed yes

Web of Science (2013): Indexed yes

BFI (2012): BFI-level 1

Scopus rating (2012): SJR 0.88 SNIP 0.749 CiteScore 2.16

ISI indexed (2012): ISI indexed yes

Web of Science (2012): Indexed yes

BFI (2011): BFI-level 1

Scopus rating (2011): SJR 0.854 SNIP 0.66 CiteScore 2.06

ISI indexed (2011): ISI indexed yes

Web of Science (2011): Indexed yes

BFI (2010): BFI-level 1

Scopus rating (2010): SJR 0.844 SNIP 0.622

BFI (2009): BFI-level 1

Scopus rating (2009): SJR 0.962 SNIP 0.662

Web of Science (2009): Indexed yes

BFI (2008): BFI-level 1

Scopus rating (2008): SJR 0.236 SNIP 0.078

Web of Science (2008): Indexed yes

Scopus rating (2007): SJR 0.286 SNIP 0.141

Scopus rating (2006): SJR 0.421 SNIP 0.125

Scopus rating (2005): SJR 0.999 SNIP 0.642

Web of Science (2005): Indexed yes
The use of quantitative PCR for identification and quantification of Brachyspira pilosicoli, Lawsonia intracellularis and Escherichia coli fimbrial types F4 and F18 in pig feces

Four quantitative PCR (qPCR) assays were evaluated for quantitative detection of Brachyspira pilosicoli, Lawsonia intracellularis, and E. coli fimbrial types F4 and F18 in pig feces. Standard curves were based on feces spiked with the respective reference strains. The detection limits from the spiking experiments were 102 bacteria/g feces for Bpilo-qPCR and Laws-qPCR, 103 CFU/g feces for F4-qPCR and F18-qPCR. The PCR efficiency for all four qPCR assays was between 0.91 and 1.01 with R2 above 0.993. Standard curves, slopes and elevation, varied between assays and between measurements from pure DNA from reference strains and feces spiked with the respective strains. The linear ranges found for spiked fecal samples differed both from the linear ranges from pure culture of the reference strains and between the qPCR tests. The linear ranges were five log units for F4- qPCR, and Laws-qPCR, six log units for F18-qPCR and three log units for Bpilo-qPCR in spiked feces. When measured on pure DNA from the reference strains used in spiking experiments, the respective log ranges were: seven units for Bpilo-qPCR, Laws-qPCR and F18-qPCR and six log units for F4-qPCR. This shows the importance of using specific standard curves, where each pathogen is analysed in the same matrix as sample DNA. The qPCRs were compared to traditional bacteriological diagnostic methods and found to be more sensitive than cultivation for E. coli and B. pilosicoli. The qPCR assay for Lawsonia was also more sensitive than the earlier used method due to improvements in DNA extraction. In addition, as samples were not analysed for all four pathogen agents by traditional diagnostic methods, many samples were found positive for agents that were not expected on the basis of age and case history. The use of quantitative PCR tests for diagnosis of enteric diseases provides new possibilities for veterinary diagnostics. The parallel simultaneous analysis for several bacteria in multi-qPCR and the determination of the quantities of the infectious agents increases the information obtained from the samples and the chance for obtaining a relevant diagnosis.

General information
State: Published
Organisations: Bacteriology & Pathology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics, Virology
Authors: Ståhl, M. (Intern), Kokotovic, B. (Intern), Hjulsager, C. K. (Intern), Breum, S. Ø. (Intern), Angen, Ø. (Intern)
Pages: 307-314
Publication date: 2011
Main Research Area: Technical/natural sciences

Publication information
Journal: Veterinary Microbiology
Volume: 151
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
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.326 SNIP 1.208
Transmission Dynamics of BVDV-1 and the Novel Atypical Bovine

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, NVRI, Lund University, SVA, VLA, Lanzhou Veterinary Research Institute
Authors: Polak, M. P. (Ekstern), Larska, M. (Ekstern), Utenthal, Å. (Intern), Alenius, S. (Ekstern), Stahl, K. (Ekstern), Belak, S. (Ekstern), Strong, R. (Ekstern), Ritho, V. (Ekstern), Yin, H. (Ekstern), Liu, L. (Ekstern)
Publication date: 2011
Event: Poster session presented at 5th Annual Meeting EPIZONE, Arnhem, Netherlands.
Main Research Area: Technical/natural sciences
Cattle, Transmission, Atypical pestivirus, BVDV
Electronic versions:
Poster ES 17.pdf
Links:
http://www.epizone-eu.net/annualmeeting/default.aspx
Source: orbit
Source-ID: 276532
Publication: Research - peer-review › Poster – Annual report year: 2011

Undersegelse af PCV2-status i danske besætninger - et års opfølgning.

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics
Authors: Kristensen, C. S. (Ekstern), Larsen, L. E. (Intern), Hjulsager, C. K. (Intern)
Number of pages: 7
Publication date: 2011

Publication information
Publisher: Videncenter for Svineproduktion
Original language: Danish
Series: Erfaring
Number: 1108
Main Research Area: Technical/natural sciences
Links:
http://vsp.lf.dk/Publikationer/Kilder/lu_erfa/2011/1108.aspx
Source: orbit
Source-ID: 283655
Publication: Research › Report – Annual report year: 2011

Unravelling evolutionary strategies of yeast for improving galactose utilization through integrated systems level analysis.
Identification of the underlying molecular mechanisms for a derived phenotype by adaptive evolution is difficult. Here, we performed a systems-level inquiry into the metabolic changes occurring in the yeast Saccharomyces cerevisiae as a result of its adaptive evolution to increase its specific growth rate on galactose and related these changes to the acquired phenotypic properties. Three evolved mutants (62A, 62B, and 62C) with higher specific growth rates and faster specific galactose uptake were isolated. The evolved mutants were compared with a reference strain and two engineered strains, SO16 and PGM2, which also showed higher galactose uptake rate in previous studies. The profile of intermediates in galactose metabolism was similar in evolved and engineered mutants, whereas reserve carbohydrates metabolism was specifically elevated in the evolved mutants and one evolved strain showed changes in ergosterol biosynthesis. Mutations were identified in proteins involved in the global carbon sensing Ras/PKA pathway, which is known to regulate the reserve carbohydrates metabolism. We evaluated one of the identified mutations, RAS2(Tyr112), and this mutation resulted in an increased specific growth rate on galactose. These results show that adaptive evolution results in the utilization of unpredictable routes to accommodate increased galactose flux in contrast to rationally engineered strains. Our study demonstrates that adaptive evolution represents a valuable alternative to rational design in bioengineering of improved strains and, that through systems biology, it is possible to identify mutations in evolved strain that can serve as unforeseen metabolic engineering targets for improving microbial strains for production of biofuels and chemicals.

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Novo Nordisk Foundation Center for Biosustainability, Fungal Cell Factories, Chalmers University of Technology
**Validation of a Taqman based real time RT-PCR assay suitable for surveillance and diagnosis of Viral Haemorrhagic Septicaemia Virus worldwide**

**General information**
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Jonstrup, S. P. (Intern), Kahns, S. (Intern), Skall, H. F. (Intern), Boutrup, T. S. (Intern), Olesen, N. J. (Intern)
Publication date: 2011
Event: Poster session presented at 15th International Conference on Diseases of Fish and Shellfish, Split, Croatia.
Main Research Area: Technical/natural sciences

**Electronic versions:**
2011 EAFP VHS qPCR A0.pdf

**Vesicular Stomatitis Virus Infection Promotes Immune Evasion by Preventing NKG2D-Ligand Surface Expression**

Vesicular stomatitis virus (VSV) has recently gained attention for its oncolytic ability in cancer treatment. Initially, we hypothesized that VSV infection could increase immune recognition of cancer cells through induction of the immune stimulatory NKG2D-ligands. Here we show that VSV infection leads to a robust induction of MICA mRNA expression, however the subsequent surface expression is potently hindered. Thus, VSV lines up with human cytomegalovirus (HCMV) and adenovirus, which actively subvert the immune system by negatively affecting NKG2D-ligand surface expression. VSV infection caused an active suppression of NKG2D-ligand surface expression, affecting both endogenous and histone deacetylase (HDAC)-inhibitor induced MICA, MICB and ULBP-2 expression. The classical immune escape mechanism of VSV (i.e., the M protein blockade of nucleocytoplasmic mRNA transport) was not involved, as the VSV mutant strain, VSV DM51, which possess a defective M protein, prevented MICA surface expression similarly to wild-type VSV. The VSV mediated down modulation of NKG2D-ligand expression did not involve apoptosis. Constitutive expression of MICA bypassed the escape mechanism, suggesting that VSV affect NKG2D-ligand expression at an early post-transcriptional level. Our results show that VSV possess an escape mechanism, which could affect the immune recognition of VSV infected cancer cells. This may also have implications for immune recognition of cancer cells after combined treatment with VSV and chemotherapeutic drugs.

**General information**
State: Published
Organisations: Department of Micro- and Nanotechnology, Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, University of Copenhagen
Authors: Jensen, H. (Ekstern), Andresen, L. (Intern), Nielsen, J. (Intern), Christensen, J. P. (Ekstern), Skov, S. (Ekstern)
Pages: e23023
Publication date: 2011
Main Research Area: Technical/natural sciences
Vildsvin uønsket i den danske natur

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Fødevarestyrelsen
Authors: Andersen, C. B. (Ekstern), Bald, C. (Ekstern), Uttenthal, Å. (Intern)
Pages: 50-53
Publication date: 2011
Main Research Area: Technical/natural sciences
Viral haemorrhagic septicaemia virus (VHSV) in rainbow trout: virulence variability within genotype Ib isolates

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Fisheries Research Agency
Authors: Ito, T. (Ekstern), Kurita, J. (Ekstern), Skall, H. F. (Intern), Lorenzen, N. (Intern), Olesen, N. J. (Intern)
Publication date: 2011
Event: Poster session presented at 15th International Conference on Diseases of Fish and Shellfish, Split, Croatia.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 316181
Publication: Research - peer-review › Poster – Annual report year: 2011

When geographic information meets molecular data

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Olesen, N. J. (Intern), Kahns, S. (Intern), Jonstrup, S. P. (Intern), Skall, H. F. (Intern)
Publication date: 2011
Event: Abstract from Annual Meeting of the National Reference Laboratories for Mollusc Diseases, Nantes, .
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 316192
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2011

An isolate and sequence database of infectious haematopoietic necrosis virus (IHNV)
In the field of fish diseases, the amount of relevant information available is enormous. Internet-based databases are an excellent tool for keeping track of the available knowledge in the field. Fishpathogens.eu was launched in June 2009 with the aim of collecting, storing and sorting data on fish pathogens. The first pathogen to be included was the rhabdovirus, viral haemorrhagic septicaemia virus (VHSV). Here, we present an extension of the database to also include infectious haematopoietic necrosis virus (IHNV). The database is developed, maintained and managed by the European Community Reference Laboratory for Fish Diseases and collaborators. It is available at http://www.fishpathogens.eu/ihnv.

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Federal Research Institute for Animal Health, U.S. Geological Survey, Symantix Ltd.
Authors: Jonstrup, S. P. (Intern), Schuetze, H. (Ekstern), Kurath, G. (Ekstern), Jensen, A. B. B. (Intern), Gray, T. (Ekstern), Olesen, N. J. (Intern)
Pages: 469-471
Publication date: 2010
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Fish Diseases
An Overview of Aquaculture in the Nordic Countries

The goal of this review was to describe in some detail the Nordic aquaculture industries in order to illuminate the similarities and differences. Information that was gathered for each country includes aquaculture history, aquaculture acts and regulations, production and production systems, environmental concerns, organic aquaculture and outlook for the future. The information will be useful for risk assessments, design of risk-based surveillance programs and for construction of comparative risk profiles for endemic and exotic diseases affecting aquaculture in the Nordic countries. Aquaculture in the Nordic countries has a long history; beginning in the 1850s when hatcheries for restocking of salmon and trout were...
established in Norway. Nowadays, Atlantic salmon is the dominant cultured species in Norway and the Faroe Islands, whereas rainbow trout dominate in Denmark, Finland, and Sweden. Arctic char and cod are most important in Iceland. Other important cultured species include eel and blue mussels. There is much diversity in Nordic aquaculture industries in terms of production, farmed species, and production systems. Although the vast majority of the Nordic aquaculture production is for human consumption, significant numbers of fish are grown for restocking of rivers, lakes, or other bodies of freshwater or seawater.

General information
State: Published
Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section of Fish Diseases, Division of Poultry, Fish and Fur Animals
Authors: Paisley, L. (Intern), Ariel, E. (Intern), Lyngstad, T. M. (Ekstern), Jónsson, G. (Ekstern), Vennerström, P. (Ekstern), Hellström, A. (Ekstern), Østergaard, P. (Ekstern)
Pages: 1 - 17
Publication date: 2010
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of the World Aquaculture Society
Volume: 41
Issue number: 1
ISSN (Print): 0893-8849
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.15 SJR 0.504 SNIP 0.826
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.552 SNIP 0.769 CiteScore 0.89
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.514 SNIP 0.794 CiteScore 1.02
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.489 SNIP 0.72 CiteScore 0.99
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.502 SNIP 0.666 CiteScore 0.83
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.542 SNIP 0.707 CiteScore 0.92
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.494 SNIP 0.684
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.558 SNIP 0.806
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.485 SNIP 0.53
Scopus rating (2007): SJR 0.443 SNIP 0.579
Scopus rating (2006): SJR 0.592 SNIP 0.817
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.588 SNIP 0.884
Scopus rating (2004): SJR 0.638 SNIP 0.983
Scopus rating (2003): SJR 0.801 SNIP 1.279
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.754 SNIP 1.174

In East Africa, the foot-and-mouth disease (FMD) virus (FMDV) isolates have over time included serotypes O, A, C, Southern African Territories (SAT) 1 and SAT 2, mainly from livestock. SAT 3 has only been isolated in a few cases and only in African buffalos (Syncerus caffer). To investigate the presence of antibodies against FMDV serotypes in wildlife in Uganda, serological studies were performed on buffalo serum samples collected between 2001 and 2003. Thirty-eight samples from African buffalos collected from Lake Mburo, Kidepo Valley, Murchison Falls and Queen Elizabeth National Parks were screened using Ceditest® FMDV NS to detect antibodies against FMDV non-structural proteins (NSP). The seroprevalence of antibodies against non-structural proteins was 74%. To characterize FMDV antibodies, samples were selected and titrated using serotype-specific solid phase blocking enzyme linked immunosorbent assay (ELISAs). High titres of antibodies (≥1 : 160) against FMDV serotypes SAT 1, SAT 2 and SAT 3 were identified. This study suggests that African buffalos in the different national parks in Uganda may play an important role in the epidemiology of SAT serotypes of FMDV.

General information
State: Published
Organisations: Sektion for Ekstotiske Virussygdomme, Division of Virology, National Veterinary Institute, Ministry of Agriculture, Animal Industry and Fisheries, Makerere University, University of Copenhagen
Authors: Ayebazibwe, C. (Ekstern), Mwine, F. N. (Ekstern), Balinda, S. N. (Ekstern), Tjørnehøj, K. (Intern), Masembe, C. (Ekstern), Muwanika, V. B. (Ekstern), Okurut, A. R. A. (Ekstern), Siegismund, H. R. (Ekstern), Alexandersen, S. (Intern)
Pages: 286-292
Publication date: 2010
Main Research Area: Technical/natural sciences

Publication information
Journal: Transboundary and Emerging Diseases
Volume: 57
Issue number: 4
ISSN (Print): 1865-1674
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.16 SJR 0.994 SNIP 1.096
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.258 SNIP 1.262 CiteScore 2.29
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.038 SNIP 1.19 CiteScore 2.23
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.953 SNIP 1.123 CiteScore 2.33
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.917 SNIP 1.149 CiteScore 2.04
Application of a pig ligated intestinal loop model for early Lawsonia intracellularis infection

Background Porcine proliferative enteropathy in pigs is caused by the obligate, intracellular bacterium Lawsonia intracellularis. In vitro studies have shown close bacterium-cell interaction followed by cellular uptake of the bacterium within 3 h post inoculation (PI). However, knowledge of the initial in vivo interaction between porcine intestinal epithelium and the bacterium is limited. The aims of the present study were to evaluate the usefulness of a ligated small intestinal loop model to study L. intracellularis infections and to obtain information on the very early L. intracellularis-enterocyte interactions. Methods A ligated small intestinal loop model using three different L. intracellularis inocula was applied to 10-11-week-old pigs. The inocula were 1) wild type bacteria derived from overnight incubation of L. intracellularis bacteria from spontaneous disease, 2) crude vaccine bacteria (Enterisol® Ileitis Vet), and 3) vaccine bacteria propagated in cell culture. The bacteria-enterocyte interaction was visualised using immunohistochemistry on specimens derived 1, 3 and 6 h PI respectively. Results Although at a low level, close contact between bacteria and the enterocyte brush border including intracellular uptake of bacteria in mature enterocytes was seen at 3 and 6 h PI for the vaccine and the propagated vaccine inocula. Interaction between the wild-type bacteria and villus enterocytes was scarce and only seen at 6 h PI, where a few bacteria were found in close contact with the brush border. Conclusions The ligated intestinal loop model was useful with respect to maintaining an intact intestinal morphology for up to 6 h. Furthermore, the study demonstrated that L. intracellularis interacts with villus enterocytes within 3 to 6 h after inoculation into intestinal loops and that the bacterium, as shown for the vaccine bacteria, propagated as well as non-propagated, was able to invade mature enterocytes. Thus, the study demonstrates the early intestinal invasion of L. intracellularis in vivo.

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, University of Copenhagen
Authors: Boutrup, T. S. (Intern), Schauser, K. (Ekstern), Agerholm, J. S. (Ekstern), Jensen, T. K. (Intern)
Pages: 1 - 22
Publication date: 2010
Main Research Area: Technical/natural sciences

Publication information
Journal: Acta Veterinaria Scandinavica (Online)
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
Authors: Holyoake, P. K. (Ekstern), Hjulsager, C. K. (Intern), Larsen, L. E. (Intern), Pedersen, K. S. (Ekstern), Johansen, M. (Ekstern), Stege, H. (Ekstern), Orchard, B. (Ekstern), Ståhl, M. (Intern), Angen, Ø. (Intern), Nielsen, J. P. (Ekstern)
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
Main Research Area: Technical/natural sciences
Conference: 21st International Pig Veterinary Society Congress, Vancouver, Canada, 18/07/2010 - 18/07/2010
Links:
http://www.ipvs2010.com/
Source: orbit
Source-ID: 282422
Publication: 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
Authors: Holyoake, P. K. (Ekstern), Hjulsager, C. K. (Intern), Larsen, L. E. (Intern), Pedersen, K. S. (Ekstern), Johansen, M. (Ekstern), Stege, H. (Ekstern), Orchard, B. (Ekstern), Ståhl, M. (Intern), Angen, Ø. (Intern), Nielsen, J. P. (Ekstern)
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
Main Research Area: Technical/natural sciences
Conference: 21st International Pig Veterinary Society Congress, Vancouver, Canada, 18/07/2010 - 18/07/2010
Links:
http://www.ipvs2010.com/
Source: orbit
Source-ID: 282425
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2011

A Single Coxsackievirus B2 Capsid Residue Controls Cytolysis and Apoptosis in Rhabdomyosarcoma Cells
Coxsackievirus B2 (CVB2), one of six human pathogens of the group B coxsackieviruses within the enterovirus genus of Picornaviridae, causes a wide spectrum of human diseases ranging from mild upper respiratory illnesses to myocarditis and meningitis. The CVB2 prototype strain Ohio-1 (CVB2O) was originally isolated from a patient with summer gripppe in the 1950s. Later on, CVB2O was adapted to cytolytic replication in rhabdomyosarcoma (RD) cells. Here, we present
analyses of the correlation between the adaptive mutations of this RD variant and the cytolytic infection in RD cells. Using reverse genetics, we identified a single amino acid change within the exposed region of the VP1 protein (glutamine to lysine at position 164) as the determinant for the acquired cytolytic trait. Moreover, this cytolytic virus induced apoptosis, including caspase activation and DNA degradation, in RD cells. These findings contribute to our understanding of the host cell adaptation process of CVB2O and provide a valuable tool for further studies of virus-host interactions.

**General information**

State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Pages: 5868-5879
Publication date: 2010
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Journal of Virology
Volume: 84
Issue number: 12
ISSN (Print): 0022-538X
Ratings:
- BFI (2018): BFI-level 2
- Web of Science (2018): Indexed yes
- BFI (2017): BFI-level 2
- Web of Science (2017): Indexed Yes
- BFI (2016): BFI-level 2
- Scopus rating (2016): SJR 3.052 SNIP 1.131 CiteScore 4.42
- Web of Science (2016): Indexed yes
- BFI (2015): BFI-level 2
- Scopus rating (2015): SJR 3.286 SNIP 1.138 CiteScore 4.42
- Web of Science (2015): Indexed yes
- BFI (2014): BFI-level 2
- Scopus rating (2014): SJR 3.168 SNIP 1.219 CiteScore 4.4
- Web of Science (2014): Indexed yes
- BFI (2013): BFI-level 2
- Scopus rating (2013): SJR 3.468 SNIP 1.26 CiteScore 4.92
- ISI indexed (2013): ISI indexed yes
- Web of Science (2013): Indexed yes
- BFI (2012): BFI-level 2
- Scopus rating (2012): SJR 3.154 SNIP 1.227 CiteScore 5.2
- ISI indexed (2012): ISI indexed yes
- Web of Science (2012): Indexed yes
- BFI (2011): BFI-level 2
- Scopus rating (2011): SJR 3.399 SNIP 1.288 CiteScore 5.37
- ISI indexed (2011): ISI indexed yes
- Web of Science (2011): Indexed yes
- BFI (2010): BFI-level 2
- Scopus rating (2010): SJR 3.532 SNIP 1.278
- Web of Science (2010): Indexed yes
- BFI (2009): BFI-level 2
- Scopus rating (2009): SJR 3.595 SNIP 1.307
- Web of Science (2009): Indexed yes
- BFI (2008): BFI-level 2
- Scopus rating (2008): SJR 3.803 SNIP 1.264
- Web of Science (2008): Indexed yes
- Scopus rating (2007): SJR 3.571 SNIP 1.311
A study on the applicability of implantable microchip transponders for body temperature measurements in pigs

Background The applicability of an electronic monitoring system using microchip transponders for measurement of body temperatures was tested in 6-week-old conventional Danish weaners infected with classical swine fever virus (CSFV). Subcutaneous tissue temperatures obtained by the implantable transponders were compared with rectal temperatures, recorded by a conventional digital thermometer. Methods In a preliminary study, transponders were inserted subcutaneously at 6 different positions of the body of 5 pigs. The transponders positioned by the ear base provided the best correlation to rectal temperature. To test the stability of the monitoring system in a larger group of pigs, transponders were therefore inserted by the left ear base in a subsequent infection experiment with 30 pigs. Results Generally, the microchip transponders measured a subcutaneous tissue temperature, which was about 1°C lower than the rectal temperature. However, a simple linear relationship between the measures of the two methods was found. Conclusions Our study showed that the tested body monitoring system may represent a promising tool to obtain an approximate correlate of body temperatures in groups of pigs. In contrast, however, the tested system did not constitute a suitable tool to measure body temperatures of individual animals in the present pig infection experiment.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research
Authors: Lohse, L. (Intern), Uttenthal, Å. (Intern), Enøe, C. (Intern), Nielsen, J. (Intern)
Publication date: 2010
Main Research Area: Technical/natural sciences

Publication information
Journal: Acta Veterinaria Scandinavica (Print Edition)
Volume: 52
Issue number: 29
ISSN (Print): 0044-605X
Ratings:
Web of Science (2018): Indexed yes
Web of Science (2017): Indexed Yes
Scopus rating (2016): CiteScore 1.01
Scopus rating (2015): CiteScore 0.98
Scopus rating (2014): CiteScore 1.54
Scopus rating (2013): CiteScore 1.41
Scopus rating (2012): CiteScore 1.26
Web of Science (2012): Indexed yes
Bluetongue in Denmark during 2008

General information
State: Published
Organisations: Sektion for Eksotiske Virusygdemme, Division of Virology, National Veterinary Institute
Authors: Rasmussen, L. D. (Intern), Rasmussen, T. B. (Intern), Belsham, G. (Intern), Strandbygaard, B. (Intern), Bøtner, A. (Intern)
Pages: 714-718
Publication date: 2010
Main Research Area: Technical/natural sciences

Publication information
Journal: Veterinary Record
Volume: 166
Issue number: 23
ISSN (Print): 0042-4900
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.442 SNIP 0.692 CiteScore 0.3
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.509 SNIP 0.794 CiteScore 0.39
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.469 SNIP 0.839 CiteScore 0.41
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.474 SNIP 0.821 CiteScore 0.5
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.491 SNIP 0.883 CiteScore 0.52
ISI indexed (2012): ISI indexed yes
Cellular and molecular immune responses of the sea bass (Dicentrarchus labrax) experimentally infected with betanodavirus

Naïve sea bass juveniles (38.4 ± 4.5 g) were intramuscularly infected with a sublethal dose of betanodavirus isolate 378/103, followed after 43 days by a similar boosting. This infection resulted in an overall mortality of 7.6%. At various intervals, sampling of fish tissues was performed to investigate: i) B and T lymphocyte content in organs and tissues; ii), proliferation of leucocytes re-stimulated in vitro with inactivated virus; iii) presence of serum antibody specific for betanodavirus; iv) expression of genes coding for the following immunoregulatory molecules involved in innate and acquired responses: type I IFN, Mx, IL-1, Cox-2; IL-10, TGF-β, TCRβ, CD4, CD8α, IgM, by using a quantitative PCR array system developed for sea bass. The obtained results showed a detectable increase of T cells and B cells in PBL during betanodavirus infection. Furthermore, leucocytes obtained from blood, head kidney, and gills showed a detectable “in vitro” increase in viability upon addition of inactivated viral particles, as determined by measuring intracellular ATP concentration. ELISA analysis of sera showed that exposure to nodavirus induced a low, but specific antibody titer measured 43 days after infection, despite the presence of measurable levels of natural antibody. Finally, a strong upregulation of genes coding for type I IFN, Mx, and IgM was identified after both infection and boosting. Interestingly, an upregulation of Cox-2 until boosting, and of TGF-β and IL-10 after boosting was also observed, while the other tested genes did not show any significant variations with respect to mock-treated fish. Overall, our work represents a first comprehensive analysis of cellular and molecular immune parameters in a fish species exposed to a pathogenic virus.

General information
State: Published
Classical swine fever infection in 6- and 11-week-old pigs: Haematological and immunological parameters are modulated in pigs with mild clinical disease

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Nielsen, J. (Intern), Lohse, L. (Intern), Rasmussen, T. B. (Intern), Uttenthal, Å. (Intern)
Pages: 159–173
Publication date: 2010
Main Research Area: Technical/natural sciences

Publication information
Journal: Veterinary Immunology and Immunopathology
Volume: 138
Issue number: 3
ISSN (Print): 0165-2427
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 1.63 SJR 0.73 SNIP 0.704
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 0.856 SNIP 0.752 CiteScore 1.67
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 0.768 SNIP 0.719 CiteScore 1.6
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 0.808 SNIP 0.805 CiteScore 1.89
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 0.837 SNIP 0.922 CiteScore 2.15
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 0.849 SNIP 0.996 CiteScore 2.16
Comparative study of ranavirus isolates from cod (Gadus morhua) and turbot (Psetta maxima) with reference to other ranaviruses

Two iridovirus isolates recovered from cod (Gadus morhua) and turbot (Psetta maxima) in Denmark were examined in parallel with a panel of other ranaviruses including frog virus 3 (FV3), the reference strain for the genus Ranavirus. The isolates were assessed according to their reactivity in immunofluorescent antibody tests (IFAT) using both homologous and heterologous antisera and their amplification in PCR using primers targeting five genomic regions. The corresponding PCR fragments were sequenced, and the sequences obtained were used in phylogenetic analysis. In addition, the pathogenicity to rainbow trout under experimental challenge conditions was investigated. The viruses were serologically and genetically closely related to highly pathogenic ranaviruses such as European catfish iridovirus (ECV), European sheatfish iridovirus (ESV) and epizootic haematopoietic necrosis virus (EHNV). The challenge trials indicate that rainbow trout fry cultured at 15°C are not target species for the virus isolates in the present panel. We suggest that the two isolates belong in the genus Ranavirus and propose the name Ranavirus maxima (Rmax) for the turbot isolate.
Issue number: 8
ISSN (Print): 0304-8608
Ratings:

BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.948 SNIP 0.879 CiteScore 2.16
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.083 SNIP 0.89 CiteScore 2.16
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.096 SNIP 1.041 CiteScore 2.37
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.002 SNIP 0.961 CiteScore 2.26
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.888 SNIP 0.943 CiteScore 2.12
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.902 SNIP 1.045 CiteScore 2.17
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.001 SNIP 0.98
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.904 SNIP 0.926
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.885 SNIP 1.023
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 0.875 SNIP 0.924
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.839 SNIP 0.97
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.883 SNIP 1.009
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.779 SNIP 0.935
Scopus rating (2003): SJR 0.807 SNIP 1.045
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.766 SNIP 0.897
Scopus rating (2001): SJR 0.752 SNIP 0.874
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 0.792 SNIP 0.939
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 0.739 SNIP 0.817
Original language: English
DOIs:
10.1007/s00705-010-0715-z
Source: orbit
Source-ID: 266359
Publication: Research - peer-review › Journal article – Annual report year: 2010
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
Authors: Belsham, G. (Intern), Polacek, C. (Intern), Breum, S. Ø. (Intern), Larsen, L. E. (Intern), Betnner, A. (Intern)
Pages: 7
Publication date: 2010
Main Research Area: Technical/natural sciences

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
Web of Science (2017): Indexed Yes
Scopus rating (2016): CiteScore 2.43 SJR 1.097 SNIP 0.894
Scopus rating (2015): SJR 1.185 SNIP 0.947 CiteScore 2.47
Scopus rating (2014): SJR 1.044 SNIP 0.911 CiteScore 2.27
Web of Science (2014): Indexed yes
Scopus rating (2013): SJR 1.031 SNIP 0.981 CiteScore 2.44
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
Scopus rating (2012): SJR 0.957 SNIP 0.866 CiteScore 2.37
ISI indexed (2012): ISI indexed yes
Scopus rating (2011): SJR 1.057 SNIP 0.9 CiteScore 2.65
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
Scopus rating (2010): SJR 1.071 SNIP 0.865
Web of Science (2010): Indexed yes
Scopus rating (2009): SJR 0.986 SNIP 0.754
Scopus rating (2008): SJR 0.618 SNIP 0.537
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 0.6 SNIP 0.562
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.845 SNIP 0.655
Scopus rating (2005): SJR 0.391 SNIP 0.358
Original language: English
Electronic versions:
Development of a monoclonal antibody against viral haemorrhagic septicaemia virus (VHSV) genotype IVa

The viral haemorrhagic septicaemia virus (VHSV) comprises 4 major genotypes and a number of subtypes with, in most cases, distinct geographical distribution. A quick and simple detection method that can discriminate the different genotypes is desirable for a quick and more efficient prevention of the spread of genotypes to new geographical areas. A monoclonal antibody (MAb) against VHSV genotype IVa was produced, with the aim of providing a simple method of discriminating this genotype from the other VHSV genotypes (I, II, III and IVb). Balb/c mice were injected with purified VHSV-JF00Ehil (genotype IVa) from diseased farmed Japanese flounder. Ten hybridoma clones secreting monoclonal antibodies (MAbs) against VHSV were established. One of these, MAb VHS-10, reacted only with genotype IVa in indirect fluorescent antibody technique (IFAT) and ELISA. Using cell cultures that were transfected with each of the viral protein genes, it was shown that the MAb VHS-10 recognizes a nonlinear genotype IVa-specific epitope on the VHSV N-protein.

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Tamaki Station, Aquatic Animal Health Division, Fisheries Research Agency
Authors: Ito, T. (Ekstern), Olesen, N. J. (Intern), Skall, H. F. (Intern), Sano, M. (Ekstern), Kurita, J. (Ekstern), Nakajima, K. (Ekstern), lida, T. (Ekstern)
Pages: 17-27
Publication date: 2010
Main Research Area: Technical/natural sciences

Publication information
Journal: Diseases of Aquatic Organisms
Volume: 89
Issue number: 1
ISSN (Print): 0177-5103
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.95 SJR 0.858 SNIP 0.929
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.949 SNIP 0.935 CiteScore 1.96
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.889 SNIP 0.881 CiteScore 1.86
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.812 SNIP 0.918 CiteScore 1.77
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.912 SNIP 1.092 CiteScore 2.04
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.11 SNIP 1.165 CiteScore 2.29
Development of a primer-probe energy transfer based real-time PCR for detection of Marek's disease virus

A real-time PCR assay, which enables simultaneous detection and differentiation of all three serotypes of Marek's disease virus, without the need for post-PCR sequencing, has been developed. The assay is based on the primer-probe energy transfer real-time PCR, which has a relatively high tolerance towards point mutations in the probe region. The PCR is followed by a probe melting point analysis, which enables confirmation of identity of amplicon and differentiation of serotypes. The assay targets the MDV031 gene, encoding UL19 major capsid protein-like protein and was shown to be quantitative, with a detection limit below 10 TCID50/ml starting material. This sensitivity is similar to the one obtained with traditional virus cultivation. However, the PCR method can provide a laboratory result within a day, while the virus cultivation method takes more than a week to perform. The new method will be useful for testing of avian live viral vaccines and screening for extraneous agents.

General information
State: Published
Organisations: National Veterinary Institute, Sektion for Eksotiske Virussygdomme, Division of Virology
Authors: Barfoed, A. M. (Intern), Østergaard, E. (Ekstern), Frandsen, P. (Ekstern), Nielsen, E. (Ekstern), Sandberg, E. (Ekstern), Rasmussen, T. B. (Intern)
Pages: 21-26
Publication date: 2010
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Virological Methods
Volume: 165
Issue number: 1
ISSN (Print): 0166-0934
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.87 SNIP 0.736 CiteScore 1.78
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.868 SNIP 0.799 CiteScore 1.68
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.893 SNIP 0.952 CiteScore 1.87
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.861 SNIP 0.91 CiteScore 1.99
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.869 SNIP 0.935 CiteScore 2.08
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.907 SNIP 0.994 CiteScore 2.23
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.892 SNIP 0.998
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.964 SNIP 1.061
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.918 SNIP 1.082
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 0.955 SNIP 1.029
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.879 SNIP 1.073
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.859 SNIP 1.005
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.715 SNIP 1.028
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.753 SNIP 1.008
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.736 SNIP 1.059
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.758 SNIP 0.949
Scopus rating (2000): SJR 0.684 SNIP 0.883
Scopus rating (1999): SJR 0.622 SNIP 0.823

Original language: English
Real-time PCR, Marek's disease virus, Primer-probe energy transfer
DOIs:
10.1016/j.viromet.2009.12.012
Source: orbit
Source-ID: 263514
Development of a real-time RT-PCR assay based on primer-probe energy transfer for the detection of all serotypes of bluetongue virus

A real-time RT-PCR assay based on the primer–probe energy transfer (PriProET) was developed to detect all 24 serotypes of bluetongue virus (BTV). BTV causes serious disease, primarily in sheep, but in other ruminants as well. A distinguishing characteristic of the assay is its tolerance toward mutations in the probe region. Furthermore, melting curve analysis following immediately PCR confirms specific probe hybridization and can reveal mutations in the probe region by showing a difference in the melting point. The assay sensitivity was in the range of 10–100 target copies and the specificity tests showed no positive results for heterologous pathogens. The assay was tested on clinical samples from BTV 8 outbreaks in Sweden and Denmark in 2008. The lowest detection limit for that serotype, determined with PCR standards, was 57 genome copies. The assay sensitivity for some other serotypes that circulate currently in Europe was also determined. BTV 2, 4, 9 and 16 were tested on available cell culture samples and the detection limits were 109, 12, 13 and 24 copies, respectively. This assay provides an important tool for early and rapid detection of a wide range of BTV strains, including emerging strains.
Development of a real-time RT-PCR assay based on primer-probe energy transfer for the detection of all twenty-four serotypes of bluetongue virus

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Leblanc, N. (Ekstern), Rasmussen, T. B. (Intern), Fernández, J. (Ekstern), Sailleau, C. (Ekstern), Rasmussen, L. D. (Intern), Uttenthal, Å. (Intern), Zientara, S. (Ekstern), Belák, S. (Ekstern), Hakhverdyan, M. (Ekstern)
Publication date: 2010
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 263936
Publication: Research - peer-review › Poster – Annual report year: 2010

Development of a real-time-RT-PCR suitable for the detection of Viral Haemorrhagic Septicaemia Virus (VHSV)

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Jonstrup, S. P. (Intern), Kahns, S. (Intern), Skall, H. F. (Intern), Olesen, N. J. (Intern)
Publication date: 2010
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 265710
Publication: Research - peer-review › Poster – Annual report year: 2010
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
Authors: Larsen, L. E. (Intern), Aastrup, P. (Ekstern), Hjulsager, C. K. (Intern), Larsen, K. V. (Ekstern)
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
Main Research Area: Technical/natural sciences
Conference: 21st International Pig Veterinary Society Congress, Vancouver, Canada, 18/07/2010 - 18/07/2010
Links:
http://www.ipvs2010.com/
Source: orbit
Source-ID: 282420
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2011

DIVA vaccination og diagnostik

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Rasmussen, T. (Intern), Uttenthal, Å. (Intern)
Pages: 21-23
Publication date: 2010
Main Research Area: Technical/natural sciences

Publication information
Journal: Dansk Veterinærtidsskrift
Volume: 92
Issue number: 22
ISSN (Print): 1600-2032
Ratings:
BFI (2008): BFI-level 1
Web of Science (2004): Indexed yes
Original language: Danish
Source: orbit
Source-ID: 270533
Publication: Communication › Journal article – Annual report year: 2010

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
Authors: Larsen, L. E. (Intern), Nielsen, C. K. (Ekstern), Aakerblom, S. (Ekstern), Hjulsager, C. K. (Intern), Nielsen, J. P. (Ekstern), Stege, H. H. (Ekstern), Kristensen, C. S. (Ekstern), Elvstrom, A. (Ekstern), Lau, L. (Ekstern)
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
Main Research Area: Technical/natural sciences
Conference: 21st International Pig Veterinary Society Congress, Vancouver, Canada, 18/07/2010 - 18/07/2010
Source: orbit
Source-ID: 282419
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2011
Early pathogenesis in porcine proliferative enteropathy caused by Lawsonia intracellularis

The intestinal bacterium Lawsonia intracellularis, the cause of proliferative enteropathy (PE) in pigs, is believed to infect mitotically active epithelial cells of the intestinal crypts and then multiply and spread in these cells as they divide. Further spread of infection is thought to occur by shedding of bacteria from infected crypts followed by infection of new crypts. The early stages of the pathogenesis of PE, from 0 to 48 hours post-infection (hpi), have not been studied in vivo. In the present study pigs were inoculated with L. intracellularis and killed from 12 hpi to 5 days post-infection (dpi). The localization of L. intracellularis was determined immunohistochemically and by fluorescence in-situ hybridization. At 12 hpi L. intracellularis was found within epithelial cells at the tips of villi, indicating infection of a range of epithelial cells including mature differentiated enterocytes. Furthermore, early invasion of the intestinal connective tissue was observed; with the presence of single bacteria in the lamina propria 12 hpi, and with a further spread of bacteria in the lamina propria observed at 5 dpi, suggesting an active role for the lamina propria in the course of infection.
Pig, Infection trial, Porcine proliferative enteropathy, Lawsonia intracellularis

DOIs:
10.1016/j.jcpa.2010.01.006

Source: orbit
Source-ID: 240896
Publication: Research - peer-review › Journal article – Annual report year: 2010


The risk that African Swine Fever virus (ASFV) remains endemic in the Trans Caucasian Countries (TCC) and the Russian Federation (RF) is moderate, while the risk of its spread in these regions is high. The resulting risk of introduction from these regions into the EU is moderate most likely through food waste. The risk of ASFV remaining endemic in wild boar and the consequent introduction into the EU was considered low in the TCC and moderate in the RF, mainly due to the higher population density in the RF and the connected wild boar populations to the EU from the RF. Within the EU, mainly domestic pigs in the free range (FR) and the limited biosecurity sector (LB) are likely to be exposed to ASFV via swill feeding, with low risk. Once infected, the risk of spread from the LB and FR sectors prior detection is high, mainly due to movement of pigs, people and vehicles and moderate from the High Biosecurity (HB) sector. The risk of endemicity in domestic pigs is considered negligible in HB and low in LB since the implementation of control measures are effective. The risk of endemicity in the FR sector is moderate due to wild boar contact, non-compliance with animal movement ban.
and difficult access to all individual pigs. The risk of ASFV becoming endemic in the wild boar population in the EU is moderate, in particular in areas with connected wild boar populations. Because of their long life, ticks of the O. erraticus complex can be important in maintaining local foci of ASFV, where pigs are kept under traditional systems. Ticks do not play an active role in the geographical spread of the virus. Wild boar have never been found infested because they do not rest inside burrows potentially infested by ticks.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, European Food Safety Authority
Authors: Betnner, A. (Intern), Peña, A. E. (Ekstern), Mannelli, A. (Ekstern), Wieland, B. (Ekstern), Potzsch, C. (Ekstern), Patta, C. (Ekstern), Albina, E. (Ekstern), Boinas, F. (Ekstern), Koenen, F. (Ekstern), Sharp, J. M. (Ekstern), Dixon, L. (Ekstern), Salmon, M. (Ekstern), Vizcaino, S. (Ekstern), Blome, S. (Ekstern), Guberti, V. (Ekstern), Dhillander, S. (Ekstern), Georgiev, M. (Ekstern), Tarres, J. (Ekstern), Goumperis, T. (Ekstern)
Number of pages: 149
Publication date: 2010

Publication information
Publisher: European Food Safety Authority
Edition: 8(3)
Original language: English
Series: EFSA Journal
Number: 1556
Main Research Area: Technical/natural sciences
DOIs: 10.2903/j.efsa.2010.1556
Source: orbit
Source-ID: 267686
Publication: Research › Report – Annual report year: 2010

Ekspertviden om svinepest

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Landbrug og Fødevarer, University of Copenhagen
Authors: Uttenthal, Å. (Intern), Nielsen, J. P. (Ekstern), Nielsen, V. (Ekstern), Westergaard, J. (Ekstern)
Pages: 10-11
Publication date: 2010
Main Research Area: Technical/natural sciences

Publication information
Journal: Dansk Veterinærtidsskrift
Volume: 93
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BFI (2008): BFI-level 1
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Original language: Danish
Source: orbit
Source-ID: 270532
Publication: Communication › Journal article – Annual report year: 2010

Evaluation of a method for recovery of noroviruses and hepatitis A virus from oysters and blue mussels

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Evaluation of a rapid method for recovery of norovirus and hepatitis A virus from oysters and blue mussels

**General information**

State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Norwegian School of Veterinary Science, University of Helsinki, Norwegian Institute of Public Health
Authors: Uhrbrand, K. (Intern), Myrmel, M. (Ekstern), Maunula, L. (Ekstern), Vainio, K. (Ekstern), Trebbien, R. (Intern), Nørrung, B. (Ekstern), Schultz, A. C. (Intern)
Publication date: 2010
Event: Abstract from 8th Symposium on Food Microbiology, Helsingør, Denmark.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 266431
Publication: Research › Conference abstract for conference – Annual report year: 2010

Foodborne outbreaks caused by noroviruses (NoVs) and hepatitis A virus (HAV) are often linked to consumption of contaminated shellfish. The objective of this study was to identify an appropriate virus recovery method for real-time reverse transcriptase (RT)-PCR detection and subsequently to evaluate this method on shellfish bioaccumulated with virus in a collaborative study. Five methods were compared for recovery of NoV GII.7 and feline calicivirus from spiked digestive tissue of oysters and mussels. A method based on proteinase K digestion followed by NucliSENS miniMAG extraction was found to be the most efficient with a 50% limit of detection (LOD50) of 62 and 12 RT-PCR U/1.5 g digestive tissue for NoV GII.7 in oysters and mussels, respectively. Evaluation of the method in four laboratories found the percentage of sensitivity, based on low/high levels of virus bioaccumulated in oysters, to be 33/80 for NoV GI.3b, 13/92 for NoV GII.4 and 50/42 for HAV. A specificity of 100% was found for all three viruses in non-bioaccumulated oysters. As process control Mengovirus (vMC0) showed an average recovery of 1.8% from oysters and 1.2% from mussels. The study demonstrates that this recovery method can be useful for harmonized data generation and routine viral analyses of shellfish.

**Publication information**

Journal: Journal of Virological Methods
Volume: 169
Issue number: 1
ISSN (Print): 0166-0934
Ratings:
  - BFI (2018): BFI-level 1
  - Web of Science (2018): Indexed yes
  - BFI (2017): BFI-level 1
  - Web of Science (2017): Indexed Yes
  - BFI (2016): BFI-level 1
  - Scopus rating (2016): SJR 0.87 SNIP 0.736 CiteScore 1.78
  - Web of Science (2016): Indexed yes
Evolutionary analysis of foot-and-mouth disease virus serotype SAT 1 isolates from east africa suggests two independent introductions from southern africa

Background: In East Africa, foot-and-mouth disease virus serotype SAT 1 is responsible for occasional severe outbreaks in livestock and is known to be maintained within the buffalo populations. Little is known about the evolutionary forces underlying its epidemiology in the region. To enhance our appreciation of the epidemiological status of serotype SAT 1...
virus in the region, we inferred its evolutionary and phylogeographic history by means of genealogy-based coalescent methods using 53 VP1 coding sequences covering a sampling period from 1948-2007. Results: The VP1 coding sequence of 11 serotype SAT 1 FMD viruses from East Africa has been determined and compared with known sequences derived from other SAT 1 viruses from sub-Saharan Africa. Purifying (negative) selection and low substitution rates characterized the SAT 1 virus isolates in East Africa. Two virus groups with probable independent introductions from southern Africa were identified from a maximum clade credibility tree. One group was exclusive to Uganda while the other was present within Kenya and Tanzania. Conclusions: Our results provide a baseline characterization of the inter-regional spread of SAT 1 in sub-Saharan Africa and highlight the importance of a regional approach to trans-boundary animal disease control in order to monitor circulating strains and apply appropriate vaccines.
Experimental vaccination of small turbot against bacterial and viral pathogens

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Bacteriology & Pathology, Division of Veterinary Diagnostics and Research, Fishlab, Intervet/Schering-Plough Animal Health, University of Copenhagen
Publication date: 2010
Event: Abstract from Dafinet-Scofda workshop, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Electronic versions:
E Lorenzen Dafinet november uændringer 2010v3[1].pdf
Source: orbit
Source-ID: 273817
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2010

Expression and characterisation of CSFV Erns protein in Pichia Pastoris

General information
State: Published
Organisations: Division of Virology, National Veterinary Institute, Sektion for Eksotiske Virussygdomme
Authors: Rasmussen, T. (Intern), Rasmussen, T. B. (Intern), Uttenthal, Å. (Intern)
Publication date: 2010
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 264098
Publication: Research - peer-review › Poster – Annual report year: 2010

Expression Profiling of Immune Response Genes in Rainbow Trout Following DNA Vaccination and VHS Virus Infection

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Rasmussen, J. S. (Intern), Christensen, M. B. (Intern), Einer-Jensen, K. (Intern), Lorenzen, E. (Intern), Lorenzen, N. (Intern)
Publication date: 2010
Event: Poster session presented at Symposium of the European Organisation of Fish Immunology, Viterbo, Italy.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 273927
Publication: Research - peer-review › Poster – Annual report year: 2010
First isolation and genotyping of viruses from recent outbreaks of viral haemorrhagic septicaemia (VHS) in Slovenia

In November and December 2007, the virus causing viral haemorrhagic septicaemia (VHS) was detected in rainbow trout Oncorhynchus mykiss from 2 fish farms in Slovenia. During 2008 and 2009 the infection spread only among rainbow trout farms and 4 new outbreaks were confirmed. High mortality and clinical signs of VHS were observed among the diseased fish. VHSV was confirmed by virus isolation, immunoperoxidase test, reverse transcriptase polymerase chain reaction (RT-PCR) and phylogenetic analysis. Based on 1 complete (1524 nucleotides [nt]) and 9 partial (600 nt) glycoprotein gene nucleotide sequences, 9 VHSV isolates from the 6 VHS outbreaks were genetically closely related (99 to 100% identity), and were classified into the Subgroup I-a of Genotype I, most closely related to the German isolates Dstg21-07, Dstg36-06, and Dstg54-1-07 (99 to 100% identity). Phylogenetic analysis and epidemiological investigations confirmed that the VHS virus had been (re)introduced with imported live fish, and that subsequent outbreaks were linked to the initial infection. Our study shows that direct nucleotide sequencing of RT-PCR products, amplified from the tissue of VHSV-infected fish, represents a reliable tool for fast routine genotyping in diagnostic laboratories. This is the first report of a natural epidemic associated with VHSV infection in Slovenia since the eradication of the disease in 1977.

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, University of Ljubljana
Authors: Toplak, I. (Ekstern), Hostnik, P. (Ekstern), Rihtaric, D. (Ekstern), Olesen, N. J. (Intern), Skall, H. F. (Intern), Jencic, V. (Ekstern)
Pages: 21-29
Publication date: 2010
Main Research Area: Technical/natural sciences

Publication information
Journal: Diseases of Aquatic Organisms
Volume: 92
Issue number: 1
ISSN (Print): 0177-5103
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.95 SJR 0.858 SNIP 0.929
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.949 SNIP 0.935 CiteScore 1.96
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.889 SNIP 0.881 CiteScore 1.86
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.812 SNIP 0.918 CiteScore 1.77
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.912 SNIP 1.092 CiteScore 2.04
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.11 SNIP 1.165 CiteScore 2.29
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.91 SNIP 0.951
Web of Science (2010): Indexed yes
Fishpathogens.eu: A database based on freeware suitable for storing isolate and sequence data of pathogens

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Symantix Ltd. UK
Authors: Jonstrup, S. P. (Intern), Jones, T. G. (Ekstern), Olesen, N. J. (Intern)
Publication date: 2010
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 268985
Publication: Research - peer-review › Journal article – Annual report year: 2010

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
Authors: Angen, Ø. (Intern), Jensen, T. K. (Intern), Melbak, L. (Intern), Larsen, L. E. (Intern), Jorsal, S. E. L. (Intern), Bækbo, P. (Ekstern)
Pages: 31
Publication date: 2010
Main Research Area: Technical/natural sciences
Generation of chimeric pestivirus mutants using Red/ET recombination-mediated mutagenesis

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Friedrich Loeffler Institute
Authors: Rasmussen, T. B. (Intern), Reimann, I. (Ekstern), Beer, M. (Ekstern)
Publication date: 2010
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 271977
Publication: Research - peer-review › Journal article – Annual report year: 2010

Generation of recombinant pestiviruses using a full-genome amplification strategy

Complete genome amplification of viral RNA provides a new tool for the generation of modified viruses. We have recently reported a full-genome amplification strategy for recovery of pestiviruses (Rasmussen et al., 2008). A full-length cDNA amplicon corresponding to the Border disease virus-Gifhorn genome was generated by long RT-PCR and then RNA transcripts derived from this amplicon were used to rescue infectious virus. Here, we have now used this full-genome amplification strategy for efficient and robust amplification of three additional pestivirus strains: the vaccine strain C and the virulent Paderborn strain of Classical swine fever virus plus the CP7 strain of Bovine viral diarrhoea virus. The amplicons were cloned directly into a stable single-copy bacterial artificial chromosome generating full-length pestivirus DNAs from which infectious RNA transcripts could be also derived.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Rasmussen, T. B. (Intern), Reimann, I. (Ekstern), Uttenthal, Å. (Intern), Leifer, I. (Ekstern), Depner, K. (Ekstern), Schirrmeier, H. (Ekstern), Beer, M. (Ekstern)
Pages: 13-17
Publication date: 2010
Main Research Area: Technical/natural sciences

Publication information
Journal: Veterinary Microbiology
Volume: 142
Issue number: 1-2
ISSN (Print): 0378-1135
Ratings:
BFI (2018): BFI-level 2
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BFI (2017): BFI-level 2
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.326 SNIP 1.208
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.393 SNIP 1.21 CiteScore 2.56
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.

**General information**
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics, Universidad Autonoma de Barcelona
Authors: Breum, S. Ø. (Intern), Hjulsager, C. K. (Intern), Deus, N. D. (Ekstern), Segalès, J. (Ekstern), Larsen, L. E. (Intern)
Publication date: 2010
Main Research Area: Technical/natural sciences

**Publication information**
Journal: Veterinary Microbiology
ISSN (Print): 0378-1135
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.326 SNIP 1.208
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.393 SNIP 1.21 CiteScore 2.56
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.281 SNIP 1.262 CiteScore 2.54
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.438 SNIP 1.484 CiteScore 3
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.437 SNIP 1.579 CiteScore 3.18
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.562 SNIP 1.738 CiteScore 3.27
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.371 SNIP 1.476
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.29 SNIP 1.472
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.169 SNIP 1.3
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.043 SNIP 1.322
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.022 SNIP 1.401
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.078 SNIP 1.262
Host response to Foot- and Mouth Disease infection in cattle; possible implications for the development of "carriers".

FMD is a viral disease with severe implications for agricultural trade in affected countries. Any cloven hoofed animal species may become infected, and ruminants, especially cattle and buffalo, may develop into "carriers" persistently shedding low amounts of virus for several years after exposure to the disease. The FMDV infection is defined as persistent when live virus can be detected for more than 28 days post infection. FMD infection in ruminants involves initial viral replication in pharyngeal epithelia, from where the virus spreads systemically. Characteristic vesicular lesions develop in the cornified stratified squamous epithelia of the coronary bands and oral cavity within a few days of infection. Viremia occurs within 2-3 days of infection, but is rapidly cleared through the effect of circulating antibodies generated by the adaptive immune response. The host response involves initial activation of the innate immune response, with activation and recruitment of effector-cells, and subsequent activation of T- and B-cells, leading to the production of circulating antibodies, as well as activation of cytotoxic T-cells. Previous experiments have indicated that the site of persistent replication of FMDV is located in pharyngeal lymphoid tissue, as well as the basal epithelia of the dorsal soft palate. A series of animal experiments, with the aim of investigating the host immune response, and sites of viral replication at different time points during both acute and persistent phases of FMDV infection in cattle has been performed. During these experiments, bull calves of 4-5 months of age were infected with FMDV O UKG 34/2001, and disease development was monitored for 32 days. Disease progression was monitored through observation of clinical signs, and analysis of serum for the presence of viral genomes as well as FMDV-specific antibodies. Viral shedding was measured through qPCR of mouth swabs and oropharyngeal fluid (probang samples). Tissue samples derived from endoscopical collection of biopsies of the dorsal soft palate from live animals at different times post infection, as well as samples of lymphoid tissue derived from staged post mortems were analysed for the presence of viral proteins through indirect immunofluorescence. These samples have also been analysed for the presence of specific populations of immune cells such as CD8+ T-cells and Dendritic cells. Biopsy samples are collected at different time points during acute and persistent infection in order to monitor the progress of viral replication, as well as the local cellular immune response, at specific sites over time. In order to measure the systemic response to infection, serum concentrations of acute phase proteins Serum Amyloid A (SAA) and Haptoglobin, as well as biologically active type 1 interferon (IFN 1) are being quantified. These markers of host immune response are also being used in order to detect any possible differences in host response throughout the infection in animals that become persistently infected compared to those that clear the infection effectively.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Innate Immunology, Division of Veterinary Diagnostics and Research, Technical University of Denmark
Authors: Stenfeldt, C. (Intern), Heegaard, P. M. H. (Intern), Tjørnehøj, K. (Ekstern), Belsham, G. (Intern)
Publication date: 2010
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 271675
Publication: Research - peer-review › Poster – Annual report year: 2010
Host response to Foot- and Mouth Disease infection in cattle; possible implications for the development of "carriers". Foot-and-mouth disease (FMD) is a viral disease with severe financial implications for agricultural industries and the trade of animal products in affected countries. Any cloven hoofed animal species may become infected, and ruminants, especially cattle and buffalo, may develop into persistently infected "carriers" shedding low amounts of virus for several years after exposure to the disease. FMD in ruminants involves initial viral replication in pharyngeal epithelia, from where the virus spreads systemically. Mortality rates are low in adult animals but the morbidity is very high and the disease spreads rapidly amongst susceptible animals. The host response involves initial activation of the innate immune response, followed by subsequent production of high titres of anti-FMDV antibodies in the circulation. Antibodies are effective in clearing virus from the circulation, but in a proportion of animals (approximately 50 % in cattle) the virus is capable of persisting at a low level within pharyngeal tissue. The animals are defined as persistently infected (« carriers ») when live virus can be detected in pharyngeal excretions for more than 28 days post infection, and the mechanisms involved in persistence of FMD in cattle are not fully known. A series of animal experiments, with the aim of investigating the innate immune response, and possible implications for the development of persistently infected FMD carrier-animals in cattle has been performed. Bull calves of 4-5 months of age were infected with FMDV O UKG 34/2001, and disease development was monitored for 35 days. Disease progression was monitored through observation of clinical signs and analysis of serum for the presence of viral genomes as well as FMDV-specific antibodies. Viral shedding was measured through qPCR of mouth swabs and oropharyngeal fluid (probang samples). Quantification of serum concentrations of acute phase proteins Serum Amyloid A (SAA) and Haptoglobulin (Hp), as well as biologically active type 1 interferon (IFN) indicated a clearly detectable acute phase response coinciding with the onset of clinical signs of disease. Results from these assays were compared to measurements of IFN α and -β, and Toll-like receptor 3 and -4 mRNA in small tissue samples derived from endoscopical collection of biopsies of the dorsal soft palate from live animals at different times post infection.

Identification of Genetic Virulence Markers in VHS Virus

Immersion exposure of rainbow trout (Oncorhynchus mykiss) fry to wildtype Flavobacterium psychrophilum induces no mortality, but protects against later intraperitoneal challenge
Flavobacterium psychrophilum, the causative agent of RTFS or rainbow trout fry syndrome, causes high mortality among hatchery reared rainbow trout (Oncorhynchus mykiss) fry in Europe and the USA. Despite several attempts, no efficient vaccines have yet been developed, the main obstacle being that the fry have to be vaccinated very early, i.e. around 0.2–0.5 g, where RTFS usually starts to give problems in the fish farms. Consequently, only oral or bath vaccines are relevant. Immersion of fry in inactivated or attenuated bacteria has resulted in RPS values of less than 50%. However, the results are biased by the fact that the fish have been challenged by intraperitoneal (ip) or subcutaneous (sc) injection against which an immersion/oral vaccine may not protect. Therefore, the present study was undertaken in order to investigate whether the presumably most potent immersion immunization, i.e. bathing in high titres of non-attenuated isolates of F. psychrophilum, was able to induce immunity to a subsequent ip challenge. Immersion in live bacteria for 30 or 50 min caused no mortality and protected a major fraction of the fry against challenges 28 and 47 days later with RPS values of 88.2 and 60.3%, respectively. Increased specific antibody titres suggested that adaptive immune mechanisms were involved in the protection.
Improved Safety for Molecular Diagnosis of Classical Rabies Viruses by Use of a TaqMan Real-Time Reverse Transcription-PCR "Double Check" Strategy

To improve the diagnosis of classical rabies virus with molecular methods, a validated, ready-to-use, real-time reverse transcription-PCR (RT-PCR) assay was developed. In a first step, primers and 6-carboxyfluorescien-labeled TaqMan probes specific for rabies virus were selected from the consensus sequence of the nucleoprotein gene of 203 different rabies virus sequences derived from GenBank. The selected primer-probe combination was highly specific and sensitive. During validation using a sample set of rabies virus strains from the virus archives of the Friedrich-Loeffler-Institut (FLI; Germany), the Veterinary Laboratories Agency (VLA; United Kingdom), and the DTU National Veterinary Institute (Lindholm, Denmark), covering the global diversity of rabies virus lineages, it was shown that both the newly developed assay and a previously described one had some detection failures. This was overcome by a combined assay that detected all samples as positive. In addition, the introduction of labeled positive controls (LPC) increased the diagnostic safety of the single as well as the combined assay. Based on the newly developed, alternative assay for the detection of rabies virus and the application of LPCs, an improved diagnostic sensitivity and reliability can be ascertained for postmortem and intra vitam real-time RT-PCR analyses in rabies reference laboratories.

General information

State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Friedrich Loeffler Institute, Veterinary Laboratories Agency
Authors: Hoffmann, B. (Ekstern), Freuling, C. M. (Ekstern), Wakeley, P. R. (Ekstern), Rasmussen, T. B. (Intern), Leech, S. (Ekstern), Fooks, A. R. (Ekstern), Beer, M. (Ekstern), Mueller, T. (Ekstern)
Pages: 3970-3978
Publication date: 2010
Main Research Area: Technical/natural sciences

Publication information

Journal: Journal of Clinical Microbiology
Volume: 48
Issue number: 11
ISSN (Print): 0095-1137
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BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.57 SJR 2.14 SNIP 1.417
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.204 SNIP 1.448 CiteScore 3.56
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.205 SNIP 1.538 CiteScore 3.84
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 2.414 SNIP 1.646 CiteScore 4.18
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.

**General information**

State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Virology
Authors: Reuter, G. (Ekstern), Zimsek-Mijovski, J. (Ekstern), Poljsak-Prijatelj, M. (Ekstern), Di Bartolo, I. (Ekstern), Ruggeri, F. (Ekstern), Kanta, T. (Ekstern), Maunula, L. (Ekstern), Kiss, I. (Ekstern), Kecskemeti, S. (Ekstern), Halaikel, N. (Ekstern), Buesa, J. (Ekstern), Johnsen, C. (Ekstern), Hjulsager, C. K. (Intern), Larsen, L. E. (Intern), Koopmans, M. (Ekstern), Bottiger, B. (Ekstern)
Pages: 363-368
Publication date: 2010
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Journal of Clinical Microbiology
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Issue number: 2
ISSN (Print): 0095-1137
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.57 SJR 2.14 SNIP 1.417
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.204 SNIP 1.448 CiteScore 3.56
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.205 SNIP 1.538 CiteScore 3.84
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 2.414 SNIP 1.646 CiteScore 4.18
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 2.114 SNIP 1.632 CiteScore 4.11
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 2.336 SNIP 1.698 CiteScore 4.27
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.303 SNIP 1.727
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 2.173 SNIP 1.694
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 2.239 SNIP 1.621
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 2.202 SNIP 1.689
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 Dyreklinitk, University of Copenhagen
Authors: Jessen, H. H. (Ekstern), Hjulsager, C. K. (Intern), Nielsen, J. P. (Ekstern), Stege, H. (Ekstern), Larsen, L. E. (Intern), Elvstrøm, A. (Ekstern)
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
Main Research Area: Technical/natural sciences
Conference: 21st International Pig Veterinary Society Congress, Vancouver, Canada, 18/07/2010 - 18/07/2010
Source: orbit
Source-ID: 263531
Publication: Research - peer-review › Journal article – Annual report year: 2010

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, Virology, Centre de Recerca en Sanitat Animal, Danish Agriculture and Food Council
Number of pages: 327
Pages: P.021
Publication date: 2010

Host publication information
Title of host publication: Proceedings of the 21st International Pig Veterinary Society Congress
Main Research Area: Technical/natural sciences
Insights into Cleavage Specificity from the Crystal Structure of Foot-and-Mouth Disease Virus 3C Protease Complexed with a Peptide Substrate

Foot-and-mouth disease (FMD) is a serious, widespread viral disease of cloven-hoofed animals, including important agricultural species such as cattle, sheep, pigs and goats (19, 45). The virus spreads rapidly and, although endemic and epidemic situations can be controlled using vaccines that are based on inactivated virus particles, political and technical difficulties with the maintenance and use of vaccine stocks has stimulated the search for alternative means of tackling the disease, such as anti-viral drugs (16). The development of such treatments will demand a detailed knowledge of the molecular basis of viral replication. In this paper we focus on the structural basis of the cleavage activity of FMDV 3Cpro; as a highly conserved viral enzyme (11), FMDV 3Cpro is a potential drug target.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Imperial College London
Authors: Zunszain, P. A. (Ekstern), Knox, S. R. (Ekstern), Sweeney, T. R. (Ekstern), Yang, J. (Ekstern), Roque-Rosell, N. (Ekstern), Belsham, G. (Intern), Leatherbarrow, R. J. (Ekstern), Curry, S. (Ekstern)
Pages: 375-389
Publication date: 2010
Main Research Area: Technical/natural sciences
In vivo screening of backbone modified siRNAs for their ability to induce interferon based off-target effects

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Aarhus University, University of Southern Denmark
Authors: Schyth, B. D. (Intern), Bramsen, J. B. (Ekstern), Kjems, J. (Ekstern), Wengel, J. (Ekstern), Lorenzen, N. (Intern)
Publication date: 2010
Main Research Area: Technical/natural sciences
Source: orbit
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Publication: Research - peer-review › Journal article – Annual report year: 2010

Joint experiences from experimental infections with CSFV Lithuania 2009

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, National Food and Veterinary Risk Assessment Institute, University of Veterinary Medicine
Authors: Uttenthal, Å. (Intern), Nielsen, J. (Intern), Lohse, L. (Intern), Strandbygaard, B. (Intern), Jaceviciene, I. (Ekstern), Morkunas, M. (Ekstern), Meindl-Böhmer, A. (Ekstern), Schmeiser, S. (Ekstern), Moennig, V. (Ekstern)
Publication date: 2010
Event: Abstract from Annual Meeting of the National Reference Laboratories of ASF, Pulawy, Poland, .
Main Research Area: Technical/natural sciences
Source: orbit
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Publication: Research - peer-review › Conference abstract for conference – Annual report year: 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
Authors: Valheim, M. (Ekstern), Gamlem, H. (Ekstern), Gjerset, B. (Ekstern), Larsen, L. E. (Intern), Lium, B. (Ekstern)
Number of pages: 588
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Title of host publication: Proceedings of the 21st International Pig Veterinary Society Congress
Main Research Area: Technical/natural sciences
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Source-ID: 282426
Publication: Research - peer-review » Conference abstract in proceedings – Annual report year: 2011

Målrettet design af DIVA vacciner gennem revers genetik

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Rasmussen, T. B. (Intern)
Number of pages: 66
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Journal: Dansk Veterinærtidsskrift
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Web of Science (2004): Indexed yes
Original language: Danish
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Publication: Research - peer-review » Journal article – Annual report year: 2010

MicroRNA regulation as a future diagnostic tool

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Schyth, B. D. (Intern)
Number of pages: 59
Publication date: 2010

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Title of host publication: 14th Annual Meeting of the National Reference Laboratories for Fish Diseases and Workshop on Use of Diagnostic kits for the Detection of Fish Diseases
Publisher: The European Union Reference Laboratory for Fish Diseases
Main Research Area: Technical/natural sciences
Conference: Annual Meeting of the National Reference Laboratories for Fish Diseases Copenhagen, Aarhus, Denmark, 01/01/2010
Electronic versions:
E61109C1d01.pdf
Source: orbit
Source-ID: 272369
Molecular epidemiology of current classical swine fever virus isolates of wild boar in Germany

Classical swine fever (CSF) has caused significant economic losses in industrialized pig production, and is still present in some European countries. Recent CSF outbreaks in Europe were mainly associated with strains of genogroup 2 (subgroup 2.3). Although there are extensive datasets regarding 2.3 strains, there is very little information available on longer fragments or whole classical swine fever virus (CSFV) genomes. Furthermore, there are no detailed analyses of the molecular epidemiology of CSFV wild boar isolates available. Nevertheless, complete genome sequences are supportive in phylogenetic analyses, especially in affected wild boar populations. Here, German CSFV strains of subgroup 2.3 were fully sequenced using two different approaches: (i) a universal panel of CSFV primers that were developed to amplify the complete genome in overlapping fragments for chain-terminator sequencing; and (ii) generation of a single full-length amplicon of the CSFV genome obtained by long-range RT-PCR for deep sequencing with next-generation sequencing technology. In total, five different strains of CSFV subgroup 2.3 were completely sequenced using these newly developed protocols. The approach was used to study virus spread and evolutionary history in German wild boar. For the first time, the results of our study clearly argue for the possibility of a long-term persistence of genotype 2.3 CSFV strains in affected regions at an almost undetectable level, even after long-term oral vaccination campaigns with intensive monitoring. Hence, regional persistence in wild boar populations has to be taken into account as an important factor in the continual outbreaks in affected areas.
Molecular epidemiology of zoonotic streptococcosis/lactococcosis in rainbow trout (Oncorhynchus mykiss) aquaculture in Iran

Background and Objectives: Streptococcosis/lactococcosis is a hyperacute systemic disease that can occur in marine and fresh waters of many species of fish. The aim of this work was to study the disease outbreak in the major rainbow trout (Oncorhynchus mykiss) production of Iran.

Materials and Methods: 108 Gram positive cocci isolates were obtained from diseased trout in seven provinces with major trout production during 2008 till 2009. These bacterial isolates were characterized using phenotypic and molecular studies. The isolates were also analysed phylogeneticaly and compared with the available data.

Results: 49 samples (45.37%) were identified as Streptococcus iniae, 37 samples (35.2%) matched with Lactococcus garvieae; and 22 samples (19.43%) were identified as members of Streptococcus genus by culture-based and biochemical tests of API 50 CH, API 20 STREP and rapid 32 STREP systems. Using universal primers for differentiation of Streptococcus sp. and Enterococcus sp, all 108 samples were identified as Streptococcus sp. with a target region of 500 bp. Single specific PCR resulted in identification of 64 (59.2%) isolates as S. iniae and 44 (40.8%) isolates as L. garvieae. The phylogenetic analysis of the S. iniae isolates resulted in maximal similarity to some strains reported from Taiwan and to all Brazilian strains. Also, one strain showed less sequence similarity values with other tested strains although this strain has high similarity with ATCC 29178 strain, all reported Chinese, and some Taiwanian strains. Also, analysis of S. iniae LctO gene sequence showed that this isolate clustered within the S. iniae group. The sequence analysis of L. garvieae strains also showed that they have maximum similarity to all Japanese and Chinese strains, but one strain has lower sequence similarity values with all other recorded strains.

Conclusion: The results of this study clearly show that trout farming in Iran is severely affected by both species of S. iniae and L. garvieae and requires serious preventive criteria.

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, University of Tehran, Inland Water Aquaculture Institute
Authors: Karsidani, S. H. (Ekstern), Soltani, M. (Ekstern), Nikbakhat-Brojeni, G. (Ekstern), Ghasemi, M. (Ekstern), Skall, H. F. (Intern)
Molecular tracing of viral haemorrhagic septicaemia viruses from Denmark provides evidence of more viral clades and cases of introduction through long distance transportation

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Kahns, S. (Intern), Skall, H. F. (Intern), Jonstrup, S. P. (Intern), Einer-Jensen, K. (Intern), Olesen, N. J. (Intern)
Publication date: 2010
Main Research Area: Technical/natural sciences
Electronic versions:
Epizone_Kahns_2011_1[1].pdf
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N-Linked Glycans on the Viral Glycoprotein are not Required for Induction of Protective Immunity to VHSV when Delivered as a DNA Vaccine

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Einer-Jensen, K. (Intern), Lorenzen, E. (Intern), Rasmussen, J. S. (Intern), Lorenzen, N. (Intern)
Publication date: 2010
Event: Abstract from 8th International Symposium on Viruses of Lower Vertebrates, Santiago de Compostela, Spain.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 273922
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2010

Novel DIVA vaccine candidates generated by recombination-mediated mutagenesis

General information
Ontogeny and characterization of blood leukocyte subsets and serum proteins in piglets before and after weaning

Existing knowledge about the development of the porcine immune system was extended by phenotypic characterization of leukocyte subsets and with assessment of Mannan-Binding Lectin (MBL) and immunoglobulin concentrations in peripheral blood of healthy piglets. Single-color and/or double-color flow cytometry using monoclonal antibodies against CD1, CD3, CD4, CD8α CD14, CD21, CD172 (SWC3a), CD284 (TLR4), SLA1, and SLA2 were performed to identify T-lymphocyte subsets, B-lymphocytes, monocytes, and granulocytes. ELISA was used to measure the concentration of serum proteins. Several of the analyzed parameters seem to be affected at the time of weaning which took place at 45 weeks of age. Using principal component analysis, all analyzed variables - except one were grouped into 8 factors with distinct developmental profiles. Several of these factors revealed an apparent suppression, a steady state or an acceleration of the developmental age profiles around weaning. In conclusion, results indicate that weaning suppresses a broad spectrum of biological functions.
of adaptive immune variables and that this was evident immediately after weaning as well as after a lag period of about one week. On the contrary, variables of the innate immune system seem to be stimulated immediately after weaning. At the time considered to have the highest infection pressure T-cells and TLR4+ cells were markedly enhanced, whereas the expression of SLA I did not seem to be affected by weaning.
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
Authors: Chriél, M. (Intern), Jensen, T. H. (Intern), Hjulsager, C. K. (Intern), Larsen, L. E. (Intern), Harslund, J. L. F. (Intern), Rangstrup-Christensen, L. (Intern), Pedersen, B. (Ekstern), Hammer, A. S. (Intern)
Publication date: 2010
Event: Abstract from FAO/OIE OFFLU Annual Technical Meeting, Rome, Italy.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 263532
Publication: Research - peer-review › Journal article – Annual report year: 2010

Patterns, risk factors and characteristics of reported and perceived foot-and-mouth disease (FMD) in Uganda

Patterns of outbreaks of foot-and-mouth disease (FMD) in Uganda were elucidated from spatial and temporal retrospective data retrieved from monthly reports from District Veterinary Officers (DVOs) to the central administration for the years spanning 2001–2008. An assessment of perceived FMD occurrence, risk factors and the associated characteristics was made based on semi-structured questionnaires administered to the DVOs. During this period, a total of 311 FMD outbreaks were reported in 56 (70%) out of Uganda’s 80 districts. The number of reported FMD outbreaks changed over time and by geographical regions. Occurrence of FMD was significantly associated with the dry season months (p = 0.0346), the time when animals movements are more frequent. The average number of FMD outbreaks was higher for some sub-counties adjacent to national parks than for other sub-counties, whilst proximity to international border only seemed to play a role at the southern border. DVOs believed that the major risk factor for FMD outbreaks was animal movements (odds ratio OR 50.8, confidence interval CI 17.8–144.6) and that most outbreaks were caused by introduction of sick animals.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Ministry of Agriculture, Animal Industry and Fisheries, Makerere University, University of Copenhagen
Authors: Ayebazibwe, C. (Ekstern), Tjørnehøj, K. (Intern), Mwiine, F. N. (Ekstern), Muwanika, V. B. (Ekstern), Ademun Okurut, A. R. (Ekstern), Siegismund, H. R. (Ekstern), Alexandersen, S. (Intern)
Pages: 1547-1559
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Main Research Area: Technical/natural sciences
Publication information
Journal: Tropical Animal Health and Production
Volume: 42
Prevalence of Antibodies Against Foot-and-Mouth Disease Virus in Cattle in Kasese and Bushenyi Districts in Uganda

Abstract: The aim of this study was to determine the seroprevalence and serotype-specificity of the circulating antibodies against Foot-and-Mouth Disease Virus (FMDV) in cattle in Kasese and Bushenyi districts in Uganda. A total of 309 serum samples were collected and tested for antibodies against Non-Structural (NS) and Structural Proteins (SP) using Ceditest® FMDV-NS and Ceditest® FMDV type O test kits. Seroprevalences were much higher in Kasese in both tests (61 and 43%, respectively) than in Bushenyi (3 and 4%, respectively). A high proportion of sera, that tested positive in the NSP test, were subjected to seven serotype specific blocking ELISAs for antibodies against the seven FMDV serotypes (O, A, C, Asia 1, SAT 1, SAT 2 and SAT 3). The study showed presence of antibodies against four FMDV serotypes with decreasing magnitude as follows: O > SAT 1 > SAT 3/SAT 2. It is recommended to develop sampling schemes to include virus recovery and identification, as well as to focus serum sampling on young unvaccinated stock.
Prevalence of *Escherichia coli* O157 and verocytotoxin producing *E. coli* (VTEC) on Danish beef carcasses

The prevalence of verocytotoxin producing *Escherichia coli* (VTEC), *E. coli* O157, and VTEC O157 in 474 swab samples from Danish beef carcasses was determined. The presence of *E. coli* O157 was determined by a culture method that included immunomagnetic separation (IMS) followed by real time PCR testing of isolates for verocytotoxin (vtx) genes. *E. coli* O157 was recovered from 4.2% of the carcass samples and VTEC O157 from 3.4% of the samples. All VTEC O157 contaminated carcasses were from bull calves and the VTEC O157 prevalence on bull calf carcasses was 7.3%. The VTEC O157 contaminated beef carcasses were sampled again after one week of cold storage, and 15 of the 16 carcasses were then VTEC O157 negative. The presence of VTEC was determined by a duplex real time PCR assay for vtx1 and vtx2 in DNA from enrichment cultures of swabs. In total 45.4% of the samples were VTEC positive. VTEC were isolated from 21% of 77 vtx-positive samples that were identified by replication of colonies on hydrophobic grid membrane filters followed by hybridisation with vtx specific DNA probes. Fourteen of the 16 VTEC isolates were non-O157 and these strains were negative for the virulence gene eae. A real time PCR assay for the *E. coli* O157 specific rfbE gene was developed. In total 22.4% of the enriched samples were positive for the O157 rfbE gene. The combined results of the vtx and rfbE real time PCR screening showed that 17.5% of the carcasses potentially were contaminated with VTEC O157. Screening of carcass swabs was expanded by real time PCR testing for eae in a subset of the samples. Of 244 samples, 25.4% were positive for both vtx and eae. The eae gene was detected in 81% of the vtx-positive samples and in 46% of 67 vtx-negative samples, indicating that bacteria harbouring eae are widespread on bovine carcasses. The present study shows that real time PCR screening of carcass samples for genes encoding virulence or other genetic markers is a reliable method for rapid identification of carcasses that potentially are contaminated with VTEC.
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Scopus rating (2016): CiteScore 3.97 SJR 1.462 SNIP 1.554
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.628 SNIP 1.694 CiteScore 4.02
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.501 SNIP 1.711 CiteScore 3.62
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.602 SNIP 1.86 CiteScore 3.8
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Scopus rating (2011): SJR 1.595 SNIP 1.717 CiteScore 3.63
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Web of Science (2009): Indexed yes
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Scopus rating (2008): SJR 1.486 SNIP 1.511
Web of Science (2008): Indexed yes
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Web of Science (2006): Indexed yes
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Web of Science (2002): Indexed yes
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Publication: Research - peer-review › Journal article – Annual report year: 2010
Protection Against Viral Haemorrhagic Septicemia Virus (VHSV) in Rainbow Trout Using a DNA Vaccine with MX1 Promotor Controlled Expression of the Viral G Protein

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

Rabies 2009 - Rabies hos dyr

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, Veterinary Laboratories Agency, Philipps-Universität Marburg, Agence Francaise de Sécurite des Aliments, Merital S.A.S., Hipra, Istituto Zooprofilattico Sperimentale della Lombardia e dell’Emilia, Central Veterinary Institute, Ghent University
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Web of Science (2017): Indexed yes
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Scopus rating (2016): CiteScore 3.11 SJR 1.201 SNIP 1.092
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.414 SNIP 1.131 CiteScore 3.32
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.545 SNIP 1.141 CiteScore 3.54
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.74 SNIP 1.147 CiteScore 3.94
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.945 SNIP 1.142 CiteScore 4.15
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 2.369 SNIP 1.23 CiteScore 4.58
ISI indexed (2011): ISI indexed no
Response to Viral Infection differs between families of Rainbow Trout

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Aarhus University, Department of Fisheries and Oceans, University of Victoria
Authors: Jørgensen, H. (Ekstern), Sørensen, P. (Ekstern), Cooper, G. (Ekstern), Lorenzen, E. (Intern), Hansen, M. (Ekstern), Koop, B. (Ekstern), Henryon, M. (Ekstern)
Publication date: 2010
Event: Abstract from Animal Genomics for Animal Health, Paris,
Main Research Area: Technical/natural sciences
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AGAH 2010 HJ abstract[1].pdf
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Source-ID: 258178
Publication: Research - peer-review › Journal article – Annual report year: 2010

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.

General information
State: Published
Organisations: National Veterinary Institute, Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, Microbial Ecology, Virology, Pig Vet Consult, Danish Pig Production
Sero-epidemiological investigation of foot-and-mouth disease virus serotypes in cattle around Lake Mburo National Park in South-Western Uganda

Foot-and-mouth disease (FMD) outbreaks in cattle occur annually in Uganda. In this study the authors investigated antibodies against FMDV in cattle in surrounding areas of Lake Mburo National Park in South-western Uganda. Two hundred and eleven serum samples from 23 cattle herds were examined for the presence of antibodies against FMDV non-structural proteins and structural proteins using Ceditest® FMDV-NS and Ceditest® FMDV type O (Cedi Diagnostics BV, Lelystad, The Netherlands). Furthermore, serotype-specific antibodies against the seven serotypes of FMDV were determined using in-house serotype-specific Solid Phase Blocking ELISAs (SPBE). Of the sera tested, 42.7% (90/211) were positive in the ELISA for antibodies against non-structural proteins, while 75.4% (159/211) had antibodies against the structural proteins of FMDV serotype O. Titres of ≥ 1:160 of serotype-specific antibodies in SPBEs were identified in 61% (19/31), 33% (5/15), 6%7 (20/30), 37% (10/27) and 12% (4/33) of the investigated samples for serotypes O, A, SAT 1, SAT 2 and SAT 3, respectively. This study indicates that most of the FMD outbreaks in the cattle herds in the investigated area were probably caused by FMDV serotype O, A and/or SAT-serotype(s). It also shows that the usage of non-purified, multivalent vaccines in Uganda obscures the serological diagnosis of FMDV outbreaks, and that the sampling strategy needs to be improved. Finally, it emphasizes the importance of isolation and characterization of FMD viruses responsible for outbreaks in the area.

General information
State: Published
Organisations: National Veterinary Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, Makerere University, Ministry of Agriculture, Animal Industry and Fisheries
Pages: 46-54
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Main Research Area: Technical/natural sciences

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Volume: 2
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Original language: English
Cattle, Antibodies, Uganda, Foot-and-mouth-disease
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Publication: Research - peer-review › Journal article – Annual report year: 2010

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, OE-Vet, Danvet K/S

Electronic versions:
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Links:
http://www.academicjournals.org/JVMAH/contents/2010%20Content/Nov.htm
Source: orbit
Source-ID: 273827
Publication: Research - peer-review › Journal article – Annual report year: 2010
Serotype Specificity of Antibodies against Foot-and-Mouth Disease Virus in Cattle in Selected Districts in Uganda

Uganda had an unusually large number of foot-and-mouth disease (FMD) outbreaks in 2006, and all clinical reports were in cattle. A serological investigation was carried out to confirm circulating antibodies against foot-and-mouth disease virus (FMDV) by ELISA for antibodies against non-structural proteins and structural proteins. Three hundred and forty-nine cattle sera were collected from seven districts in Uganda, and 65% of these were found positive for antibodies against the non-structural proteins of FMDV. A subset of these samples were analysed for serotype specificity of the identified antibodies. High prevalences of antibodies against non-structural proteins and structural proteins of FMDV serotype O were demonstrated in herds with typical visible clinical signs of FMD, while prevalences were low in herds without clinical signs of FMD. Antibody titres were higher against serotype O than against serotypes SAT 1, SAT 2 and SAT 3 in the sera investigated for serotype-specific antibodies. Only FMDV serotype O virus was isolated from one probang sample. This study shows that the majority of the FMD outbreaks in 2006 in the region studied were caused by FMDV serotype O; however, there was also evidence of antibodies to both SAT 1 and SAT 3 in one outbreak in a herd inside Queen Elizabeth national park area.

General Information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Mwine, F. (Ekstern), Ayebazibwe, C. (Ekstern), Olaho-Mukani, W. (Ekstern), Alexandersen, S. (Ekstern), Balinda, S. (Ekstern), Masembe, C. (Ekstern), Okurut, A. (Ekstern), Christensen, L. S. (Intern), Sørensen, K. (Ekstern), Tjørnehøj, K. (Intern)
Pages: 365-374
Publication date: 2010
Main Research Area: Technical/natural sciences

Publication information
Journal: Transboundary and Emerging Diseases
Volume: 57
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BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.16 SJR 0.994 SNIP 1.096
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.258 SNIP 1.262 CiteScore 2.29
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.038 SNIP 1.19 CiteScore 2.23
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.953 SNIP 1.123 CiteScore 2.33
Strategies for differentiating infection in vaccinated animals (DIVA) for foot-and-mouth disease, classical swine fever and avian influenza

The prophylactic use of vaccines against exotic viral infections in production animals is undertaken exclusively in regions where the disease concerned is endemic. In such areas, the infection pressure is very high and so, to assure optimal protection, the most efficient vaccines are used. However, in areas considered to be free from these diseases and in which there is the possibility of only limited outbreaks, the use of Differentiation of Infected from Vaccinated Animals (DIVA) or marker vaccines allows for vaccination while still retaining the possibility of serological surveillance for the presence of infection. This literature review describes the current knowledge on the use of DIVA diagnostic strategies for three important transboundary animal diseases: foot-and-mouth disease in cloven-hoofed animals, classical swine fever in pigs and avian influenza in poultry.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, The Pirbright Institute, Friedrich Loeffler Institute, Instituto Zooprofilattico Sperimentale delle Venezie
Authors: Uttenthal, Å. (Intern), Parida, S. (Ekstern), Rasmussen, T. B. (Intern), Paton, D. (Ekstern), Haas, B. (Ekstern), Dundon, W. (Ekstern)
Pages: 73-87
Publication date: 2010
Main Research Area: Technical/natural sciences

Publication information
Journal: Expert Review of Vaccines
Volume: 9
Issue number: 1
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
Authors: Breum, S. Ø. (Intern), Hjulsager, C. K. (Intern), Trebbien, R. (Intern), Larsen, L. E. (Intern)
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
Main Research Area: Technical/natural sciences
Conference: The International Symposium on Neglected Influenza Viruses, Amelia Island, Florida, USA, 01/01/2010
Source: orbit
Source-ID: 265784
Publication: Research - peer-review › Conference abstract in proceedings – Annual report year: 2010

**Studies on herd-immunity and primary versus secondary infection of VHSV in challenge and vaccination trials with rainbow trout**

**General information**
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Lorenzen, E. (Intern), Kjær, T. E. (Intern), Lorenzen, N. (Intern)
Publication date: 2010
Event: Abstract from Symposium of the European Organization of Fish Immunology, Viterbo, Italy,
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 273823
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2010

**Svineinfluenza – status og afklaring af nomenclatur**

**General information**
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics
Authors: Larsen, L. E. (Intern), Hjulsager, C. K. (Intern)
Publication date: 2010
Main Research Area: Technical/natural sciences

**Publication information**
Journal: Dansk Veterinærtidsskrift
Volume: 93
Issue number: 10
ISSN (Print): 1600-2032
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BFI (2008): BFI-level 1
Web of Science (2004): Indexed yes
Original language: Danish
Source: orbit
Source-ID: 282203
Publication: Research - peer-review › Journal article – Annual report year: 2011

**Temperature effects on vaccine induced immunity to viruses in fish**
Abstract In poikilothermic vertebrates such as teleost fishes, temperature affects all physiological processes including host-pathogen interactions like immune response and propagation of infection. Whether an infection with a pathogenic virus in fish results in development of clinical disease often depends on the balance between virus multiplication and anti viral immune reactions in the host. Water temperature is one of the most important factors influencing the balance between the fish and its environment. Usually, an optimal immune response of a particular fish species is obtained at its normal summer temperature whereas low temperatures may be immunosuppressive. Although innate and adaptive immune response mechanisms should be considered as integrated parts of the immunedefence, low temperatures appears to affect (inhibit) adaptive mechanisms more than innate mechanisms. This might represent a problem in terms of inducing a
protective immune response by vaccination in aquaculture, since it is often desirable to vaccinate fish during autumn, winter, or spring. In experimental vaccination trials with rainbow trout (Oncorhynchus mykiss) using a DNA-vaccine encoding the viral glycoprotein of viral haemorrhagic septicaemia virus (VHSV), non-specific as well as specific immune mechanisms seemed to be delayed at low temperature. At five weeks post vaccination fish kept at 5°C had no detectable response of neutralising antibodies while two thirds of the fish kept at 15°C had sero-converted. While protective immunity was still established at both temperatures, specificity analysis suggested that protection at the lower temperature was mainly due to non-specific innate antiviral mechanisms, which appeared to last longer at low temperature. This was presumably related to a prolonged persistence of the vaccine. In DNA vaccination trials with spring viremia of carp (SVC) in common carp (Cyprinus carpio), protection at low temperature (10°C) appeared to require considerably longer time to develop compared to at 19°C, stressing that determination of optimal vaccination strategies in terms of temperature related effects need to be based on experimental evidence with the actual host and pathogen species rather on general principles.

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Veterinary Research Institute, Brno, Czech Republic
Publication date: 2010
Event: Abstract from 8th International Symposium on Viruses of Lower Vertebrates, Santiago de Compostela, Spain.
Main Research Area: Technical/natural sciences
Electronic versions: NLorenzen VLV 2010 abstract[1].pdf
Source: orbit
Source-ID: 273834
Publication: Research › Conference abstract for conference – Annual report year: 2010

The role of African buffalos (Syncerus caffer) in the maintenance of foot-and-mouth disease in Uganda
Background To study the role of African buffalos (Syncerus caffer) in the maintenance of foot-and-mouth disease in Uganda, serum samples were collected from 207 African buffalos, 21 impalas (Aepyceros melampus), 1 giraffe (Giraffa camelopardalis), 1 common eland (Taurotragus oryx), 7 hartebeests (Alcelaphus buselaphus) and 5 waterbucks (Kobus ellipsiprymnus) from four major National Parks in Uganda between 2005 and 2008. Serum samples were screened to detect antibodies against foot-and-mouth disease virus (FMDV) non-structural proteins (NSP) using the Ceditest FMDV NS ELISA. Solid Phase Blocking ELISAs (SPBE) were used to determine the serotype-specificity of antibodies against the seven serotypes of FMDV among the positive samples. Virus isolation and sequencing were undertaken to identify circulating viruses and determine relatedness between them. Results Among the buffalo samples tested, 85% (95% CI = 80-90%) were positive for antibodies against FMDV non-structural proteins while one hartebeest sample out of seven (14.3%; 95% CI = -11.6-40.2%) was the only positive from 35 other wildlife samples from a variety of different species. In the buffalo, high serotype-specific antibody titres (equal to or greater than 80) were found against the four serotypes O (7/27 samples), SAT 1 (23/29 samples), SAT 2 (18/32 samples) and SAT 3 (16/30 samples). Among the samples titrated for antibodies against the four serotypes O, SAT 1, SAT 2 and SAT 3, 17/22 (77%; CI = 59.4-94.6%) had high titres against at least two serotypes. FMDV isolates of serotypes SAT 1 (1 sample) and SAT 2 (2 samples) were obtained from buffalo probang samples collected in Queen Elizabeth National Park (QENP) in 2007. Sequence analysis and comparison of VP1 coding sequences showed that the SAT 1 isolate belonged to topotype IV while the SAT 2 isolates belonged to different lineages within the East African topotype X. Conclusions Consistent detection of high antibody titres in buffalos supports the view that African buffalos play an important role in the maintenance of FMDV infection within National Parks in Uganda. Both SAT 1 and SAT 2 viruses were isolated, and serological data indicate that it is also likely that FMDV serotypes O and SAT 3 may be present in the buffalo population. Detailed studies should be undertaken to define further the role of wildlife in the epidemiology of FMDV in East Africa.

General information
State: E-pub ahead of print
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Ministry of Agriculture, Animal Industry and Fisheries, Makerere University, Ministry of Agriculture, Water and Forestry, University of Copenhagen
Authors: Ayebazibwe, C. (Ekstern), Mwine, F. N. (Ekstern), Tjarnehej, K. (Intern), Balinda, S. N. (Ekstern), Muwanika, V. B. (Ekstern), Okurut, A. R. A. (Ekstern), Belsham, G. (Intern), Normann, P. (Intern), Siegismund, H. R. (Ekstern), Alexandersen, S. (Intern)
Publication date: 2010
Main Research Area: Technical/natural sciences

Publication information
Journal: B M C Veterinary Research
Volume: 6
Issue number: 54
Tidlig varsling af sygdom med microchip transponder

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research
Authors: Lohse, L. (Intern), Nielsen, J. (Intern), Enøe, C. (Intern), Uttenthal, Å. (Intern)
Pages: 12-14
Publication date: 2010
Main Research Area: Technical/natural sciences
Using small interfering RNAs (siRNAs) to combat a fish pathogenic virus

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Schyth, B. D. (Intern), Lorenzen, N. (Intern)
Publication date: 2010
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 270995
Publication: Communication › Journal article – Annual report year: 2010

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, OE-Vet, Danvet K/S
Authors: Haugegaard, J. (Ekstern), Astrup, P. (Ekstern), Haugegaard, S. (Ekstern), Larsen, C. B. (Ekstern), Hjulsager, C. K. (Intern), Larsen, L. E. (Intern)
Pages: 24-28
Publication date: 2010
Main Research Area: Technical/natural sciences
Publication information
Journal: Dansk Veterinaertidsskrift
Volume: 93
Issue number: 5
ISSN (Print): 0106-6854
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BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
ISI indexed (2012): ISI indexed no
BFI (2011): BFI-level 1
Validation of real-time RT-PCR for molecular diagnosis of classical rabies virus in brain samples from Greenland

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Rasmussen, T. B. (Intern)
Publication date: 2010
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 282041
Publication: Research › Journal article – Annual report year: 2011

Viral diseases of fish and a possible role for small regulatory RNAs in their antiviral defence

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, University of Tehran
Authors: Schyth, B. D. (Intern), Jalali, S. A. H. (Ekstern), Kristensen, L. B. J. (Intern), Lorenzen, N. (Intern)
Publication date: 2010
Event: Abstract from Theme 5 Annual Meeting : Intervention Strategies, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 265705
Publication: Research › Poster – Annual report year: 2010

Viral haemorrhagic septicaemia virus (VHSV) genotype II isolated from European river lamprey Lampetra fluviatilis in Finland during surveillance from 1999 to 2008

We examined the occurrence of viral haemorrhagic septicaemia virus (VHSV) in the main spawning stocks of wild European river lamprey Lampetra fluviatilis in the rivers of Finland from 1999 to 2008. Pooled samples of internal organs (kidney, liver and heart or brain) from 2621 lampreys were examined for the presence of VHSV by standard virological techniques. VHSV was isolated from 5 samples from the rivers Lestijoki and Kalajoki, which flow from Finland into the Bothnian Bay of the Baltic Sea. The presence of VHSV was confirmed by immunofluorescent antibody technique (IFAT), ELISA and RT-PCR. Phylogenetic analysis based on the full-length VHSV glycoprotein (G) gene sequence revealed that the isolates were most closely related to the VHSV strain isolated in 1996 from herring Clupea harengus and sprat Sprattus sprattus in the Eastern Gotland Basin of the Baltic Sea, and were therefore assigned to VHSV genotype II. The partial G gene sequences obtained (nt 1 to 672–1129) of all 5 lamprey VHSV isolates were identical, and so were the entire G genes (nt 1 to 1524) of 2 isolates sequenced. The virulence of one of the lamprey isolates was evaluated by an experimental infection trial in rainbow trout Oncorhynchus mykiss fry. No mortality was induced postinfection by waterborne and intraperitoneal challenge, respectively, while 2 genotype Id isolates originating from Finnish rainbow trout caused marked mortality under the same conditions. The infection in the European river lamprey is thought to be independent from the epidemic in farmed rainbow trout in Finnish brackish waters, because the isolates from rainbow trout were of a different genotype. This is the first report of VHSV found in the European river lamprey. The role of wild river lampreys in maintaining the infection in the marine environment remains unclear.

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Finnish Food Safety Authority
Authors: Gadd, T. (Ekstern), Jakava-Viljanen, M. (Ekstern), Einer-Jensen, K. (Intern), Ariel, E. (Intern), Koski, P. (Ekstern), Sihovnen, L. (Ekstern)
A dominant negative mutant of rab5 inhibits infection of cells by foot-and-mouth disease virus; implications for virus entry.

Foot-and-mouth disease virus (FMDV) can use a number of different integrins (alphavβ1, alphavβ3, alphavβ6, and alphavβ8) as receptors to initiate infection. Infection mediated by alphavβ6 is known to occur by clathrin-mediated endocytosis and is dependent on the acidic pH within endosomes. On internalization, virus is detected rapidly in early endosomes (EE) and subsequently in perinuclear recycling endosomes (PNRE), but not in late endosomal compartments. Due to the extreme sensitivity of FMDV to acidic pH, it is thought that EE can provide a pH low enough for infection to occur; however, definitive proof that infection takes place from within these compartments is still lacking. Here we have investigated the intracellular transport steps required for FMDV infection of IBRS-2 cells, which express vβ8 as their FMDV receptor. These experiments confirmed that FMDV infection mediated by alphavβ8 is also dependent on clathrin-mediated endocytosis and an acidic pH within endosomes. Also, the effect on FMDV infection of dominant-negative (DN) mutants of cellular rab proteins that regulate endosomal traffic was examined. Expression of DN rab5 reduced the number of FMDV-infected cells by 80%, while expression of DN rab4 or DN rab7 had virtually no effect on infection. Expression of DN rab11 inhibited infection by FMDV, albeit to a small extent (35%). These results demonstrate that FMDV infection takes place predominantly from within EE and does not require virus trafficking to the late endosomal compartments. However, our results suggest that infection may not be exclusive to EE and that a small amount of infection could occur from within PNRE.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, The Pirbright Institute
Authors: Johns, H. (Ekstern), Berryman, S. (Ekstern), Monaghan, P. (Ekstern), Belsham, G. (Intern), Jackson, T. (Ekstern)
Pages: 6247-6256
Publication date: 2009
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Virology
Volume: 83
Issue number: 12
ISSN (Print): 0022-538X
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): SJR 3.052 SNIP 1.131 CiteScore 4.42
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 3.286 SNIP 1.138 CiteScore 4.42
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 3.168 SNIP 1.219 CiteScore 4.4
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 3.468 SNIP 1.26 CiteScore 4.92
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
Adptive versus innate immune mechanisms in trout responding to rhabdovirus antigens.

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Lorenzen, N. (Intern)
Publication date: 2009
Event: Abstract from Dafinet & Scofda Symposium, University of Copenhagen, Faculty of Life Sciences, .
Main Research Area: Technical/natural sciences
Electronic versions:
NLorenzen Dafinet abstract 160409_e.doc
Source: orbit
Source-ID: 255125
Publication: Research › Conference abstract for conference – Annual report year: 2009
Antibody response of rainbow trout with single or double infections involving viral haemorrhagic septicaemia virus and infectious haematopoietic necrosis virus

Juvenile rainbow trout Oncorhynchus mykiss were experimentally infected by immersion with viral haemorrhagic septicaemia virus (VHSV), infectious haematopoietic necrosis virus (IHNV) or with both viruses. The presence of neutralizing antibodies in the sera of infected fish were analysed by 50% plaque neutralization tests (50%PNT). In Group 1 (infected with VHSV) and Group 2 (infected with IHNV) neutralizing antibodies were found in 41% and 21% of the serum samples, respectively. No cross-reacting antibodies were found in these 2 groups. In Group 3 (infected with both viruses) 30% of the samples showed neutralizing antibodies against VHSV, 21% against IHNV and 12% against both viruses. Fish in Group 3 developed a double specific antibody reaction whose kinetics and intensity (mean of log10 titres) were similar to the antibody response of the single infected groups.

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Fregeneda-Grandes, J. M. (Ekstern), Skall, H. F. (Intern), Olesen, N. J. (Intern)
Pages: 23-29
Publication date: 2009
Main Research Area: Technical/natural sciences

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Journal: Diseases of Aquatic Organisms
Volume: 83
Issue number: 1
ISSN (Print): 0177-5103
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.95 SJR 0.858 SNIP 0.929
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.949 SNIP 0.935 CiteScore 1.96
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.889 SNIP 0.881 CiteScore 1.86
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.812 SNIP 0.918 CiteScore 1.77
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.912 SNIP 1.092 CiteScore 2.04
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.11 SNIP 1.165 CiteScore 2.29
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.91 SNIP 0.951
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.889 SNIP 0.99
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Bluetongue in Denmark 2008

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Rasmussen, L. D. (Intern), Rasmussen, T. B. (Intern), Belsham, G. (Intern), Strandbygaard, B. (Intern), Bøtner, A. (Intern)
Publication date: 2009
Main Research Area: Technical/natural sciences

Publication information
Journal: Bovilogisk
Volume: 2
ISSN (Print): 0906-009X
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Original language: Danish
Source: orbit
Source-ID: 238759
Publication: Communication › Journal article – Annual report year: 2009

Bluetongue in Denmark 2008

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Rasmussen, L. D. (Intern), Rasmussen, T. B. (Intern), Belsham, G. (Intern), Strandbygaard, B. (Intern), Bøtner, A. (Intern)
Publication date: 2009
Event: Poster session presented at 3rd Annual Meeting of EPIZONE, Antalya, Turkey.
Main Research Area: Technical/natural sciences
Electronic versions:
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General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Rasmussen, L. D. (Intern), Bøtner, A. (Intern)
Pages: 29
Publication date: 2009
Main Research Area: Technical/natural sciences

Publication information
Journal: Dansk Veterinaertidsskrift
Volume: 9
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BFI (2017): BFI-level 1
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
ISI indexed (2012): ISI indexed no
BFI (2011): BFI-level 1
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
BFI (2009): BFI-level 1
BFI (2008): BFI-level 1
Original language: Danish
Source: orbit
Source-ID: 242384
Publication: Communication › Journal article – Annual report year: 2009

Challenge studies of European stocks of redfin perch, Perca fluviatilis L., and rainbow trout, Oncorhynchus mykiss (Walbaum), with epizootic haematopoietic necrosis virus
A challenge model for comparison of the virulence of epizootic haematopoietic necrosis virus (EHNV) to European stock of redfin perch, Perca fluviatilis L., and rainbow trout, Oncorhynchus mykiss (Walbaum), was tested. The model investigated intraperitoneal (IP), bath and cohabitation routes at 10, 15 and 20 C for 5–6 g fish and 15 C for 20 g perch. In the IP challenges of perch, significant mortality occurred at 15 C and 20 C. In challenge trials for rainbow trout, significant mortalities were observed in IP and bath challenges at 20 C. The mortality observed in IP-challenged 20 g perch was not significantly different from that recorded for 6 g fish challenged IP. No significant mortality was observed in any other treatment groups. Re-isolation of ranavirus was confirmed by IFAT and was consistently associated with dead or moribund fish in the trial groups challenged with EHNV. The findings indicate that EHNV does not pose a high risk for wild perch and trout populations in Europe by natural exposure. Mortality appears to be primarily a function of environmental factors, with temperature playing an important role, and not just the presence of the virus in the fish.

General information
State: Published
Organisations: National Veterinary Institute, Section of Fish Diseases, Division of Poultry, Fish and Fur Animals
Authors: Ariel, E. (Intern), Jensen, A. B. B. (Intern)
Pages: 1017 - 1025
Publication date: 2009
Main Research Area: Technical/natural sciences
Publication information
Pigs are considered intermediate hosts for the transmission of avian influenza viruses (AIVs) to humans but the basic organ pathogenesis of AIVs in pigs has been barely studied. We have used 42 four-week-old influenza naive pigs and two different inoculation routes (intranasal and intratracheal) to compare the pathogenesis of a low pathogenic (LP) H5N2 AIV with that of an H1N1 swine influenza virus. The respiratory tract and selected extra-respiratory tissues were examined for virus replication by titration, immunofluorescence and RT-PCR throughout the course of infection. Both viruses caused a productive infection of the entire respiratory tract and epithelial cells in the lungs were the major target. Compared to the
swine virus, the AIV produced lower virus titers and fewer antigen positive cells at all levels of the respiratory tract. The respiratory part of the nasal mucosa in particular showed only rare AIV positive cells and this was associated with reduced nasal shedding of the avian compared to the swine virus. The titers and distribution of the AIV varied extremely between individual pigs and were strongly affected by the route of inoculation. Gross lung lesions and clinical signs were milder with the avian than with the swine virus, corresponding with lower viral loads in the lungs. The brainstem was the single extra-respiratory tissue found positive for virus and viral RNA with both viruses. Our data do not reject the theory of the pig as an intermediate host for AIVs, but they suggest that AIVs need to undergo genetic changes to establish full replication potential in pigs. From a biomedical perspective, experimental LP H5 AIV infection of pigs may be useful to examine heterologous protection provided by H5 vaccines or other immunization strategies, as well as for further studies on the molecular pathogenesis and neurotropism of AIVs in mammals.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Ghent University, Veterinary & Agrochemical Research Centre, Brussels
Authors: De Vleeschauwer, A. (Ekstern), Atanasova, K. (Ekstern), Van Borm, S. (Ekstern), van den Berg, T. (Ekstern), Rasmussen, T. B. (Intern), Uttenthal, Å. (Intern), Van Reeth, K. (Ekstern)
Pages: e6662
Publication date: 2009
Main Research Area: Technical/natural sciences

Publication information
Journal: PLoS One
Volume: 4
Issue number: 8
ISSN (Print): 1932-6203
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BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.11 SJR 1.201 SNIP 1.092
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.414 SNIP 1.131 CiteScore 3.32
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.545 SNIP 1.141 CiteScore 3.54
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.74 SNIP 1.147 CiteScore 3.94
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.945 SNIP 1.142 CiteScore 4.15
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 2.369 SNIP 1.23 CiteScore 4.58
ISI indexed (2011): ISI indexed no
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.631 SNIP 1.161
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 2.473 SNIP 0.985
Web of Science (2009): Indexed yes
Comparing the epidemiological and economic effects of control strategies against classical swine fever in Denmark

In 2006, total Danish pork exports were valued at (sic)3.8 billion, corresponding to approximately 5% of the total Danish exports, and an outbreak of a notifiable disease would have dramatic consequences for the agricultural sector in Denmark. Several outbreaks of classical swine fever (CSF) have occurred in Europe within the last decade, and different control strategies have been suggested. The objective of this study was to simulate the epidemiological and economic consequences of such control strategies in a CSF epidemic under Danish conditions with respect to herd demographics and geography and to investigate the effect of extra biosecurity measures on farms. We used InterSpread Plus to model the effect of nine different control strategies: the minimum measures required by the EU plus depopulation of contact herds (EUplus), extra depopulation of neighbouring herds, extra surveillance within the protection and surveillance zones, extra biosecurity in SPF herds-or in all herds, vaccination of all pigs in the 1 or 2 km zones using live vaccine as a protective measure (vaccination-to-kill), vaccination of all weaners and finishers in the 1 or 2 km zones using an E2 marker vaccine as a suppressive measure (vaccination-to-live). Each epidemic was simulated to start in four different index herds: production herds located in low, medium and high pig density areas, respectively; and a nucleus herd in an area of high pig density. For each control strategy and index case, we calculated the size and duration of the epidemic, the number of depopulated and/or vaccinated herds and animals, the control costs borne by the public and the pig industry, respectively, as well as the loss of exports associated with the epidemic. The simulations showed that the EUplus strategy is the most effective of the evaluated strategies with respect to limiting the size, duration and cost of the epidemic, regardless of the index case. However, regarding the number of slaughtered animals, the vaccination-to-live strategies appeared to be more effective. Epidemics become larger and last longer if the index case is a nucleus herd. This implies that biosecurity in nucleus herds is extremely important to avoid transmission of CSF to these herds. Simulations showed that a Danish CSF epidemic will be moderate in most cases and will include fewer than 10 cases and last less than 2 weeks on average. However, for some iterations, long-lasting and large epidemics were observed. Irrespective of the size and duration, an epidemic is expected to be very costly due to the export losses.
Complete genome amplification of Classical swine fever virus

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Friedrich Loeffler Institute
Authors: Rasmussen, T. B. (Intern), Leifer, I. (Ekstern), Reimann, I. (Ekstern), Uttenthal, Å. (Intern), Beer, M. (Ekstern)
Publication date: 2009
Event: Abstract from Annual Meeting of the National Reference Laboratories of CSF, Valdeolmos, Spain, .
Main Research Area: Technical/natural sciences
pestivirus, virus, CSFV, genome amplification
Source: orbit
Source-ID: 249979
Publication: Research › Conference abstract for conference – Annual report year: 2009

Contingency plans for the control and eradication of diseases in aquaculture

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Olesen, N. J. (Intern), Skall, H. F. (Intern), Møllergaard, S. (Ekstern), Korsholm, H. (Ekstern), Håstein, T. (Ekstern)
Pages: 28-29
Publication date: 2009
Host publication information
Title of host publication: International aquaculture biosecurity conference : Proceedings
Main Research Area: Technical/natural sciences
Conference: International aquaculture biosecurity conference : Practical approaches for the prevention, control, and eradication of disease, 01/01/2009
aquaculture, eradication, contingency plans, disease control
Source: orbit
Source-ID: 254962
Publication: Research › Conference abstract in proceedings – Annual report year: 2009

CSFV DIVA diagnostic using Pichia pastoris as expression system

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: von Rosen, T. (Intern), Rasmussen, T. B. (Intern), Uttenthal, Å. (Intern)
Publication date: 2009
Event: Poster session presented at Theme 5 Meeting EPIZEONE, Maisons-Alfort, France, .
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 254943
Publication: Research › Poster – Annual report year: 2009

CSFV DIVA diagnostic using Pichia pastoris as expression system

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: von Rosen, T. (Intern), Rasmussen, T. B. (Intern), Uttenthal, Å. (Intern)
Publication date: 2009
Event: Poster session presented at 1st European Symposium on Porcine Health Management (ESPVM 2009), Frederiksberg, Denmark.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 249607
Publication: Research › Poster – Annual report year: 2009
Detection of infectious pancreatic necrosis virus from rainbow trout, Oncorhynchus mykiss (Walbaum), using the macrophage lysis method

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Technical University of Denmark
Authors: Johansson, T. (Ekstern), Olesen, N. J. (Intern)
Pages: 563-566
Publication date: 2009
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Fish Diseases
Volume: 32
Issue number: 6
ISSN (Print): 0140-7775
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.12
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 1.71
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 1.99
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 1.74
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 1.7
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.09
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Web of Science (2008): Indexed yes
Web of Science (2007): Indexed yes
Web of Science (2006): Indexed yes
Web of Science (2005): Indexed yes
Web of Science (2004): Indexed yes
Web of Science (2003): Indexed yes
Web of Science (2001): Indexed yes
A real-time PCR assay, based on Primer-Probe Energy Transfer (PriProET), was developed to improve the detection and quantification of porcine circovirus type 2 (PVC2). PCV2 is recognised as the essential infectious agent in post-weaning multisystemic wasting syndrome (PMWS) and has been associated with other disease syndromes such as porcine dermatitis and nephropathy syndrome (PDNS) and porcine respiratory disease complex (PRDC). Since circoviruses commonly occur in the pig populations and there is a correlation between the severity of the disease and the viral load in the organs and blood, it is important not only to detect PCV2 but also to determine the quantitative aspects of viral load. The PriProET real-time PCR assay described in this study was tested on various virus strains and clinical forms of PMWS in order to investigate any correlation between the clinical signs and viral loads in different organs. The data obtained in this study correlate with those described earlier; namely, the viral load in 1 ml plasma and in 500 ng tissue DNA exceeds $10^7$ copies in the case of PMWS. The results indicate that the new assay provides a specific, sensitive and robust tool for the improved detection and quantification of PCV2.

**General information**

State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Swedish University of Agricultural Sciences, Central Agricultural Office, Szent Istvan University, Institute for Veterinary Medicinal Products
Authors: Balint, A. (Ekstern), Tenk, M. (Ekstern), Deim, Z. (Ekstern), Rasmussen, T. B. (Intern), Uttenthal, Å. (Intern), Csagola, A. (Ekstern), Tuboly, T. (Ekstern), Farsang, A. (Ekstern), Berg, M. (Ekstern), Belak, S. (Ekstern)
Pages: 441-452
Publication date: 2009
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Acta Veterinaria Hungarica
Volume: 57
Issue number: 3
ISSN (Print): 0236-6290
Ratings:
- BFI (2018): BFI-level 1
- Web of Science (2018): Indexed yes
- BFI (2017): BFI-level 1
- Web of Science (2017): Indexed Yes
- BFI (2016): BFI-level 1
- Scopus rating (2016): SJR 0.336 SNIP 0.483 CiteScore 0.88
- BFI (2015): BFI-level 1
- Scopus rating (2015): SJR 0.317 SNIP 0.38 CiteScore 0.75
- BFI (2014): BFI-level 1
- Scopus rating (2014): SJR 0.322 SNIP 0.607 CiteScore 0.79
- BFI (2013): BFI-level 1
- Scopus rating (2013): SJR 0.286 SNIP 0.651 CiteScore 0.83
- ISI indexed (2013): ISI indexed yes
- BFI (2012): BFI-level 1
- Scopus rating (2012): SJR 0.422 SNIP 0.957 CiteScore 1.13
- ISI indexed (2012): ISI indexed yes
- BFI (2011): BFI-level 1
- Scopus rating (2011): SJR 0.421 SNIP 0.708 CiteScore 0.86
- ISI indexed (2011): ISI indexed yes
- BFI (2010): BFI-level 1
Distinction of genotypes of viral haemorrhagic septicaemia virus (VHSV) by monoclonal antibodies

VHSV isolates can be divided into 4 major genotypes and a number of subtypes with an almost distinct geographical distribution. Host range and pathogenicity appear to some extent to be linked with genotypes. Once new genotypes of VHSV will be introduced into new areas, they can cause severe outbreaks of VHS among susceptible fishes. According to the OIE Aquatic Animal Health Code, even if the same disease agent is present in both the import and the export country, the importing country can demand health certificate of the exporting country for imports when the pathogenicity or host range of the strain in the exporting country is significantly higher or larger than that in the importing country. In order to prevent introduction to or spreading in a country of new genotypes of VHSV and to facilitate the responsibilities of exporting and importing countries, such as issuing health certificates and carry out quarantine and disease control programs, a quick and simple detection method for discriminating between each the genotypes of VHSV is strongly desired. Monoclonal antibodies (MAbs) VHS-10 and VHS-5.18 specifically recognizing VHSV genotypes IVa and Ib respectively, as well as MAb IP5B11 recognizing all known VHSV isolates, were prepared earlier. In the present study, more new genotype specific monoclonal antibodies against VHSV were produced, aiming at establishing a complete immunoassay for typing of VHSV according to genotype. BALb-c mice were immunized with purified preparations of 7 different genotypes of VHSV (I, Ia, Ib, II, III, IVa and IVb). Six MAbs from these hybridoma clones were selected and their MAbs reactivity in IFAT and ELISA tested against a large panel of 79 VHSV isolates. The isolates representing all known geno- and subgenotypes of VHSV. Among the new MAbs, VHS-1.24, reacted with all types except genotype Ie (the Black Sea variant of VHSV), while MAb VHS-9.23 reacted with all genotypes except genotype III. MAb VHS-3.80 reacted with genotypes Ib, Ic, Id and II, only. MAb VHS-7.57 reacted with genotype II and IVa. Interestingly, MAb VHS-3.75 reacted with all genotype III isolates except the rainbow trout pathogenic isolate from Norway (NO-2007-50-385) (Dale et al. in press), but did react with the New Brunswick VHSV IVb isolate (Oliver 2002, Gagné et al. 2007). Another MAb (VHS-1.88) reacted with genotype IVb only, except with the New Brunswick isolate. The present findings support a phenotypic difference between NO-2007-50-385 and the other virus representatives in genotype III, and genotype IVb may eventually be split up in two subgroups (the Great Lakes isolates and New Brunswick isolate). In conclusion, we can now distinguish between all genotypes and some of subtypes of VHSV by testing isolates in IFAT or ELISA with 9 MAbs (Table 1).
Dual DNA vaccination of rainbow trout (Oncorhynchus mykiss) against two different rhabdoviruses, VHSV and IHNV, induces specific divalent protection

DNA vaccines encoding the glycoprotein genes of the salmonid rhabdoviruses VHSV and IHNV are very efficient in eliciting protective immune responses against their respective diseases in rainbow trout (Oncorhynchus mykiss). The early anti-viral response (EAVR) provides protection by 4 days post vaccination and is non-specific and transient while the specific anti-viral response (SAVR) is long lasting and highly specific. Since both VHSV and IHNV are endemic in rainbow trout in several geographical regions of Europe and Atlantic salmon (Salmo salar) on the Pacific coast of North America, co-vaccination against the two diseases would be a preferable option. In the present study we demonstrated that a single injection of mixed DNA vaccines induced long-lasting protection against both individual and a simultaneous virus challenge 80 days post vaccination. Transfected muscle cells at the injection site expressed both G proteins. This study confirms the applied potential of using a combined DNA vaccination for protection of fish against two different rhabdoviral diseases.
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

Authors: Norder, H. (Ekstern), Sundqvist, L. (Ekstern), Magnusson, L. (Ekstern), Breum, S. Ø. (Intern), Lofdahl, M. (Ekstern), Larsen, L. E. (Intern), Hjulsager, C. K. (Intern), Magnus, L. (Ekstern), Bottiger, B. (Ekstern), Widen, F. (Ekstern)

Pages: 20-28

Publication date: 2009

Main Research Area: Technical/natural sciences

**Publication information**

Journal: Eurosurveillance (Online Edition)

Volume: 14

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BFI (2018): BFI-level 1

Web of Science (2018): Indexed yes

BFI (2017): BFI-level 1

Web of Science (2017): Indexed Yes

BFI (2016): BFI-level 1

Scopus rating (2016): CiteScore 3.05

BFI (2015): BFI-level 1

Scopus rating (2015): CiteScore 2.69

Web of Science (2015): Indexed yes

BFI (2014): BFI-level 1

Scopus rating (2014): CiteScore 2.83

BFI (2013): BFI-level 1

Scopus rating (2013): CiteScore 2.62

ISI indexed (2013): ISI indexed yes

Web of Science (2013): Indexed yes

BFI (2012): BFI-level 1

Scopus rating (2012): CiteScore 3.02

ISI indexed (2012): ISI indexed no

BFI (2011): BFI-level 1

Scopus rating (2011): CiteScore 3.27

ISI indexed (2011): ISI indexed no

Web of Science (2011): Indexed yes

BFI (2010): BFI-level 1

BFI (2009): BFI-level 1

Web of Science (2009): Indexed yes

BFI (2008): BFI-level 1

Web of Science (2007): Indexed yes

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http://www.eurosurveillance.org/ViewArticle.aspx?ArticleId=19211

Source: orbit

Source-ID: 249535

Publication: Research - peer-review › Journal article – Annual report year: 2009
Evaluation of automated nucleic acid extraction methods for virus detection in a multicenter comparative trial

Five European veterinary laboratories participated in an exercise to compare the performance of nucleic acid extraction robots. Identical sets of coded samples were prepared using serial dilutions of bovine viral diarrhoea virus (BVDV) from serum and cell culture propagated material. Each laboratory extracted nucleic acid from this panel using available robotic equipment (12 separate instruments, comprising 8 different models), after which the processed samples were frozen and sent to a single laboratory for subsequent testing by real-time RT-PCR. In general, there was good concordance between the results obtained for the different automated extraction platforms. In particular, the limit of detection was identical for 9/12 and 8/12 best performing robots (using dilutions of BVDV infected-serum and cell culture material, respectively), which was similar to a manual extraction method used for comparison. The remaining equipment and protocols used were less sensitive, in an extreme case for serum, by a factor of 1000. There was no evidence for cross-contamination of RNA template in any of the negative samples included in these panels. These results are not intended to replace local optimisation and validation, but provide reassurance to laboratories to indicate that the best performing optimised nucleic acid extraction systems can have similar performance.

General information

State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Rasmussen, T. B. (Intern), Uttenthal, Å. (Intern), Hakhverdyan, M. (Ekstern), Belak, S. (Ekstern), Wakeley, P. R. (Ekstern), Reid, S. M. (Ekstern), Ebert, K. (Ekstern), King, D. P. (Ekstern)
Pages: 87-90
Publication date: 2009
Main Research Area: Technical/natural sciences

Publication information

Journal: Journal of Virological Methods
Volume: 155
Issue number: 1
ISSN (Print): 0166-0934
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.87 SNIP 0.736 CiteScore 1.78
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.868 SNIP 0.799 CiteScore 1.68
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.893 SNIP 0.952 CiteScore 1.87
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.861 SNIP 0.91 CiteScore 1.99
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.869 SNIP 0.935 CiteScore 2.08
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.907 SNIP 0.994 CiteScore 2.23
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.892 SNIP 0.998
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Evaluation of CSFV Antibody ELISAs for the differentiation of infected from vaccinated animals

Classical swine fever (CSF) is one of the most important epizootic diseases of pigs. With few exceptions the Member States of the European Union (EU) are currently considered to be free of CSF in domestic pigs. However, the disease is still endemic in the wild boar populations of several European countries and out-breaks occurred recently e.g. in Germany, France, Hungary, Romania, Bulgaria, and the Slovak Republic. Preventive vaccination is prohibited within the EU, but emergency vaccination can be part of the strategy in case of a contingency. Using conventional vaccines, differentiation of vaccinated from infected animals (DIVA) is not possible. Newly developed modified live marker vaccines allow a DIVA strategy based on the use of enzyme linked immunosorbent assay (ELISA) tests. The aim of this study was to evaluate CSF virus (CSFV) Antibody ELISAs, commercially available in Europe, for their diagnostic sensitivity as well as for their potential in differentiating between infected and marker vaccinated animals. Two newly available ELISAs were included into the tests, the Priocheck® CSFV Erns ELISA, a special DIVA test, and the LDL Pigtype® CSFV Antibody ELISA. An inter-laboratory comparison test with four EU national CSF reference laboratories and one EU reference laboratory participating was organized. Seven different CSFV antibody ELISA test kits, targeting distinct antibodies (against E2, Erns, NS3) were provided to the participating laboratories together with a set of 41 samples. This set included the following, well characterized samples derived from animal experiments: CSFV antibody positive sera with low, medium and high titers, sera free of CSF antibodies, sera from pigs infected with pestiviruses other than CSFV (Bovine viral diarrhoea type I and II and Border disease virus), sera from pigs vaccinated with conventional vaccines (C-strain, GPE-), sera from pigs vaccinated with E2 subunit vaccine and recent 3rd generation marker vaccines (cp7E2Alf, cp7E2gif, pRiensABCgif, FLC11, FLc9), as well as sera from pigs vaccinated and afterwards challenged with CSFV. In addition each of the laboratories was asked to additionally test approximately 50 samples from their national pig herds, which were regarded to be negative and approximately 100 samples from DIVA experiments to assure a wide coverage of different serum samples. Practicability, diagnostic sensitivity, specificity, repeatability, and reproducibility were calculated and conclusions were drawn on the feasibility of using existing Ab-ELISAs for DIVA testing. The results will be presented at the meeting.

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General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, University of Veterinary Medicine, Friedrich Loeffler Institute, Centrum voor Onderzoek in Diergeneeskunde en Agrochemie, Central Veterinary Institute
Authors: Schroeder, S. (Ekstern), Blome, S. (Ekstern), Koenen, F. (Ekstern), Loeffen, W. (Ekstern), Rasmussen, T. (Intern), Haegemann, A. (Ekstern), Uttenthal, Å. (Intern)
FishPathogens.eu/vhsv: a user-friendly viral haemorrhagic septicaemia virus isolate and sequence database

A database has been created, http://www.FishPathogens.eu, with the aim of providing a single repository for collating important information on significant pathogens of aquaculture, relevant to their control and management. This database will be developed, maintained and managed as part of the European Community Reference Laboratory for Fish Diseases function. This concept has been initially developed for viral haemorrhagic septicaemia virus and will be extended in future to include information on other significant aquaculture pathogens. Information included for each isolate comprises sequence, geographical origin, host origin and useful key literature. Various search mechanisms make it easy to find specific groups of isolates. Search results can be presented in several different ways including table-based, map-based and graph-based outputs. When retrieving sequences, the user is given freedom to obtain data from any selected part of the genome of interest. The output of the sequence search can be readily retrieved as a FASTA file ready to be imported into a sequence alignment tool of choice, facilitating further molecular epidemiological study.

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Jonstrup, S. P. (Intern), Gray, T. (Ekstern), Kahns, S. (Intern), Skall, H. F. (Intern), Snow, M. (Ekstern), Olesen, N. J. (Intern)
Publication date: 2009
Main Research Area: Technical/natural sciences
A database has been created, www.FishPathogens.eu, with the aim of providing a single repository for collating important information on significant pathogens of aquaculture, relevant to their control and management. This database will be developed, maintained and managed as part of the European Community Reference Laboratory for Fish Diseases function. This concept has been initially developed for VHSV and will be extended in future to include information on other viral haemorrhagic septicaemia virus, fish pathogens, database
significant aquaculture pathogens. Information included for each isolate comprises sequence, geographic origin, host origin and useful key literature. Various search mechanisms make it easy to find specific groups of isolates. Search results can be presented in several different ways including table based, map based, and graph based outputs. When retrieving sequences, the user is given freedom to obtain data from any selected part of the genome of interest. The output of the sequence search can be readily retrieved as a FASTA file ready to be imported into a sequence alignment tool of choice, facilitating further molecular epidemiological study.

**General information**
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Jonstrup, S. P. (Intern), Gray, T. (Ekstern), Kahns, S. (Intern), Skall, H. F. (Intern), Snow, M. (Ekstern), Schuetze, H. (Ekstern), Kurath, G. (Ekstern), Stone, D. (Ekstern), Agapow, P. (Ekstern), Bashiruddin, J. (Ekstern), Jensen, A. B. B. (Intern), Olesen, N. J. (Intern)
Publication date: 2009
Event: Poster session presented at 14th EAFP International Conference on Diseases of Fish and Shellfish, Prague, Czech Republic.
Main Research Area: Technical/natural sciences

**Foot-and-mouth disease**
Foot-and-mouth disease is an economically important, highly contagious, disease of cloven-hoofed animals characterized by the appearance of vesicles (blisters) on the feet and in and around the mouth. The causative agent, foot-and-mouth disease virus, was the first mammalian virus to be discovered. It has a ribonucleic acid (RNA) genome enclosed within a protein coat. The virus replicates very rapidly within the cytoplasm of cells. The RNA genome has to function both as a messenger RNA and as a template for RNA replication. The RNA encodes a single polyprotein which is processed, by virus-encoded proteases, to about 12 mature products which are required for virus replication and assembly. Some of these viral proteins modify host cell activities to block anti-virus defence systems. Thus, this small virus displays a remarkably complex array of biological activities.

**General information**
State: E-pub ahead of print
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Institute for Animal Health
Authors: Belsham, G. (Intern), Charleston, B. (Ekstern), Jackson, T. (Ekstern), Paton, D. J. (Ekstern)
Publication date: 2009
Main Research Area: Technical/natural sciences

**Functional demonstration of adaptive immunity in zebrafish using DNA vaccination.**
Due to the well characterized genome, overall highly synteny with the human genome and its suitability for functional genomics studies, the zebrafish is considered to be an ideal animal model for basic studies of mechanisms of diseases and immunity in vertebrates including humans. While several studies have documented existence of a classical innate immune response, there is mainly indirect evidence of functional adaptive immunity. To address this aspect, groups of zebrafish were vaccinated with DNA-vaccines against the rhabdoviruses VHSV, IHNV and SVCV. Seven weeks later, the fish were challenged with SVCV by immersion. Despite some variability between replicate aquaria, there was a protective effect of the homologous vaccine and no effect of the heterologous vaccines. The results therefore confirm the existence of not only a well developed but also a fully functional adaptive immune system in zebrafish.

**General information**
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Veterinary Research Institute, Brno
Further evaluation of the DIVA vaccine properties of the chimeric pestivirus CP7-E2gif using commercially available CSFV ELISA kit systems

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Rasmussen, T. (Intern), Rasmussen, T. B. (Intern), Utenthal, Å. (Intern)
Publication date: 2009
Event: Poster session presented at 3rd Annual Meeting of EPIZONE, Antalya, Turkey.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 236990
Publication: Research - peer-review › Poster – Annual report year: 2009

Genetic stability of pestivirus genomes cloned into BACs
Infectious cDNA clones are a prerequisite for directed genetic manipulations of pestivirus genomes to obtain attenuated pestiviruses designed as new modified live DIVA vaccine candidates against classical swine fever. However, the construction of new infectious pestivirus cDNA clones has been hampered due to the large size of the pestivirus genome and due to genetic instability of the cloned cDNA, which in combination with plasmid vectors tend to be unstable and deleterious in the bacterial host. Therefore, new strategies are needed to facilitate construction of stable infectious cDNA clones of pestivirus strains. In a collaborative research project, between DTU Vet and FLI, on the establishment of genetically modified pestiviruses engineered specifically for the DIVA principle, we cloned a series of complete pestivirus cDNA clones, obtained by full-length RT-PCR, directly into the bacterial artificial chromosome (BAC) vector “pBeloBAC11”. This BAC vector provides a markedly higher stability of cloned sequences in E. coli compared to plasmids that form the basis for the existing pestivirus cDNA clones. In this study, two of the newly constructed BAC clones were analysed for genetic stability of the cloned pestivirus genomes to demonstrate the suitability of the BAC vector for harbouring pestivirus genomes. Two BAC clones, comprising the complete genomes of BDV Gifhorn (pBeloGif3) and CSFV Paderborn (pBeloPader10) were passaged 15 times in E. coli representing at least 360 bacteria generations. From 15th passage of the BAC clones, the entire 5' and 3' ends of the cloned genomes and parts of the open reading frame were sequenced and compared to the sequences of the parent BAC clones. The sequenced areas represent approximately 20 % of the cloned genome. No mutations were observed after the extensive passaging of the cDNA clones in the bacterial host, indicating a highly stable system for cloning and maintenance of complete pestivirus genomes. This work was supported by the by the Danish Research Council for Technology and Production Sciences (DRCTPS grant 274-07-0198) and the EU Network of Excellence, EPIZONE (Contract No FOOD-CT-2006-016236).

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Friedrich Loeffler Institute
Authors: Rasmussen, T. B. (Intern), Reimann, I. (Ekstern), Uttenthal, Å. (Intern), Martin, B. (Ekstern)
Publication date: 2009
Event: Abstract from 3rd Annual Meeting of EPIZONE, Antalya, Turkey.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 243445
Publication: Research - peer-review › Conference abstract for conference – 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
Authors: Larsen, L. E. (Intern)
HEPATITIS E VIRUS IS PREVALENT IN THE DANISH PIG POPULATION

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics, Universidad Autonoma de Barcelona, Swedish Institute for Infectious Disease Control, Statens Serum Institut
Authors: Breum, S. Ø. (Intern), Hjulsager, C. K. (Intern), Deus, N. D. (Ekstern), Segalès, J. (Ekstern), Norder, H. (Ekstern), Böttiger, B. (Ekstern), Larsen, L. E. (Intern)
Number of pages: 114
Publication date: 2009

Host publication information
Title of host publication: 8th International Congress of Veterinary Virology: Integrating classical and molecular virology
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 254908
Publication: Research - peer-review › Article in proceedings – Annual report year: 2009

Identifying potential virulence determinants in viral haemorrhagic septicaemia virus (VHSV) for rainbow trout

We identified viral haemorrhagic septicaemia virus (VHSV) isolates classified within Genotype Ib which are genetically similar (>99.4% glycoprotein amino acid identity) yet, based on their isolation history, were suspected to differ in virulence in juvenile rainbow trout. The virulence of an isolate recovered in 2000 from a viral haemorrhagic septicaemia disease episode in a marine rainbow trout farm in Sweden (SE-SVA-1033) was evaluated in juvenile rainbow trout via intraperitoneal injection and immersion challenge alongside 3 isolates recovered from wild-caught marine fish (DK-4p37, DK-5e59 and UKMLA98/6HE1) suspected of being of low pathogenicity to trout. Mortality data revealed that isolate SE-SVA-1033 caused VHSV-specific mortality in both intraperitoneal and immersion challenges (75.0 and 15.4%, respectively). The remaining Genotype Ib isolates caused significantly lower mortalities using the same experimental infection routes.

General information
State: Published
Organisations: National Veterinary Institute, Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, Marine Scotland Science, University of Aberdeen
Authors: Campbell, S. (Ekstern), Collet, B. (Ekstern), Einer-Jensen, K. (Intern), Secombes, C. J. (Ekstern), Snow, M. (Ekstern)
Pages: 205-212
Publication date: 2009
Main Research Area: Technical/natural sciences

Publication information
Journal: Diseases of Aquatic Organisms
Volume: 86
Issue number: 3
ISSN (Print): 0177-5103
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.95 SJR 0.858 SNIP 0.929
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.949 SNIP 0.935 CiteScore 1.96
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.889 SNIP 0.881 CiteScore 1.86
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.812 SNIP 0.918 CiteScore 1.77
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.912 SNIP 1.092 CiteScore 2.04
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.11 SNIP 1.165 CiteScore 2.29
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.91 SNIP 0.951
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.889 SNIP 0.99
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.859 SNIP 0.998
Scopus rating (2007): SJR 0.949 SNIP 1.054
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.868 SNIP 0.964
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.898 SNIP 1.046
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.972 SNIP 1.105
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.931 SNIP 1.187
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 1.083 SNIP 1.187
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 1.347 SNIP 1.197
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.091 SNIP 1.221
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 1.192 SNIP 1.136
Original language: English
VHSV, Rainbow trout, Pathogenicity, Sequencing, Virulence determinants
DOIs:
10.3354/dao02127
Source: orbit
Source-ID: 231914
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 Virussygdomme, Division of Virology, Division of Microbiology and Risk Assessment, National Food Institute, Section for Veterinary Epidemiology and public sector consultancy, Virology, Danish Pig Production
Authors: Kristensen, C. S. (Ekstern), Bækbo, P. (Ekstern), Bille-Hansen, V. (Intern), Bøtner, A. (Intern), Vigre, H. (Intern), Enøe, C. (Intern), Larsen, L. E. (Intern)
Pages: 244-250
Publication date: 2009
Main Research Area: Technical/natural sciences

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Journal: Veterinary Microbiology
Volume: 138
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Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
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Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.326 SNIP 1.208
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.393 SNIP 1.21 CiteScore 2.56
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.281 SNIP 1.262 CiteScore 2.54
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.438 SNIP 1.484 CiteScore 3
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.437 SNIP 1.579 CiteScore 3.18
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.562 SNIP 1.738 CiteScore 3.27
ISI indexed (2011): ISI indexed yes
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.
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
Main Research Area: Technical/natural sciences

**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
- Web of Science (2017): Indexed Yes
- BFI (2016): BFI-level 1
- Scopus rating (2016): SJR 0.442 SNIP 0.692 CiteScore 0.3
- BFI (2015): BFI-level 1
- Scopus rating (2015): SJR 0.509 SNIP 0.794 CiteScore 0.39
- BFI (2014): BFI-level 1
- Scopus rating (2014): SJR 0.469 SNIP 0.839 CiteScore 0.41
- Web of Science (2014): Indexed yes
- BFI (2013): BFI-level 1
- Scopus rating (2013): SJR 0.474 SNIP 0.821 CiteScore 0.5
- ISI indexed (2013): ISI indexed yes
- Web of Science (2013): Indexed yes
- BFI (2012): BFI-level 1
- Scopus rating (2012): SJR 0.491 SNIP 0.883 CiteScore 0.52
- ISI indexed (2012): ISI indexed yes
- Web of Science (2012): Indexed yes
- BFI (2011): BFI-level 1
- Scopus rating (2011): SJR 0.563 SNIP 0.9 CiteScore 0.62
- ISI indexed (2011): ISI indexed yes
Influenzavirus hos svin

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Dansk Veterinaertidsskrift
Authors: Dalsgård, A. (Ekstern), Larsen, L. E. (Intern)
Pages: 6-9
Publication date: 2009
Main Research Area: Technical/natural sciences

Publication information
Journal: Dansk Veterinaertidsskrift
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
Publication: Communication › Journal article – Annual report year: 2009

Interference of an ERM-vaccine with a VHS-DNA vaccine in rainbow trout
Simultaneous vaccination of fish against several diseases is often desirable in order to minimise cost and handling of the fish. Intramuscular DNA-vaccination of rainbow trout against viral haemorrhagic septicaemia virus (VHSV) has proved to provide very good protection. However, preliminary results showed that intraperitoneal injection of a commercial vaccine
against Enteric Redmouth Disease (ERM) based on formalin-killed bacteria in oil adjuvant immediately followed by intramuscular injection of an experimental DNA-vaccine against VHSV, decreased the protective effect of the DNA-vaccine against challenge with VHSV 11 weeks post vaccination (pv). This experiment was performed with rainbow trout of 30 g injected with 0.5 g VHS-DNA vaccine. The experiment was later repeated with smaller fish (2.5 g) and using two different doses of DNA-vaccine, 1 g and 0.05 g. Both doses provided good protection in the control groups not given the ERM vaccine. But among fish given both vaccines, those vaccinated with the lower DNA dose had significantly higher mortality when challenged with VHSV 9 weeks pv. When challenged with VHSV 8 days pv, not even the 1 µg DNA dose protected such fish. A plasmid dose of 0.05 g VHSV DNA vaccine would normally induce good protection in small fish (2-3 g). To ensure complete protection in larger fish, higher doses are needed. This could explain the negative effect of ERM vaccination observed in the 30 g fish described above. It thus appears, that if the fish are vaccinated with a VHS-DNA vaccine dose according to their size, a simultaneous intraperitoneal vaccination against ERM can compromise the protective effect of the DNA-vaccine. The negative effect appears to be strongest in the early phase following vaccination. The immune mechanisms behind this interference will be discussed.

**General information**

**State:** Published  
**Organisations:** Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Marine Scotland, Norwegian School of Veterinary Medicine  
**Authors:** Lorenzen, E. (Intern), Einer-Jensen, K. (Intern), Rasmussen, J. S. (Intern), Lorenzen, N. (Intern), Ellis, T. (Ekstern), McLauchlan, P. (Ekstern), Evensen, Ø. (Ekstern)  
**Publication date:** 2009  
**Event:** Abstract from The ontogeny of the fish immune system : Abildgaard Symposium & Research School Scofd, University of Copenhagen, Faculty of Life Sciences,  
**Main Research Area:** Technical/natural sciences  
**Source:** orbit  
**Source-ID:** 255110  
**Publication:** Research › Conference abstract for conference – Annual report year: 2009

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**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 it 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  
**Authors:** Hjulsager, C. K. (Intern), Grau-Roma, L. (Ekstern), Sibila, M. (Ekstern), Enøe, C. (Intern), Larsen, L. E. (Intern), Segales, J. (Ekstern)  
**Pages:** 172-178  
**Publication date:** 2009  
**Main Research Area:** Technical/natural sciences

**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
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
Inter-laboratory proficiency tests to detect viral fish diseases.

An inter-laboratory proficiency test has been provided by the European Community Laboratory (CRL) for Fish Diseases every year since 1996. The test is provided to all European National Reference Laboratories (NRLs) that are obliged to participate and to a limited number of non-European NRLs, making the total number of participating laboratories 35. The test is primarily designed to assess the ability of participating laboratories to identify and quantify the notifiable non-exotic fish pathogenic viruses: Viral haemorrhagic septicaemia virus (VHSV) and infectious haematopoietic necrosis virus (IHNV) but also to assess their ability to differentiate other fish viruses as spring viraemia of carp virus, infectious pancreatic necrosis virus, perch rhabdovirus etc. Five coded ampoules are provided to participants containing lyophilised supernatant from infected cell cultures. The CRL collect the data and provide a statistically and graphically picture of the performance of the individual laboratory relative to other participants. The proficiency test has been used for additional purposes. Participants have been asked to genotype virus isolates and have been encouraged to submit full-length G-gene sequences of the rhabdoviruses identified in order to analyse the inter-laboratory quality of sequencing results. Such results are very important for assessing how sequence data can be used in e.g. molecular tracing. Here we present results and experiences obtained from these additional studies.

IN VIVO SCREENING OF CHEMICAL MODIFICATIONS OF siRNAs FOR EFFECT ON THE INNATE IMMUNE RESPONSE IN FISH

Abstract Due to their sequence specific gene silencing activity siRNAs are regarded as promising new active compounds in gene medicine and functional studies. But one serious problem with delivering siRNAs as treatment is the now well-established non-specific activities of some RNA duplexes. Cellular reactions towards double stranded RNAs include the 2’-5’ oligoadenylate synthetase system, the protein kinase R, RIG-I and Toll-like receptor activated pathways all resulting in antiviral defence mechanism. We have previously shown that antiviral innate immune reactions against injected siRNAs could be detected in vivo as reduced susceptibility to a fish pathogenic virus. This protection corresponded with an interferon response. Here we use this fish model to screen siRNAs containing various chemical modifications of the RNA backbone and find that is possible to differentiate between the antiviral activities of these duplexes. We conclude that the fish in vivo model is a potent tool for gaining insight into the overall triggering of antiviral reactions by siRNAs in vertebrates. The perspective is to learn how to avoid triggering of non-specific antiviral responses and still allow uptake of siRNAs into RISC for specific gene silencing.
MicroRNA Expression during Viral Infection or PolyI:C Stimulation in a Fish Model

Fish are important as small vertebrate models for studying various aspects of development and disease. MicroRNA regulation in fish has so far received attention especially in studies of their expression and function during embryonic development. In the studies carried out at the National Veterinary Institute in Århus we aim at using fish models for studying microRNA regulation during viral infection. In the studies presented here we make use of a qPCR method to detect miRNAs in fish cells. We present results regarding the expression of the immunologically relevant microRNAs, miR-155, miR-146a and miR-146b in fish cells during infection with the fish pathogenic virus viral hemorrhagic septicemia virus (VHSV) and during immune stimulation with double stranded RNA (polyI:C). We highlight the need of finding stable normalization genes for microRNA detection.

New tools to study RNA interference to fish viruses: Fish cell lines permanently expressing siRNAs targeting the viral polymerase of viral hemorrhagic septicemia virus

Previous studies have indicated that low transfection efficiency can be a major problem when gene inhibition by the use of small interfering RNAs (siRNAs) is attempted in fish cells. This may especially be true when targeting genes of viruses which are fast replicating and which can still infect cells that have not been transfected with the antiviral siRNAs. To increase the amount of antiviral siRNAs per cell a different strategy than transfection was taken here. Thus, we describe carp epithelioma papulosum cyprinid (EPC) cell clones expressing siRNAs designed to target the L polymerase gene of the viral hemorrhagic septicemia virus (VHSV), a rhabdovirus affecting fish. Eight siRNA sequences were first designed, synthesized and screened for inhibition of in vitro VHSV infectivity. Small hairpin (sh) DNAs corresponding to three selected siRNAs were then cloned into pRNA-CMV3.1/puro plasmids, transfected into EPC cells and transformed clones were obtained by puromycin selection. Sequence-specific interference with VHSV could only be observed with EPC clones transformed with a mixture of the three shDNAs, rather than with those clones obtained with individual sh DNAs. However, interference was not specific for VHSV as infection with an heterologous fish rhabdovirus, was also reduced to a similar extent. It was shown that this reduction was not due to an Mx response in the transformed cell clones. Here, we discuss some of the possible reasons for such data and future work directions. EPC clones stably expressing rhabdoviral specific siRNA sequences could be a strategy to further investigate the use of RNA interference for targeting costly fish pathogenic viruses.
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

Authors: Angen, Ø. (Intern), Jorsal, S. E. L. (Intern), Larsen, L. E. (Intern), Hjulsager, C. K. (Intern), Ståhl, M. (Intern)
Nyt fra Veterinærinstituttet: VHS er en trussel for havbrug - særlig om vinteren

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Skall, H. F. (Intern), Olesen, N. J. (Intern)
Pages: 28
Publication date: 2009
Main Research Area: Technical/natural sciences

Publication information
Journal: Dansk Veterinaertidsskrift
Volume: 92
Issue number: 1
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
ISI indexed (2012): ISI indexed no
BFI (2011): BFI-level 1
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
BFI (2009): BFI-level 1
BFI (2008): BFI-level 1
Original language: Danish
Source: orbit
Source-ID: 235062
Publication: Communication › Journal article – Annual report year: 2009

O-005: Detection of antibodies against VHSV and IHNV in rainbow trout (Oncorhychus mykiss)

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Olesen, N. J. (Intern), Castric, J. (Ekstern)
Number of pages: 489
Publication date: 2009
O-021: A retrospective cluster-analysis of the occurrence of viral haemorrhagic septicemia in Denmark

General information
State: Published
Organisations: National Veterinary Institute, Section of Fish Diseases, Division of Poultry, Fish and Fur Animals
Authors: Jensen, A. B. B. (Intern), Olesen, N. J. (Intern), Ersbøll, A. K. (Ekstern)
Number of pages: 489
Publication date: 2009

O-114: Distinction between genotypes of viral haemorrhagic septicemia virus (VHSV) using monoclonal antibodies

General information
State: Published
Organisations: National Veterinary Institute, Section of Fish Diseases, Division of Poultry, Fish and Fur Animals
Authors: Ito, T. (Intern), Kurita, J. (Ekstern), Sano, M. (Ekstern), Iida, T. (Ekstern), Skall, H. F. (Intern), Lorenzen, N. (Intern), Olesen, N. J. (Intern)
Number of pages: 489
Publication date: 2009

Outbreak of viral haemorrhagic septicemic (VHS) in seawater-farmed rainbow trout in Norway caused by VHS virus genotype III

We describe the finding of a novel viral haemorrhagic septicemia virus (VHSV) Genotype III strain that caused disease of both a neurological and septicemic nature in seawater-farmed rainbow trout Oncorhynchus mykiss in Storfjorden, Norway. In November 2007, an outbreak of VHS associated with slightly elevated mortality was confirmed at a seawater site rearing rainbow trout (90 to 440 g). Within 3 to 4 mo, the disease was recognised in 3 neighbouring sea sites with on-growing rainbow trout. The clinical, gross pathological and histopathological findings were in accordance with VHS, and the diagnosis was confirmed by the detection of VHSV in brain and internal tissues by immunohistochemistry, cell culture and reverse transcriptase PCR (RT-PCR). Sequence analysis of the G-gene revealed that the isolated virus clustered with VHSV Genotype III and that the Norwegian isolate represents a unique strain of VHSV. The pathogenicity of the virus
strain to rainbow trout and Atlantic salmon Salmo salar was examined using infection experiments. In immersion trials, the Norwegian isolate produced a cumulative mortality of 70% in rainbow trout, while nearly 100% mortality was obtained after intraperitoneal injection of the virus. For Atlantic salmon, no mortality was observed in immersion trials, whereas 52% mortality was observed after intraperitoneal injection. The Norwegian isolate thus represents the first VHSV of Genotype III pathogenic to rainbow trout.
Scopus rating (2005): SJR 0.898 SNIP 1.046
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.972 SNIP 1.105
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.931 SNIP 1.187
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 1.083 SNIP 1.187
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 1.347 SNIP 1.197
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.091 SNIP 1.221
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 1.192 SNIP 1.136
Original language: English
VHSV, sea farm, VHS, rainbow trout, genotype III
DOIs:
10.3354/dao02065
Links:
Source: orbit
Source-ID: 244877
Publication: Research - peer-review › Journal article – Annual report year: 2009

P-001: Koi herpes virus world wide: results of the global KHV questionnaire 2007-2009

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Haenen, O. (Ekstern), Olesen, N. J. (Intern)
Number of pages: 489
Publication date: 2009
Event: Poster session presented at 14th EAFP International Conference on Diseases of Fish and Shellfish, Prague, Czech Republic.
Main Research Area: Technical/natural sciences
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PATHOLOGY AND EPIDEMIOLOGY OF VIRAL HAEMORRHAGIC SEPTICAEMIA OUTBREAKS IN POLAND

General information
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Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Reichert, M. (Ekstern), Matras, M. (Ekstern), Kahns, S. (Intern), Antychowicz, J. (Ekstern), Olesen, N. J. (Intern)
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PCV2 dynamik

General information
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Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Virology, Dansk Svineproduktion, Centre de Recerca en Sanitat Animal
Authors: Kristensen, C. S. (Ekstern), Grau-Roma, L. (Ekstern), Segales, J. (Ekstern), Bækbo, P. (Ekstern), Hjulsager, C. K. (Intern), Larsen, L. E. (Intern)
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PCV-2 og diarresygdomme hos svin

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Authors: Larsen, L. E. (Intern)
Pages: 2 - 4
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Persistance of foot-and mouth disease virus in ruminants.
During the spring of 2008, a new clinical project, with the aim of investigating mechanisms involved in development of FMD carrier animals, has been launched in the new FMD facilities of the Danish Veterinary Institute located at Lindholm Island. The project is based on a series of animal experiments, investigating the host response to FMD infection in sheep and cattle. FMD infection in ruminants involves initial viral replication in pharyngeal epithelia, from where the virus spreads systemically via the lymphatic system. Characteristic vesicular lesions develop in the cornified stratified squamous epithelia of the coronary bands and oral cavity within a few days of infection. Viremia occurs within 2-3 days of infection, but is rapidly cleared through the effect of circulating antibodies of the adaptive immune response. The host response involves initial activation of the innate immune response, with activation and recruitment of effector-cells, and subsequent activation of T- and B-cells, leading to the production of circulating antibodies, as well as activation of cytotoxic T-cells. In ruminants, approximately 50% of animals infected with FMDV develop into persistently infected carrier animals, with intermittent excretion of live virus, whilst remaining animals clear the infection effectively. Previous experiments have indicated that the site of persistent viral replication is located in pharyngeal lymphoid tissue, as well as the basal epithelia of the dorsal soft palate. In these locations, FMDV is capable of persistent replication, without being detected by the host cellular immune response, which would normally be expected to clear virus infected cells. In an ongoing series of experiments, animals of 4-5 moths of age are infected with FMD O UKG 34/2001, either through subepidermo-lingual injection or direct contact with inoculated animals. Animals are kept for approximately 2 to 4 months, and the progression of infection is monitored through samples of oropharyngeal fluid (probang samples) and serum, which are analysed for presence of live virus and development of antibodies. During different fixed time points of the infection, biopsy samples of epithelial and lymphoid tissues from the pharynx and dorsal soft palate are collected with the use of an endoscope equipped with biopsy forceps. Biopsy samples are used to investigate the host’s cellular immune response at different time points during the infection, as well as the presence of FMDV antigen using immunohistochemistry. Samples will also be used to investigate expression of genes related to the innate and adaptive immune responses through qPCR at the mRNA level.

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Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Stenfeldt, C. (Intern), Belsham, G. (Intern), Tjørnehøj, K. (Intern), Alexandersen, S. (Intern)
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Event: Poster session presented at 3rd Annual Meeting of EPIZONE, Antalya, Turkey.
Photobacterium damselae subsp. damselae, an emerging pathogen in Danish rainbow trout, Oncorhynchus mykiss (Walbaum), mariculture

A selection of 16 field isolates of Photobacterium damselae from marine rainbow trout farms in Denmark was subjected to phenotypic and genotypic characterization and pathogenicity to fish. All isolates belonged to the subspecies damselae, being positive for haemolysis, motility and urease. There were considerable differences in haemolytic properties, some isolates presenting a broad zone of haemolysis and others only a narrow zone. Pulsed-field gel electrophoresis revealed a high diversity indicating that P. damselae subsp. damselae is an opportunistic, not clonal pathogen in Danish marine rainbow trout. Virulence of the strains to rainbow trout was highly variable with LD50 values ranging from $3.9 \times 10^3$ to $1.5 \times 10^8$ cfu at 20 degrees C. The virulence was significantly higher at 20 degrees C than at 13 degrees C. The strains with the strongest haemolytic properties were the most virulent suggesting a strong involvement of haemolysin in the pathogenesis. The pathological changes were consistent with a bacterial septicaemia and the haemorrhages were more pronounced than for most other bacterial infections.
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


General information

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Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Virology
Authors: Hjulsager, C. K. (Intern), Breum, S. Ø. (Intern), Larsen, L. E. (Intern)
Publication date: 2009
Event: Abstract from 8th International Congress of Veterinary Virology, Budapest, Hungary.
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Phylogenetic characterisation of European fresh water viral haemorrhagic septicaemia virus (VHSV) isolates

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Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Kahns, S. (Intern), Jonstrup, S. P. (Intern), Jensen, A. B. B. (Intern), Skall, H. F. (Intern), Olesen, N. J. (Intern)
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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 0.001) 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, Rise National Laboratory for Sustainable Energy, Virology, Centre de Recerca en Sanitat Animal
Authors: Grau-Roma, L. (Ekstern), Heegaard, P. M. H. (Intern), Hjulsager, C. K. (Intern), Sibila, M. (Ekstern), Kristensen, C. S. (Ekstern), Allepuz, A. (Ekstern), Pineiro, M. (Ekstern), Larsen, L. E. (Intern), Segales, J. (Ekstern), Fraile, L. (Ekstern)
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Poster: Detection of antibodies against VHSV and IHNV in rainbow trout

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Proficiency testing of national reference laboratories for fish diseases

General information
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Organisations: National Veterinary Institute, Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, Department of Informatics and Mathematical Modeling
Authors: Ariel, E. (Intern), Nicolajsen, N. (Intern), Skall, H. F. (Intern), Andersen, J. S. (Intern), Madsen, S. (Intern), Olesen, N. J. (Intern)
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Scopus rating (2014): SJR 1.002 SNIP 1.34 CiteScore 2.16
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ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.151 SNIP 1.394
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.941 SNIP 1.263
Web of Science (2009): Indexed yes
Propagation and isolation of ranaviruses in cell culture
The optimal in vitro propagation procedure for a panel of ranavirus isolates and the best method for isolation of Epizootic haematopoietic necrosis virus (EHNV) from organ material in cell-culture were investigated. The panel of ranavirus isolates included: Frog virus 3 (FV3), Bohle iridovirus (BIV), Pike-perch iridovirus (PPIV), European catfish virus (ECV), European sheatfish virus (ESV), EHNV, Doctor fish virus (DFV), Guppy virus 6 (GF6), short-finned eel virus (SERV) and Rana esculenta virus Italy 282/102 (REV 282/102). Each isolate was titrated in five cell lines: bluegill fry (BF-2), epithelioma papulosum cyprini (EPC), chinook salmon embryo (CHSE-214) rainbow trout gonad (RTG-2) and fathead minnow (FHM), and incubated at 10, 15, 20, 24 and 28 °C for two weeks. BF-2, EPC and CHSE-214 cells performed well and titers obtained in the three cell lines were similar, whereas FHM and RTG-2 cells consistently produced lower titers than the other cell lines at all temperatures. The optimal temperature for propagating the isolates collectively to high titers in vivo was 24 °C. Additionally, three established methods for re-isolation of virus from EHNV-infected organ material were compared. Challenged fish were sampled twice weekly and 7 organs were processed separately according to the three methods. Samples incubated on BF-2 cells at 22 °C for 2 weeks+1 week sub-cultivation (method 1) provided more positive results than the other 2 methods and when using the EPC cell line. Virus was most frequently isolated from the kidney, followed by brain, muscle, heart, liver, gills and lastly spleen.

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Main Research Area: Technical/natural sciences
A survey for the amphibian pathogens ranavirus and Batrachochytrium dendrobatidis (Bd) was conducted in Denmark during August and September 2008. The public was encouraged via the media to register unusual mortalities in a web-based survey. All members of the public that registered cases were interviewed by phone and 10 cases were examined on suspicion of disease-induced mortality. All samples were negative for Bd. Ranavirus was isolated from 2 samples of recently dead frogs collected during a mass mortality event in an artificial pond near Slagelse, Denmark. The identity of the virus was confirmed by immunofluorescent antibody test. Sequencing of the major capsid protein gene showed the isolate had more than 97.3% nucleotide homology to 6 other ranaviruses.
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
Authors: Angen, Ø. (Intern), Thomsen, J. (Ekstern), Larsen, L. E. (Intern), Larsen, J. (Ekstern), Kokotovic, B. (Intern), Heegaard, P. M. H. (Intern), Enemark, J. M. D. (Ekstern)
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Screening of Modified RNA duplexes

Because of sequence specific gene targeting activity siRNAs are regarded as promising active compounds in gene medicine. But one serious problem with delivering siRNAs as treatment is the now well-established non-specific activities of some RNA duplexes. Cellular reactions towards double stranded RNAs include the 2′-5′ oligoadenylate synthetase system, the protein kinase R, RIG-I and Toll-like receptor activated pathways all resulting in antiviral defence mechanism.

We have previously shown that antiviral innate immune reactions against double stranded RNAs could be detected in vivo as partial protection against a fish pathogenic virus. This protection corresponded with an interferon response in the fish. Here we use this fish model to screen siRNAs containing various chemical modifications of the RNA backbone for their antiviral activity, the overall aim being identification of an siRNA form with minimal immunostimulatory effects.

General information
**Studies on herd-immunity and primary versus secondary infection of VHSV in challenge and vaccination trials with rainbow trout**

Abstract for Scofda meeting 4-5.11.09 Studies on herd-immunity effect and primary versus secondary infection of VHSV by Ellen Lorenzen, Torben Eigil Kjær & Niels Lorenzen, National Veterinary Laboratory, Århus

The phenomenon of “herd-immunity” is one of the basal principles behind vaccination as well as selective breeding, i.e. the more non-susceptible individuals in a population, the lower the risk of disease among susceptible individuals. Thus as part of a recent field trial with a VHS-DNA-vaccine vaccinated as well as naïve fish from a Danish fish farm were brought to the laboratory at a size of 24g to be subjected to an experimental challenge with VHSV. The setup included 7 aquaria with 100 fish in each: 2 aquaria with 100 vaccinated fish (+VHS-challenge), 2 aquaria with 100 naïve fish (+ VHS-challenge), 2 aquaria with 50 vaccinated + 50 naïve fish (+VHS-challenge), and 1 aquarium with non-challenged control fish (vaccinated + naïve).

Mortality in the aquaria with only vaccinated fish was 2-3 %. Mortality in the aquaria with only naïve fish was 60-70 %. However, mortality among naïve fish in the mixed aquaria was only 6-18 %, the mortality among vaccinated fish being 0-6 %, and we interpreted this as an effect of herd-immunity, where the vaccinated fish protected the naïve fish, probably by secreting less virus compared to the naïve fish. We tried to demonstrate this phenomenon in 3 later experiments, but without success, probably due to a too high challenge load in relation to the susceptibility of the fish included in these studies, i.e. it was shown that the challenged vaccinated fish secreted large amounts of virus, although still less than challenged naïve fish. However, these results led to the question if the fish die due to the challenge virus or due to the virus secreted from fish in the same aquarium that become diseased at an early time point. This question was addressed in 3 subsequent parallel challenge experiments (3 different virus doses) including only one fish in 24 aquaria and 24 fish in 3 aquaria. The study showed, that at high challenge doses, mortality was comparable in the single-fish group (24 aquaria) and the group with 24 fish in each of 3 aquaria. At lower challenge doses, however, the survival rate increased in the single fish group the lower the virus titer during challenge. i.e. at lower challenge doses, secondary infections seem more pronounced. These results will be presented and discussed.

**General information**

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Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Lorenzen, E. (Intern), Kjaer, T. E. (Intern), Lorenzen, N. (Intern)
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**Susceptibility of pike Esox lucius to a panel of Ranavirus isolates**

In order to study the pathogenicity of ranaviruses to a wild European freshwater fish species, pike Esox lucius fry were challenged with the following Ranavirus isolates: epizootic haematopoietic necrosis virus (EHNV), European sheatfish virus (ESV), European catfish virus (ECV), pike-perch iridovirus (PPIV), New Zealand eel virus (NZeelV) and frog virus 3 (FV3). The fry were infected using bath challenge at 12 and 22 degrees C. Significant mortalities were observed at 12 degrees C for EHNV, ETV, PPIV and NZeelV. Background mortality was too high in the experiments performed at 22 degrees C for any conclusions about viral pathogenicity at this temperature to be drawn. Viruses could be re-isolated from samples from all challenged groups, and their presence in infected tissue was demonstrated using immunohistochemistry. The findings suggest that pike fry are susceptible to EHNV, ETV, PPIV and NZeelV and can be a vector for ECV and FV3. Statistical analysis of the factors associated with positive virus re-isolation showed that the number of fish in the sample influenced the outcome of virus re-isolation. Moreover, the likelihood of positive virus re-isolation significantly differed among the 6 viral isolates. The temperature from where the sample was taken and the number of days after infection were not associated with the probability of a positive virus re-isolation.

**General information**

State: Published
Susceptibility testing of fish cell lines for virus isolation

Passage of cell cultures may adversely influence cell susceptibility to virus infection through selection of cell clones that thrive in vitro but may not necessarily display high sensitivity to virus infection. Susceptibility to a given virus can therefore vary not only between cell lines and laboratories, but also between lineages of the same cell line. To minimise the occurrence of false negatives in a cell culture based surveillance system, we have investigated methods to select cell lineages that are relatively superior in their susceptibility to a panel of virus isolates. The procedures compare susceptibility between cell lines and between lineages within a laboratory and between laboratories (Inter-laboratory Proficiency Test). The objective being that the most sensitive cell line and lineages are routinely selected for diagnostic purposes. In comparing cell lines, we simulated "non-cell-culture-adapted" virus by propagating the virus in heterologous cell lines to the one tested. A stock of test virus was produced and stored at -80 °C and tests were conducted biannually. This procedure becomes complicated when several cell lines are in use and does not account for variation among lineages. In comparing cell lineages, we increased the number of isolates of each virus, propagated stocks in a given cell line and tested all lineages of that line in use in the laboratory. Testing of relative cell line susceptibility between laboratories is carried out annually via the Inter-laboratory Proficiency Test (Ariel et al., in press), which is organised by the European Community Reference Laboratory for Fish Diseases (CRL) in Denmark. In the year 2000, infected organ material rather than cell-culture-adapted virus was included in the test, to approach a realistic assessment of the variability in cell sensitivity for surveillance purposes within a cell line and between laboratories. In terms of economic and practical considerations as well as attempting to approach a realistic test system, we suggest the optimal procedure for susceptibility testing of fish cell lines for virus isolation to be a combination of biannual tests within the laboratory to compare cell lineages combined with the Inter-laboratory Proficiency Test.
The protective mechanisms induced by a fish rhabdovirus DNA vaccine depend on temperature

DNA vaccines encoding the viral glycoproteins of viral haemorrhagic septicaemia virus (VHSV) and infectious haematopoietic necrosis Virus (IHNV) have proved highly efficient in rainbow trout (Oncorhynchus mykiss) under experimental conditions. Non-specific as well as specific immune mechanisms seem to be activated. Temperature is an
important external parameter affecting the immune response in fish. The present study aimed at determining the effectiveness of a DNA vaccine against VHS at different temperatures. Rainbow trout fingerlings acclimated at 5 degrees C, 10 degrees C or 15 degrees C, were given an intramuscular injection of 1 μg purified plasmid DNA and challenged with virulent VHSV 8 or 36-40 days later. The vaccine protected the fish well at all three temperatures, but the involvement of innate and adaptive mechanisms differed: at low temperature, non-specific protection lasted longer and at 36 dpv fish kept at 5 degrees C had no detectable response of neutralizing antibodies while 67% of the fish kept at 15 degrees C had seroconverted. Induction of Mx as measured in liver samples was delayed at 5 degrees C with no detectable response 7 dpv whereas fish maintained at 10 C had significantly elevated levels of Mx3-transcripts at that time point. Immunohistochemical studies of the injection site of vaccinated fish also showed a clear effect of temperature: in fish maintained at 15 degrees C the vhsG-protein appeared earlier on the surface of transfected myocytes and the inflammatory response clearing away these myocytes arose earlier Compared to fish kept at the lower temperatures of 5 and 10 degrees C.

**General information**

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Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Lorenzen, E. (Intern), Einer-Jensen, K. (Intern), Rasmussen, J. S. (Intern), Kjær, T. E. (Intern), Collet, B. (Ekstern), Secombes, C. (Ekstern), Lorenzen, N. (Intern)
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Scopus rating (2014): SJR 2.05 SNIP 1.231 CiteScore 3.57
Web of Science (2014): Indexed yes
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Scopus rating (2013): SJR 1.73 SNIP 1.126 CiteScore 3.43
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Web of Science (2013): Indexed yes
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Scopus rating (2012): SJR 1.634 SNIP 1.159 CiteScore 3.56
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
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Scopus rating (2011): SJR 1.74 SNIP 1.274 CiteScore 3.86
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.636 SNIP 1.207
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Scopus rating (2009): SJR 1.428 SNIP 1.21
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.327 SNIP 1.025
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Scopus rating (2006): SJR 1.305 SNIP 1.154
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Web of Science (2005): Indexed yes
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Web of Science (2004): Indexed yes
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**THE PROTECTIVE MECHANISMS INDUCED BY A FISH RHABDOVIRUS DNA-VACCINE DEPENDS ON TEMPERATURE**

DNA-vaccines encoding the viral glycoproteins of viral haemorrhagic septicaemia virus (VHSV) and infectious haematopoietic necrosis virus (IHNV) have proved highly efficient in rainbow trout (Oncorhynchus mykiss) under experimental conditions. In the early phase following vaccination, innate cross-protective mechanisms are dominating but the protection becomes highly specific within 3-4 weeks at 12-15°C. Temperature is known as an important external parameter affecting the immune response in fish and the present study aimed at characterizing temperature effects on the immune response to a VHS DNA vaccine. Rainbow trout fingerlings acclimated at 5°C, 10°C or 15°C, were given an intramuscular injection of 1g purified plasmid DNA and challenged with virulent VHSV 9 or 36-40 days later. The vaccine protected the fish well at all three temperatures, however the non-specific mechanisms lasted for a longer period of time at lower temperatures, hereby apparently compensating for a delayed adaptive response. At 36 dpv fish kept at 5C thus had no detectable response of neutralising antibodies while 67% of the fish kept at 15C had seroconverted.

Immunohistochemical time-course studies of the injection site of vaccinated fish also showed a clear effect of temperature: in fish maintained at 15°C the vhsG-protein occurred earlier on the surface of transfected myocytes than in fish kept at the lower temperatures and the inflammatory response clearing away these myocytes similarly arose earlier at high temperature. Long persistence of transfected myocytes expressing the vaccine antigen might explain the prolonged stimulation of innate protective mechanisms at low temperature. From a practical point of view the results suggest that DNA vaccination against rhabdoviruses might be applied as a prophylactic measure within a broad temperature range.

**General information**

State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, University of Aberdeen
Authors: Lorenzen, N. (Intern), Lorenzen, E. (Intern), Einer-Jensen, K. (Intern), Rasmussen, J. S. (Intern), Kjær, T. E. (Intern), Collet, B. (Ekstern), Secombes, C. J. (Ekstern)
Publication date: 2009
Event: Abstract from 11th Congress of the International Society of Developmental and Comparative Immunology (ISDCI), Prague, Poland.
Main Research Area: Technical/natural sciences
Electronic versions:
NLorenzen-abstract2-ISDCI09.doc
Source: orbit
Source-ID: 255127
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2009
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.
Vaccination af slagtekalve mod BRSV: Et feltforsøg i 16 danske slagtekalvebesætninger i perioden 2006 - 2008

General information
State: Published
Organisations: National Veterinary Institute, Division of Veterinary Diagnostics and Research, Virology, AgroTech
Authors: Graumann, A. M. (Ekstern), Larsen, L. E. (Intern)
Number of pages: 45
Publication date: 2009
Antibody titers against swine influenza subtypes determined by the hemagglutination inhibition test are highly dependent on the strain

In Denmark there are three circulating strains of swine influenza H1N1, H1N2 and H3N2. The H1N2 is different from the H1N2 subtypes circulating in other European countries. The Danish subtype is a reassortment between the two Danish circulating swine influenza subtypes H1N1 and H3N2. From a diagnostic and epidemiological point of view it is crucial to clarify whether the immunological response to one subtype protects against infection with the other subtype. The hemagglutination inhibition test (HI-test) has been used widely to determine the presence of antibodies in serum against influenza viruses. In the present study the HI-test was used to determine antibody response from experimental infected pigs. The aim of the study was to evaluate the antibody response against the new Danish influenza subtype H1N2 (H1N2dk) and to examine the level of crossprotection/reaction between the two influenza subtypes.
Bakterier i svin

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics
Authors: Mølbak, L. (Intern), Jensen, T. K. (Intern), Boye, M. (Intern)
Pages: 46 - 48
Publication date: 2008
Main Research Area: Technical/natural sciences

Publication information
Journal: Hyologisk
Volume: 30
Issue number: 9
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: 223529
Publication: Research › Journal article – Annual report year: 2008

Bedre identifikation af VHS-virus i havet

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Einer-Jensen, K. (Intern)
Pages: 31
Publication date: 2008
Main Research Area: Technical/natural sciences

Publication information
Journal: Dansk Veterinærtidsskrift
Issue number: 15/16
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
ISI indexed (2012): ISI indexed no
BFI (2011): BFI-level 1
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
BFI (2009): BFI-level 1
BFI (2008): BFI-level 1
Original language: Danish
Source: orbit
Source-ID: 233505
Publication: Communication › Journal article – Annual report year: 2008
Classical swine fever in one-week-old piglets

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Uttenthal, Å. (Intern), Rasmussen, T. B. (Intern), Nielsen, J. (Intern)
Number of pages: 125
Publication date: 2008

Host publication information
Title of host publication: Proceedings of the 7th ESVV Pestivirus Symposium
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 242280
Publication: Research › Article in proceedings – 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, Universidad Autonoma de Barcelona
Authors: Hjulsager, C. K. (Intern), Grau-Roma, L. (Ekstern), Sibila, M. (Ekstern), Enøe, C. (Intern), Larsen, L. E. (Intern), Segales, J. (Ekstern)
Publication date: 2008
Event: Abstract from 20th International Pig Veterinary Society Congress, Durban, South Africa.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 224289
Publication: 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
Authors: Larsen, L. E. (Intern), Bødker, R. (Intern)
Publication date: 2008
Event: Poster session presented at RUFF-møde om klimaændringer, Krogerup Avlsgård, Humlebæk.
Differences in Virulence of Marine and Freshwater Isolates of Viral Hemorrhagic Septicemia Virus In Vivo Correlate with In Vitro Ability To Infect Gill Epithelial Cells and Macrophages of Rainbow Trout (Oncorhynchus mykiss)

Two strains of viral hemorrhagic septicemia virus (VHSV) with known different virulence characteristics in vivo were studied (by a time course approach) for their abilities to infect and translocate across a primary culture of gill epithelial cells (GEC) of rainbow trout (RBT; Oncorhynchus mykiss). The strains included one low-virulence marine VHSV (ma-VHSV) strain, ma-1p8, and a highly pathogenic freshwater VHSV (fw-VHSV) strain, fw-DK-3592B. Infectivities toward trout head kidney macrophages were also studied (by a time course method), and differences in in vivo virulence were reconfirmed, the aim being to determine any correlation between in vivo virulence and in vitro infectivity. The in vitro studies showed that the fw-VHSV isolate infected and caused a cytotoxic effect in monolayers of GEC (demonstrating virulence) at an early time point (2 h postinoculation) and that the same virus strain had translocated over a confluent, polarized GEC layer by 2 h postinoculation. The marine isolate did not infect monolayers of GEC, and delayed translocation across polarized GEC was seen by 48 h postinoculation. Primary cultures of head kidney macrophages were also infected with fw-VHSV, with a maximum of 9.5% virus-positive cells by 3 days postinfection, while for the ma-VHSV strain, only 0.5% of the macrophages were positive after 3 days of culture. In vivo studies showed that the fw-VHSV strain was highly virulent for RBT fry and caused high mortality, with classical features of viral hemorrhagic septicemia. The ma-VHSV showed a very low level of virulence (only one pool of samples from the dead fish was VHSV positive). This study has shown that the differences in virulence between marine and freshwater strains of VHSV following the in vivo infection of RBT correlate with in vitro abilities to infect primary cultures of GEC and head kidney macrophages of the same species.

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, PHARMAQ AS, Norwegian School of Veterinary Science
Authors: Brudeseth, B. E. (Ekstern), Skall, H. F. (Intern), Evensen, Ø. (Ekstern)
Pages: 10359-10365
Publication date: 2008
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Virology
Volume: 82
Issue number: 21
ISSN (Print): 0022-538X
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Web of Science (2016): Indexed yes
Scopus rating (2016): SJR 3.052 SNIP 1.131 CiteScore 4.42
Web of Science (2015): Indexed yes
BFI (2015): BFI-level 2
Web of Science (2015): Indexed yes
Scopus rating (2015): SJR 3.286 SNIP 1.138 CiteScore 4.42
Web of Science (2014): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 3.168 SNIP 1.219 CiteScore 4.4
Web of Science (2013): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 3.468 SNIP 1.26 CiteScore 4.92
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 3.154 SNIP 1.227 CiteScore 5.2
ISI indexed (2012): ISI indexed yes
Differentiating infected from vaccinated animals: WP 4.3 DIVA diagnostics

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Uttenthal, Å. (Intern)
Publication date: 2008
Event: Poster session presented at 2nd Annual Meeting EPIZONE, Brescia, Italy.
Main Research Area: Technical/natural sciences
DIVA, virus, Pig
Electronic versions:
Progress poster WP4.3 2008.pdf
Source: orbit
Source-ID: 241320
Publication: Research › Poster – Annual report year: 2008
Direct recovery of infectious Pestivirus from a full-length RT-PCR amplicon

This study describes the use of a novel and rapid long reverse transcription (RT)-PCR for the generation of infectious full-length cDNA of pestiviruses. To produce rescued viruses, full-length RT-PCR amplicons of 12.3 kb, including a T7-promoter, were transcribed directly in vitro, and the resulting RNA transcripts were electroporated into ovine cells. Infectious virus was obtained after one cell culture passage. The rescued viruses had a phenotype similar to the parental Border Disease virus strain. Therefore, direct generation of infectious pestiviruses from full-length RT-PCR cDNA products could be a valuable instrument for virus rescue, conservation and further characterization.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Friedrich Loeffler Institute
Authors: Rasmussen, T. B. (Intern), Reimann, I. (Ekstern), Hoffmann, B. (Ekstern), Depner, K. (Ekstern), Uttenthal, Å. (Intern), Beer, M. (Ekstern)
Pages: 330-330
Publication date: 2008
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Virological Methods
Volume: 149
Issue number: 2
ISSN (Print): 0166-0934
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.87 SNIP 0.736 CiteScore 1.78
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.868 SNIP 0.799 CiteScore 1.68
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.893 SNIP 0.952 CiteScore 1.87
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.861 SNIP 0.91 CiteScore 1.99
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.869 SNIP 0.935 CiteScore 2.08
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.907 SNIP 0.994 CiteScore 2.23
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.892 SNIP 0.998
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.964 SNIP 1.061
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.918 SNIP 1.082
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 0.955 SNIP 1.029
Disminuye la distancia entre el cerdo y el laboratorio: Proyecto Lab-On-Site

General information
State: Published
Organisations: National Veterinary Institute, Section for Virology, Universidad Complutense, SVA, Sverige
Authors: Uttenthal, Å. (Intern), Rodriguez, B. (Ekstern), Belak, S. (Ekstern), Sánchez-Viscaino, J. M. (Ekstern), Rasmussen, T. B. (Intern)
Pages: 22-23
Publication date: 2008
Main Research Area: Technical/natural sciences

Publication information
Journal: Anaporc
Volume: 52
Issue number: 5
ISSN (Print): 1577-8568
Original language: Spanish
Source: orbit
Source-ID: 228441
Publication: Communication › Journal article – Annual report year: 2008

DIVA diagnostics.: Different approaches towards the same goal.

General information
State: Published
Organisations: National Veterinary Institute, Division of Virology, Sektion for Eksotiske Virusygdommen
Authors: Uttenthal, Å. (Intern)
Publication date: 2008
Event: Paper presented at EPIZONE Theme 5 meeting : Young EPIZONE meeting, El Escorial, Madrid, Spain,
Main Research Area: Technical/natural sciences
Classical Swine Fever, Foot and Mouth Disease, Avian Influenza Virus, DIVA Diagnostics
Source: orbit
Source-ID: 233201
Publication: Research › Paper – Annual report year: 2008

DIVA properties of the chimeric pestivirus CP7_E2gif

General information
DIVA properties of the chimeric pestivirus CP7_E2

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Friedrich Loeffler Institute
Authors: Rasmussen, T. B. (Intern), Reimann, I. (Ekstern), Beer, M. (Ekstern), Uttenthal, Å. (Intern)
Publication date: 2008
Event: Poster session presented at 2nd Annual Meeting EPIZONE, Brescia, Italy.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 232551
Publication: Research - peer-review › Poster – Annual report year: 2008

Dromedaries (Camelus dromedarius) are of Low Susceptibility to Inoculation with Foot-and-Mouth Disease Virus Serotype O

Two sheep and five dromedaries were inoculated with a high dose of a cattle-passaged type O strain of foot-and-mouth disease virus (FMDV). The sheep developed typical FMD. The inoculated camels, which were placed in contact with five further dromedaries and four sheep, showed no visible signs of illness or vesicular lesions. However, one of them had a raised body temperature at 3 days post-inoculation (pi) and a viraemia from days 2 to 10; probang samples from this animal were negative for infections virus, but a low level of FMDV RNA was detected in a sample taken on day 6 pi, five other samples taken from days 3 to 28 being negative. Examination of mouth swabs indicated a low level of FMDV RNA at days 1-5 pi in four of the five inoculated camels, but no infectious FMDN7 or FMDV RNA was detected in serum, probang or month swab samples from contact-exposed animals (camels and sheep). All the contact-exposed camels and sheep and two of the inoculated camels were serologically negative for FMD when tested up to day 28. In contrast, the camel with viraemia became serologically positive from day 14, and the other two inoculated camels (which had been exposed to FMDV in an earlier experiment) became serologically positive from day 10. The experiment suggested that dromedaries (1) are of low susceptibility to FMDV serotype O, (2) do not transmit infection, even by close contact, and (3) are unlikely to play a significant epidemiological role in FMD.

General information
State: Published
Organisations: National Veterinary Institute, Sektion for Eksotiske Virussygdomme, Division of Virology
Authors: Alexandersen, S. (Intern), Wernery, U. (Ekstern), Nagy, P. (Ekstern), Frederiksen, T. (Intern), Normann, P. (Intern)
Pages: 187-193
Publication date: 2008
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Comparative Pathology
Volume: 139
Issue number: 4
ISSN (Print): 0021-9975
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Dynamics of porcine circovirus type 2 infection and excretion in pigs from postweaning multisystemic wasting syndrome affected farms from Spain and Denmark

Serological 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.
Early Administration of Probiotics Alters Bacterial Colonization and Limits Diet-Induced Gut Dysfunction and Severity of Necrotizing Enterocolitis In Preterm Pigs

Following preterm birth, bacterial colonization and enteral formula feeding predispose neonates to gut dysfunction and necrotizing enterocolitis (NEC), a serious gastrointestinal inflammatory disease. We hypothesized that administration of probiotics would beneficially influence early bacterial colonization, thereby reducing the susceptibility to formula-induced gut atrophy, dysfunction, and NEC. Caesarean-delivered preterm pigs were provided total parenteral nutrition (1.5 d) followed by enteral feeding (2d) with porcine colosstrum (COLOS; n= 5), formula (FORM; n = 9), or formula with probiotics (FORM-P, Bifidobacterium animalis and Lactobacillus: L. acidophilus, L. casei, L. pentosus, L. planterum; n=13). Clinical NEC scores were reduced (P
Egtvedsyge og frontforskning i fiskevacciner. Århusafdelingens indsats har været meget vigtig for forskningen i og bekæmpelsen af Egtvedsyge, en alvorlig sygdom hos dambrugsfisk i Europa og USA

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Olesen, N. J. (Intern), Lorenzen, N. (Intern)
Pages: 10-13
Publication date: 2008
Main Research Area: Technical/natural sciences

Publication information
Journal: DTU Vet 100 års jubilæumsskrift
Original language: Danish
Source-ID: 241565
Publication: Research › Journal article – 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, Centre de Recerca en Sanitat Animal
Authors: Kristensen, C. S. (Ekstern), Roma, L. G. (Ekstern), Larsen, L. E. (Intern)
Pages: 1-4
Publication date: 2008
Main Research Area: Technical/natural sciences

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

Evaluation of automated nucleic acid extraction methods in a multicentre comparative trial.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Institute for Animal Health, Lund University, Veterinary Laboratories Agency
Authors: Ebert, K. (Ekstern), Rasmussen, T. B. (Intern), Uttenthal, Å. (Intern), Reid, S. M. (Ekstern), Hakhverdyan, M. (Ekstern), Belak, S. (Ekstern), Wakeley, P. R. (Ekstern), King, D. P. (Ekstern)
Publication date: 2008
Event: Poster session presented at EUFMD Meeting 2008, Sicily, Italy.
Main Research Area: Technical/natural sciences
Source-ID: 232553
Publication: Research - peer-review › Poster – Annual report year: 2008

Examination for a viral co-factor in postweaning multisystemic wasting syndrome (PMWS)

In order to test the hypothesis that a putative co-factor for the development of postweaning multisystemic wasting syndrome (PMWS) in pigs could be of viral origin, we performed extensive virological examinations on organ material from pigs diagnosed with PMWS originating from within a Danish PMWS-transmission study. Virus isolation attempts were carried out on a large panel of different cell types including primary pig kidney cells and lung macrophages, primary rabbit kidney cells and seven established cell lines (MARC-145, ST117, PK15, BHK21, HeLa, Vero, and MDCK). Although these represent cells with susceptibility to a wide range of known viruses, the results did not provide evidence for a specific virus other than PCV2 contributing to the development of PMWS. Furthermore, in order to test whether specific genotypes of PCV2 may trigger the switch from PCV2 infection to clinical disease, we compared complete DNA genome sequences of PCV2 derived from PMWS-positive as well as PMWS-negative pigs. On the basis of the DNA sequences, the PCV2 isolates were divided into two groups. Group 1 consisting of one isolate originating from a herd unaffected by PMWS, with
group 2 consisting of nine isolates originating from four PMWS-affected herds, four PMWS-positive pigs plus one
unaffected herd. The PCV2 genomes from the two groups showed 95.5% identity. Alignment analyses of the sequences
encoding the replicase and capsid protein from group 1 and group 2 PCV2 isolates showed two amino acid differences
encoded in the replicase protein, while 19 amino acid differences were predicted among the capsid protein sequences.
The PCV2 DNA sequence analysis supports recent observations from studies in USA as well as Europe, which suggest
that strain variations may influence the clinical outcome of PCV2 infection.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Microbial Ecology,
Division of Veterinary Diagnostics and Research, Technical University of Denmark
Authors: Lohse, L. (Intern), Bøtner, A. (Intern), Hansen, A. L. (Ekstern), Frederiksen, T. (Intern), Dupont, K. (Intern),
Christensen, C. S. (Ekstern), Bækbo, P. (Ekstern), Nielsen, J. (Intern)
Pages: 97-107
Publication date: 2008
Main Research Area: Technical/natural sciences

Publication information
Journal: Veterinary Microbiology
Volume: 129
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
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.326 SNIP 1.208
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.393 SNIP 1.21 CiteScore 2.56
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.281 SNIP 1.262 CiteScore 2.54
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.438 SNIP 1.484 CiteScore 3
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.437 SNIP 1.579 CiteScore 3.18
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.562 SNIP 1.738 CiteScore 3.27
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.371 SNIP 1.476
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.29 SNIP 1.472
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.169 SNIP 1.3
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.043 SNIP 1.322
Foot-and-mouth disease virus infection in young lambs: pathogenesis and tissue tropism

Foot-and-mouth disease (FMD) in adult sheep usually causes milder clinical signs than in cattle or pigs, and is often subtle enough to go undiagnosed. In contrast, FMD in lambs has been reported to cause high mortality during field outbreaks. In order to investigate the pathogenesis of FMD in lambs, two groups, aged 10–14 days, were infected with foot-and-mouth disease virus (FMDV) type O UKG. One group of lambs (n = 8) was inoculated with FMDV in the coronary band, while the other (n = 4) was infected by direct contact with FMDV-inoculated ewes. Daily serum samples and temperature
measurements were taken. Lambs were killed sequentially and tissue samples taken for analysis. Using real-time RT-PCR, viral RNA levels in tissue samples and serum were measured, and a novel strand-specific real-time RT-PCR assay was used to quantify viral replication levels in tissues. Tissue sections were examined for histopathological lesions, and in situ hybridisation (ISH) was used to localise viral RNA within histological sections. The contact-infected lambs became infected approximately 24 h after the ewes were inoculated. Vesicular lesions developed on the feet of all lambs and on the caudo-lateral part of the tongues of six of the eight inoculated lambs and three of the four contact-infected lambs. Although no lambs developed severe clinical signs, one of the contact-infected lambs died acutely at 5 days post-exposure. Histological examination of the heart from this lamb showed multi-focal areas of lymphocytic-plasmacytic myocarditis; similar lesions were also observed in the hearts of three of the inoculated lambs. Using ISH, viral RNA was localised within cardiac and skeletal muscle cells from the lamb which had died, and also from vesicular lesions on the coronary band and tongue of inoculated lambs. These results provide a detailed description of the pathogenesis of the disease in lambs.

General information
State: Published
Organisations: Section of Vesicular virus diseases, Division of Virology, National Veterinary Institute, The Pirbright Institute, Royal Veterinary College
Authors: Ryan, E. (Ekstern), Horsington, J. (Ekstern), Durand, S. (Ekstern), Brooks, H. (Ekstern), Alexandersen, S. (Intern), Brownlie, J. (Ekstern), Zhang, Z. (Ekstern)
Pages: 258-274
Publication date: 2008
Main Research Area: Technical/natural sciences

Publication information
Journal: Veterinary Microbiology
Volume: 127
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
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.326 SNIP 1.208
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.393 SNIP 1.21 CiteScore 2.56
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.281 SNIP 1.262 CiteScore 2.54
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.438 SNIP 1.484 CiteScore 3
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.437 SNIP 1.579 CiteScore 3.18
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.562 SNIP 1.738 CiteScore 3.27
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.371 SNIP 1.476
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.29 SNIP 1.472
Generation of recombinant pestiviruses using a full genome amplification strategy.

Aim Complete genome amplification of viral RNA provides a new tool for generation of modified pestiviruses. We have recently reported a full genome amplification strategy for direct recovery of infectious pestivirus (Rasmussen et al., 2008). This comprised rescue of BDV strain “Gifhorn” from a full-length RT-PCR amplicon demonstrating that long RT-PCR can be used for direct generation of an infectious pestivirus. The strategy is not limited to amplification of BDV “Gifhorn”, but can be further utilized for amplification of a diverse selection of pestivirus strains and for the generation of modified pestiviruses. Methods Pestivirus genomes were amplified from either total RNA preparations using long RT-PCR or from infectious cDNA clones using long PCR. Viral RNA was extracted from cell cultures inoculated with pestivirus (e.g. BDV “Gifhorn” or BVDV “CP7”) using a combined Trizol/RNeasy protocol. Total RNA was reverse transcribed to cDNA at 50°C for 90 minutes using SuperScript III reverse transcriptase (Invitrogen). Full-length PCR amplification was performed using specific primers for complete genome amplification of the different pestivirus strains. Amplicons were prepared for cloning into low-copy vectors to produce new infectious cDNA clones. Conclusions Using this full genome amplification strategy the efforts in producing new viral variants can be expedited and focused on a variety of other viral strains and hence is not limited to the availability of an existing infectious clone. The long RT-PCR strategy significantly simplifies and streamlines the workflow and facilitates generation of new modified pestiviruses and also allows direct full-length sequence analysis. References Rasmussen et al., J. Virol. Methods 149(2), 330 (2008).
Global situation concerning CSFV

General information
State: Published
Organisations: National Veterinary Institute, Division of Virology, Sektion for Eksotiske Virussygdomme
Authors: Uttenthal, Å. (Intern)
Publication date: 2008
Event: Abstract from 7th ESVV Pestivirus Symposium, Uppsala, Sweden.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 232550
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2008

Helicobacter spp. present in the small intestine of pigs having proliferative enteropathy

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics
Authors: Mølbak, L. (Intern), Giovalle, E. (Intern), Jensen, T. K. (Intern), Boye, M. (Intern)
Publication date: 2008
Event: Abstract from Building bridges : EPISODE Workshop: Research in Swine Viral Diseases, Shanghai, China.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 229173
Publication: Research › Conference abstract for conference – 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
Authors: Breum, S. Ø. (Intern), Hjulsager, C. K. (Intern), Larsen, L. E. (Intern)
Publication date: 2008
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 232979
Publication: 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
Authors: Breum, S. Ø. (Intern), Hjulsager, C. K. (Intern), Larsen, L. E. (Intern)
Publication date: 2008
Main Research Area: Technical/natural sciences

Publication information
Journal: Dansk Veterinaertidsskrift
Issue number: 7
ISSN (Print): 0106-6854
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.

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, Universidad Autonoma de Barcelona
Authors: Breum, S. Ø. (Intern), Hjulsager, C. K. (Intern), De Deus, N. (Ekstern), Segales, J. (Ekstern), Enøe, C. (Intern), Larsen, L. E. (Intern)
Publication date: 2008
Event: Abstract from 20th International Pig Veterinary Society Congress, Durban, South Africa.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 224421
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2008

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.

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, Universidad Autonoma de
Identification of a new porcine circovirus type 2 (PCV2) genotype in Danish archive pig samples

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.

Improved diagnosis for nine viral diseases considered as notifiable by the World Organization for Animal Health

General information
State: Published
Organisations: Section for Exotic Viral Diseases, Division of Virology, National Veterinary Institute, Universidad Complutense, SVA Sweden, The Pirbright Institute, National Veterinary Institute, ISZ, Research Center Borstel, SVA, Sverige, Queen's University Belfast
Authors: Rodriguez-Sanchez, B. (Ekstern), Sanchez-Vizcaino, J. M. (Ekstern), Uttenthal, Å. (Intern), Rasmussen, T. B. (Intern), Hakverdyan, M. (Ekstern), King, D. P. (Ekstern), Ferris, N. P. (Ekstern), Ebert, K. (Ekstern), Reid, S. M. (Ekstern), Kiss, I. (Ekstern), Brocchi, E. (Ekstern), Cordioli, P. (Ekstern), Hjertner, B. (Ekstern), McMenamy, M. (Ekstern), McMillan, J. (Ekstern), Ahmed, J. (Ekstern), Belak, S. (Ekstern)
Pages: 215-225
Publication date: 2008
Main Research Area: Technical/natural sciences

Journal: Transboundary and Emerging Diseases
Volume: 55
Issue number: 5-6
ISSN (Print): 1865-1674
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.16 SJR 0.994 SNIP 1.096
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.258 SNIP 1.262 CiteScore 2.29
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.038 SNIP 1.19 CiteScore 2.23
Intra-laboratory evaluation of two commercial DIVA kits for Avian influenza

General information
State: Published
Organisations: Section of Poultry Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, ISZ, CVI, Friedrich Loeffler Institute, VLA, Weybridge, UK, Agence Française de Sécurité Sanitaire des Aliments, National Veterinary Institute, Centrum voor Onderzoek in Diergeneeskunde en Agrochemie
Authors: Dundon, W. (Ekstern), Pizzuto, M. (Ekstern), Koch, G. (Ekstern), Kuehn, K. (Ekstern), Harder, T. (Ekstern), Mahmood, S. (Ekstern), Slomka, M. (Ekstern), Schmitz, A. (Ekstern), Jestin, V. (Ekstern), Jørgensen, P. H. (Intern), Stahl, K. (Ekstern), Marche, S. (Ekstern), Van Den Berg, T. (Ekstern), Capua, I. (Ekstern), Uttenthal, Å. (Intern)
Event: Abstract from 2nd Annual Meeting EPIZONE, Brescia, Italy.
Main Research Area: Technical/natural sciences
DIVA diagnostics, Intra laboratory evaluation, Avian Influenza
Source: orbit
Source-ID: 232051
Publication date: 2008
Publication: Research - peer-review › Journal article – Annual report year: 2008
Jagten på virus-genet

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Technical University of Denmark
Authors: Hoffmann, P. (Ekstern), Einer-Jensen, K. (Intern)
Publication date: 2008
Main Research Area: Technical/natural sciences

LabOnSite - at bringe laboratoriet ud i felten

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Universidad Complutense, Queen's University Belfast, Centro de Investigación en Sanidad Animal, National Veterinary Institute
Authors: Uttenthal, Å. (Intern), Rodriguez, B. (Ekstern), Hjertner, B. (Ekstern), Fernandez, J. (Ekstern), Belak, S. (Ekstern), Rasmussen, T. B. (Intern)
Publication date: 2008
Main Research Area: Technical/natural sciences
Monocistronic mRNAs containing defective hepatitis C virus-like picornavirus internal ribosome entry site elements in their 5' untranslated regions are efficiently translated in cells by a cap-dependent mechanism

The initiation of protein synthesis on mRNAs within eukaryotic cells is achieved either by a 5' cap-dependent mechanism or through internal initiation directed by an internal ribosome entry site (IRES). Picornavirus IRES elements, located in the 5' untranslated region (5'UTR), contain extensive secondary structure and multiple upstream AUG codons. These features can be expected to inhibit cap-dependent initiation of translation. However, we have now shown that certain mutant hepatitis C virus-like picornavirus IRES elements (from porcine teschovirus-1 and avian encephalomyelitis virus), which are unable to direct internal initiation, are not significant barriers to efficient translation of capped monocistronic mRNAs that contain these defective elements within their 5'UTRs. Moreover, the translation of these mRNAs is highly sensitive to the expression of an enterovirus 2A protease (which induces cleavage of eIF4G) and is also inhibited by hippuristanol, a specific inhibitor of eIF4A function, in contrast to their parental wild-type IRES elements. These results provide a possible basis for the evolution of viral IRES elements within the context of functional mRNAs that are translated by a cap-dependent mechanism.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Belsham, G. (Intern), Nielsen, I. (Intern), Normann, P. (Intern), Royall, E. (Ekstern), Roberts, L. (Ekstern)
Pages: 1671-1680
Publication date: 2008
Main Research Area: Technical/natural sciences

Publication information
Journal: Rna-a Publication of the Rna Society
Volume: 14
Issue number: 8
ISSN (Print): 1355-8382
Ratings:
National biosecurity approaches, plans and programmes in response to diseases in farmed aquatic animals: evolution, effectiveness and the way forward

The rapid increase in aquaculture production and trade, and increased attention to the negative effects of disease, are becoming stimuli for developing national biosecurity strategies for farmed fisheries, for which the World Organisation for Animal Health (OIE) Aquatic Animal Health Code and Manual of Diagnostic Tests for Aquatic Animals serve as an excellent framework. Using examples from a few countries and selected diseases, this paper provides a general overview of the development of approaches to implementing biosecurity strategies, including those emerging in the national legislation and regulations of some countries, and those being initiated by industries themselves. The determination of disease status in different epidemiological units (from a farm to a nation), appropriate approaches for preventing the introduction of disease and developing contingencies for disease control and eradication are also discussed. Important to
the effectiveness of such strategies are provision of financial, personnel and other resources to implement them, including incentives such as indemnification or compensation in eradication programmes, and practical linkage to regulatory or government policy initiatives.

**General information**

State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, National Veterinary Institute, Biosecurity New Zealand, Norwegian Food Safety Authority, Marine Scotland, American Veterinary Medical Association, Australian Government Department of Agriculture
Authors: Håstein, T. (Ekstern), Binde, M. (Ekstern), Hine, M. (Ekstern), Johnsen, S. (Ekstern), Lillehaug, A. (Ekstern), Olesen, N. J. (Intern), Purvis, N. (Ekstern), Scarfe, A. (Ekstern), Wright, B. (Ekstern)
Pages: 125-145
Publication date: 2008
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Rev Sci Tech Off Int Epizoot
Volume: 27
Issue number: 1
ISSN (Print): 0253-1933
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.24 SJR 0.575 SNIP 0.758
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.554 SNIP 0.759 CiteScore 1.11
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.543 SNIP 0.738 CiteScore 1.12
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.432 SNIP 0.56 CiteScore 0.99
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.521 SNIP 0.516 CiteScore 1.03
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.609 SNIP 0.617 CiteScore 1.39
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.624 SNIP 0.627
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.436 SNIP 0.629
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.393 SNIP 0.721
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 0.437 SNIP 0.793
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.411 SNIP 0.618
Scopus rating (2005): SJR 0.464 SNIP 0.757
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.585 SNIP 0.947
Scopus rating (2003): SJR 0.607 SNIP 1.184
New and emerging technologies: Improved laboratory and on-site detection of OIE List A viruses in animals and animal products

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, National Veterinary Institute, Universidad Complutense, Veterinary Institute of Debrecen, Hungary, SVANOVA Biotech AB, Sweden , ISZ, Ghent University, The Pirbright Institute, Queen's University Belfast
Authors: Belak, S. (Ekstern), Uttenthal, Å. (Intern), Hakhverdyan, M. (Ekstern), Allan, G. (Ekstern), Sanchez-Vizcaino, J. M. (Ekstern), Istvan, K. (Ekstern), Merza, M. (Ekstern), Brocchi, E. (Ekstern), van Reeth, K. (Ekstern), King, D. (Ekstern)
Publication date: 2008
Event: Poster session presented at 2nd Annual Meeting EPIZONE, Brescia, Italy.
Main Research Area: Technical/natural sciences
Classical swine fever, Foot and Mouth Disease, Virus, OIE listed diseases
Source: orbit
Source-ID: 232060
Publication: Research › Poster – Annual report year: 2008

Nye anmeldepligtige fiskesygdomme

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Olesen, N. J. (Intern)
Publication date: 2008
Main Research Area: Technical/natural sciences

Publication information
Journal: Dansk Veterinær Tidsskrift
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
ISI indexed (2012): ISI indexed no
BFI (2011): BFI-level 1
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
BFI (2009): BFI-level 1
BFI (2008): BFI-level 1
Original language: Danish
Source: orbit
Source-ID: 241564
Publication: Research › Journal article – Annual report year: 2008
Orf som differential diagnose til mund- og klovesyge.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Tjørnehøj, K. (Intern), Bøtner, A. (Intern), Belsham, G. (Intern), Alexandersen, S. (Intern)
Pages: 33
Publication date: 2008
Main Research Area: Technical/natural sciences

Publication information
Journal: Dansk veterinærtidsskrift
Issue number: 4, 15. februar
ISSN (Print): 1902-3715
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
ISI indexed (2012): ISI indexed no
BFI (2011): BFI-level 1
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
BFI (2009): BFI-level 1
BFI (2008): BFI-level 1
Original language: Danish
Source: orbit
Source-ID: 232990
Publication: Communication › Journal article – Annual report year: 2008

Organisation of rabies control and rabies prevention in Denmark

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Rasmussen, T. B. (Intern), Strandbygaard, B. (Intern)
Publication date: 2008

Publication information
Original language: English
Main Research Area: Technical/natural sciences
Rabies
Source: orbit
Source-ID: 243442
Publication: Research › Sound/Visual production (digital) – 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, Universidad Autonoma de Barcelona, Merial S.A.S., Ghent University, Institute of Virology and Immunoprophylaxis, University of Saskatchewan, Ohio State University, Robert Koch Institute, Lund University, Devenish Nutrition, BPEX, Agence Française de Sécurité Sanitaire des Aliments, Danish Pig Production, University of Copenhagen, Queen's University Belfast, Wageningen University & Research
Authors: Segalés, J. (Ekstern), Olvera, A. (Ekstern), Grau-Roma, L. (Ekstern), Charreyre, C. (Ekstern), Nauwynck, H. (Ekstern), Larsen, L. E. (Intern), Dupont, K. (Intern), McCullough, K. (Ekstern), Ellis, J. (Ekstern), Krakowka, S. (Ekstern),
Phenotypic and genetic characterization of a novel phenotype in pigs characterized by juvenile hairlessness and age dependent emphysema.

General Information
State: Published
Organisations: Sektion for Eksotiske Virusygdomme, Division of Virology, National Veterinary Institute, University of Copenhagen
Authors: Bruun, C. S. (Ekstern), Jørgensen, C. B. (Ekstern), Bay, L. (Ekstern), Cirera, S. (Ekstern), Jensen, H. E. (Ekstern), Leifsson, P. S. (Ekstern), Nielsen, J. (Intern), Christensen, K. (Ekstern), Fredholm, M. (Ekstern)
Pages: 283
Publication date: 2008
Main Research Area: Technical/natural sciences

Publication information
Journal: BMC Genomics
Volume: 9
ISSN (Print): 1471-2164
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 4.05 SJR 2.065 SNIP 1.122
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.287 SNIP 1.172 CiteScore 4.3
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.297 SNIP 1.205 CiteScore 4.18
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 2.141 SNIP 1.174 CiteScore 4.39
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 2.181 SNIP 1.225 CiteScore 4.61
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 2.271 SNIP 1.197 CiteScore 4.38
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.109 SNIP 1.038
Web of Science (2010): Indexed yes
PMWS smitter via luften

General information
State: Published
Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics, Virology, Dansk Svineproduktion
Authors: Sonne Kristensen, C. (Ekstern), Vestergaard, K. (Ekstern), Bækbo, P. (Ekstern), Enøe, C. (Intern), Bille-Hansen, V. (Intern), Jorsal, S. E. L. (Intern), Larsen, L. E. (Intern)
Pages: 1 - 8
Publication date: 2008
Main Research Area: Technical/natural sciences

Publication information
Journal: Dansk Svineproduktion
Issue number: 822
Original language: Danish
Source: orbit
Source-ID: 232555
Publication: Research - peer-review › Journal article – Annual report year: 2008

PMWS smitter via luften

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Authors: Kristensen, C. S. (Ekstern), Larsen, L. E. (Intern)
Publication date: 2008
Main Research Area: Technical/natural sciences

Publication information
Journal: Fagbladet Svin
Original language: Danish
Source: orbit
Postweaning multisystematic wasting syndrome in Danish pig herds: productivity, clinical signs and pathology

A case-control study of 74 herds with postweaning multisystemic wasting syndrome (PMWS) and 74 matched control herds was carried out. In the case herds the mortality rates of weaner and finisher pigs were 11.2 and 5.2 per cent respectively, compared with 3.1 and 3.2 per cent in the control herds. In most case herds, PMWS developed within the first four weeks after weaning. Wasting, diarrhoea and respiratory signs were observed in 10 per cent of the weaner pigs (7 to 30 kg) in the case herds compared with 7 per cent in the control herds. The average daily gains of the weaner pigs and finisher pigs were 36 g and 52 g less in the case herds than in the control herds. By examining three weaner pigs from each herd the PMWS diagnosis was confirmed by histopathology and immunohistochemistry in 78 per cent of the case herds, but at least one PMWS-positive weaner pig was found in 19 of the control herds. The prevalence of PMWS-positive pigs among illthriven weaner pigs was 45 per cent (101/222) in the case herds, and 12 per cent (27/222) in the control herds. Specific gross pathological findings were associated with a positive PMWS diagnosis; pigs with heavy, rubber-like lungs, atonic intestines, and enlarged bronchial and inguinal lymph nodes, had a 0.7 probability of a positive PMWS diagnosis by laboratory examinations. However, for illthriven pigs, this probability of having PMWS was equal in the case herds and the control herds.

General information
State: Published
Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics, Section of Swine fever etc., Division of Virology, Danish Pig Production, Danske Slagterier
Authors: Okholm Nielsen, E. (Ekstern), Enøe, C. (Intern), Jorsal, S. E. L. (Intern), Barfod, K. (Ekstern), Svensmark, B. (Ekstern), Bille-Hansen, V. (Intern), Vigre, H. (Intern), Bøtner, A. (Intern), Baekbo, P. (Ekstern)
Pages: 505-508
Publication date: 2008
Main Research Area: Technical/natural sciences

Publication information
Journal: Veterinary Record
Volume: 162
Issue number: 16
ISSN (Print): 0042-4900
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.442 SNIP 0.692 CiteScore 0.3
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.509 SNIP 0.794 CiteScore 0.39
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.469 SNIP 0.839 CiteScore 0.41
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.474 SNIP 0.821 CiteScore 0.5
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.491 SNIP 0.883 CiteScore 0.52
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.563 SNIP 0.9 CiteScore 0.62
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Post-weaning multisystemic wasting syndrome (PMWS) in Danish pig herds: productivity, clinical symptoms, and pathology

A case-control study of 74 herds with postweaning multisystemic wasting syndrome (PMWS) and 74 matched control herds was carried out. In the case herds the mortality rates of weaner and finisher pigs were 11.2 and 5.2 per cent respectively, compared with 3.1 and 3.2 per cent in the control herds. In most case herds, PMWS developed within the first four weeks after weaning. Wasting, diarrhoea and respiratory signs were observed in 10 per cent of the weaner pigs (7 to 30 kg) in the case herds compared with 7 per cent in the control herds. The average daily gains of the weaner pigs and finisher pigs were 36 g and 52 g less in the case herds than in the control herds. By examining three weaner pigs from each herd the PMWS diagnosis was confirmed by histopathology and immunohistochemistry in 78 per cent of the case herds, but at least one PMWS-positive weaner pig was found in 19 of the control herds. The prevalence of PMWS-positive pigs among illthriven weaner pigs was 45 per cent (101/222) in the case herds, and 12 per cent (27/222) in the control herds. Specific gross pathological findings were associated with a positive PMWS diagnosis; pigs with heavy, rubber-like lungs, atonic intestines, and enlarged bronchial and inguinal lymph nodes, had a 0.7 probability of a positive PMWS diagnosis by laboratory examinations. However, for illthriven pigs, this probability of having PMWS was equal in the case herds and the control herds.
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.
Reduction of Classical swine fever virus infectivity by anaesthesia or heat treatment

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Utenthal, Å. (Intern), Rasmussen, T. B. (Intern), Nielsen, J. (Intern)
Publication date: 2008

Host publication information
Title of host publication: Annual meeting of the National Swine Fever Laboratories
Publisher: CRL, Hannover
Main Research Area: Technical/natural sciences
Conference: Annual Meeting of the National Reference Laboratories of CSF, Hannover, Germany, 01/01/2008
Classical swine fever
Source: orbit
Source-ID: 233215
Publication: Research › Article in proceedings – Annual report year: 2008

Regnbærredens redning

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Dynamo
Authors: Vinge, T. (Ekstern), Lorenzen, N. (Intern)
Pages: 28-31
Publication date: 2008
Main Research Area: Technical/natural sciences

Publication information
Journal: Dynamo
Issue number: 12
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: 233520
Publication: Communication › Journal article – Annual report year: 2008

RNAi-mediated gene silencing in fishes?

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Schyth, B. D. (Intern)
Pages: 1890-1906
Publication date: 2008
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Fish Biology
Volume: 72
Robotter gode til automatiseret ekstraktion af virus RNA.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Rasmussen, T. B. (Intern), Uttenthal, Å. (Intern)
Pages: 33
Publication date: 2008
Main Research Area: Technical/natural sciences

Publication information
Journal: Dansk Veterinaertidsskrift
Volume: 91
Issue number: 23
ISSN (Print): 1902-3715
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
ISI indexed (2012): ISI indexed no
BFI (2011): BFI-level 1
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
BFI (2009): BFI-level 1
BFI (2008): BFI-level 1
Original language: Danish
Source: orbit
Source-ID: 224293
Publication: Research - peer-review › Journal article – Annual report year: 2008

Sapovirus fundet i danske grise

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Virology
Authors: Hjulsager, C. K. (Intern), Breum, S. Ø. (Intern), Larsen, L. E. (Intern)
Pages: 41
Publication date: 2008
Main Research Area: Technical/natural sciences

Publication information
Journal: Dansk Veterinaertidsskrift
Issue number: 18
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
Simulating the spread of classical swine fever virus between a hypothetical wild-boar population and domestic pig herds in Denmark

Denmark has no free-range wild-boar population. However, Danish wildlife organizations have suggested that wild boar should be reintroduced into the wild to broaden national biodiversity. Danish pig farmers fear that this would lead to a higher risk of introduction of classical swine fever virus (CSFV), which could have enormous consequences in terms of loss of pork exports. We conducted a risk assessment to address the additional risk of introducing and spreading CSFV due to the reintroduction of wild boar. In this paper, we present the part of the risk assessment that deals with the spread of CSFV between the hypothetical wild-boar population and the domestic population. Furthermore, the economic impact is assessed taking the perspective of the Danish national budget and the Danish pig industry. We used InterSpreadPlus to model the differential classical swine fever (CSF) risk due to wild boar. Nine scenarios were run to elucidate the effect of: (a) presence of wild boar (yes/no), (b) locations for the index case (domestic pig herd/wild-boar group).

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Danish Meat Association
Authors: Boklund, A. (Intern), Goldbach, S. G. (Ekstern), Uttenthal, Å. (Intern), Alban, L. (Ekstern)
Pages: 187-206
Surveillance of health status on eight marine rainbow trout, Oncorhynchus mykiss (Walbaum), farms in Denmark in 2006

General information
State: Published
Organisations: National Veterinary Institute, Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, Section of Poultry Diseases, AquaSearch Vet, Danish Aquaculture Organisation
Authors: Pedersen, K. (Intern), Skall, H. F. (Intern), Lassen-Nielsen, A. M. (Intern), Nielsen, T. (Ekstern), Henriksen, N. (Ekstern), Olesen, N. J. (Intern)
Pages: 659-667
Publication date: 2008
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Fish Diseases
Volume: 31
Issue number: 9
ISSN (Print): 0140-7775
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.12
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 1.71
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 1.99
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 1.74
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 1.7
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 2.09
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Testing immunogenicity of Mycoplasma hyosynoviae vaccine candidates; Induction of antibodies and IFNγ response

General information
State: Published
Organisations: Adaptive Immunology & Parasitology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Sektion for Eksotiske Virussygdomme, Division of Virology
Publication date: 2008
Event: Poster session presented at Workshop: Laying the foundations for rationally designed vaccines in veterinary medicine, National Veterinary Institute, Copenhagen, .
Main Research Area: Technical/natural sciences
Mycoplasma hyosynoviae, Swine, Vaccine
Source: orbit
Source-ID: 240779
Publication: Research › Poster – Annual report year: 2008

The picornavirus avian encephalomyelitis virus possesses a hepatitis C virus-like internal ribosome entry site element

Avian encephalomyelitis virus (AEV) is a picornavirus that causes disease in poultry worldwide, and flocks must be vaccinated for protection. AEV is currently classified within the hepatovirus genus, since its proteins are most closely related to those of hepatitis A virus (HAV). We now provide evidence that the 494-nucleotide-long 5’ untranslated region of the AEV genome contains an internal ribosome entry site (IRES) element that functions efficiently in vitro and in mammalian cells. Unlike the HAV IRES, the AEV IRES is relatively short and functions in the presence of cleaved eIF4G and it is also resistant to an inhibitor of eIF4A. These properties are reminiscent of the recently discovered class of IRES elements within certain other picornaviruses, such as porcine teschovirus 1 (PTV-1). Like the PTV-1 IRES, the AEV IRES shows significant similarity to the hepatitis C virus (HCV) IRES in sequence, function, and predicted secondary structure. Furthermore, mutational analysis of the predicted pseudoknot structure at the 3’ end of the AEV IRES lends support to the secondary structure we present. AEV is therefore another example of a picornavirus harboring an HCV-like IRES element within its genome, and thus, its classification within the hepatovirus genus may need to be reassessed in light of these findings.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Bakhshesh, M. (Ekstern), Groppelli, E. (Ekstern), Willcocks, M. (Ekstern), Royall, E. (Ekstern), Belsham, G. (Intern), Roberts, L. (Ekstern)
Pages: 1993-2003
Publication date: 2008
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Virology
Volume: 82
Issue number: 4
ISSN (Print): 0022-538X
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): SJR 3.052 SNIP 1.131 CiteScore 4.42
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 3.286 SNIP 1.138 CiteScore 4.42
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 3.168 SNIP 1.219 CiteScore 4.4
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 3.468 SNIP 1.26 CiteScore 4.92
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 3.154 SNIP 1.227 CiteScore 5.2
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 3.399 SNIP 1.288 CiteScore 5.37
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 3.532 SNIP 1.278
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 3.595 SNIP 1.307
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 3.803 SNIP 1.264
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 3.571 SNIP 1.311
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 3.76 SNIP 1.255
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 3.374 SNIP 1.243
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 3.382 SNIP 1.32
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 3.425 SNIP 1.331
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 3.242 SNIP 1.254
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 3.577 SNIP 1.357
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 3.543 SNIP 1.394
Web of Science (2000): Indexed yes
Vacciner til kvæg - status og perspektiver

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Adaptive Immunology & Parasitology
Authors: Larsen, L. E. (Intern), Jungersen, G. (Intern)
Pages: 12-14
Publication date: 2008
Main Research Area: Technical/natural sciences

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

Validation of a PriProET real-time PCR assay for the detection of African Swine Fever Virus (ASFV).

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Centro de Investigación en Sanidad Animal
Authors: Fernandez, J. (Ekstern), Rasmussen, T. B. (Intern), Callardo, C. (Ekstern), Uttenthal, Á. (Intern)
Publication date: 2008
Event: Abstract from Annual Meeting of the National Reference Laboratories of ASF, Hannover, Germany.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 232552
Publication: Research › Conference abstract for conference – 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
Authors: Ståhl, M. (Intern), Hjulsager, C. K. (Intern), Breum, S. Ø. (Intern), Larsen, L. E. (Intern), Jorsal, S. E. L. (Intern), Angen, Ø. (Intern)
Publication date: 2008
Event: Poster session presented at Advances in qPCR, Stockholm, Sweden.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 224219
Publication: Research - peer-review › Poster – Annual report year: 2008
The Specifics and Non-Specifics of using Small Interfering RNAs for Targeting of Viral Genes in a Fish Model

A novel in vivo model composed of small juvenile rainbow trout and a fish-pathogenic virus is suggested to analyze delivery and antiviral effect of formulated siRNAs. This model was used for testing delivery of intraperitoneally injected siRNAs formulated in polycationic liposomes. These, and to a lesser degree naked siRNAs, primarily entered free intraperitoneal cells including macrophage-like cells. Furthermore uptake correlated with antiviral activity seen as reduced mortality of fish challenged with VHSV. Protection at the disease level was not dependent upon which one of three tested siRNAs was used and protection correlated with up-regulation of an interferon-related gene in the liver indicating a systemic interferon response. The results show the validity of the fish model for testing delivery and non-specific effects of siRNAs in a high throughput vertebrate model. The purchase of chemically synthesized siRNAs is expensive why the use of in vitro transcribed siRNAs was initially tested in fish cell culture. Transfection with three different in vitro transcribed siRNAs specific to the viral glycoprotein gene of the target-virus efficiently inhibited viral multiplication in infected cell cultures, while two of three corresponding control siRNAs, containing four mismatches compared to the target, did not have this effect. This suggested specific interference, but similar results were obtained when the same siRNAs were tested against a heterologous virus. Further analyses revealed that the siRNAs induced a non-target-specific anti-viral effect, which correlated with an upregulation of the interferon induced Mx gene. Accordingly inclusion of a heterologous virus as target control was essential for verification of the specificity of siRNA-induced interference with virus multiplication. Current work on studying the action of chemically synthesized siRNAs designed to suppress expression of the surface glycoprotein G and the large polymerase L of the rhabdoviral target virus is also presented. The results emphasize the use of controls, choice of target gene, type of siRNA and the compromise in using transfection reagents for improved uptake of siRNAs, where these reagents also increase the risk of the siRNAs ending up in a cellular compartment in which stimulation of non-specific anti-viral defence mechanisms will be initiated.

Afrikansk svinepest truer svineproduktionen i Georgien

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Schyth, B. D. (Intern)
Number of pages: 103
Publication date: Sep 2007

Publication information
Place of publication: Aarhus
Original language: English
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 250970
Publication: Research › Ph.D. thesis – Annual report year: 2007
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
Authors: Kristensen, C. (Ekstern), Bille-Hansen, V. (Intern), Vestergaard, K. (Ekstern), Jorsal, S. E. L. (Intern), Bækbo, P. (Ekstern), Enøe, C. (Intern), Larsen, L. E. (Intern)
Publication date: 2007
Event: Abstract from 5th International Symposium on Emerging and Re-emerging Pig Diseases, Krakow, Poland.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 240807
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2007

Bluetongue in Europe with focus on the recent introduction of bluetongue virus in north-western Europe

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Bøtner, A. (Intern)
Pages: 58-60
Publication date: 2007
Host publication information
Title of host publication: Proceedings of Cattle Consultancy Days
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 241780
Publication: Research › Article in proceedings – Annual report year: 2007

Bluetongue: The virus, clinical signs, transmission and diagnosis

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Bøtner, A. (Intern)
Cell-mediated cytotoxicity in rainbow trout, Oncorhynchus mykiss, infected with viral haemorrhagic septicemia virus

Mammalian cytotoxic T cells as part of the adaptive immune system recognize virus-infected target cells by binding of their T-cell receptors (TCR) to classical MHC class I molecules loaded with viral peptides. Our previous studies have shown that the allele of the single dominant polymorphic classical MHC class I locus Onmy-UBA is identical in the rainbow trout clone C25 and in the permanent rainbow trout cell line RTG-2. This enabled us to develop an assay to measure antiviral cytotoxicity in rainbow trout using a system of MHC class I-matched effector and target cells. Peripheral blood leucocytes
(PBL) isolated from low dose viral haemorrhagic septicaemia virus (VHSV)-infected rainbow trout killed MHC class I-matched and later also xenogeneic MHC class I-mismatched VHSV-infected cells. When compared to PBL from uninfected control fish PBL from infected fish showed a higher transcriptional level of the CD8 alpha gene which is a typical marker for mammalian cytotoxic T cells. Concurrently, the expression of the natural killer cell enhancement factor (NKEF)-like gene was enhanced as measured by real-time RT-PCR. Taken together, these results suggest that both innate and adaptive cell-mediated immune responses represented by NK and cytotoxic T cells, respectively, are triggered after VHSV infection. PBL that were able to kill VHSV-infected MHC class I-mismatched xenogeneic cells were generated later during infection than PBL capable of lysing VHSV-infected MHC class I-matched targets. This is contradictory to the generally accepted rule that innate immune mechanisms represent the first line of defence after viral infections.

**General information**

State: Published  
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute  
Authors: Utke, K. (Ekstern), Bergmann, S. (Ekstern), Lorenzen, N. (Intern), Kollner, B. (Ekstern), Ototake, M. (Ekstern), Fischer, U. (Ekstern)  
Pages: 182-196  
Publication date: 2007  
Main Research Area: Technical/natural sciences

**Publication information**  
Journal: Fish and Shellfish Immunology  
Volume: 22  
Issue number: 3  
ISSN (Print): 1050-4648  
Ratings:  
BFI (2018): BFI-level 1  
Web of Science (2018): Indexed yes  
BFI (2017): BFI-level 1  
Web of Science (2017): Indexed Yes  
BFI (2016): BFI-level 1  
Scopus rating (2016): CiteScore 3.36 SJR 1.114 SNIP 1.16  
Web of Science (2016): Indexed yes  
BFI (2015): BFI-level 1  
Scopus rating (2015): SJR 1.268 SNIP 1.171 CiteScore 3.19  
Web of Science (2015): Indexed yes  
BFI (2014): BFI-level 1  
Scopus rating (2014): SJR 1.138 SNIP 1.089 CiteScore 2.92  
Web of Science (2014): Indexed yes  
BFI (2013): BFI-level 1  
Scopus rating (2013): SJR 1.001 SNIP 1.149 CiteScore 3.11  
ISI indexed (2013): ISI indexed yes  
Web of Science (2013): Indexed yes  
BFI (2012): BFI-level 1  
Scopus rating (2012): SJR 1.151 SNIP 1.174 CiteScore 3.02  
ISI indexed (2012): ISI indexed yes  
Web of Science (2012): Indexed yes  
BFI (2011): BFI-level 1  
Scopus rating (2011): SJR 1.196 SNIP 1.265 CiteScore 3.52  
ISI indexed (2011): ISI indexed yes  
Web of Science (2011): Indexed yes  
BFI (2010): BFI-level 1  
Scopus rating (2010): SJR 1.131 SNIP 1.056  
Web of Science (2010): Indexed yes  
BFI (2009): BFI-level 1  
Scopus rating (2009): SJR 0.96 SNIP 1.101  
Web of Science (2009): Indexed yes  
BFI (2008): BFI-level 2  
Scopus rating (2008): SJR 0.952 SNIP 1.062
Development of a novel recombinant encapsidated RNA particle: evaluation as an internal control for diagnostic RT-PCR

This report describes the generation of novel encapsidated RNA particles and their evaluation as in-tube internal controls in diagnostic real-time reverse-transcription PCR (rRT-PCR) assays for the detection of RNA viruses. A cassette containing sequences of 2 diagnostic primer sets for foot-and-mouth disease virus (FMDV) and a set for swine vesicular disease virus (SVDV) was engineered into a full-length cDNA clone containing the RNA-2 segment of Cowpea Mosaic Virus (CPMV). After co-inoculation with a plasmid that expressed CPMV RNA-1, recombinant virus particles were rescued from cowpea plants (Vigna unguiculata). RNA contained in these particles was amplified in diagnostic rRT-PCR assays used for detection of FMDV and SVDV. Amplification of these internal controls was used to confirm that rRT-PCR inhibitors were absent from clinical samples, thereby verifying negative assay results. The recombinant CPMVs did not reduce the analytical sensitivity of the rRT-PCRs when amplification of the insert was performed in the same tube as the diagnostic target. This system provides an attractive solution to the production of internal controls for rRT-PCR assays since CPMV grows to high yields in plants, the particles are thermostable, RNase resistant and simple purification of RNA-2 containing capsids yields a preparation which is non-infectious.

General information
State: Published
Organisations: Section of Vesicular virus diseases, Division of Virology, National Veterinary Institute, The Pirbright Institute, John Innes Centre
Authors: King, D. P. (Ekstern), Montague, N. (Ekstern), Ebert, K. (Ekstern), Reid, S. M. (Ekstern), Dukes, J. P. (Ekstern), Schhdlich, L. (Ekstern), Belsham, G. (Intern), Lomonossoff, G. P. (Ekstern)
Pages: 218-225
Publication date: 2007
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of virological methods
Volume: 146
Issue number: 1-2
ISSN (Print): 0166-0934
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.87 SNIP 0.736 CiteScore 1.78
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.868 SNIP 0.799 CiteScore 1.68
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.893 SNIP 0.952 CiteScore 1.87
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.861 SNIP 0.91 CiteScore 1.99
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.869 SNIP 0.935 CiteScore 2.08
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.907 SNIP 0.994 CiteScore 2.23
ISI indexed (2011): ISI indexed yes
Reverse transcription polymerase chain reaction, Virology, Real time, Method, Capsid, Microbiology

DOIs:
10.1016/j.jviromet.2007.07.002

Links:
http://www.sciencedirect.com/science?_ob=ArticleURL&_udi=B6T96-4PHSF5T-1&_user=6461462&_coverDate=12%2F31%2F2007&_alid=799597841&_rdoc=1&_fmt=high&_orig=search&_cdi=5106&_sort=d&_docanchor=&view=c&_ct=1&_acct=C000034418&_version=1&_userid=6461462&md5=dee73c18b654a34a6920011f19bde7de#cor1

Source: orbit
Source-ID: 224088
Publication: Research - peer-review › Journal article – 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
Event: Abstract from 5th International Symposium on Emerging and Re-emerging Pig Diseases, Krakow, Poland.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 241481
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2007

Faktorer af betydning for sundheden hos kalve

General information
Genetic characterisation of the recent foot-and-mouth disease virus subtype A/IRN/2005

Background According to the World Reference Laboratory for FMD, a new subtype of FMDV serotype A was detected in Iran in 2005. This subtype was designated A/IRN/2005, and rapidly spread throughout Iran and moved westwards into Saudi Arabia and Turkey where it was initially detected from August 2005 and subsequently caused major disease problems in the spring of 2006. The same subtype reached Jordan in 2007. As part of an ongoing project we have also detected this subtype in Pakistan with the first positive samples detected in April 2006. To characterise this subtype in detail, we have sequenced and analysed the complete coding sequence of three subtype A/IRN/2005 isolates collected in Pakistan in 2006, the complete coding sequence of one subtype A/IRN/2005 isolate collected during the first outbreak in Turkey in 2005 and, in addition, the partial 1D coding sequence derived from 4 epithelium samples and 34 swab-samples from Asian buffaloes or cattle subsequently found to be infected with the A/IRN/2005 subtype. Results The phylogenies of the genome regions encoding for the structural proteins, displayed, with the exception of 1A, distinct, serotype-specific clustering and an evolutionary relationship of the A/IRN/2005 sublineage with the A22 sublineage. Potential recombination events have been detected in parts of the genome region coding for the non-structural proteins of FMDV. In addition, amino acid substitutions have been detected in the deduced VP1 protein sequence, potentially related to clinical or subclinical outcome of FMD. Indications of differential susceptibility for developing a subclinical course of disease between Asian buffaloes and cattle have been detected. Furthermore, hitherto unknown insertions of 2 amino acids before the second start codon, as well as sublineage specific amino acids have been detected in the genome region encoding for the leader proteinase of A/IRN/2005 sublineage. Conclusion Our findings indicate that the A/IRN/2005 sublineage has undergone two different paths of evolution for the structural and non-structural genome regions. The structural genome regions have had their evolutionary starting point in the A22 sublineage. It can be assumed that, due to the quasispecies structure of FMDV populations and the error-prone replication process, advantageous mutations in a changed environment have been fixed and lead to the occurrence of the new A/IRN/2005 sublineage. Together with this mechanism, recombination within the non-structural genome regions, potentially modifying the virulence of the virus, may be involved in the success of this new sublineage. The possible origin of this recombinant virus may be a co-infection with Asia1 and a serotype A precursor of the A/IRN/2005 sublineage potentially within Asian Buffaloes, as these appears to relatively easy become infected, but usually without developing clinical disease and consequently showing not a strong acute inflammatory immune response against a second FMDV infection.

General information
State: Published
Organisations: Section of Vesicular virus diseases, Division of Virology, National Veterinary Institute. Sektion for Eksotiske Virussygdomme, Food and Agriculture Organization of the United Nations, Ministry of Food, Agriculture & Livestock
Authors: Klein, J. (Intern), Hussain, M. (Ekstern), Ahmad, M. (Ekstern), Normann, P. (Intern), Afzal, M. (Ekstern), Alexandersen, S. (Intern)
Pages: 122
Publication date: 2007
Main Research Area: Technical/natural sciences

Publication information
Journal: Virology Journal
Volume: 4
ISSN (Print): 1743-422X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
Web of Science (2017): Indexed Yes
Scopus rating (2016): CiteScore 2.43 SJR 1.097 SNIP 0.894
Scopus rating (2015): SJR 1.185 SNIP 0.947 CiteScore 2.47
Scopus rating (2014): SJR 1.044 SNIP 0.911 CiteScore 2.27
Web of Science (2014): Indexed yes
Identification of minimal sequences of the Rhopalosiphum padi virus 5' untranslated region required for internal initiation of protein synthesis in mammalian, plant and insect translation systems

Rhopalosiphum padi virus (RhPV) is a member of the family Dicistroviridae. The genomes of viruses in this family contain two open reading frames, each preceded by distinct internal ribosome entry site (IRES) elements. The RhPV 5' IRES is functional in mammalian, insect and plant translation systems and can form 48S initiation complexes in vitro with just the mammalian initiation factors eIF2, eIF3 and eIF1. Large regions of the 5' untranslated region (UTR) can be deleted without affecting initiation-complex formation. The minimal sequences required for directing internal initiation in mammalian (rabbit reticulocyte lysate), plant (wheatgerm extract) and insect (Sf21 cells) translation systems have now been defined. A fragment (nt 426–579) from the 3' portion of the 5' UTR can direct translation in each of these translation systems. In addition, a distinct region (nt 300–429) is also active. Thus, unstructured regions within the 5' UTR seem to be critical for IRES function.
Inhibition of the Secretory pathway by Foot-and-Mouth disease virus 2BC protein is reproduced by co-expression of 2B with 2C, and the site of inhibition is determined by the subcellular location of 2C.
Infection of cells with picornviruses can lead to a block in protein secretion. For poliovirus this is achieved by the 3A protein, and the consequent reduction in secretion of proinflammatory cytokines and surface expression of major histocompatibility complex class I proteins may inhibit host immune responses in vivo. Foot-and-mouth disease virus (FMDV), another picornavirus, can cause persistent infection of ruminants, suggesting it too may inhibit immune responses. Endoplasmic reticulum (ER)-to-Golgi apparatus transport of proteins is blocked by the FMDV 2BC protein. The observation that 2BC is processed to 2B and 2C during infection and that individual 2B and 2C proteins are unable to block secretion stimulated us to study the effects of 2BC processing on the secretory pathway. Even though 2BC was processed rapidly to 2B and 2C, protein transport to the plasma membrane was still blocked in FMDV-infected cells. The block could be reconstituted by coexpression of 2B and 2C, showing that processing of 2BC did not compromise the ability of FMDV to slow secretion. Under these conditions, 2C was located to the Golgi apparatus, and the block in transport also occurred in the Golgi apparatus. Interestingly, the block in transport could be redirected to the ER when 2B was coexpressed with a 2C protein fused to an ER retention element. Thus, for FMDV a block in secretion is dependent on both 2B and 2C, with the latter determining the site of the block.
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
Authors: Dupont, K. (Intern), Kristensen, C. S. (Ekstern), Hjulsager, C. K. (Intern), Bækbo, P. (Ekstern), Bille-Hansen, V. (Intern), Larsen, L. E. (Intern)
Publication date: 2007
Event: Poster session presented at 5th International Symposium on Emerging and Re-emerging Pig Diseases, Krakow, Poland.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 240808
Publication: Research - peer-review › Poster – Annual report year: 2007

Molecular and phylogentic studies of perch rhabdoviruses (P-11)

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Johansson, T. (Ekstern), Skall, H. F. (Intern), Olesen, N. J. (Intern)
Publication date: 2007
Event: Poster session presented at 13th International Conference on Diseases of Fish and Shellfish, Grado, Italy.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 242047
Publication: Research › Poster – Annual report year: 2007
Molecular studies of perch rhabdoviruses

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Johansson, T. (Ekstern), Skall, H. F. (Intern), Olesen, N. J. (Intern)
Publication date: 2007
Event: Abstract from 13th International Conference on Diseases of Fish and Shellfish, Grado, Italy.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 242041
Publication: Research › Conference abstract for conference – Annual report year: 2007

Myxomatose hos kaniner

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Authors: Larsen, L. E. (Intern)
Publication date: 2007
Main Research Area: Technical/natural sciences
Publication information
Journal: Dansk Veterinærtidsskrift
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
Publication: Research › Journal article – Annual report year: 2007

Myxomatose hos kaniner på Sjælland og Lolland

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Hammer, A. S. (Ekstern), Betner, A. (Intern)
Publication date: 2007
Main Research Area: Technical/natural sciences
Publication information
Journal: DVT
Original language: Danish
Source: orbit
Source-ID: 241781
Publication: 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
Authors: Kristensen, S. L. S. (Ekstern), Hjulsager, C. K. (Intern), Larsen, L. E. (Intern)
Publication date: 2007
Main Research Area: Technical/natural sciences
Publication information
Journal: Norovirus hyppig hos kalve
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
Authors: Böttiger, B. (Ekstern), Johnsen, C. K. (Ekstern), Midgley, S. (Ekstern), Hjulsager, C. K. (Intern), Larsen, L. E. (Intern)
Publication date: 2007
Event: Poster session presented at EVENT meeting, Pesc, Hungary.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 240986
Publication: Research - peer-review › Poster – Annual report year: 2007

One-step primer-probe energy transfer (PriProET) real-time RT-PCR detection of SVDV using Rotor Gene 6000

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Hakhverdyan, M. (Ekstern), Rasmussen, T. B. (Intern), Uttenthal, Å. (Intern), Belák, S. (Ekstern)
Publication date: 2007
Event: Poster session presented at International Symposium for the WAVLD : World Association of Veterinary Laboratory Diagnosticians, Melbourne, Australia.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 242286
Publication: Research › Poster – Annual report year: 2007

Pathology and diagnosis of PMWS in a Danish case – control study

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, Sektion for Eksotiske Virussygdomme, Division of Virology, Section for Veterinary Epidemiology and public sector consultancy
Authors: Jorsal, S. E. L. (Intern), Bille-Hansen, V. (Intern), Nielsen, E. O. (Ekstern), Svensmark, B. (Ekstern), Holm, G. (Ekstern), Barfod, K. (Intern), Vigre, H. (Intern), Bøtner, A. (Intern), Enøe, C. (Intern), Bækbo, P. (Ekstern)
Real-time laboratory exercises to test contingency plans for classical swine fever: experiences from two national laboratories

In order to adequately and efficiently handle outbreaks of contagious diseases such as classical swine fever (CSF), foot and mouth disease or highly pathogenic avian influenza, competent authorities and the laboratories involved have to be well prepared and must be in possession of functioning contingency plans. These plans should ensure that in the event of an outbreak access to facilities, equipment, resources, trained personnel, and all other facilities needed for the rapid and efficient eradication of the outbreak is guaranteed, and that the procedures to follow are well rehearsed. It is essential that these plans are established during ‘peace-time’ and are reviewed regularly. This paper provides suggestions on how to perform laboratory exercises to test preparedness and describes the experiences of two national reference laboratories for CSF. The major lesson learnt was the importance of a well-documented laboratory contingency plan. The major pitfalls encountered were shortage of space, difficulties in guaranteeing biosecurity and sufficient supplies of sterile equipment.
and consumables. The need for a standardised laboratory information management system, that is used by all those involved in order to reduce the administrative load, is also discussed.

**General information**

**State:** Published  
**Organisations:** Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Centrum voor Onderzoek in Diergeneeskunde en Agrochemie, University of Veterinary Medicine  
**Authors:** Koenen, K. (Ekstern), Uttenthal, Å. (Intern), Meindl-Böhmer, A. (Ekstern)  
**Pages:** 629-638  
**Publication date:** 2007  
**Main Research Area:** Technical/natural sciences

**Publication information**

**Journal:** O I E Revue Scientifique et Technique  
**Volume:** 26  
**Issue number:** 3  
**ISSN (Print):** 0253-1933  
**Ratings:**  
BFI (2018): BFI-level 1  
Web of Science (2018): Indexed yes  
BFI (2017): BFI-level 1  
Web of Science (2017): Indexed Yes  
BFI (2016): BFI-level 1  
Scopus rating (2016): CiteScore 1.24 SJR 0.575 SNIP 0.758  
BFI (2015): BFI-level 1  
Scopus rating (2015): SJR 0.554 SNIP 0.759 CiteScore 1.11  
BFI (2014): BFI-level 1  
Scopus rating (2014): SJR 0.543 SNIP 0.738 CiteScore 1.12  
BFI (2013): BFI-level 1  
Scopus rating (2013): SJR 0.432 SNIP 0.56 CiteScore 0.99  
ISI indexed (2013): ISI indexed yes  
Web of Science (2013): Indexed yes  
BFI (2012): BFI-level 1  
Scopus rating (2012): SJR 0.521 SNIP 0.516 CiteScore 1.03  
ISI indexed (2012): ISI indexed yes  
Web of Science (2012): Indexed yes  
BFI (2011): BFI-level 1  
Scopus rating (2011): SJR 0.609 SNIP 0.617 CiteScore 1.39  
ISI indexed (2011): ISI indexed yes  
Web of Science (2011): Indexed yes  
BFI (2010): BFI-level 1  
Scopus rating (2010): SJR 0.624 SNIP 0.627  
BFI (2009): BFI-level 1  
Scopus rating (2009): SJR 0.436 SNIP 0.629  
BFI (2008): BFI-level 1  
Scopus rating (2008): SJR 0.393 SNIP 0.721  
Web of Science (2008): Indexed yes  
Scopus rating (2007): SJR 0.437 SNIP 0.793  
Web of Science (2007): Indexed yes  
Scopus rating (2006): SJR 0.411 SNIP 0.618  
Scopus rating (2005): SJR 0.464 SNIP 0.757  
Web of Science (2005): Indexed yes  
Scopus rating (2004): SJR 0.585 SNIP 0.947  
Scopus rating (2003): SJR 0.607 SNIP 1.184  
Scopus rating (2002): SJR 0.591 SNIP 0.924  
Scopus rating (2001): SJR 0.452 SNIP 0.666  
Scopus rating (2000): SJR 0.278 SNIP 0.334
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
Authors: Enæe, C. (Intern), Bækbo, P. (Ekstern), Vigre, H. (Intern), Larsen, L. E. (Intern), Jorsal, S. E. L. (Intern), Nielsen, E. (Ekstern)
Publication date: 2007
Event: Abstract from 5th International Symposium on Emerging and Re-emerging Pig Diseases, Krakow, Poland.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 224078
Publication: Research - peer-review › Journal article – Annual report year: 2007

Significance of Arginine 20 in the 2A protease for swine vesicular disease virus pathogenicity
Pathogenic and attenuated strains of swine vesicular disease virus (SVDV), an enterovirus, have been characterized previously and, by using chimeric infectious cDNA clones, the key determinants of pathogenicity in pigs have been mapped to the coding region for 1D–2A. Within this region, residue 20 of the 2A protease is particularly significant. Inoculation of pigs with mutant viruses containing single amino acid substitutions at this residue leads to the appearance of revertants, often containing an arginine at this position encoded by an AGA codon, one of six codons for this residue. The properties in pigs of two chimeric viruses, each with an arginine residue at this position but encoded by different codons, have been investigated in parallel with the parental pathogenic and attenuated strains. Presence of the arginine residue, but not of the AGA codon, is essential for induction of high viraemia and appearance of significant disease.

General information
State: Published
Organisations: Section of Vesicular virus diseases, Division of Virology, National Veterinary Institute, National Institute of Animal Health, The Pirbright Institute
Authors: Inoue, T. (Ekstern), Zhang, Z. (Ekstern), Wang, L. (Ekstern), West, L. (Ekstern), Bashiruddin, J. B. (Ekstern), Belsham, G. (Intern)
Pages: 2275-2279
Publication date: 2007
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of General Virology
Volume: 88
ISSN (Print): 0022-1317
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.93 SJR 1.499 SNIP 0.886
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.729 SNIP 1.007 CiteScore 3.26
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.683 SNIP 1.059 CiteScore 3.25
Web of Science (2014): Indexed yes

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Uttenthal, Å. (Intern), Rasmussen, T. B. (Intern)
Publication date: 2007
Survey and diagnosis summary: 1) status and emergence of VHS and IHN in Europe. 2) other fish disease monitoring programmes in EU

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Olesen, N. J. (Intern), Jensen, B. (Ekstern), Skall, H. F. (Intern), Nicolajsen, N. (Intern)
Publication date: 2007
Event: Abstract from Annual Meeting for DTU-National Veterinary Institute in Copenhagen, Copenhagen, .
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 242039
Publication: Research › Conference abstract for conference – Annual report year: 2007

Temperate phages TP901-1 and phi LC3, belonging to the P335 species, apparently use different pathways for DNA injection in Lactococcus lactis subsp cremoris 3107

Five mutants of Lactococcus lactis subsp. cremoris 3107 resistant to phage TP901-1 were obtained after treatment with ethyl methanesulfonate. Two of the mutants were also resistant to phage phi LC3. The remaining three mutants were as sensitive as 3107. Mutants E46 and E100 did not adsorb the two phages. Mutants E119, E121 and E126 adsorbed phage phi LC3 as well as 3107 but phage TP901-1 with significantly reduced efficiency. All, except E46, could be lysogenized with phage TP901-BC1034, a derivative of TP901-1 harboring an erythromycin-resistance marker. However, the lysogenization frequency was 10(3)-10(4) fold higher for 3107 than for the mutants. Mitomycin C induction of lysogenized mutants 3107 indicated that phage propagation was not affected in these four mutants. Electron microscopy and analysis of total DNA of infected cells showed that DNA was liberated from the phage particle during infection of strain 3107 with TP901-1 and that intracellular phage DNA replication occurred. This was not the case for mutants E121 and E126. This strongly suggests that some step starting with triggering DNA release and ending with DNA injection is impaired during infection with TP901-1. As such impairment was not seen when infecting E119, E121 and E126 with phi LC3, we conclude that TP901-1 and phi LC3 either are differently triggered by their receptor or utilize different pathways of injection.

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Authors: Breum, S. Ø. (Intern), Neve, H. (Ekstern), Heller, K. J. (Ekstern), Vogensen, F. K. (Ekstern)
Pages: 156-164
Publication date: 2007
Main Research Area: Technical/natural sciences

Publication information
Journal: Fems Microbiology Letters
Volume: 276
Issue number: 2
ISSN (Print): 0378-1097
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.76 SJR 0.747 SNIP 0.597
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.131 SNIP 0.752 CiteScore 2.08
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Testing immunogenicity of Mycoplasma hyosynoviae vaccine candidates; induction of antibodies and IFNγ response

General information
State: Published
Organisations: Adaptive Immunology & Parasitology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Sektion for Eksotiske Virussygdomme, Division of Virology
Publication date: 2007
Event: Poster session presented at 8th International Veterinary Immunology Symposium, Ouro Preto, Brazil.
Main Research Area: Technical/natural sciences
Source: orbit

Original language: English
Lactococcus lactis, phage adsorption, DNA injection, phage P335 species, TP901-1
Source: orbit
Source-ID: 214267
Publication: Research - peer-review › Journal article – Annual report year: 2007
Virulence, immunogenicity and vaccine properties of a novel chimeric pestivirus

A chimeric pestivirus of border disease virus Gifhorn and bovine viral diarrhea virus CP7 (Meyers et al., 1996) was constructed. Virulence, immunogenicity and vaccine properties of the chimeric virus were studied in a vaccination–challenge experiment in pigs. The chimeric virus proved to be avirulent and neither chimeric virus nor viral RNA was detected in serum after vaccination. The safety of the vaccine was tested by horizontal transmission to sentinel pigs, which remained uninfected. The vaccine efficacy was examined by challenge infection with classical swine fever

virus (CSFV) Eystrup. In 'challenge controls', the viral load of CSFV coincided with the development of pronounced clinical symptoms. In contrast, the vaccinated pigs showed transient and weak clinical signs. Analysis of the viral load in these pigs showed 1000-fold lower viral RNA levels compared to 'challenge controls' and horizontal transmission of challenge virus to sentinel pigs was not observed. A supplementary figure is available in JGV Online.
Virus isolation vs RT-PCR: which method is more successful in detecting VHSV and IHNV in fish tissue sampled under field conditions?

This study compared the results of reverse transcription-polymerase chain reaction (RT-PCR) and traditional virus isolation on cell culture in detection of viral haemorrhagic septicemia virus (VHSV) and infectious haematopoietic necrosis virus (IHNV). RT-PCR was used for 172 tissue sample pools (total of 859 fish) originating from a field survey on the occurrence of VHSV and IHNV in farmed and wild salmonids in Switzerland. These samples represented all sites with fish that were either identified as virus-positive by means of virus isolation (three sites, four positive tissue sample pools) and/or demonstrated positive anti-VHSV-antibody titres (83 sites, 121 positive blood samples) in a serum plaque neutralization test (SPNT). The RT-PCR technique confirmed the four VHSV-positive tissue sample pools detected by virus isolation and additionally identified one VHSV-positive sample that showed positive anti-VHSV-AB titres, but was negative in virus isolation. With IHNV, RT-PCR detected two positive samples not identified by virus isolation while in these fish the SPNT result had been questionable. One of the IHNV-positive samples represents the first detection of IHNV-RNA in wild brown trout in Switzerland. Compared to SPNT, the RT-PCR method detected, as with virus isolation, a much lower number of positive cases; reasons for this discrepancy are discussed. Our results indicate that RT-PCR can not only be successfully applied in field surveys, but may also be slightly more sensitive than virus isolation. However, in a titration experiment under laboratory conditions, the sensitivity of RT-PCR was not significantly higher when compared with virus isolation.
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
Authors: Segalés, J. (Ekstern), Larsen, L. E. (Intern), Wallgren, P. (Ekstern), Rose, N. (Ekstern), Grau-Roma, L. (Ekstern), Sibila, M. (Ekstern), Fraile, L. (Ekstern), Casal, J. (Ekstern), Bækbo, P. (Ekstern)
Publication date: 2007
Event: Abstract from 5th International Symposium on Emerging and Re-emerging Pig Diseases, Krakow, Poland.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 240811
Publication: Research - peer-review › Journal article – Annual report year: 2007
**Absence of PCV2-neutralizing antibodies in PMWS-affected pigs**

**General information**
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Lefebvre, D. (Ekstern), Meerts, P. (Ekstern), Misinzo, G. (Ekstern), Nielsen, J. (Ekstern), Bøtner, A. (Intern), Kristensen, C. S. (Ekstern), Nauwynck, H. J. (Ekstern)
Number of pages: 175
Publication date: 2006

**Host publication information**
Title of host publication: Proceeding of the 19th International Pig Veterinary Congress
Main Research Area: Technical/natural sciences
Conference: The 19th International Pig Veterinary Congress, 01/01/2006
Source: orbit
Source-ID: 241731
Publication: Research › Article in proceedings – Annual report year: 2006

**A Danish case-control study on risk factors for PMWS – bio security in the herd**

**General information**
State: Published
Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, Section for Veterinary Diagnostics
Authors: Enøe, C. (Intern), Vigre, H. (Intern), Nielsen, E. O. (Ekstern), Larsen, P. (Ekstern), Bøtner, A. (Intern), Bille-Hansen, V. (Intern), Jorsal, S. E. L. (Intern), Bækbo, P. (Ekstern)
Number of pages: 163
Publication date: 2006

**Host publication information**
Title of host publication: Proceeding of the 19th International Pig Veterinary Congress
Main Research Area: Technical/natural sciences
Conference: The 19th International Pig Veterinary Congress, Copenhagen, 01/01/2006
Source: orbit
Source-ID: 241733
Publication: Research › Article in proceedings – Annual report year: 2006

**A Danish case-control study on risk factors for PMWS-biosecurity in the herd**

**General information**
State: Published
Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Division of Microbiology and Risk Assessment, National Food Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, Section for Veterinary Diagnostics
Authors: Enøe, C. (Intern), Vigre, H. (Intern), Nielsen, E. O. (Ekstern), Larsen, P. (Ekstern), Bøtner, A. (Intern), Bille-Hansen, V. (Intern), Jorsal, S. E. L. (Intern), Bækbo, P. (Ekstern)
Publication date: 2006
Event: Abstract from 19th International Pig Veterinary Society Congress, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 241478
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2006

**An epidemiological study of the occurrence of Viral Haemorrhagic Septicaemia in Denmark during 1982-2005**

**General information**
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Jensen, B. (Ekstern), Erbsøll, A. (Ekstern), Korsholm, H. (Ekstern), Olesen, N. J. (Intern)
Number of pages: 3
Publication date: 2006
Antiviral activity of Small interfering RNAs: Specificity testing using heterologous virus reveals interferon-related effects overlooked by conventional mismatch controls

RNA interference by small interfering RNAs (siRNAs) is considered to be a highly specific method for knockdown of gene expression in eukaryotic cells via degradation of target mRNA. Mutated siRNA molecules with 1–4 mismatching nucleotides compared to the target mRNA are regularly used as specificity controls. Using siRNAs for inhibition of a fish-pathogenic rhabdovirus, we report that inclusion of a heterologous virus, as target control is essential for verification of the specificity of siRNA-induced interference with virus multiplication. Transfection with three different siRNAs specific to the viral glycoprotein gene of the target-virus efficiently inhibited viral multiplication in infected cell cultures, while two of three corresponding mismatched siRNAs did not have this effect. This suggested specific interference, but similar results were obtained when the same siRNAs were tested against a heterologous virus. Further analyses revealed that the siRNAs induced a non-target-specific anti-viral effect correlating with upregulation of the interferon induced Mx gene.
Association between PMWS and PRRSV

General information
State: Published
Organisations: National Veterinary Institute, Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, Sektion for Eksotiske Virussygdomme, Division of Virology, Section for Veterinary Diagnostics
Authors: Vigre, H. (Intern), Enøe, C. (Intern), Bøtner, A. (Intern), Jorsal, S. E. L. (Intern), Bækbo, P. (Ekstern), Okholm, E. (Ekstern)
Number of pages: 174
Publication date: 2006

Host publication information
Title of host publication: Proceeding of the 19th International Pig Veterinary Congress
Main Research Area: Technical/natural sciences
Conference: The 19th International Pig Veterinary Congress, Copenhagen, 01/01/2006
Source: orbit
Source-ID: 241739
Publication: Research - Article in proceedings – Annual report year: 2006

Aviær influenza i svin

General information
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics
Authors: Larsen, L. E. (Intern), Hjulsager, C. K. (Intern)
Pages: 2-4
Publication date: 2006
Main Research Area: Technical/natural sciences
Avian Influenza in wild birds: Evaluation of the risk of transmission to swine

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Paisley, L. (Ekstern), Vigre, H. (Intern), Bøtner, A. (Intern)
Publication date: 2006

Publication information
Publisher: Danmarks Fødevareforskning
Original language: English
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 242218
Publication: Research › Report – Annual report year: 2006

Caliciviruses differ in their functional requirements for eIF4F components

Two classes of viruses, namely members of the Potyviridae and Caliciviridae, use a novel mechanism for the initiation of protein synthesis that involves the interaction of translation initiation factors with a viral protein covalently linked to the viral RNA, known as VPg. The calicivirus VPg proteins can interact directly with the initiation factors eIF4E and eIF3.

Translation initiation on feline calicivirus (FCV) RNA requires eIF4E because it is inhibited by recombinant 4E-BP1. However, to date, there have been no functional studies carried out with respect to norovirus translation initiation, because of a lack of a suitable source of VPg-linked viral RNA. We have now used the recently identified murine norovirus (MNV) as a model system for norovirus translation and have extended our previous studies with FCV RNA to examine the role of the other eIF4F components in translation initiation. We now demonstrate that, as with FCV, MNV VPg interacts directly with eIF4E, although, unlike FCV RNA, translation of MNV RNA is not sensitive to 4E-BP1, eIF4E depletion, or foot-and-mouth disease virus Lb protease-mediated cleavage of eIF4G. We also demonstrate that both FCV and MNV RNA translation require the RNA helicase component of the eIF4F complex, namely eIF4A, because translation was sensitive (albeit to different degrees) to a dominant negative form and to a small molecule inhibitor of eIF4A (hippuristanol). These results suggest that calicivirus RNAs differ with respect to their requirements for the components of the eIF4F translation initiation complex.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Chaudhry, Y. (Ekstern), Nayak, A. (Ekstern), Bordeleau, M. (Ekstern), Tanaka, J. (Ekstern), Pelletier, J. (Ekstern), Belsham, G. (Intern), Roberts, L. O. (Ekstern), Goodfellow, I. G. (Ekstern)
Pages: 25315-25325
Publication date: 2006
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Biological Chemistry
Volume: 281
Issue number: 35
ISSN (Print): 0021-9258
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
Circulation of bovine respiratory syncytial virus in Brazil

**General information**
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Authors: Almeida, R. (Ekstern), Domingues, H. (Ekstern), Spilki, F. (Ekstern), Larsen, L. E. (Intern), Hagglund, S. (Ekstern), Belak, S. (Ekstern), Arns, C. (Ekstern)
Pages: 632-634
Publication date: 2006
Main Research Area: Technical/natural sciences

**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
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.442 SNIP 0.692 CiteScore 0.3
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.509 SNIP 0.794 CiteScore 0.39
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.469 SNIP 0.839 CiteScore 0.41
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.474 SNIP 0.821 CiteScore 0.5
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.491 SNIP 0.883 CiteScore 0.52
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.563 SNIP 0.9 CiteScore 0.62
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.574 SNIP 0.835
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.642 SNIP 0.996
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 0.553 SNIP 0.854
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 0.498 SNIP 0.814
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.64 SNIP 0.949
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.582 SNIP 0.923
Clinical suspicion for classical swine fever, how reliable is it?

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Uttenthal, Å. (Intern), Nielsen, J. (Ekstern), Lohse, L. (Ekstern)
Publication date: 2006

Host publication information
Title of host publication: NSFL 2006
Main Research Area: Technical/natural sciences
Conference: NSFL 2006, Brussels, Belgium, 01/01/2006
Source: orbit
Source-ID: 240950
Publication: Research › Article in proceedings – Annual report year: 2006

Comparison between molecular beacon and PriProET real-time PCR assays based on detection ability of different SVDV strains

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Hakhverdyan, M. (Ekstern), Rasmussen, T. B. (Intern), Uttenthal, Å. (Intern), Belák, S. (Ekstern)
Number of pages: 219
Publication date: 2006

Host publication information
Title of host publication: Proceedings at the international congress of Veterinary Virology
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 242293
Publication: Research › Article in proceedings – Annual report year: 2006

Coordination action for foot-and mouth disease and classical swine fever

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Meindl-Böhmer, A. (Ekstern), Moennig, V. (Ekstern), Thuer, B. (Ekstern), Uttenthal, Å. (Intern), Loeffen, W. L. (Ekstern)
Publication date: 2006
Correlation between the presence of neutralizing antibodies against porcine circovirus 2 (PCV2) and protection against replication of the virus and development of PCV2-associated disease

General information
State: Published
Organisations: Sektion for Eksotiske Virusyngdomme, Division of Virology, National Veterinary Institute
Authors: Meerts, P. (Ekstern), Misinzo, G. (Ekstern), Lefebvre, D. (Ekstern), Nielsen, J. (Intern), Bøtner, A. (Intern), Kristensen, C. (Ekstern), Nauwynck, H. (Ekstern)
Pages: 6
Publication date: 2006
Main Research Area: Technical/natural sciences

Publication information
Journal: BMC Veterinary Research
Volume: 2
ISSN (Print): 1746-6148
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.83 SJR 0.847 SNIP 0.983
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.925 SNIP 0.97 CiteScore 1.86
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.885 SNIP 0.987 CiteScore 1.81
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.829 SNIP 0.833 CiteScore 1.85
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.743 SNIP 1.043 CiteScore 1.94
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.157 SNIP 1.455 CiteScore 2.66
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.072 SNIP 1.4
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.931 SNIP 0.984
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.512 SNIP 0.814
Scopus rating (2007): SJR 0.537 SNIP 0.882
Scopus rating (2006): SJR 0.361 SNIP 1.104
Cultivation of hard-to-culture mercury resistant subsurface soil bacteria using a soil slurry membrane growth system

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Microbial Ecology, Division of Veterinary Diagnostics and Research
Authors: Kroer, N. (Ekstern), Rasmussen, L. D. (Intern), Boye, M. (Intern), Binnerup, S. (Ekstern)
Publication date: 2006
Event: Abstract from 11th International Symposium on Microbial Ecology, Vienna, Austria.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 241065
Publication: Research › Conference abstract for conference – Annual report year: 2006

Cultivation of hard-to-culture subsurface mercury resistant bacteria from Lower East Fork Poplar Creek Floodplain, Oak Ridge

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Kroer, N. (Ekstern), Rasmussen, L. D. (Intern), Binnerup, S. (Ekstern), Sørensen, S. J. (Ekstern), Øregaard, G. (Ekstern)
Publication date: 2006
Event: Poster session presented at DOE-NABIR PI workshop, Warrenton, VA, United States.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 242409
Publication: Research - peer-review › Poster – Annual report year: 2006

Cytokine and C-reactive protein profiles induced by porcine circovirus type 2 experimental infection in 3-week-old piglets
The purpose of this study was to determine serum profiles of cytokines at a protein level and C-reactive protein (CRP) during the development of postweaning multisystemic wasting syndrome (PMWS) in experimentally inoculated pigs. Levels of serum IFN-alpha, IL-6, IL-10, and CRP were examined for a 35-day period in 10 piglets experimentally infected with PCV2 at 3 weeks of age. Four of the infected piglets developed severe PMWS at 14 to 21 days post-infection (d.p.i.) and died prior to termination of the experiment. The remaining six PCV2-infected piglets experienced transient fever, but did not display overt clinical signs of PMWS and were considered as subclinically infected. A bioassay was used to detect IL-6 and ELISAs were used to detect IFN-a, IL-10, and CRP. There were no significant differences in cytokine or CRP expression from 0 to 7 d.p.i. between the PMWS-affected and the subclinically infected piglets. Levels of IL-10 and CRP were elevated from 10 and 14 d.p.i. respectively in the PMWS-affected piglets compared to the subclinically infected piglets. There were no significant differences in IFN-a and IL-6 expression between the PMWS-affected piglets and the subclinically infected piglets. The present study shows that elevated levels of serum CRP and IL-10 were associated with PCV2-infected piglets that subsequently developed severe PMWS. This may help to provide further insight into the immunopathogenesis of this syndrome.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Stevenson, L. (Ekstern), McCullough, K. (Ekstern), Vincent, I. (Ekstern), Gilpin, D. (Ekstern), Summerfield, A. (Ekstern), Nielsen, J. (Intern), McNeilly, F. (Ekstern), Adair, B. (Ekstern), Allan, G. (Ekstern)
Pages: 189-195
Publication date: 2006
Main Research Area: Technical/natural sciences
Detection of three porcine vesicular viruses using multiplex real-time primer-probe energy transfer

Rapid identification of the etiologic agent in infected animals is important for the control of an outbreak of vesicular disease in livestock. We have in the present study developed a multiplex real-time reverse transcription-PCR, based on primer-probe energy transfer (PriProET), for simultaneous detection and differentiation of three Office International des Epizooties (OIE) classified vesicular viruses: foot-and-mouth disease virus, vesicular stomatitis virus and swine vesicular disease, causing clinically indistinguishable vesicular diseases in swine. The multiplex assay consists of extraction of total RNA
from clinical samples; reverse transcription to cDNA using random primers and one-tube real-time amplification of cDNA using multiplex PriProET with specific fluorescent-labelled primers and probes for detection of the three viruses from the vesicular disease complex. The probes are labelled with unique reporter fluorophores, which during amplification are excited by donor fluorophores incorporated in the 5’ end of specific amplicons by primer extension. The sensitivity of the multiplex assay was approximately 100 TCID50, which is 10-fold lower compared to the individual PriProET assays for the three vesicular viruses.
Development of a real-time PCR assay based on primer-probe energy transfer for the detection of swine vesicular disease virus

A real-time PCR assay based on primer-probe energy transfer (PriProET) was developed to detect swine vesicular disease virus (SVDV). Specificity tests of SVDV and heterologous virus showed specific amplification of SVDV strains only. The amplification plot for the closely related Coxsackievirus B5 remained negative. The sensitivity of assay was five copies of viral genome equivalents. A key point of the assay is tolerance toward mutations in the probe region. Melting curve analysis directly after PCR, with determination of probe melting point, confirmed specific hybridisation of the SVDV strains. Eight of twenty SVDV strains tested, revealed shifted melting points that indicated mutations in the probe region. All predicted mutations were confirmed by nucleotide sequencing. With the PriProET system there is a chance to identify phylogenetically divergent strains of SVDV, which may appear negative in other probe-based real-time PCR assays. At the same time, any difference in melting points may provide an indication of divergence in the probe region. The high sensitivity, specificity, and tolerance toward mutations in the probe region of the SVDV PriProET assay may improve the early and rapid detection of a wide range of SVDV strains, allowing reduced turnaround time and the use of high-throughput, automated technology.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Hakhverdyan, M. (Ekstern), Rasmussen, T. B. (Intern), Thoren, P. (Ekstern), Uttenthal, Å. (Intern), Belak, S. (Ekstern)
Pages: 2365-2376
Publication date: 2006
Main Research Area: Technical/natural sciences

Publication information
Journal: Archives of Virology
Volume: 151
Issue number: 12
ISSN (Print): 0304-8608
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.948 SNIP 0.879 CiteScore 2.16
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.083 SNIP 0.89 CiteScore 2.16
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.096 SNIP 1.041 CiteScore 2.37
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
- Authors: Tråvén, M. (Ekstern), Verdier, K. (Ekstern), Larsen, L. E. (Intern), Thorén, P. (Ekstern)
- Publication date: 2006
- Event: Abstract from 7th International Congress of Veterinary Virology, Lisboa, Portugal
- Main Research Area: Technical/natural sciences

**Effect of PMWS pig serum and PCV2 specific serum on mortality and weight gain in PMWS affected herds**
Expression of the glycoprotein of viral haemorrhagic septicaemia virus (VHSV) on the surface of the fish cell line RTG-P1 induces type 1 interferon expression in neighbouring cells

In the present study using a luciferase/Mx promoter reporter system, it was shown that the rainbow trout gonad cell line (RTG-P1), a fibroblastic cell line, produces IFN when transfected with a plasmid encoding the glycoprotein of VHSV but not with plasmid vector alone. Only a small percentage of the cells expressed the G protein on the surface membrane as indicated by immunostaining of transfected cells. When transfection was performed in the presence of monoclonal antibodies (Mab) to the glycoprotein, the production of interferon mRNA transcripts was reduced by over 50%. This indicates that the surface expression of G protein was the major mechanism of interferon induction and that most of the interferon was being expressed by cells neighbouring the transfected cells. Crown
Full genome amplification of border disease virus strain Gifhorn

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Rasmussen, T. B. (Intern), Reimann, I. (Ekstern), Hoffmann, B. (Ekstern), Depner, K. (Ekstern), Utenthal, Å. (Intern), Beer, M. (Ekstern)
Number of pages: 243
Publication date: 2006

Host publication information
Title of host publication: ESVV, 7th international congress of Veterinary Virology
Main Research Area: Technical/natural sciences
Conference: 7th International Congress of Veterinary Virology, Lisboa, Portugal, 01/01/2006
Source: orbit
Source-ID: 240949
Publication: Research › Article in proceedings – Annual report year: 2006

Genetic stability of the VHSV consensus sequence of G-gene in diagnostic samples from an acute outbreak
The negative stranded RNA virus viral haemorrhagic septicaemia virus (VHSV) is an important disease-causing agent in aquacultured fish and internationally harmonized diagnostic procedures are continuously under development. The present
study concerns the suitability of genotyping by sequencing of RT-PCR products for epidemiological analysis. Focus was put on a specific case story involving an acute outbreak of VHS in a Danish rainbow trout farm which otherwise had been free of VHSV during the previous 5 years. Tissue materials from individual fish were collected during routine inspection and the initial diagnosis was based on isolation of the virus by cell cultivation and subsequent identification by ELISA. Additional tissue samples were collected 25 days after the initial sampling. RT-PCR amplification and sequencing of the entire glycoprotein-gene (1524 nt) was performed on RNA purified from collected tissue material as well as from inoculated cell culture. No nucleotide substitutions were identified when aligning the obtained sequence data for the two sample types. The presented data indicate that the overall consensus sequence of the virus outbreak was stable during the survey, and that initial passage of the virus on BF-2 cells did not result in changes within the G-gene at a detectable level. The results suggest that genotyping of VHSV isolates based on RT-PCR products amplified from infected primary tissues material is a reliable tool for epidemiological studies.

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Einer-Jensen, K. (Intern), Ahrens, P. (Intern), Lorenzen, N. (Intern)
Pages: 62-67
Publication date: 2006
Main Research Area: Technical/natural sciences

Publication information
Journal: Bulletin of the European Association of Fish Pathologists
Volume: 26
Issue number: 2
ISSN (Print): 0108-0288
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 0.49 SJR 0.234 SNIP 0.421
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.27 SNIP 0.496 CiteScore 0.64
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.32 SNIP 0.414 CiteScore 0.68
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.365 SNIP 0.431 CiteScore 0.62
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.257 SNIP 0.49 CiteScore 0.47
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.236 SNIP 0.364 CiteScore 0.41
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.34 SNIP 0.469
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.292 SNIP 0.459
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.325 SNIP 0.373
Scopus rating (2007): SJR 0.31 SNIP 0.386
Scopus rating (2006): SJR 0.436 SNIP 0.592
Web of Science (2006): Indexed yes
Histopathologic findings in a case control study of PMWS in Danish pig herds

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Virology
Authors: Bille-Hansen, V. (Intern), Jorsal, S. E. L. (Intern), Vigre, H. (Intern), Larsen, L. E. (Intern)
Publication date: 2006
Event: Abstract from 19th International Pig Veterinary Society Congress, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 230107
Publication: Research - peer-review › Journal article – Annual report year: 2006

Immunological traits have the potential to improve selection of pigs for resistance to clinical and subclinical disease

It was reasoned that, if we used a large sample of pigs, we could demonstrate that total and differential numbers of leukocytes, expression levels of swine leukocyte antigens (SLA) I and II, and serum concentrations of IgG and haptoglobin show additive genetic variation and are, therefore, potentially useful as criteria to improve selection of pigs for resistance to clinical and subclinical disease. We tested this premise by assessing 4204 male pigs from the Duroc, Landrace, and Yorkshire breeds for total and differential numbers of leukocytes and serum concentrations of IgG and haptoglobin; 1217 of the Duroc and Landrace pigs were also assessed for expression levels of SLA I and II. We estimated the amount of additive genetic variation by fitting linear animal models to the total and differential numbers of leukocytes and serum concentrations of IgG and haptoglobin. We fitted linear sire models to the expression levels of SLA I and II. We detected additive genetic variation for each group of traits. Total and differential numbers of leukocytes were moderately heritable ($h^2 = 0.22$ to 0.30), expression levels of SLA I and II were moderate-to-highly heritable ($h^2 = 0.46$ to 1.23), while serum concentrations of IgG and haptoglobin were lowly heritable ($h^2 = 0.14$ to 0.16). The additive genetic variation shown for the immunological traits is encouraging for pig breeders. It indicates that these traits are potentially useful as criteria to improve selection of pigs for resistance to clinical and subclinical disease.

General information
State: Published
Organisations: Innate Immunology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Sektion for Eksotiske Virussygdomme, Division of Virology
Authors: Henryon, M. (Ekstern), Heegaard, P. M. H. (Intern), Nielsen, J. (Intern), Berg, P. (Ekstern), Juul-Madsen, H. (Ekstern)
Pages: 597-606
Publication date: 2006
Main Research Area: Technical/natural sciences

Publication information
Journal: Animal Science
Volume: 82
ISSN (Print): 1357-7298
Ratings:
Scopus rating (2009): SJR 1.004 SNIP 1.769
BFI (2008): BFI-level 1
Investigation of the endosperm-specific sucrose synthase promoter from rice using transient expression of reporter genes in guar seed tissue

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Rasmussen, T. B. (Intern), Donaldson, I. A. (Ekstern)
Pages: 1035-1042
Publication date: 2006
Main Research Area: Technical/natural sciences

Publication information
Journal: Plant Cell Reports
Volume: 25
Issue number: 10
ISSN (Print): 0721-7714
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 1.242 SNIP 1.044 CiteScore 3.13
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.234 SNIP 1.265 CiteScore 3.11
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.24 SNIP 1.3 CiteScore 3.19
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.059 SNIP 1.264 CiteScore 2.98
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.992 SNIP 1.161 CiteScore 2.63
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.963 SNIP 1.434 CiteScore 2.57
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.014 SNIP 1.328
Isolation and genetic characterization of new reassortant H1N2 swine influenza A virus from pigs in Denmark

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, Virology
Authors: Hjulsager, C. K. (Intern), Bragstad, K. (Ekstern), Bøtner, A. (Intern), Larsen, L. E. (Intern)
Publication date: 2006
Event: Poster session presented at 7th International Congress of Veterinary Virology, Lisboa, Portugal.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 240806
Publication: Research - peer-review › Poster – Annual report year: 2006

Isolation and genetic characterization of new reassortant H1N2 swine influenza A virus from pigs in Denmark

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Hjulsager, C. K. (Ekstern), Bragstad, K. (Ekstern), Bøtner, A. (Intern), Larsen, L. E. (Ekstern)
Publication date: 2006
Event: Abstract from 7th International Congress of Veterinary Virology, Lisboa, Portugal.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 241742
Publication: Research › Conference abstract for conference – Annual report year: 2006

Long-term treatment of pigs with low doses of monoclonal antibodies against porcine CD4 and CD8 antigens

In vivo depletion of lymphocyte subsets allows investigation of the role of specific subsets in protective immunity. In the present study we evaluated the effects of long-term, low-dose treatment with murine monoclonal antibodies (mAbs) against porcine CD4 and CD8 surface antigens on lymphocyte subsets in pigs. Four-week-old pigs were treated by intramuscular injections of hybridoma cell culture supernatants containing anti-CD mAbs twice a week for a period of 5 weeks. The immunomodulatory effects of the treatments were assessed by flow cytometry (FCM) analysis of peripheral blood lymphocytes. Treatment with the anti-CD4 mAb almost completely eliminated the CD4(+) T-cell subset from the circulation after 2 weeks of therapy. This depletion persisted until the end of the experimental period 5 weeks after initiated therapy. Treatment with the anti-CD8 mAb was less effective, reducing the CD8(+) T-cell subset in peripheral blood by approximately 50% of the initial level after 3 weeks of therapy. Further, the anti-CD8 mAb-treated pigs showed a parallel increase in the CD4(+) T-cell subset from day 7. Two-colour FCM analysis indicated that a shift in phenotype from single-positive CD4(+)/CD8(-) to double-positive CD4(+)/CD8(+) T-cells might have occurred in these pigs. In the present experiment we demonstrated specific modulation of the peripheral blood T-lymphocyte population in pigs with continuous
low-dose injections of specific mAb. The ability to modulate individual T-cell subsets should provide a method to elucidate their functionality in protection against infectious disease.
Mercury affects the distribution of culturable species of Pseudomonas in soil

Pseudomonas bacteria isolated during 52 days on Gould's S1 agar from soil spiked with 0, 3.5 and 15 mg Hg(II) kg soil(-1) were characterised to reveal whether mercury affected them differently. Isolates from the treatments with 0 and 15 mg Hg kg(-1) were characterised using FT-IR characterisation and subsequent 16S rDNA partial sequencing of representative isolates. To verify the selectivity of Gould's S1 agar and the FT-IR characterisation, all 450 isolates were subjected to the following tests: Gram-determination, catalase and oxidase activity, pigment production on PDA and growth at different temperatures. Furthermore, the isolates were tested for their ability to grow on agar amended with 10 mg Hg kg(-1) as an indication of mercury resistance. We found that up to 80% of the isolates in soil amended with 15 mg Hg kg(-1) were mercury-resistant, whereas only up to 20% were resistant in the treatments with 0 and 3.5 mg Hg kg(-1). We found two groups of Pseudomonas, which probably represent non-described species since they did not group closely with any known species of Pseudomonas in the dendrogram. Hg-enhanced isolates were closely related to P. frederiksbergensis. Furthermore, Hg resistance was almost exclusively restricted to P. frederiksbergensis and P. migulae groups. We conclude that Hg caused a shift in the dominating species of culturable Pseudomonas.
Molecular characterization of a new porcine skin and lung phenotype: a potential model of human lung emphysema

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Bruun, C. S. (Ekstern), Jørgensen, C. B. (Ekstern), Jensen, H. E. (Ekstern), Nielsen, J. (Ekstern), Lohse, L. (Intern), Salicio, S. C. (Ekstern), Christensen, K. (Ekstern), Fredholm, M. (Ekstern)
Publication date: 2006
Event: Poster session presented at 30th ISAG congress, Brazil.
Main Research Area: Technical/natural sciences

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
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Authors: Liu, L. (Ekstern), Häggglund, S. (Ekstern), Hakhverdyan, M. (Ekstern), Alenius, S. (Ekstern), Larsen, L. E. (Intern), Belak, S. (Ekstern)
Pages: 957-960
Publication date: 2006
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Clinical Microbiology
Volume: 44
Issue number: 3
ISSN (Print): 0095-1137
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.57 SJR 2.14 SNIP 1.417
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.204 SNIP 1.448 CiteScore 3.56
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.205 SNIP 1.538 CiteScore 3.84
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 2.414 SNIP 1.646 CiteScore 4.18
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 2.114 SNIP 1.632 CiteScore 4.11
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 2.336 SNIP 1.698 CiteScore 4.27
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.303 SNIP 1.727
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 2.173 SNIP 1.694
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 2.239 SNIP 1.621
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 2.202 SNIP 1.689
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 2.187 SNIP 1.642
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 2.012 SNIP 1.655
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 1.678 SNIP 1.701
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 1.845 SNIP 1.855
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 1.947 SNIP 1.722
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 2.076 SNIP 1.808
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.945 SNIP 1.938
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 1.851 SNIP 2.036

Original language: English
DOIs:
Monitoring of the immune system in fish and shellfish

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Pages: 48-49
Publication date: 2006
Main Research Area: Technical/natural sciences

Publication information
Journal: Bulletin of the European Association of Fish Pathologists
Volume: 26
Issue number: 1
ISSN (Print): 0108-0288
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 0.49 SJR 0.234 SNIP 0.421
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.27 SNIP 0.496 CiteScore 0.64
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.32 SNIP 0.414 CiteScore 0.68
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.365 SNIP 0.431 CiteScore 0.62
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.257 SNIP 0.49 CiteScore 0.47
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.236 SNIP 0.364 CiteScore 0.41
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.34 SNIP 0.469
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.292 SNIP 0.459
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.325 SNIP 0.373
Scopus rating (2007): SJR 0.31 SNIP 0.386
Scopus rating (2006): SJR 0.436 SNIP 0.592
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.623 SNIP 0.672
Scopus rating (2004): SJR 0.602 SNIP 0.796
Natural and experimental infection of sheep with European bat lyssavirus type-1 of Danish bat origin

In 1998 and 2002, European bat lyssavirus type-1 (EBLV-1) was demonstrated in brain tissue of five Danish sheep suffering from micrological disorders. Four of the five sheep also had encephalic listeriosis. The animals originated from four flocks on pastures within a limited area of western Jutland. In a serological investigation in two of the herds, from which three of the diseased animals originated, EBLV-1 neutralizing antibodies were detected in only one of 69 sheep. Ill follow-up surveys, 2110 sheep sera collected at Danish slaughterhouses during 2000 were all negative for EBLV-1-antibodies, and EBLV-1 was not demonstrated in 87 ruminants displaying neurological symptoms. To investigate the pathogenic effects of EBLV-1, four sheep were inoculated intralabially with either brain material from one of the naturally infected sheep or virus isolated from the same sheep. These animals developed EBLV-1 neutralizing antibodies at 5-9 weeks post-inoculation but did not exhibit neurological signs during a 33-week observation period. It was speculated that the immune response prevented viral dissemination to the brain, resulting in an abortive peripheral infection. It was concluded that EBLV-1 can infect sheep under natural conditions as an incidental event.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Technical University of Denmark
Authors: Tjørnehøj, K. (Intern), Fooks, A. (Ekstern), Agerholm, J. (Ekstern), Rønsholt, L. (Ekstern)
Pages: 190-201
Publication date: 2006
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Comparative Pathology
Volume: 134
Issue number: 2-3
ISSN (Print): 0021-9975
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.655 SNIP 0.685 CiteScore 1.17
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.686 SNIP 0.837 CiteScore 1.23
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.562 SNIP 0.775 CiteScore 1.17
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.628 SNIP 0.89 CiteScore 1.32
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.728 SNIP 1.059 CiteScore 1.57
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
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
Event: Abstract from 19th International Pig Veterinary Society Congress, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 230117
Publication: Research - peer-review › Journal article – Annual report year: 2006

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
Event: Abstract from 19th International Pig Veterinary Society Congress, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 240801
Publication: Research › Conference abstract for conference – Annual report year: 2006
New swine influenza A H1N2 reassortment found in Danish swine

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Division of Microbiology and Risk Assessment, Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research
Number of pages: 265
Publication date: 2006

Host publication information
Title of host publication: Proceeding of the 19th International Pig Veterinary Congress
Main Research Area: Technical/natural sciences
Conference: The 19th International Pig Veterinary Congress, Copenhagen, 01/01/2006
Source: orbit
Source-ID: 241727
Publication: Research › Article in proceedings – 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
Authors: Kristensen, S. S. (Ekstern), Hjulsager, C. K. (Intern), Larsen, L. E. (Intern)
Publication date: 2006
Main Research Area: Technical/natural sciences

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
Publication: 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
Authors: Bøtner, A. (Intern), Vigre, H. (Intern), Jorsal, S. E. L. (Intern), Nielsen, J. (Intern), Lohse, L. (Intern), Bille-Hansen, V. (Intern), Larsen, L. E. (Intern), Baekbo, P. (Ekstern), Kristensen, C. S. (Ekstern), Nielsen, E. O. (Ekstern), Enæe, C. (Intern)
Publication date: 2006

Host publication information
Title of host publication: PCVD...Coming Full Circle
Place of publication: Merial Write Book
PMWS in Denmark: Epidemiology, Diagnosis and Control: Merial White Book

**General information**

State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research
Authors: Bøtner, A. (Intern), Vigre, H. (Intern), Jorsal, S. E. L. (Intern), Nielsen, J. (Ekstern), Lohse, L. (Ekstern), Bille-Hansen, V. (Intern), Larsen, L. E. (Ekstern), Bækbo, P. (Ekstern)
Pages: 9-22
Publication date: 2006

**Host publication information**

Title of host publication: Proceeding of the 19th International Pig Veterinary Congress
Main Research Area: Technical/natural sciences
Conference: The 19th International Pig Veterinary Congress, 01/01/2006
Source: orbit
Source-ID: 241741
Publication: Research › Article in proceedings – Annual report year: 2006

PMWS - Laboratory Diagnosis on Herd and Pig Level in a Danish Case-Control Study

**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
Authors: Jorsal, S. E. L. (Intern), Bille-Hansen, V. (Intern), Vigre, H. (Intern), Larsen, P. (Ekstern), Bøtner, A. (Intern), Nielsen, E. O. (Ekstern), Enøe, C. (Intern), Bækbo, P. (Ekstern)
Number of pages: 270
Publication date: 2006

**Host publication information**

Title of host publication: Proceeding of the 19th International Pig Veterinary Congress
Main Research Area: Technical/natural sciences
Conference: The 19th International Pig Veterinary Congress, 01/01/2006
Source: orbit
Source-ID: 241728
Publication: Research › Article in proceedings – Annual report year: 2006

PMWS-laboratory diagnosis on herd and pig level in a Danish case-study

**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, Sektion for Eksotiske Virussygdomme, Division of Virology, Section for Veterinary Epidemiology and public sector consultancy
Authors: Jorsal, S. E. L. (Intern), Bille-Hansen, V. (Intern), Vigre, H. (Intern), Larsen, P. B. (Ekstern), Bøtner, A. (Intern), Nielsen, E. O. (Ekstern), Enæe, C. (Intern), Bækbo, P. (Ekstern)
Publication date: 2006
Event: Abstract from 19th International Pig Veterinary Society Congress, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 241477
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2006

Repeated vaccinations by live African swine fever virus (ASFV) does not east the course of ASFV infections in pigs

**General information**
Role of RNA structure and RNA binding activity of foot-and-mouth disease virus 3C protein in VPg uridylylation and virus replication

The uridylylation of the VPg peptide primer is the first stage in the replication of picornavirus RNA. This process can be achieved in vitro using purified components, including 3B (VPg) with the RNA dependent RNA polymerase (3D(pol)), the precursor 3CD, and an RNA template containing the cre/bus. We show that certain RNA sequences within the foot-and-mouth disease virus (FMDV) 5’ untranslated region but outside of the cre/bus can enhance VPg uridylylation activity. Furthermore, we have shown that the FMDV X protein alone can substitute for 3CD, albeit less efficiently. In addition, the VPg precursors, 3B(3)3C and 3B(123)3C, can function as substrates for uridylylation in the absence of added 3C or 3CD. Residues within the FMDV 3C protein involved in interaction with the cre/bus RNA have been identified and are located on the face of the protein opposite from the catalytic site. These residues within 3C are also essential for VPg uridylylation activity and efficient virus replication.
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): SJR 3.052 SNIP 1.131 CiteScore 4.42
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 3.286 SNIP 1.138 CiteScore 4.42
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 3.168 SNIP 1.219 CiteScore 4.4
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 3.468 SNIP 1.26 CiteScore 4.92
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 3.154 SNIP 1.227 CiteScore 5.2
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 3.399 SNIP 1.288 CiteScore 5.37
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 3.532 SNIP 1.278
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 3.595 SNIP 1.307
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 3.803 SNIP 1.264
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 3.571 SNIP 1.311
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 3.76 SNIP 1.255
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 3.374 SNIP 1.243
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 3.382 SNIP 1.32
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 3.425 SNIP 1.331
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 3.242 SNIP 1.254
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 3.577 SNIP 1.357
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 3.543 SNIP 1.394
Web of Science (2000): Indexed yes
Original language: English
DOIs:
10.1128/JVI.00561-06
Sammenhæng mellem besætningsforhold og PMWS sygdomsudbrud – foreløbige resultater

General information
State: Published
Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Division of Microbiology and Risk Assessment, National Food Institute, Section for Veterinary Diagnostics, Sektion for Eksotiske Virussygdomme, Division of Virology
Authors: Okholm Nielsen, E. (Ekstern), Enøe, C. (Intern), Bækbo, P. (Ekstern), Vigre, H. (Intern), Jorsal, S. E. L. (Intern), Betner, A. (Intern)
Pages: 726
Publication date: 2006
Main Research Area: Technical/natural sciences

Publication information
Journal: Månedsbladet Svin
Original language: Danish
Source: orbit
Source-ID: 242217
Publication: Research › Journal article – Annual report year: 2006

Simulation model estimates of test accuracy and predictive values for the Danish Salmonella surveillance program in dairy herds
The Danish government and cattle industry instituted a Salmonella surveillance program in October 2002 to help reduce Salmonella enterica subsp. enterica serotype Dublin (S. Dublin) infections. All dairy herds are tested by measuring antibodies in bulk tank milk at 3-month intervals. The program is based on a well-established ELISA, but the overall test program accuracy and misclassification was not previously investigated. We developed a model to simulate repeated bulk tank milk antibody measurements for dairy herds conditional on true infection status. The distributions of bulk tank milk antibody measurements for infected and noninfected herds were determined from field study data. Herd infection was defined as having either >= 1 Salmonella culture-positive fecal sample or >= 5% within-herd prevalence based on antibody measurements in serum or milk from individual animals. No distinction was made between Dublin and other Salmonella serotypes which cross-react in the ELISA. The simulation model was used to estimate the accuracy of herd classification for true herd-level prevalence values ranging from 0.02 to 0.5. Test program sensitivity was 0.95 across the range of prevalence values evaluated. Specificity was inversely related to prevalence and ranged from 0.83 to 0.98. For a true herd-level infection prevalence of 15%, the estimate for specificity (Sp) was 0.96. Also at the 15% herd-level prevalence, approximately 99% of herds classified as negative in the program would be truly noninfected and 80% of herds classified as positive would be infected. The predictive values were consistent with the primary goal of the surveillance program which was to have confidence that herds classified negative would be free of Salmonella infection.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Warnick, L. (Ekstern), Nielsen, L. (Ekstern), Nielsen, J. (Intern), Greiner, M. (Ekstern)
Pages: 284-303
Publication date: 2006
Main Research Area: Technical/natural sciences

Publication information
Journal: Preventive Veterinary Medicine
Volume: 77
Issue number: 3-4
ISSN (Print): 0167-5877
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.2 SJR 1.185 SNIP 1.329
Web of Science (2016): Indexed yes
The effects of PMWS on productivity and clinical expression in Danish herds from a case-control study

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research
The effects of PMWS on productivity and clinical expression on Danish herds from a case-control study

General information
State: Published
Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, Section for Veterinary Diagnostics
Authors: Nielsen, E. O. (Ekstern), Bækbo, P. (Ekstern), Enøe, C. (Ekstern), Hassing, A. (Ekstern), Bøtner, A. (Intern), Jorsal, S. E. L. (Intern), Bille-Hansen, V. (Intern)
Publication date: 2006
Event: Abstract from 19th International Pig Veterinary Society Congress, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 241480
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2006

The effects of zonation of the pen and grouping in intact litters on use of pen, immune competence and health of pigs

The effects of pen design and group composition were examined with respect to activity, use of pen, floor conditions, health condition and immune competence for groups of 60 pigs. The experiment was designed with the two factors with zones/without zones and divided litters/intact litters. The experiment included a total of 1440 pigs from weaning at the age of 4 weeks to the age of 18 weeks after weaning. In pens with zones, the selection of different areas for different activities was improved. Pens with zones were more dirty in the elimination and open areas than pens without zones. In pens with zones, the number of lymphocytes was decreased, the ability to respond to an additional challenge by a model infection was decreased and the number of neutrophils was increased in intact litters. In week 9, the health condition was better with a group composition consisting of intact litters compared to divided litters. The health condition of the pigs was unaffected by pen design, but noninfectious health condition was improved in pens with zones.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Damgaard, B. (Ekstern), Studnitz, M. (Ekstern), Nielsen, J. (Intern), Moustsen, V. (Ekstern), Jorgensen, E. (Ekstern), Jensen, K. (Ekstern)
Pages: 203-216
Publication date: 2006
Main Research Area: Technical/natural sciences

Publication information
Journal: Livestock Science
Volume: 104
Issue number: 1-2
ISSN (Print): 1871-1413
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.812 SNIP 1.085 CiteScore 1.58
BFI (2015): BFI-level 1
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
Authors: Holm, E. (Intern), Voss, H. (Intern), Jensen, N. (Ekstern), Larsen, L. E. (Intern), Uttenthal, Å. (Intern)
Publication date: 2006
Event: Abstract from International Pestivirus Symposium, Uppsala, Sweden
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 230024
Publication: Research - peer-review › Journal article – Annual report year: 2006

floor condition, pen design, group composition, health, large groups, activity

DOIs:
10.1016/j.livsci.2006.04.023
Source: orbit
Source-ID: 240805
Publication: 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
Authors: Kristensen, C. (Ekstern), Bille-Hansen, V. (Intern), Vigre, H. (Intern), Bøtner, A. (Intern), Bækbo, P. (Ekstern), Enøe, C. (Intern), Larsen, L. E. (Intern)
Publication date: 2006
Event: Abstract from 19th International Pig Veterinary Society Congress, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 240802
Publication: Research › Conference abstract for conference – Annual report year: 2006

Vaccination af Kalve mod lungebetændelse

**General information**
State: Published
Organisations: Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Authors: Larsen, L. E. (Intern)
Publication date: 2006
Publication information
Source/Publisher: www.kvaegforskning.dk
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 242197
Publication: Research › Internet publication – Annual report year: 2006

Validated CSFV and BVDV Taqman RT-PCRs for combined pestivirus diagnostics

**General information**
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Rasmussen, T. B. (Intern), Uttenthal, Å. (Intern)
Publication date: 2006

Host publication Information
Title of host publication: NSFL 2006
Main Research Area: Technical/natural sciences
Conference: Annual Meeting of National Classical Swine Fever Laboratories, Brussels, Belgium, 01/01/2006
Source: orbit
Source-ID: 240951
Publication: Research › Article in proceedings – 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.

**General information**
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Virology, Division of Veterinary Diagnostics and Research
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 antepartum 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.

General information

State: Published
Organisations: Microbial Ecology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Section for Veterinary Diagnostics, Virology, Royal Veterinary and Agricultural University
Pages: 146-152
Publication date: 2006
Main Research Area: Technical/natural sciences

Publication information

Journal: Acta Pathologica Microbiologica et Immunologica Scandinavica
Volume: 114
Issue number: 2
ISSN (Print): 0903-4641
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.87
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 1.92
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 1.95
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.07
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.06
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 1.97
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
Viral haemorrhagic septicaemia (VHS) outbreaks in Finnish-rainbow trout farms

In Finland, viral haemorrhagic septicaemia virus (VHSV) was diagnosed for the first time in 2000 from 4 rainbow trout farms in brackish water. Since then the infection has spread and, by the end of 2004, VHSV had been isolated from 24 farms in 3 separate locations: 2 in the Baltic Sea and 1 in the Gulf of Finland. The pathogenicity of 3 of these isolates from 2 separate locations was analysed in infection experiments with rainbow trout fry. The cumulative mortalities induced by waterborne and intraperitoneal challenge were approximately 40 and 90%, respectively. Pair-wise comparisons of the G and NV gene regions of Finnish VHSV isolates collected between 2000 and 2004 revealed that all isolates were closely related, with 99.3 to 100% nucleotide identity, which suggests the same origin of infection. Phylogenetic analysis revealed that they were closely related to the old freshwater isolates from rainbow trout in Denmark and to one old marine isolate from cod in the Baltic Sea, and that they were located close to the presumed ancestral source. As the Finnish isolates induce lower mortality than freshwater VHSV isolates in infection experiments, they could represent an intermediate stage of marine isolates evolving towards pathogenicity in rainbow trout.

General information

State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Raja-Halli, M. (Ekstern), Vehmas, T. (Ekstern), Rimaila-Parnanen, E. (Ekstern), Sainmaa, S. (Ekstern), Skall, H. F. (Intern), Olesen, N. J. (Intern), Tapiovaara, H. (Ekstern)
Pages: 201-211
Publication date: 2006
Main Research Area: Technical/natural sciences

Publication information
Journal: Diseases of Aquatic Organisms
Volume: 72
Issue number: 3
ISSN (Print): 0177-5103
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.95 SJR 0.858 SNIP 0.929
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.949 SNIP 0.935 CiteScore 1.96
A Danish study on FRNA Coliphages as source specific indicator of faecal pollution in shellfish harvest areas

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Authors: Schultz, A. C. (Intern), Trebbien, R. (Intern)
A Danish study on FRNA Coliphages as source specific indicator of faecal pollution in shellfish harvest areas

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Virology, Division of Veterinary Diagnostics and Research, National Veterinary Institute
Authors: Schultz, A. C. (Intern), Trebbien, R. (Intern)
Publication date: 2005
Event: Poster session presented at 13th International Symposium on Health-related Water Microbiology, Swansea, United Kingdom.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 239510
Publication: Research › Poster – Annual report year: 2005

Advances in surveillance and control of viral diseases in rainbow trout

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Olesen, N. J. (Intern)
Publication date: 2005
Event: Abstract from COE Marine Bio-manipulation Frontier for Food Production, Hokkaido University, Kinki University, Ehime University and University of the Ryukyus.
Main Research Area: Technical/natural sciences

Bibliographical note
Reproductive, Genetic and Disease Management in Aquaculture and Ocean Ranching
Source: orbit
Source-ID: 241722
Publication: Research › Conference abstract for conference – Annual report year: 2005

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 TNFa levels and less virus-specific IFN gamma 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
Authors: Grell, S. (Ekstern), Riber, U. (Intern), Tjørnehøj, K. (Intern), Larsen, L. E. (Intern), Heegaard, P. M. H. (Intern)
Pages: 3412-3423
Publication date: 2005
Main Research Area: Technical/natural sciences

Publication information
Journal: Vaccine
Volume: 23
Issue number: 26
ISSN (Print): 0264-410X
Ratings:
bovine respiratory syncytial virus, age-dependent immunity

DOIs:
10.1016/j.vaccine.2005.01.094
Analyse af BVD-virus subtyper isoleret fra danske kvægbesætninger gennem 10 år

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Uttenthal, Å. (Intern), Nylin, B. (Ekstern)
Pages: 28-29
Publication date: 2005
Main Research Area: Technical/natural sciences

Publication information
Journal: Dansk Veterinærtidsskrift
Volume: 88
Issue number: 21
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
ISI indexed (2012): ISI indexed no
BFI (2011): BFI-level 1
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
BFI (2009): BFI-level 1
BFI (2008): BFI-level 1
Original language: Danish
Source: orbit
Source-ID: 240941
Publication: Research › Journal article – Annual report year: 2005

Analysis of the epidemiological dynamics during the 1982-1983 epidemic of foot-and-mouth disease in Denmark based on molecular high-resolution strain identification

An epidemic of foot-and-mouth disease (FMD) causing a total of 23 cases in 1982-1983, primarily on the island of Funen, Denmark, was subjected to molecular epidemiological investigations. In an attempt to exploit the quasi-species nature of foot-and-mouth disease virus strains for molecular high-resolution strain identification in order to analyse the dynamics of this epidemic, full-length VP1 coding regions were sequenced for 17 isolates collected at different farms during the epidemic. The sequence information together with epidemiological information gathered during the epidemic suggests that the epidemic was caused by at least three introductions across Danish borders and one case of airborne transmission between two islands in Denmark over a distance of 70 km. The assortment of nucleotide markers among the three strains is indicative of common recombination events in their evolutionary history, and the prerequisite of co- or superinfection of animals with variant strains in turn implies that they have a common source or epidemiologically related sources originating from an area with endemic FMD.

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Meteorology, Wind Energy Division, Risø National Laboratory for Sustainable Energy
Authors: Christensen, L. S. (Intern), Normann, P. (Intern), Thykier-Nielsen, S. (Intern), Sorensen, J. (Ekstern), de Stricker, K. (Ekstern), Rosenorn, S. (Ekstern)
Pages: 2577-2584
Publication date: 2005
Main Research Area: Technical/natural sciences
Characterisation of European perch rhabdoviruses (O-143): Abstract Book p. 147.

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Olesen, N. J. (Intern), Skall, H. F. (Intern), Johansson, T. (Ekstern)
Publication date: 2005
Event: Abstract from 12th International Conference on Diseases of Fish and Shellfish, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences

Danmark fri for bovin virus diarre (BVD) i 2005?

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Uttenthal, Å. (Intern), Voss, H. B. (Ekstern), Vestergaard, P. (Ekstern), Steffensen, M. (Ekstern), Nielsen, J. (Ekstern), Holm, E. (Ekstern), Grubbe, T. (Ekstern), Chriel, M. (Ekstern)
Pages: 10-12
Publication date: 2005
Main Research Area: Technical/natural sciences

Danmark fri for bovin virus diarre (BVD) virus i 2005?

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Laboratory Service, Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, Division of Microbiology and Risk Assessment, National Food Institute
Detection of swine vesicular disease virus (SVDV) using PriProET real-time PCR assay

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Hakverdyan, M. (Ekstern), Rasmussen, T. B. (Intern), Uttenthal, Å. (Intern), Belák, S. (Ekstern)
Publication date: 2005

Host publication information
Title of host publication: Proceedings of the IUMS 2005 conference: Microbes in a changing world
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 242304
Publication: Research › Article in proceedings – Annual report year: 2005

Development of a multiplex real-time RT-PCR method for simultaneous detection and differentiation of pestiviruses

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Stadejek, T. (Ekstern), Storgaard, T. (Ekstern), Jensen, T. (Ekstern), Rasmussen, T. B. (Intern), Uttenthal, Å. (Intern)
Number of pages: 97
Publication date: 2005

Host publication information
Title of host publication: Proceedings of the ESVV Pestivirus Symposium
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 242302
Publication: Research › Article in proceedings – Annual report year: 2005

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
Authors: Larsen, L. E. (Intern), Batner, A. (Intern)
Publication date: 2005
Main Research Area: Technical/natural sciences

Publication information
Diagnostik af svineinfluenza og påvisning af ny subtype i Danmark

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Larsen, L. E. (Ekstern), Bøtner, A. (Intern)
Publication date: 2005
Main Research Area: Technical/natural sciences

Publication information
Journal: DVT
Volume: 8
Original language: English
Source: orbit
Source-ID: 241776
Publication: Research › Journal article – Annual report year: 2005

Diagnostik af svineinfluenza og påvisning af ny subtype i Danmark

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Larsen, L. E. (Ekstern), Bøtner, A. (Intern)
Publication date: 2005
Main Research Area: Technical/natural sciences

Publication information
Source/Publisher: DFVF’s hjemmeside
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 242214
Publication: Research › Internet publication – Annual report year: 2005

DNA vaccines for aquacultured fish
Deoxyribonucleic acid (DNA) vaccination is based on the administration of the gene encoding the vaccine antigen, rather than the antigen itself. Subsequent expression of the antigen by cells in the vaccinated hosts triggers the host immune system. Among the many experimental DNA vaccines tested in various animal species as well as in humans, the vaccines against rhabdovirus diseases in fish have given some of the most promising results. A single intramuscular (IM) injection of microgram amounts of DNA induces rapid and long-lasting protection in farmed salmonids against economically important viruses such as infectious haematopoietic necrosis virus (IHNV) and viral haemorrhagic septicaemia virus (VHSV). DNA vaccines against other types of fish pathogens, however, have so far had limited success. The most efficient delivery route at present is IM injection, and suitable delivery strategies for mass vaccination of small fish have yet to be developed. In terms of safety, no adverse effects in the vaccinated fish have been observed to date. As DNA vaccination is a relatively new technology, various theoretical and long-term safety issues related to the environment and the consumer remain to be fully addressed, although inherently the risks should not be any greater than with the commercial fish vaccines that are currently used. Present classification systems lack clarity in distinguishing DNA-vaccinated animals from genetically modified organisms (GMOs), which could raise issues in terms of licensing and public acceptance of the technology. The potential benefits of DNA vaccines for farmed fish include improved animal welfare, reduced environmental impacts of aquaculture activities, increased food quality and quantity, and more sustainable production. Testing under commercial production conditions has recently been initiated in Canada and Denmark.
field-testing glycoprotein plasmid, deoxyribonucleic acid vaccine, safety, regulatory issues, animal welfare, farmed fish, viral diseases, protective mechanisms, cost-benefit, delivery, consumer perceptions

Source: orbit
Source-ID: 230236
Endosperm specific Promoter from Rice – High level expression linked to carbohydrate metabolism

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Rasmussen, T. B. (Intern), Donaldson, I. A. (Ekstern)
Publication date: 2005
Event: Abstract from IP pragmatics.
Main Research Area: Technical/natural sciences
Source-ID: 242305
Publication: Research › Conference abstract for conference – Annual report year: 2005

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
Authors: Hakhverdyan, M. (Ekstern), Hägglund, S. (Ekstern), Larsen, L. E. (Intern), Belák, S. (Ekstern)
Publication date: 2005
Main Research Area: Technical/natural sciences
Experiences on the application of various nucleic acid amplification systems for the improved diagnosis of vesicular diseases

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Hakhverdyan, M. (Ekstern), Rasmussen, T. B. (Intern), Uttenthal, Å. (Intern), Thóren, P. (Ekstern), Bélak, S. (Ekstern)
Publication date: 2005
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 229494
Publication: Research - peer-review › Journal article – Annual report year: 2005

Experimental reproduction of postweaning multisystemic wasting syndrome (PMWS) in pigs in Sweden and Denmark with a Swedish isolate of porcine circovirus type 2

An experimental model using 3-day-old snatch-farrowed colostrum-deprived piglets co-infected with porcine circovirus type 2 (PCV2) and porcine parvovirus (PPV) is at present one of the best methods to study factors affecting development of postweaning multisystemic wasting syndrome (PMWS). A Swedish isolate of PCV2 (S-PCV2) retrieved in 1993 from a healthy pig has been used in this model to reproduce PMWS in pigs from Northern Ireland. This virus has been present in the Swedish pig population for at least a decade without causing any known PMWS disease problems, despite its potential pathogenicity. The reasons for this are unknown, but could be related to genetics, absence of triggers for PCV2 upregulation (infectious agent and/or management forms) within Swedish pig husbandry. In order to confirm the pathogenicity of S-PCV2, Swedish and Danish pigs were experimentally infected with this isolate according to the established model. Swedish pigs were also infected with a reference isolate of PCV2 (PCV2-1010) to compare the severity of disease caused by the two isolates in Swedish pigs. Both Danish and Swedish pigs developed PMWS after the experimental infection with S-PCV2. Antibodies to PCV2 developed later and reached lower levels in serum from pigs infected with S-PCV2 than in pigs inoculated with PCV2-1010. In general, pigs infected with S-PCV2 showed more severe clinical signs of disease than pigs infected with PCV2-1010, but pigs from all PCV2-inoculated groups displayed gross and histological lesions consistent with PMWS. All pigs inoculated with PPV, alone or in combination with PCV2, displayed interleukin-10 responses in serum while only pigs infected with PPV in combination with PCV2 showed interferon-a in serum on repeated occasions. Thus, the pathogenicity of S-PCV2 was confirmed and a role for cytokines in the etiology of PMWS was indicated.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Technical University of Denmark
Authors: Hasslung, F. (Ekstern), Wallgren, P. (Ekstern), Hansen, A. L. (Ekstern), Batnner, A. (Intern), Nielsen, J. (Intern), Wattrag, E. (Ekstern), Allan, G. (Ekstern), McNeilly, F. (Ekstern), Ellis, J. (Ekstern), Timmusk, S. (Ekstern), Belak, K. (Ekstern), Segal, T. (Ekstern), Melin, L. (Ekstern), Berg, M. (Ekstern), Fossum, C. (Ekstern)
Pages: 49-60
Publication date: 2005
Main Research Area: Technical/natural sciences

Publication information
Journal: Veterinary Microbiology
Volume: 106
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
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<td>SJR 1.393 SNIP 1.21 CiteScore 2.56</td>
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<td>SJR 1.437 SNIP 1.579 CiteScore 3.18</td>
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<td>2012</td>
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<td>2004</td>
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<td>BFI-level 2</td>
<td>SJR 0.833 SNIP 1.058</td>
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<tr>
<td>2000</td>
<td>Indexed yes</td>
<td>BFI-level 2</td>
<td>SJR 0.82 SNIP 1.088</td>
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<tr>
<td>1999</td>
<td>Indexed yes</td>
<td>BFI-level 2</td>
<td>SJR 0.703 SNIP 1.078</td>
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</tbody>
</table>

Original language: English

PCV2, experimental infection, PMWS, Denmark, Sweden


Source: orbit

Source-ID: 230300
Genetic diversity of bovine viral diarrhoea viruses (BVDV) in Denmark during a 10-year eradication period

A 243 base-pair fragment of the 5'- untranslated region (5'-UTR) of bovine viral diarrhoea virus (BVDV) was RT-PCR amplified from tissue samples (after one passage) or from plasma collected from Danish cattle in 1962 (1), 1993 (7), or in 2002-03 (28) when BVD was almost extinct as a result of a 6-year eradication programme. The PCR products were sequenced and phylogenetically analysed. All 36 samples were BVDV species I (BVDV-1), 29 sequences belonged to the BVDV Id subtype, 6 to the BVDV 1b subtype, and one sequence to the BVDV le subtype. While all samples from 1993 and 1962 were of Id subtype, the samples collected in 2002-2003 belonged to Id (22 samples), 1b (5 samples) and le (1 sample) subtypes. In five herds, materials from two animals were obtained for PCR analysis. In four of five herds the sequences of the two viruses were identical, but in one herd the obtained sequences belonged to two different subtypes. Routine analysis detected I I PI calves older than 2 months of age. For early detection of infected calves it is recommended that antigen ELISA be replaced by PCR detection. Here we present the first sequence analysis of Danish BVDV strains.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Utenthal, Å. (Intern), Stadejek, T. (Ekstern), Nylin, B. (Ekstern)
Pages: 536-541
Publication date: 2005
Main Research Area: Technical/natural sciences

Publication information
Journal: Apmis
Volume: 113
Issue number: 7-8
ISSN (Print): 0903-4641
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Genotyping of the fish rhabdovirus, viral haemorrhagic septicaemia virus, by restriction fragment length polymorphisms

The aim of this study was to develop a standardized molecular assay that used limited resources and equipment for routine genotyping of isolates of the fish rhabdovirus, viral haemorrhagic septicaemia virus (VHSV). Computer generated restriction maps, based on 62 unique full-length (1524 nt) sequences of the VHSV glycoprotein (G) gene, were used to predict restriction fragment length polymorphism (RFLP) patterns that were subsequently grouped and compared with a phylogenetic analysis of the G-gene sequences of the same set of isolates. Digestion of PCR amplicons from the full-length G-gene by a set of three restriction enzymes was predicted to accurately enable the assignment of the VHSV isolates into the four major genotypes discovered to date. Further sub-typing of the isolates into the recently described sub-lineages of genotype I was possible by applying three additional enzymes. Experimental evaluation of the method consisted of three steps: (i) RT-PCR amplification of the G-gene of VHSV isolates using purified viral RNA as template, (ii) digestion of the PCR products with a panel of restriction endonucleases and (iii) interpretation of the resulting RFLP profiles. The RFLP analysis was shown to approximate the level of genetic discrimination obtained by other, more labour-intensive, molecular techniques such as the ribonuclease protection assay or sequence analysis. In addition, 37 previously uncharacterised isolates from diverse sources were assigned to specific genotypes. While the assay was able to distinguish between marine and continental isolates of VHSV, the differences did not correlate with the pathogenicity of the isolates.
Kinetics of Mx expression in rainbow trout (Oncorhynchus mykiss) and Atlantic salmon (Salmo salar L.) parr in response to VHS-DNA vaccination

The duration of the Mx mRNA response to an intramuscular injection of the viral haemorrhagic septicaemia virus (VHSV) glycoprotein (G) gene DNA vaccine as well as to the control plasmid was determined in rainbow trout at 14 degreesC over a period of 11 weeks. The Mx response was detectable on day 7, peaked on day 14 and returned to pretreatment levels on day 21 and thereafter. No increase in Mx expression was detectable to the control plasmid. In further experiments, the kinetics of the Mx response were compared in rainbow trout and Atlantic salmon parr kept at 10 degreesC and injected with the DNA vaccine or the synthetic double-stranded RNA, poly LC. In both species there was a rapid response to poly LC detectable from day 1, reaching maximum from days 3 to 9 and decreasing to background level by day 12. The peak level and return to background was reached slightly later in salmon. In both species the response to the VHS/DNA vaccine was slower to begin, not being detectable on days 1 and 3, but elevated levels were found on day 6. However, in the salmon part, the peak level was on day 6 and the signal disappeared by day 12, while in the rainbow trout, the response peaked at day 12 and lasted until day 21. The kinetics of the Mx response to the VHS/DNA vaccine in rainbow trout correlate with the early non-specific protection against VHS in this species following vaccination. It is speculated that the more transient Mx response in Atlantic salmon parr to the DNA vaccine may be related to the innate resistance of salmon to VHS.
Low-dose effects of anti-androgens in male rat offspring after perinatal exposure

**General information**
State: Published
Organisations: Division of Toxicology and Risk Assessment, National Food Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Hass, U. (Intern), Christiansen, S. (Intern), Dalgaard, M. (Ekstern), Filinska, M. (Intern), Borch, J. (Intern), Vinggaard, A. (Intern), Metzdorff, S. B. (Intern)
Publication date: 2005
Event: Abstract from The CREDO Cluster Workshop on Endocrine Disrupters: Exposure Assessment, Epidemiology, Low-dose and Mixture Effects, Prague, .
Main Research Area: Technical/natural sciences
Source: orbit
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 die, 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 reinfection 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 tot-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
Authors: Grell, S. N. (Ekstern), Tjørnehøj, K. (Intern), Larsen, L. E. (Intern), Heegaard, P. M. H. (Intern)
Pages: 235-245
Publication date: 2005
Main Research Area: Technical/natural sciences

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
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 1.63 SJR 0.73 SNIP 0.704
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 0.856 SNIP 0.752 CiteScore 1.67
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 0.768 SNIP 0.719 CiteScore 1.6
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 0.808 SNIP 0.805 CiteScore 1.89
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 0.837 SNIP 0.922 CiteScore 2.15
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 0.849 SNIP 0.996 CiteScore 2.16
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Parallel phylogenetic analyses using the N, G or Nv gene from a fixed group of VHSV isolates reveal the same overall genetic typing

Different genetic regions representing the viral phospho-(P), nucleocapsid-(N) or glyco-protein (G) gene have been used for phylogenetic studies of viral haemorrhagic septicaemia virus (VHSV). Since these analyses were performed on
different virus isolates using various genomic regions, it has been difficult to evaluate how the choice of target region affects the output of the analyses. To address this, we sequenced and performed parallel phylogenetic analysis of an N gene fragment, the entire Nv (non-structural protein) and G genes, and 4 different fragments of the G gene from a fixed virus panel. The overall genotyping of the selected isolates was identical for the 7 target regions, but separation of Genotype I sub-lineages was best when the analysis was performed on the full length G gene (1524 nucleotides, nt). Good resolution was furthermore obtained using smaller sequencing windows represented by a G gene fragment (nt 360 to 720) or the Nv gene (366 nt), although these regions had different characteristics with respect to resolution of Genotype I sublineages and resolution within Sub-lineage Ia. Phylogenetic analysis based on the deduced amino acid sequences was also performed. The phylogenetic relationship between the nucleotide and amino acid sequences of the isolates corresponded best in the case of the N gene/protein. For the 6 other genomic regions, genetically distant isolates occasionally grouped together when compared at protein levels. No clear relationship between the G gene genotyping and serotyping with neutralising (G protein specific) antibodies was observed, stressing that epidemiological analysis based on phenotypic characteristics such as serotype could be misleading.

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Einer-Jensen, K. (Intern), Ahrens, P. (Intern), Lorenzen, N. (Intern)
Pages: 39-45
Publication date: 2005
Main Research Area: Technical/natural sciences

Publication information
Journal: Diseases of Aquatic Organisms
Volume: 67
Issue number: 1-2
ISSN (Print): 0177-5103
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.95 SJR 0.858 SNIP 0.929
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.949 SNIP 0.935 CiteScore 1.96
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.889 SNIP 0.881 CiteScore 1.86
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.812 SNIP 0.918 CiteScore 1.77
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.912 SNIP 1.092 CiteScore 2.04
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.11 SNIP 1.165 CiteScore 2.29
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.91 SNIP 0.951
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.889 SNIP 0.99
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Persistent BVDV infection in mousedeer infects calves - Do we know the reservoirs for BVDV?

Bovine virus diarrhea 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
Authors: Uttenthal, Å. (Intern), Grøndahl, M. (Ekstern), Houe, H. (Intern), Van Maanen, C. (Ekstern), Rasmussen, T. B. (Intern), Larsen, L. E. (Intern)
Pages: 87-91
Publication date: 2005
Main Research Area: Technical/natural sciences

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
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.2 SJR 1.185 SNIP 1.329
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.26 SNIP 1.23 CiteScore 2.1
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
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
Authors: Uttenthal, Å. (Intern), Grøndahl, C. (Ekstern), Hoyer, M. (Ekstern), Houe, H. (Intern), van Maanen, K. (Ekstern), Rasmussen, T. B. (Intern), Larsen, L. E. (Intern)

DOI: 10.1016/j.prevetmed.2005.08.006
Source: orbit
Source-ID: 233574
Publication: Research - peer-review › Journal article – Annual report year: 2005

Scopus rating (2014): SJR 1.267 SNIP 1.421 CiteScore 2.37
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.247 SNIP 1.552 CiteScore 2.49
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.274 SNIP 1.452 CiteScore 2.45
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.211 SNIP 1.303 CiteScore 2.24
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.155 SNIP 1.28
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.022 SNIP 1.34
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.066 SNIP 1.273
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.006 SNIP 1.36
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.056 SNIP 1.305
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.926 SNIP 1.438
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.807 SNIP 1.147
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.865 SNIP 1.346
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.924 SNIP 1.423
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 1.044 SNIP 1.415
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 0.945 SNIP 1.272
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 0.639 SNIP 1.008

Original language: English
pestivirus, reservoir, BVDV, Tragulus javanicus

Source: orbit
Source-ID: 233574
Publication: Research - peer-review › Journal article – Annual report year: 2005

Persistant 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
Authors: Uttenthal, Å. (Intern), Grøndahl, C. (Ekstern), Hoyer, M. (Ekstern), Houe, H. (Intern), van Maanen, K. (Ekstern), Rasmussen, T. B. (Intern), Larsen, L. E. (Intern)
Phylogeography, population dynamics, and molecular evolution of European bat lyssaviruses

European bat lyssaviruses types 1 and 2 (EBLV-1 and EBLV-2) are widespread in Europe, although little is known of their evolutionary history. We undertook a comprehensive sequence analysis to infer the selection pressures, rates of nucleotide substitution, age of genetic diversity, geographical origin, and population growth rates of EBLV-1. Our study encompassed data from 12 countries collected over a time span of 35 years and focused on the glycoprotein (G) and nucleoprotein (N) genes. We show that although the two subtypes of EBLV-1-EBLV-1a and EBLV-lb-have both grown at a low exponential rate since their introduction into Europe, they have differing population structures and dispersal patterns. Furthermore, there were strong constraints against amino acid change in both EBLV-1 and EBLV-2, as reflected in a low ratio of nonsynonymous to synonymous substitutions per site, particularly in EBLV-1b. Our inferred rate of nucleotide substitution in EBLV-1, approximately $5 \times 10^{-5}$ substitutions per site per year, was also one of the lowest recorded for RNA viruses and implied that the current genetic diversity in the virus arose 500 to 750 years ago. We propose that the slow evolution of EBLVs reflects their distinctive epidemiology in bats, where they occupy a relatively stable fitness peak.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Davis, P. (Ekstern), Holmes, E. (Ekstern), Larrous, F. (Ekstern), Van der Poel, W. (Ekstern), Tjørnehøj, K. (Intern), Alonso, W. (Ekstern), Bourhy, H. (Ekstern)
Pages: 10487-10497
Publication date: 2005
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Virology
Volume: 79
Issue number: 16
ISSN (Print): 0022-538X
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): SJR 3.052 SNIP 1.131 CiteScore 4.42
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 3.286 SNIP 1.138 CiteScore 4.42
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 3.168 SNIP 1.219 CiteScore 4.4
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 3.468 SNIP 1.26 CiteScore 4.92
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 3.154 SNIP 1.227 CiteScore 5.2
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 3.399 SNIP 1.288 CiteScore 5.37
ISI indexed (2011): ISI indexed yes
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
Authors: Jensen, T. K. (Intern), Vigre, H. (Intern), Svensmark, B. (Ekstern), Larsen, L. E. (Intern), Bille-Hansen, V. (Intern)
Publication date: 2005
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 230242
Publication: Research - peer-review › Journal article – Annual report year: 2005

Porcine humoral immune responses to multiple injections of murine monoclonal antibodies
In humans and cattle, multiple injections of murine monoclonal antibodies (m-mAbs) induce anti-mouse antibody responses. The objectives of the present study were to investigate whether a similar response could be seen when pigs were subjected to m-mAb therapy, and to study the kinetics of such a response. In two separate animal experiments, long-term treatment was performed with m-mAbs at low-dose levels and therapeutic levels, respectively. Two specific m-mAbs that recognized cognate antigen in the pigs (CD4 and CD8 surface antigens on T-lymphocytes) and two irrelevant control m-mAbs having no cognate antigen in the pigs were used. Enzyme-linked immunosorbent assays (ELISA) were used to quantify the circulating m-mAbs, as well as the induced pig anti-mouse antibodies (PAMA). In serum samples from m-mAb-treated pigs. As expected, we generally saw vigorous PAMA responses within 10 days after the start of m-mAb treatment with the specific m-mAbs. However, the different mAbs showed striking differences in the kinetics and levels of...
PAMA responses, differences that might be ascribed to the m-mAb formulation and epitope specificity. In conclusion, treatment of pigs with m-mAbs against T-cell surface antigens induced rapid PAMA responses. This may influence and possibly decrease the effect of the m-mAb treatment by narrowing the time period where m-mAbs can efficiently be used for cell depletion.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Lohse, L. (Intern), Nielsen, J. (Intern), Kamstrup, S. (Intern), Oleksiewicz, M. (Ekstern), Eriksen, L. (Ekstern)
Pages: 489-496
Publication date: 2005
Main Research Area: Technical/natural sciences

Publication information
Journal: Apmis
Volume: 113
Issue number: 7-8
ISSN (Print): 0903-4641
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.87
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 1.92
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 1.95
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 2.07
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 2.06
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 1.97
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Web of Science (2008): Indexed yes
Web of Science (2007): Indexed yes
Web of Science (2006): Indexed yes
Web of Science (2005): Indexed yes
Web of Science (2004): Indexed yes
Web of Science (2003): Indexed yes
Web of Science (2002): Indexed yes
Web of Science (2001): Indexed yes
Web of Science (2000): Indexed yes
Original language: English
immunoglobulin, mAb, immunotherapy, IgG, ELISA, anti-mouse response, CD4, CD8, pig
DOIs:
Prevalence of viral haemorrhagic septicaemia virus in Danish marine fishes and its occurrence in new host species

In order to analyse the occurrence of viral haemorrhagic septicaemia virus (VHSV) in the marine waters around Denmark, staff from the Danish Institute for Food and Veterinary Research participated in 5 research cruises during 1998 to 2002 as a follow-up to 4 research cruises performed in 1996 to 1997. In total, 16 655 fish were examined virologically as 3569 samples. Forty fish species and 3 invertebrate species were represented. VHSV was isolated from 133 samples representing 8 species: herring Clupea harengus, sprat Sprattus sprattus, dab Limanda limanda, flounder Platichthys flesus, plaice Pleuronectes platessa, cod Gadus morhua, sand eel Ammodytes sp. and sand goby Pomatochistus minutus. Calculations showed that VHSV was more prevalent in the Baltic Sea in an area between Zealand and the island of Bornholm and the waters surrounding Bornholm than in the Kattegat, Skagerrak and along the North Sea coast of Denmark. This is the first report on the isolation of VHSV from dab, flounder and plaice and the first publication on VHSV from sand eel from Europe and sand goby.

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Skall, H. F. (Intern), Olesen, N. J. (Intern), Mellergaard, S. (Intern)
Pages: 145-151
Publication date: 2005
Main Research Area: Technical/natural sciences

Publication information
Journal: Diseases of Aquatic Organisms
Volume: 66
Issue number: 2
ISSN (Print): 0177-5103
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.95 SJR 0.858 SNIP 0.929
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.949 SNIP 0.935 CiteScore 1.96
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.889 SNIP 0.881 CiteScore 1.86
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.812 SNIP 0.918 CiteScore 1.77
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.912 SNIP 1.092 CiteScore 2.04
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.11 SNIP 1.165 CiteScore 2.29
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.91 SNIP 0.951
Web of Science (2010): Indexed yes
Quantitative multiplex assay for simultaneous detection and identification of Indiana and New Jersey serotypes of vesicular stomatitis virus

In order to establish a rapid and reliable system for the detection of vesicular stomatitis virus (VSV), we developed a quantitative reverse transcription-PCR assay for the detection, quantification, and differentiation of the major serotypes, VSV Indiana and VSV New Jersey, using a closed-tube multiplex format. The detection system is based on the recently invented primer-probe energy transfer (PriProET) system. A region of the gene encoding the RNA-dependent RNA polymerase was amplified by using VSV-specific primers in the presence of two serotype-specific fluorescent probes. By incorporating nucleotide analogues in the primers, both serotypes were amplified with similar efficiencies. The generation of specific amplicons resulted in fluorescent signals for either of the two serotypes, and the specificities of the reactions were confirmed from the melting temperature profiles of the fluorescent probes. The limits of detection were found to be less than 10^5 50% tissue culture infective doses/ml for both serotypes. The diagnostic value of the new method was tested with clinical materials from experimentally infected pigs, and it is concluded that the method is a powerful tool for the rapid identification of VSV.
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.57 SJR 2.14 SNIP 1.417
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.204 SNIP 1.448 CiteScore 3.56
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.205 SNIP 1.538 CiteScore 3.84
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 2.414 SNIP 1.646 CiteScore 4.18
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 2.114 SNIP 1.632 CiteScore 4.11
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 2.336 SNIP 1.698 CiteScore 4.27
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 2.303 SNIP 1.727
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 2.173 SNIP 1.694
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 2.239 SNIP 1.621
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 2.202 SNIP 1.689
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 2.187 SNIP 1.642
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 2.012 SNIP 1.655
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 1.678 SNIP 1.701
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 1.845 SNIP 1.855
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 1.947 SNIP 1.722
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 2.076 SNIP 1.808
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.945 SNIP 1.938
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 1.851 SNIP 2.036
Original language: English
DOIs:
10.1128/JCM.43.1.356-362.2005
Selective breeding provides an approach to increase resistance of rainbow trout (Onchorhynchus mykiss) to the diseases, enteric redmouth disease, rainbow trout fry syndrome, and viral haemorrhagic septicemia

In this study, we reasoned that if we challenged rainbow trout with the causative agents of enteric redmouth disease (ERM), rainbow trout fry syndrome (RTFS), and viral haemorrhagic septicemia (VHS), we would: 1) detect additive genetic variation for resistance to ERM, RTFS, and VHS; and 2) find that resistance of the trout to ERM and RTFS are favourably correlated genetically, while resistance to VHS is unfavourably correlated with resistance to ERM and RTFS. We tested these premises by challenging 63 full-sib families of rainbow trout (50 sires, 38 dams) with Yersinia ruckeri, Flavobacterium psychrophilum, and VHS virus, the causative agents of ERM, RTFS, and VHS. Resistance to each disease was assessed as both a binary trait (i.e., died/survived) and a longitudinal trait (i.e., time until death following challenge). Additive genetic variation and genetic correlations for resistance to ERM, RTFS, and VHS were estimated by fitting a threshold liability model to resistance assessed as a binary trait. As a longitudinal trait, additive genetic variation and genetic correlations were estimated by fitting a Weibull frailty model to the times until death. Our findings support the first of our premises as we detected additive genetic variation for resistance to ERM, RTFS, and VHS. The heritability for resistance to ERM, RTFS, and VHS ranged between 0.42 and 0.57 on the underlying liability scale when resistance was assessed as a binary trait. As a longitudinal trait, the heritabilities ranged between 0.07 and 0.21 for time until death on the logarithmic-time scale. We were, however, unable to support our second premise as we found that resistance to each of the diseases tended to be weakly correlated genetically. The genetic correlations between the resistances ranged between -0.11 and 0.15 when resistance was assessed as a binary trait, and between -0.23 and 0.16 when resistance was assessed as a longitudinal trait. These findings are encouraging for commercial trout production. The additive genetic variation detected for resistance demonstrates that selectively breeding trout for resistance to ERM, RTFS, and VHS will be successful, providing a complementary approach to control these diseases. The weak genetic correlations suggest that
it should be relatively easy to improve resistance to each of the diseases simultaneously.

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Section for Aquaculture, National Institute of Aquatic Resources
Pages: 621-636
Publication date: 2005
Main Research Area: Technical/natural sciences

Publication information
Journal: Aquaculture
Volume: 250
Issue number: 3-4
ISSN (Print): 0044-8486
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.75 SJR 1.101 SNIP 1.524
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.103 SNIP 1.254 CiteScore 2.12
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.002 SNIP 1.34 CiteScore 2.16
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.136 SNIP 1.3 CiteScore 2.18
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.212 SNIP 1.487 CiteScore 2.32
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.294 SNIP 1.542 CiteScore 2.39
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.151 SNIP 1.394
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.941 SNIP 1.263
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 0.909 SNIP 1.173
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.019 SNIP 1.318
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.008 SNIP 1.689
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.915 SNIP 1.236
Significance of Mobile Genetic Elements for Microbial Community Adaptation to Pollutant Stress

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Sørensen, S. J. (Ekstern), de Lipthay, J. R. (Ekstern), Øregaard, G. (Ekstern), Kroer, N. (Ekstern), Rasmussen, L. D. (Intern)
Publication date: 2005
Event: Poster session presented at DOE-NABIR PI workshop, Warrenton, VA, United States.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 242408
Publication: Research - peer-review › Poster – Annual report year: 2005

Smittarisiko ved separering 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
Main Research Area: Technical/natural sciences

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 titel: Infection risk in relation to manure separation
Source: orbit
Source-ID: 241862
Spatial and temporal patterns of pig herds diagnosed with Postweaning Multisystemic Wasting Syndrome (PMWS) during the first two years of its occurrence in Denmark

The clinical syndrome Postweaning Multisystemic Wasting Syndrome (PMWS) in pigs has emerged globally during the last decade. In October 2001, the first pig herd diagnosed with PMWS was reported in Denmark, and since then the number of herds diagnosed with PMWS has increased markedly. The etiology of PMWS is not well understood, but increased knowledge of the causal factors is prerequisite for applying preventive interventions. In this study we described the temporal (time of diagnosis), spatial (location of herds) and spatio-temporal pattern of Danish pig herds diagnosed with PMWS during the first two years after the first herd was diagnosed, and we tested for spatial and spatio-temporal clustering using scan statistics. The study population consisted of pig herds that during the study period (October 2001 - September 2003) performed diagnostic submissions to the two major veterinary diagnostic laboratories in Denmark (6724 herds). Of these, 277 herds were diagnosed with PMWS. Two statistically significant spatial clusters of herds diagnosed with PMWS were identified. These clusters included 11% and 8% of the study herds, respectively. Within these two clusters the relative risk for a herd to be diagnosed with PMWS was twice as high as expected. One statistically significant spatio-temporal cluster was identified between February and May 2002. We discuss different hypotheses that could explain why pig herds diagnosed with PMWS were clustered both spatially and spatio-temporally, and conclude that the results support the hypothesis that PMWS is caused by introduction of a new, unidentified, pathogen into the Danish pig production. (c) 2005 Elsevier B.V. All rights reserved.
Time course study of in situ expression of antigens following DNA-vaccination against VHS in rainbow trout (Oncorhynchus mykiss Walbaum) fry

The present study was performed as a time course study of fish vaccinated with 20 μg plasmid DNA vaccine encoding either the VHSV G-protein or the VHSV N-protein. Samples of the injection site were collected sequentially over a 7-week period. The study revealed an intense positive staining by immunohistochemistry for the viral G-protein mainly in the membrane of intact myocytes, most prominent by days 10-27, and with concomitant infiltration of inflammatory cells by days 13-38 that subsequently lead to a marked reduction in the number of myocytes expressing the G-protein. By immunofluorescence, infiltrating cells positive for MHC II, IgM, and C3 were demonstrated. By contrast, in fish vaccinated with the VHSV-N construct, fewer, diffusely positive myocytes were found, most prominent by days 13-38, these having a positive reaction for the N-protein mainly in the cytoplasm and variably in the membrane. N-protein positive myocytes did not attract infiltrating cells to the same degree. Positive reaction for the N-protein almost ceased by day 48 post-vaccination.

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Lorenzen, E. (Intern), Lorenzen, N. (Intern), Einer-Jensen, K. (Intern), Brudeseth, B. (Ekstern), Evensen, O. (Ekstern)
Pages: 27-41
Publication date: 2005
Main Research Area: Technical/natural sciences
Uniform extraction of RNA and DNA for quantitative multiplex PCR detection of classical and African swine fevers in blood or meat juice

General information
State: Published
Organisations: Sektion for Eksotiske Virusyngdomme, Division of Virology, National Veterinary Institute
Authors: Uttenthal, Å. (Intern), Jensen, T. (Ekstern), Rasmussen, T. B. (Intern)
Number of pages: 50
Publication date: 2005

Host publication information
Title of host publication: Proceedings of the 6th ESVV Pestivirus Symposium
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 242301
Publication: Research › Article in proceedings – Annual report year: 2005

Viral haemorrhagic septicaemia virus in marine fish and its implications for fish farming - a review
Viral haemorrhagic septicaemia virus (VHSV) has, in recent decades, been isolated from an increasing number of free-living marine fish species. So far, it has been isolated from at least 48 fish species from the northern hemisphere, including North America, Asia and Europe, and fifteen different species including herring, sprat, cod, Norway pout and flatfish from northern European waters. The high number of VHSV isolations from the Baltic Sea, Kattegat, Skagerrak, the North Sea and waters around Scotland indicate that the virus is endemic in these waters. The VHSV isolates originating from wild marine fish show no to low pathogenicity to rainbow trout and Atlantic salmon, although several are pathogenic for turbot. Marine VHSV isolates are so far serologically indistinguishable from freshwater isolates. Genotyping based on VHSV G- and N-genes reveals four groups indicating the geographical origin of the isolates, with one group representing traditional European freshwater isolates and isolates of north European marine origin, a second group of marine isolates from the Baltic Sea, a third group of isolates from the North Sea, and a group representing North American isolates. Examples of possible transfer of virus from free-living marine fish to farmed fish are discussed, as are measures to prevent introduction of VHSV from the marine environment to aquaculture.

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Skall, H. F. (Intern), Olesen, N. J. (Intern), Mellergaard, S. (Intern)
Pages: 509-529
Publication date: 2005
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Fish Diseases
Volume: 28
Issue number: 9
ISSN (Print): 0140-7775
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.12
Web of Science (2016): Indexed yes
Virulence, immunogenicity and vaccine properties of a novel chimeric pestivirus

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Rasmussen, T. B. (Intern), Uttenthal, Å. (Intern), Nielsen, J. (Intern), Beer, M. (Ekstern), Depner, K. (Ekstern), Reimann, I. (Ekstern)
Number of pages: 85
Publication date: 2005

Host publication information
Title of host publication: Proceedings of the ESVV Pestivirus Symposium
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 240963
Publication: Research › Article in proceedings – Annual report year: 2005
Wildrisk: Classical swine fever and wild boar in Denmark: A risk analysis

General information
State: Published
Organisations: National Veterinary Institute, Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, Sektion for Eksotiske Virussygdomme, Division of Virology, Danish Bacon and Meat Council, National Environmental Research Institute, Centre for Environmental Research Leipzig-Halle, Danish Institute for Food and Veterinary Research, Danish Veterinary and Food Administration
Authors: Alban, L. (Ekstern), andersen, M. M. (Ekstern), Asferg, T. (Ekstern), Boklund, A. (Intern), Fernandez, N. (Ekstern), Goldbach, S. (Ekstern), Greiner, M. (Ekstern), Hejgaard, A. (Ekstern), Kramer-Schadt, S. (Ekstern), Stockmarr, A. (Intern), Thulke, H. H. (Ekstern), Utenthal, Å. (Intern), Ydesen, B. (Ekstern)
Number of pages: 118
Publication date: 2005

Publication information
Publisher: Danish Institute for Food and Veterinary Research
ISBN (Print): 87-91-58701-8
Original language: English
Main Research Area: Technical/natural sciences
Risk analysis, virus, wildrisk, wild boar
Electronic versions:
WILDRISK_2005.pdf
Links:
Source: orbit
Source-ID: 240540
Publication: Research › Report – Annual report year: 2005

Work package 1 report: Hazard identification for vertical transfer of fish disease agents

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Bovo, G. (Ekstern), Hæstein, T. (Ekstern), Hill, B. (Ekstern), LaPatra, S. (Ekstern), Michel, C. (Ekstern), Olesen, N. J. (Intern), Shchelkunov, I. (Ekstern), Storset, A. (Ekstern), Wolffrom, T. (Ekstern), Midtlyng, P. J. (Ekstern)
Number of pages: 35
Publication date: 2005

Publication information
Place of publication: Oslo, Norway
Publisher: VESO
ISBN (Print): 82-91-74334-7
Original language: English
Series: VESO
Number: VESO-1601
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 241531
Publication: Research › Report – Annual report year: 2005

Work package 3 report: Pathogen survival outside the host, and susceptibility to disinfection

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Bovo, G. (Ekstern), Hill, B. (Ekstern), Husby, A. (Ekstern), Hæstein, T. (Ekstern), Michel, C. (Ekstern), Olesen, N. J. (Intern), Storset, A. (Ekstern), Midtlyng, P. J. (Ekstern)
Number of pages: 41
Publication date: 2005

Publication information
Place of publication: Oslo, Norway
Work package 4 report: Broodfish testing for viral infections

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Olesen, N. J. (Intern), Bovo, G. (Ekstern), Dannevig, B. (Ekstern), Hill, B. (Ekstern), Håstein, T. (Ekstern), Munro, E. (Ekstern), Midtlyng, P. J. (Ekstern)
Number of pages: 20
Publication date: 2005

Antibodies to EBLV-1 in a domestic cat in Denmark

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Tjørnehøj, K. (Intern), Ronsholt, L. (Ekstern), Fooks, A. (Ekstern)
Pages: 571-572
Publication date: 2004
Main Research Area: Technical/natural sciences

Publication information
Journal: Veterinary Record
Volume: 155
Issue number: 18
ISSN (Print): 0042-4900
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.442 SNIP 0.692 CiteScore 0.3
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.509 SNIP 0.794 CiteScore 0.39
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.469 SNIP 0.839 CiteScore 0.41
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
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
Authors: Hjulsager, C. K. (Intern), Jørgensen, P. H. (Intern), Larsen, L. E. (Intern), Storgaard, T. (Ekstern), Bøtner, A. (Intern)
Publication date: 2004
Event: Poster session presented at International qPCR Symposium & Application Workshop, Freising-Weihenstephan, Germany
Main Research Area: Technical/natural sciences
Source: orbit
Behandling med serum i PMWS besætninger

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, Division of Microbiology and Risk Assessment, National Food Institute
Authors: Hassing, A. (Ekstern), Bækbo, P. (Ekstern), Bøtner, A. (Intern), Jorsal, S. E. L. (Intern), Wachmann, H. (Ekstern) , Vigre, H. (Intern)
Publication date: 2004
Main Research Area: Technical/natural sciences

Publication information
Journal: DVHS efterårsmøde
Original language: Danish
Source: orbit
Source-ID: 242211
Publication: Research › Conference abstract in journal – Annual report year: 2004

Behandling med serum i PMWS besætninger

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, Division of Microbiology and Risk Assessment, National Food Institute
Authors: Hassing, A. (Ekstern), Bækbo, P. (Ekstern), Bøtner, A. (Intern), Jorsal, S. E. L. (Intern), Wachmann, H. (Ekstern) , Vigre, H. (Intern)
Pages: 675
Publication date: 2004
Main Research Area: Technical/natural sciences

Publication information
Journal: LU meddelelse
Original language: Danish
Source: orbit
Source-ID: 242210
Publication: Research › Journal article – 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
Authors: Larsen, L. E. (Intern), Pedersen, R. E. (Ekstern), Lauridsen, B. H. (Ekstern), Steffensen, M. A. (Intern), Trinderup, M. (Ekstern), Jensen, A. M. (Ekstern)
Publication date: 2004
Main Research Area: Technical/natural sciences

Publication information
Journal: Dansk Veterinaridsskrift
ISSN (Print): 1600-2032
Ratings:
BFI (2008): BFI-level 1
Web of Science (2004): Indexed yes
Original language: Danish
Source: orbit
Source-ID: 242181
Publication: 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 (n = 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
Authors: Hägglund, S. (Ekstern), Hu, K. (Ekstern), Larsen, L. E. (Intern), Hakhverdyan, M. (Ekstern), Valarcher, J. (Ekstern), Taylor, G. (Ekstern), Morein, B. (Ekstern), Belák, S. (Ekstern), Alenius, S. (Ekstern)
Pages: 646-655
Publication date: 2004
Main Research Area: Technical/natural sciences

Publication information
Journal: Vaccine
Volume: 23
Issue number: 5
ISSN (Print): 0264-410X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.33 SJR 1.956 SNIP 1.155
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.068 SNIP 1.259 CiteScore 3.45
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.05 SNIP 1.231 CiteScore 3.57
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.73 SNIP 1.126 CiteScore 3.43
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.634 SNIP 1.159 CiteScore 3.56
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.74 SNIP 1.274 CiteScore 3.86
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.636 SNIP 1.207
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.428 SNIP 1.21
Web of Science (2009): Indexed yes
Cellular immune responses in the lungs of pigs infected in utero with PRRSV: An immunohistochemical study

The cellular response in the lungs of pigs transplacentally infected with porcine reproductive and respiratory syndrome virus (PRRSV) was examined by immunohistochemistry. Double staining for the T-cell marker antigen CD3 and PRRSV demonstrated that the appearance and distribution of T-cells homing to the lungs of infected pigs correlated well with the presence and location of virus-infected cells. Single stainings showed that cells positive for the CD2 and CD8 antigen were almost as numerous in pneumonic lesions as CD3 positive cells whereas cells expressing the CD4 antigen were rare. The morphology and the distribution pattern of the CD2 and CD8 positive cells were similar to that of the CD3 positive cells suggesting coexpression of all three antigens within the majority of the recruited T-lymphocytes. The presence of cells consistent with the phenotype of cytotoxic T-lymphocytes (CTL) close to virus infected macrophages strongly indicate an important role of CTLs in the PRRSV-specific pulmonary immune response.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Tingstedt, J. E. (Ekstern), Nielsen, J. (Intern)
Pages: 558-564
Publication date: 2004
Main Research Area: Technical/natural sciences

Publication information
Journal: Viral Immunology
Volume: 17
Issue number: 4
ISSN (Print): 0882-8245
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.686 SNIP 0.392 CiteScore 1.26
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.75 SNIP 0.55 CiteScore 1.34
Characterisation of a new type O lineage of FMDV from Uganda with atypical clinical manifestations in domestic cattle

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Veterinary Institute, Sektion for Eksotiske Virusssygdomme, Division of Virology
Authors: Christensen, L. S. (Intern), Okorut, R. (Ekstern), Tjørnehøj, K. (Intern), Normann, P. (Intern), Sørensen, K. J. (Ekstern), Esau, M. (Ekstern)
Pages: 159-162
Publication date: 2004

Host publication information
Title of host publication: Report of the Open Session of the Research Group of the Standing Technical Committee of the European Commission for the control of Foot-and-Mouth disease
Place of publication: Crete, Greece
Main Research Area: Technical/natural sciences
Electronic versions:
Johan.pdf
Source: orbit
Source-ID: 229499
Publication: Research › Journal article – Annual report year: 2004
Composting rapidly degrades DNA from genetically modified plants

**General information**
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Rasmussen, L. D. (Intern), Møller, J. (Ekstern), Magid, J. (Ekstern)
Publication date: 2004
Main Research Area: Technical/natural sciences

**Publication information**
Journal: Dacofa enews Newsletter
Volume: 2
Original language: English
Source: orbit
Source-ID: 242385
Publication: Research › Journal article – Annual report year: 2004

Development of a European resource on the origins of pathogens of aquaculture: The Europa Project
This workshop described the EUROPA project, an EU-funded program aimed at creating a web-based database of molecular sequence data-sets related to significant pathogens of aquaculture. The project aims to focus the efforts of fish health researchers into generating large, evolving and readily available data-sets suited to the purpose of molecular epidemiology. This workshop reviewed the progress of this project, demonstrated the scope of the database developed to date, and sought input regarding the future development of this resource.

**General information**
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Number of pages: 84
Pages: 54-57
Publication date: 2004

**Host publication information**
Title of host publication: European Association of Fish Pathologists. Bulletin
Volume: 24/1
Place of publication: Scotland
Publisher: European Association of Fish Pathologists
Edition: 1
Main Research Area: Technical/natural sciences
Conference: European Association of Fish Pathologists, Copenhagen, 01/01/2005
Source: orbit
Source-ID: 233066
Publication: Research › Article in proceedings – Annual report year: 2004

DFVF indfører en ny serologiske metode til undersøgelse for antistoffer mod PCV2 fra 1.12.04

**General information**
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Klausen, J. (Ekstern), Nielsen, J. (Ekstern), Bøtner, A. (Intern)
Publication date: 2004
Main Research Area: Technical/natural sciences

**Publication information**
Journal: DFVF-nyt
Original language: English
Source: orbit
Source-ID: 241774
Publication: Research › Journal article – Annual report year: 2004

DNA vaccination of pigs with open reading frame 1-7 of PRRS virus
We cloned all open reading frames of a Danish isolate of porcine reproductive and respiratory syndrome (PRRS) virus in DNA vaccination vectors. Pigs were vaccinated using a gene gun with each single construct (ORF1, ORF2, ORF3, ORF4,
ORF5, ORF6, or ORF7) or combinations thereof. Vaccination with ORF7 consistently induced antibodies after three vaccinations, while antibodies were only sporadically detected in the remaining groups. After six vaccinations, all pigs were inoculated with PRRS virus and the post-inoculation antibody response was studied. Pigs vaccinated with ORF1 or ORF4 were primed for antibody response against NSP2 or GP4, respectively. Neutralising antibodies were detected in all pigs, with ORF5 vaccinated pigs showing the highest titres.

**General information**
State: Published
Organisations: National Veterinary Institute, Sektion for Ekotiske Virussygdomme, Division of Virology
Authors: Barfoed, A. M. (Intern), Blixenkrone-Møller, M. (Ekstern), Jensen, M. H. (Ekstern), Bøtner, A. (Intern), Kamstrup, S. (Intern)
Pages: 3628-3641
Publication date: 2004
Main Research Area: Technical/natural sciences

**Publication information**
Journal: Vaccine
Volume: 22
Issue number: 27-28
ISSN (Print): 0264-410X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.33 SJR 1.956 SNIP 1.155
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.068 SNIP 1.259 CiteScore 3.45
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.05 SNIP 1.231 CiteScore 3.57
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.73 SNIP 1.126 CiteScore 3.43
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.634 SNIP 1.159 CiteScore 3.56
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.74 SNIP 1.274 CiteScore 3.86
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.636 SNIP 1.207
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.428 SNIP 1.21
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.327 SNIP 1.025
Scopus rating (2007): SJR 1.286 SNIP 1.112
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.305 SNIP 1.154
Evolution of the fish rhabdovirus viral haemorrhagic septicaemia virus

Viral haemorrhagic septicaemia (VHS) caused by the rhabdovirus VHSV is economically the most important viral disease in European rainbow trout farming. Until 1989, this virus was mainly isolated from freshwater salmonids but in the last decade, it has also been isolated from an increasing number of free-living marine fish species. To study the genetic evolution of VHSV, the entire G gene from 74 isolates was analysed. VHSV from wild marine species caught in the Baltic Sea, Skagerrak, Kattegat, North Sea, and English Channel and European freshwater isolates, appeared to share a recent common ancestor. Based on the estimated nucleotide substitution rate, the ancestor of the European fresh water isolates was dated some 50 years ago. This finding fits with the initial reports in the 1950s on clinical observations of VHS in Danish freshwater rainbow trout farms. The study also indicates that European marine VHSV and the North American marine line separated approx. 500 years ago. The codon substitution rate among the freshwater VHSV isolates was found to be 2-5 times faster than among marine isolates. The data support the hypothesis of the marine environment being the original reservoir of VHSV and that the change in host range (to include rainbow trout) may have occurred several times. Virus from the marine environment will therefore continue to represent a threat to the trout aquaculture industry.

General information

State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Einer-Jensen, K. (Intern), Ahrens, P. (Intern), Forsberg, R. (Ekstern), Lorenzen, N. (Intern)
Pages: 1167-1179
Publication date: 2004
Main Research Area: Technical/natural sciences

Publication information

Journal: Journal of General Virology
Volume: 85
Issue number: 5
ISSN (Print): 0022-1317
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.93 SJR 1.499 SNIP 0.886
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.729 SNIP 1.007 CiteScore 3.26
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.683 SNIP 1.059 CiteScore 3.25
Web of Science (2014): Indexed yes
**Experimental airborne transmission of PRRS virus**

A series of three experiments, differing primarily in airflow volume, were performed to evaluate the likelihood of airborne transmission of Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) from infected to non-infected pigs. Pigs were housed in two units (unit A and unit B) located 1 m apart and connected by pipes. The air pressure and diameter of the pipes, depending on experiments, were strictly controlled to allow desired airflow volumes from unit A to unit B. Either 25 (experiment 1 and experiment 3) or 26 (experiment 2) pigs infected recently with PRRSV, and either 25 (experiment 1 and experiment 3) or 17 (experiment 2) pigs from a PRRSV-free herd, were housed in unit A. Either 50 pigs (experiment 1 and experiment 3) or 43 pigs (experiment 2) from a PRRSV-free herd were housed in unit B. The amount of air transmitted from unit A to unit B, expressed as a percentage of ventilation intake, was approximately 70, 10, and 1% for experiment 1, experiment 2 and experiment 3, respectively. Blood samples were collected from all pigs once per week and analyzed for antibodies against PRRSV. Based on these methods, airborne transmission of PRRSV from infected to non-infected pigs was confirmed in each of the three experiments.
Experimental infection of rainbow trout Oncorhynchus mykiss with viral haemorrhagic septicaemia virus isolates from European marine and farmed fishes

The susceptibility of rainbow trout Oncorhynchus mykiss to infection with various isolates of viral haemorrhagic septicaemia virus (VHSV) was examined. A total of 8 experiments with rainbow trout ranging from 0.6 to 6.2 g was conducted for 139 isolates originating from wild marine fishes in European waters (115 isolates), farmed turbot from Scotland and Ireland (2 isolates), and farmed rainbow trout (22 isolates). The isolates were tested by immersion and/or intraperitoneal injection either as pooled or single isolates. The isolates from wild marine fishes did not cause mortality by immersion while some of the isolates caused mortality when injected. All VHSV isolates from farmed rainbow trout caused significant mortality by immersion. Currently, pathogenicity trials are the only way to differentiate VHSV isolates from wild marine fishes and farmed rainbow trout. The 2 farmed turbot isolates did not cause mortality by immersion, supporting the view that they originated from the marine environment.

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Skall, H. F. (Intern), Slierendrecht, W. (Ekstern), King, J. (Ekstern), Olesen, N. J. (Intern)
Pages: 99-110
Publication date: 2004
Main Research Area: Technical/natural sciences

Publication information
Journal: Diseases of Aquatic Organisms
Volume: 58
Issue number: 2-3
ISSN (Print): 0177-5103
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.95 SJR 0.858 SNIP 0.929
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.949 SNIP 0.935 CiteScore 1.96
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.889 SNIP 0.881 CiteScore 1.86
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.812 SNIP 0.918 CiteScore 1.77
Første fund af infektion med Lactococcus garvieae i et dansk dambrug

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Olesen, N. J. (Intern)
Publication date: 2004
Main Research Area: Technical/natural sciences

Publication information
Journal: Ferskvandsfiskeribladet
ISSN (Print): 0015-0223
Ratings:
ISI indexed (2013): ISI indexed no
Genetic population structure of marine viral haemorrhagic septicaemia virus (VHSV)

The nucleotide sequences of a specific region of the nucleoprotein gene were compared in order to investigate the genetic population structure of marine viral haemorrhagic septicaemia virus (VHSV). Analysis of the sequence from 128 isolates of diverse geographic and host origin renders this the most comprehensive molecular epidemiological study of marine VHSV conducted to date. Phylogenetic analysis of nucleoprotein gene sequences confirmed the existence of the 4 major genotypes previously identified based on N- and subsequent G-gene based analyses. The range of Genotype I included subgroups of isolates associated with rainbow trout aquaculture (Genotype la) and those from the Baltic marine environment (Genotype lb) to emphasise the relatively close genetic relationship between these isolates. The existence of an additional genotype circulating within the Baltic Sea (Genotype II) was also confirmed. Genotype III included marine isolates from around the British Isles in addition to those associated with turbot mariculture, highlighting a continued risk to the development of this industry. Genotype IV consisted of isolates from the marine environment in North America. Taken together, these findings suggest a marine origin of VHSV in rainbow trout aquaculture. The implications of these findings with respect to the future control of VHSV are discussed. The capacity for molecular phylogenetic analysis to resolve complex epidemiological problems is also demonstrated and its likely future importance to disease management issues highlighted.

General information

State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Snow, M. (Ekstern), Bain, N. (Ekstern), Black, J. (Ekstern), Taupin, V. (Ekstern), Cunningham, C. (Ekstern), King, J. (Ekstern), Skall, H. F. (Intern), Raynard, R. (Ekstern)
Pages: 11-21
Publication date: 2004
Main Research Area: Technical/natural sciences

Publication information

Journal: Diseases of Aquatic Organisms
Volume: 61
Issue number: 1-2
ISSN (Print): 0177-5103
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.95 SJR 0.856 SNIP 0.929
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.949 SNIP 0.935 CiteScore 1.96
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.889 SNIP 0.881 CiteScore 1.86
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.812 SNIP 0.918 CiteScore 1.77
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.912 SNIP 1.092 CiteScore 2.04
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
Genotyping of viral haemorrhagic septicaemia virus from worldwide using the non-virion gene

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Johansson, T. (Ekstern), Einer-Jensen, K. (Intern), Ahrens, P. (Intern), Lorenzen, N. (Intern), Olesen, N. J. (Intern)
Publication date: 2004
Event: Abstract from Symposium on Viruses of Lower Vertebrates, Hakodate, Hokkaido, Japan
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 229502
Publication: Research › Journal article – Annual report year: 2004

High-resolution molecular analysis of the 1982-3 FMD epidemic in Denmark

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Veterinary Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, Technical University of Denmark
Authors: Christensen, L. S. (Intern), Normann, P. (Intern), de Stricker, K. (Ekstern), Rosenorn, S. (Ekstern)
Pages: 173-178
Publication date: 2004
Immunisation against PCV2 structural protein by DNA vaccination of mice

Porcine circovirus type 2 (PCV2) is the causative agent of an emerging swine disease, postweaning multisystemic wasting syndrome (PMWS). The disease affects primarily 5-12-weeks-old pigs which might suggest that infection with PCV2 occurs when the level of maternal antibodies have declined to sub-protective levels around weaning at 3-5-weeks of age. If immunoprophylaxis is to be effective, an immunisation method capable of breaking through maternal immunity must be employed. In this study, we have developed and investigated the potential of a DNA vaccination approach to be one such method. The gene encoding the capsid protein of PCV2 was cloned in a DNA vaccination plasmid and expression of capsid protein was demonstrated in vitro. Mice were gene gun vaccinated three times and all mice responded serologically by raising antibodies against PCV2. The results suggest, that DNA based vaccination might offer opportunities for vaccination of piglets against PCV2.
Influence of routes and administration parameters on antibody response of pigs following DNA vaccination

Using the nucleoprotein of porcine reproductive and respiratory syndrome virus as model antigen, we optimised parameters for gene gun vaccination of pigs, including firing pressure and vaccination site. As criteria for optimisation, we characterised particle penetration and local tissue damage by histology. For selected combinations, vaccination efficiency in terms of antibody response was studied. Gene gun vaccination on ear alone was as efficient as a multi-site (ear, thorax, inguinal area, tongue mucosa) gene gun approach, and more efficient than combined intramuscular (i.m.)/intradermal (i.d.) injection of plasmid DNA. This indicates, that the ear is an attractive site for gene gun vaccination of pigs.

General information
State: Published
Organisations: National Veterinary Institute, Sektion for Ekotiske Virussygdomme, Division of Virology
Authors: Barfoed, A. M. (Intern), Kirstensen, B. (Ekstern), Dannemann-Jensen, T. (Ekstern), Viuff, B. (Ekstern), Bøtner, A. (Intern), Kamstrup, S. (Intern), Møller, M. B. (Ekstern)
Pages: 1395-1405
Publication date: 2004
Main Research Area: Technical/natural sciences

Publication information
Journal: Vaccine
Volume: 22
Issue number: 11-12
ISSN (Print): 0264-410X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.33 SJR 1.956 SNIP 1.155
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.068 SNIP 1.259 CiteScore 3.45
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.05 SNIP 1.231 CiteScore 3.57
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.73 SNIP 1.126 CiteScore 3.43
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.634 SNIP 1.159 CiteScore 3.56
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.74 SNIP 1.274 CiteScore 3.86
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.636 SNIP 1.207
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.428 SNIP 1.21
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.327 SNIP 1.025
Scopus rating (2007): SJR 1.286 SNIP 1.112
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.305 SNIP 1.154
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.194 SNIP 1.065
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 1.142 SNIP 1.128
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 1.142 SNIP 1.129
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 1.118 SNIP 0.996
Scopus rating (2001): SJR 1.018 SNIP 1.043
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.027 SNIP 1.009
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 0.982 SNIP 1.252
Original language: English
gene gun, DNA vaccination, CpG
DOIs:
10.1016/j.vaccine.2003.10.032
Interlaboratory testing of porcine sera for antibodies to porcine circovirus type 2

A panel of 20 porcine sera was distributed to 5 laboratories across Europe and Canada. Each center was requested to test the sera for the presence of porcine circovirus type 2 antibodies using the routine assays, indirect immunofluorescence assay (IFA) and indirect immunoperoxidase monolayer assay (IPMA), and to determine the titer of each serum. Results from all centers were then compiled and correlated. They demonstrate a wide variation in the titers obtained between laboratories. These differences were dependent on the assay used and the choice of fixative. In general, IPMA gave higher titers than did IFA, and paraformaldehyde gave higher titers than did acetone or ethyl alcohol. This report highlights the need for standardized procedures and biologicals for this virus.
Introduction of mercury resistant bacterial strains to Hg(II) amended soil microcosms increases the resilience of the natural microbial community to mercury stress

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: de Lipthay, J. R. (Ekstern), Rasmussen, L. D. (Intern), Sørensen, S. J. (Ekstern)
Publication date: 2004
Event: Poster session presented at DOE-NABIR PI workshop, Warrenton, VA, United States.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 229522
Publication: Research - peer-review › Journal article – Annual report year: 2004

In utero infection with PRRS virus modulates cellular functions of blood monocytes and alveolar lung macrophages in piglets

The putative immunosuppressive effect of PRRS virus (PRRSV) on innate immune responses was studied in piglets infected in utero with PRRSV. Phagocytosis and oxidative burst capacities in 2-, 4- and 6-week-old in utero infected piglets were investigated and compared with age-matched control piglets. Phagocytic capacity of blood monocytes against Salmonella bacteria was investigated by flow cytometry. Oxidative burst in blood monocytes and in alveolar lung macrophages was investigated by luminol- and lucigenin-enhanced chemiluminescence, respectively. Decreased phagocytosis against Salmonella was found in blood monocytes from 4- and 6-week-old infected piglets compared to controls. In contrast, 2-week-old infected piglets showed phagocytic responses comparable to age matched control piglets. While oxidative burst capacity was increased in blood (PBMC) from in utero PRRSV infected piglets, the oxidative burst capacity of alveolar macrophages was decreased, especially in 2- and 4-week-old piglets, compared to age-matched control piglets. The present results indicate that in utero infection with PRRSV inhibits phagocytosis against Salmonella in blood monocytes as well as the oxidative burst capacity of alveolar macrophages. These observations indicate that PRRSV in utero infection induces a state of immunosuppression in piglets paving the way for enhanced secondary infections.

General information
State: Published
Organisations: Adaptive Immunology & Parasitology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, Section for Veterinary Epidemiology and public sector consultancy
Investigation of wild caught whitefish, Coregonus lavaretus (L.), for infection with viral haemorrhagic septicaemia virus (VHSV) and experimental challenge of whitefish with VHSV

One hundred and forty-eight wild whitefish, Coregonus lavaretus (L.), were caught by electrofishing and sampled for virological examination in December 1999 and 2000, during migration from the brackish water feeding grounds to the freshwater spawning grounds, where the whitefish may come into contact with farmed rainbow trout. All samples were examined on cell cultures. No viruses were isolated. Three viral haemorrhagic septicaemia virus (VHSV) isolates of different origin were tested in infection trials by immersion and intraperitoneal (IP) injection, using 1.5 g farmed whitefish: an isolate from wild caught marine fish, a farmed rainbow trout isolate with a suspected marine origin and a classical freshwater isolate. The isolates were highly pathogenic by IP injection where 99-100% of the whitefish died. Using an immersion challenge the rainbow trout isolates were moderately pathogenic with approximately 20% mortality, whereas the marine isolate was virtually non-pathogenic. At the end of the experiment it was possible to isolate VHSV from survivors infected with the marine and suspected marine isolates. Because of the low infection rate in wild whitefish in Denmark, the role of whitefish in the spread of VHSV in Denmark is probably not significant. The experimental studies, however, showed that whitefish are potential carriers of VHSV as they suffer only low mortality after infection but continue to carry virus.

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Skall, H. F. (Intern), Kjær, T. E. (Intern), Olesen, N. J. (Intern)
Pages: 401-408
Publication date: 2004
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Fish Diseases
Volume: 27
Issue number: 7
ISSN (Print): 0140-7775
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.12
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 1.71
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 1.99
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 1.74
ISI indexed (2013): ISI indexed yes
ITIH4 (inter-alpha-trypsin inhibitor heavy chain 4) is a new acute-phase protein isolated from cattle during experimental infection

We have isolated from calf serum a protein with an apparent M, of 120,000. The protein was detected by using antibodies against major acute-phase protein in pigs with acute inflammation. The amino acid sequence of an internal fragment revealed that this protein is the bovine counterpart of ITIH4, the heavy chain 4 of the inter-alpha-trypsin inhibitor family. The response of this protein in the sera was determined for animals during experimental bacterial and viral infections. In the bacterial model, animals were inoculated with a mixture of Actinomyces pyogenes, Fusobacterium necrophorum, and Peptostreptococcus indolicus to induce an acute-phase reaction. All animals developed moderate to severe clinical mastitis and exhibited remarkable increases in ITIH4 concentration in serum (from 3 to 12 times the initial values, peaking at 48 to 72 h after infection) that correlated with the severity of the disease. Animals with experimental infections with bovine respiratory syncytial virus (BRSV) also showed increases in ITIH4 concentration (from two- to fivefold), which peaked at around 7 to 8 days after inoculation. Generally, no response was seen after a second infection of the same animals with the virus. Because of the significant induction of the protein in the animals in the mastitis and BRSV infection models, we can conclude that ITIH4 is a new positive acute-phase protein in cattle.

General information
State: Published
Organisations: Innate Immunology, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Sektion for Eksotiske Virussygdomme, Division of Virology
Authors: Pineiro, M. (Ekstern), Andres, M. (Ekstern), Iturralde, M. (Ekstern), Carmona, S. (Ekstern), Hirvonen, J. (Ekstern), Pyorala, S. (Ekstern), Heegaard, P. M. H. (Intern), Tjørnehøj, K. (Intern), Lampreave, F. (Ekstern), Pineiro, A. (Ekstern), Alava, M. (Ekstern)
Pages: 3777-3782
Publication date: 2004
Main Research Area: Technical/natural sciences

Publication information
Journal: Infection and Immunity
Volume: 72
Issue number: 7
Measuring degradation of transgenic DNA and screening for horizontal gene transfer from GMO-plant material during composting

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Magid, J. (Ekstern), Rasmussen, L. D. (Intern), Møller, J. (Ekstern)
Publication date: 2004
Event: Poster session presented at International Conference on Soil and Compost Eco-biology, León, Spain.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 242407
Publication: Research - peer-review › Journal article – Annual report year: 2004

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
Authors: Angen, Ø. (Intern), Enemark, J. M. (Ekstern), Larsen, L. E. (Intern), Thomsen, J. (Ekstern)
Publication date: 2004
Event: Abstract from ASM General Meeting.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 242084
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2004

Monoclonal antibody induced T-cell depletion in pigs

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Lohse, L. (Intern)
Publication date: 2004

Publication information
Place of publication: Kgs. Lyngby, Denmark
Original language: English
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 241258
Publication: Research › Ph.D. thesis – Annual report year: 2004

PCV2-associated disease following intrauterine infection

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
Authors: Nielsen, J. (Ekstern), Ladekjær Hansen, A. S. (Ekstern), Bille-Hansen, V. (Intern), Lohse, L. (Intern)
Publication date: 2004
Event: Abstract from 18th International Pig Veterinary Society Congress, Hamburg, Germany.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 241263
Publication: Research › Conference abstract for conference – Annual report year: 2004
Phage display of the Equine arteritis virus nsp1 ZF domain and examination of its metal interactions

A putative zinc finger (ZF) domain in the Equine arteritis virus (EAV) nsp 1 protein was described recently to be required for viral transcription. The nsp 1 ZF (50 aa) was expressed on the surface of M13KE gIII phage, fused to the N terminus of the phage pIII protein. To evaluate the functionality of the ZF domain, a binding assay was developed, based on the use of immobilized Ni2+ ions (Ni-NTA). Phages displaying ZF bound significantly better to Ni-NTA than did phages displaying negative-control peptides, which also contained metal-coordinating residues. Also, binding of ZF-displaying phages could be inhibited by an anti-nsp 1 serum, or by mutation of residues predicted to be important for zinc coordination. Finally, binding was abolished by low concentrations (0.1%) Tween 20, and rescued by including Zn2+, Ni2+ or Cu2+, but not Mg2+, in the binding buffer, suggesting that formation of secondary structure was involved in binding of the ZF to Ni-NTA. These findings provide the first experimental evidence that the putative nsp 1 ZF domain can coordinate divalent metal ions, and that this property is associated with the secondary structure of the domain. The Ni-NTA binding assay developed in the present study may have general applications in the study of other ZF domains.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Technical University of Denmark
Authors: Oleksiewicz, M. B. (Ekstern), Snijder, E. (Ekstern), Normann, P. (Intern)
Pages: 159-169
Publication date: 2004
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Virological Methods
Volume: 119
Issue number: 2
ISSN (Print): 0166-0934
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.87 SNIP 0.736 CiteScore 1.78
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.868 SNIP 0.799 CiteScore 1.68
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.893 SNIP 0.952 CiteScore 1.87
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.861 SNIP 0.91 CiteScore 1.99
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.869 SNIP 0.935 CiteScore 2.08
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.907 SNIP 0.994 CiteScore 2.23
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.892 SNIP 0.998
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.964 SNIP 1.061
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Porcine circovirus type 2 (PCV2) is now recognised as the causal agent of porcine multisystemic wasting syndrome (PMWS), an economically important wasting disease of young pigs [J. Vet. Diagn. Invest. 12 (2000) 3]. Gross lesions of PMWS include generalised lymphadenopathy, hepatitis, nephritis and pneumonia and typical histological lesions include lymphocytic depletion and multinucleated giant cell formation in lymph nodes, degeneration and necrosis of hepatocytes, and multifocal lymphohistocytic interstitial pneumonia. This communication will review the results of experimental infections of gnotobiotic (GN), colostrum-deprived (CD) and colostrum-fed (CF) pigs within our group, and elsewhere, with PCV2 and the conclusions that can be drawn from this work.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Allan, G. M. (Ekstern), McNeilly, F. (Ekstern), Ellis, J. (Ekstern), Krakowka, S. (Ekstern), Betner, A. (Intern), McCullough, K. (Ekstern), Nauwynck, H. (Ekstern), Kennedy, S. (Ekstern), Meehan, B. (Ekstern), Charreyre, C. (Ekstern)
Pages: 165-168
Publication date: 2004
Main Research Area: Technical/natural sciences

Publication information
Journal: Veterinary Microbiology
Volume: 98
Issue number: 2
ISSN (Print): 0378-1135
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.326 SNIP 1.208
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.393 SNIP 1.21 CiteScore 2.56
Rapport om laboratorieberedskabsøvelse vedrørende mund- og klovesyge

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Bøtner, A. (Intern)
Temporary CD8(+) T-cell depletion in pigs does not exacerbate infection with porcine reproductive and respiratory syndrome virus (PRRSV)

Several studies have demonstrated a consistent increase in the CD8(+) T-cell subset of pigs following infection with porcine reproductive and respiratory virus (PRRSV). Consequently, it has been suggested that CD8(+) T-cells may play an important role in protection against this infection. In order to test this hypothesis, we examined five 5-week-old pigs, which had been depleted for CD8(+) T-cells by treatment with anti-CD8 mAb injections, starting 2 days before inoculation with PRRSV. Virus-inoculated and sham-inoculated age-matched pigs served as controls. Blood samples were collected continuously, together with organ material at necropsy, to study kinetics of leukocyte subpopulations, antibody production and virus persistence in individual pigs. Significant lower CD8(+) T-cell counts on day 0, that is, before virus challenge, in the anti-CD8 mAb treated pigs compared to the control pigs, confirmed the depletion effect of specific mAb therapy. Almost complete depletion of cell subsets expressing the CD8(+) antigen was obtained on day 2 and 5 post infection (PI) with nadir less than 1 % of peripheral blood mononuclear cells (PBMC). One week PI, an increase in T-cell subsets was observed for both anti-CD8 mAb treated pigs and virus-inoculated control pigs. T-memory cells and cytotoxic T-cells reached levels comparative with the virus-inoculated control pigs on days 8 and 12 PI, respectively, whereas NK-cells remained suppressed for the rest of the experimental period. An extraordinary increase of T-helper cells in the anti-CD8 mAb treated pigs with a significantly higher level than in the virus-inoculated and sham-inoculated control pigs, was observed from day 12 PI. In conclusion, it was established that CD8(+) T-cell depletion in the early phase of PRRSV infection neither caused increased disease nor influenced the ability to clear virus in the treated pigs.
The emergence of koi herpesvirus and its significance to European aquaculture

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Haenen, O. (Ekstern), Way, K. (Ekstern), Bergmann, S. (Ekstern), Ariel, E. (Intern)
Pages: 293-307
Publication date: 2004
Main Research Area: Technical/natural sciences

Publication information
Journal: Bulletin of the European Association of Fish Pathologists
Volume: 24
Issue number: 6
ISSN (Print): 0108-0288
Ratings:
The use of different diagnostic tests in a herd with an unexpected case of a BVD virus positive calf

General information
State: Published
Organisations: Sektion for Eksotiske Virusssygdomme, Division of Virology, National Veterinary Institute
Authors: Uttenthal, Å. (Intern), Holm, E. (Ekstern), Voss, H. B. (Ekstern), Jensen, N. P. (Ekstern), Larsen, L. E. (Ekstern)
Publication date: 2004
Transmission of PMWS

General information
State: Published
Organisations: Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Sektion for Eksotiske Virusssygdomme, Division of Virology
Authors: Kristensen, C. S. (Ekstern), Bækbo, P. (Ekstern), Bille-Hansen, V. (Intern), Hassing, A. G. (Ekstern), Batner, A. (Intern)
Publication date: 2004
Event: Abstract from 18th International Pig Veterinary Society Congress, Hamburg, Germany.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 241474
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2004

Use of plasmid DNA for induction of protective immunity

Vaccines based on plasmid DNA have been tested for a number of fish pathogens but so far it is only in case of the rhabdoviruses, where the technology has been a real break through in vaccine research. Aspects of dose, time-course and mechanisms of protection, as well as practical use are discussed.

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Lorenzen, N. (Intern)
Pages: 11-15
Publication date: 2004
Main Research Area: Technical/natural sciences

Publication information
Journal: European Association of Fish Pathologists. Bulletin
Volume: 24
Issue number: 1
ISSN (Print): 0108-0288
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2016): CiteScore 0.49 SJR 0.234 SNIP 0.421
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.27 SNIP 0.496 CiteScore 0.64
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.32 SNIP 0.414 CiteScore 0.68
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.365 SNIP 0.431 CiteScore 0.62
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Zoo-sanitary controls in trade and transfer of fish eggs and sperm

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Midtlyng, P. (Ekstern), Wolffrom, T. (Ekstern), Bovo, G. (Ekstern), Husby, A. (Ekstern), Håstein, T. (Ekstern), Hill, B. (Ekstern), Storset, A. (Ekstern), Michel, C. (Ekstern), Olesen, N. J. (Intern)
Pages: 571-572
Publication date: 2004
Main Research Area: Technical/natural sciences

Publication information
Journal: European Aquaculture Society. Special Publications
Issue number: 34
ISSN (Print): 0774-0689
Ratings:
Web of Science (2018): Indexed yes
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Original language: English
Source: orbit
Source-ID: 241530
Publication: Research › Journal article – Annual report year: 2004

A DNA vaccine directed against a rainbow trout rhabdovirus induces early protection against a nodavirus challenge in turbot
A DNA vaccine encoding the envelope glycoprotein from a fish rhabdovirus, viral hemorrhagic septicemia virus (VHSV), has previously been shown to induce both early and long time protection against the virus in rainbow trout. Challenge
experiments have revealed that the immunity established shortly after vaccination is cross-protective against heterologous fish rhabdoviruses. In this study, we show that the DNA vaccine encoding the VHSV glycoprotein also induces early protection against a non-enveloped, positive-sense RNA virus belonging to the Nodavirus family, the Atlantic halibut nodavirus (AHNV). In a vaccine, efficacy test using juvenile turbot as model fish, the fish injected with the VHSV vaccine were completely protected against a nodavirus challenge performed 8 days post vaccination, while the cumulative mortality in the control group reached 54%. A DNA vaccine carrying the gene encoding the capsid protein of AHNV revealed no protective properties against the nodavirus challenge. Histological examination of muscle tissue sections from the vaccine injection site showed that the DNA vaccine against VHSV triggered a pronounced inflammatory response in turbot similar to what has earlier been observed in rainbow trout.

**General information**
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Sommerset, I. (Ekstern), Lorenzen, E. (Intern), Lorenzen, N. (Intern), Bleie, H. (Ekstern), Nerland, A. (Ekstern)
Pages: 4661-4667
Publication date: 2003
Main Research Area: Technical/natural sciences

**Publication information**
Journal: Vaccine
Volume: 21
Issue number: 32
ISSN (Print): 0264-410X
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.33 SJR 1.956 SNIP 1.155
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 2.068 SNIP 1.259 CiteScore 3.45
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 2.05 SNIP 1.231 CiteScore 3.57
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.73 SNIP 1.126 CiteScore 3.43
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.634 SNIP 1.159 CiteScore 3.56
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.74 SNIP 1.274 CiteScore 3.86
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.636 SNIP 1.207
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.428 SNIP 1.21
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.327 SNIP 1.025
Scopus rating (2007): SJR 1.286 SNIP 1.112
Age- and weight-dependent susceptibility of rainbow trout Oncorhynchus mykiss to isolates of infectious haematopoietic necrosis virus (IHNV) of varying virulence

The virulence of 5 European and 1 North American isolate of infectious haematopoietic necrosis virus (IHNV) was compared by infecting female sibling rainbow trout ('Isle of Man' strain) of different weights and ages (2, 20 and 50 g). The fish were exposed to 104 TCID50 IHNV per ml of water by immersion, and the mortality was recorded for 28 d. Two new IHNV isolates from Germany were included in the investigation. One was isolated from European eels kept at 23\textdegree\textpm 2\textdegree\textC, and the other was not detectable by immunofluorescence with commercially available monoclonal antibodies recognising the viral G protein. The results showed that IHNV isolates of high or low virulence persisted in rainbow trout of all ages/weights for 28 d, with the exception of fish over 15 g in the eel IHNV (DF [diagnostic fish] 13/98)-infected groups from which the virus could not be reisolated on Day 28. The smallest fish were most susceptible to an infection with any of the IHNV isolates. The lowest cumulative mortality (18%) was observed in fingerlings infected with the North American isolate HAG (obtained from Hagerman Valley), and the highest mortality (100%) in DF 04/99 infected fish. The DF 04/99 and O-13/95 viruses caused mortality in fish independent of their weight or age. The isolates FR-32/87 and I-4008 were virulent in fish up to a weight of 20 g and caused no mortality in larger fish. In the IHNV HAG- and DF 13/98 (eel)-infected rainbow trout, no signs of disease were observed in fish weighing between 15 and 50 g. An age/weight related susceptibility of rainbow trout was demonstrated under the defined conditions for all IHNV isolates tested.

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Bergmann, S. (Ekstern), Fichtner, D. (Ekstern), Skall, H. F. (Intern), Schlotfeldt, H. (Ekstern), Olesen, N. J. (Intern)
Pages: 205-210
Publication date: 2003
Main Research Area: Technical/natural sciences

Publication information
Journal: Diseases of Aquatic Organisms
Volume: 55
Issue number: 3
ISSN (Print): 0177-5103
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Airborne transmission of Porcine Reproductive and Respiratory Syndrome Virus between pig units located at close range

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research
Authors: Kristensen, C. S. (Ekstern), Bøtner, A. (Intern), Nielsen, J. P. (Ekstern), Jorsal, S. E. L. (Intern)
Publication date: 2003
Event: Abstract from 4th International Symposium on Emerging and Re-emerging Pig Diseases, Rome, Italy.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 241706
Publication: Research › Conference abstract for conference – Annual report year: 2003

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 Virussygdomme, Division of Virology, National Veterinary Institute, Virology, Division of Veterinary Diagnostics and Research
Authors: Tjørnehøj, K. (Intern), Utenthal, Å. (Intern), Viuff, B. (Ekstern), Larsen, L. E. (Intern), Rontved, C. (Ekstern), Ronsholt, L. (Ekstern)
Pages: 55-65
Publication date: 2003
Main Research Area: Technical/natural sciences

Publication information
Journal: Research in Veterinary Science
Volume: 74
Issue number: 1
ISSN (Print): 0034-5288
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): SJR 0.613 SNIP 0.807 CiteScore 1.46
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 0.761 SNIP 0.936 CiteScore 1.57
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 0.685 SNIP 0.893 CiteScore 1.58
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 0.676 SNIP 0.952 CiteScore 1.62
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 0.631 SNIP 1.073 CiteScore 1.63
ISI indexed (2012): ISI indexed yes
Association of lymphopenia with porcine circovirus type 2 induced postweaning multisystemic wasting syndrome (PMWS)

**General information**
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Nielsen, J. (Intern), Vincent, I. (Ekstern), Ladekjær-Mikkelsen, A. (Ekstern), Allan, G. (Ekstern), McCullough, K. (Ekstern), Bøtner, A. (Intern)
Pages: 97-111
Publication date: 2003
Main Research Area: Technical/natural sciences

**Publication information**
Journal: Veterinary Immunology and Immunopathology
Volume: 92
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
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 1.63 SJR 0.73 SNIP 0.704
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 0.856 SNIP 0.752 CiteScore 1.67
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 0.768 SNIP 0.719 CiteScore 1.6
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 0.808 SNIP 0.805 CiteScore 1.89
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 0.837 SNIP 0.922 CiteScore 2.15
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 0.849 SNIP 0.996 CiteScore 2.16
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 0.77 SNIP 0.945
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 0.768 SNIP 0.852
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 0.69 SNIP 0.866
Scopus rating (2007): SJR 0.77 SNIP 0.925
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.784 SNIP 0.993
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.676 SNIP 0.937
Bovine respiratory syncytial virus immunostimulating complexes (BRSV-ISCOMS) provided protection against a virulent challenge

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

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.
Characterisation of The First Cases of PMWS in Denmark

General information
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, Technical University of Denmark
Authors: Grøndahl, C. (Ekstern), Uttenthal, Å. (Intern), Houec, H. (Ekstern), Rasmussen, T. B. (Intern), Høyer, M. J. (Ekstern), Larsen, L. E. (Intern)
Publication date: 2003
Event: Abstract from International Congress for Zoo Animals, Rom, Italy.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 240799
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2003

Determination of the sequence of the complete open reading frame and the 5' NTR of the Paderborn isolate of classical swine fever virus

The classical swine fever (CSF) epidemic in the Netherlands in 1997-1998 lasted 14 months, during which 429 infected and 1300 at risk herds were culled, at an estimated economical cost of 2 billion US dollars. Despite the overwhelming scale of the epizootic, the CSF virus (CSFV) strain causing the outbreak has remained largely uncharacterized. The Dutch epizootic is epidemiologically linked to a small CSF outbreak in 1997, in Paderborn in Germany. E2 and partial 5' NTR sequencing has shown that the index Paderborn isolate, and several Dutch isolates taken during the 1997-1998 epizootic, are virtually identical, confirming that the Paderborn isolate triggered the Dutch outbreak, and furthermore showing that this single isolate was stable throughout the whole Dutch outbreak (the above reviewed in [C. Terpstra, A. J. de Smit, Veterinary Microbiol. 77 (2000) 3-15]). We determined the nucleotide sequence of the 5' NTR (by 5' RACE) and the complete open reading frame of the Paderborn isolate (GenBank AY072924). Our sequence was identical to previously published partial 5'NTR and E2 sequences for the index Paderborn 1997 and Dutch 1997 (Venhorst) isolates, confirming the identity of the virus we sequenced. Phylogenetic analysis based on the complete open reading frame showed that Paderborn is genetically very different from common European laboratory reference strains. Neutralization studies showed that Paderborn is also antigenically very different from common laboratory strains such as Alfort 187. Paderborn is the only recent European CSFV field isolate for which a complete sequence is available, and given Paderborns genetic and antigenic uniqueness, the Paderborn sequence may have practical use for diagnostic and vaccine antigen development.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Technical University of Denmark
Authors: Oleksiewicz, M. B. (Ekstern), Rasmussen, T. B. (Intern), Normann, P. (Intern), Uttenthal, Å. (Intern)
Pages: 311-325
Publication date: 2003
Main Research Area: Technical/natural sciences

Publication information
Journal: Veterinary Microbiology
Volume: 92
Issue number: 4
ISSN (Print): 0378-1135
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
pestivirus, pig virus, hog cholera, Paderborn isolate, classical swine fever virus (CSFV), whole genome sequence

DOIs:
10.1016/S0378-1135(02)00424-8

Source: orbit
Source-ID: 229844
Development of a novel quantitative real-time RT-PCR assay for the simultaneous detection of all serotypes of Foot-and-mouth disease virus

Foot-and-mouth disease virus (FMDV) spreads extremely fast and the need for rapid and robust diagnostic virus detection systems was obvious during the recent European epidemic. Using a novel real-time RT-PCR system based on primer-probe energy transfer (PriProET) we present here an assay targeting the 3D gene of FMDV. The assay was validated for the efficacy to detect all known FMDV serotypes. The test method was linear over a range of at least 7 orders of magnitude and the detection limit was below the equivalent of 10 genomic copies. Analysing recent African probang samples the method was able to detect FMDV in materials from both cattle and buffalo. When compared to traditional virus cultivation the virus detection sensitivity was similar but the RT-PCR method can provide a laboratory result much faster than virus cultivation. The real-time PCR method confirms the identity of the amplicon by melting point analysis for added specificity and at the same time allows the detection of mutations in the probe region. As such, the described new method is suitable for the robust real-time detection of index cases caused by any serotype of FMDV.
DNA vaccination against viral haemorrhagic septicaemia (VHS) in rainbow trout: size, dose, route of injection and duration of protection—early protection correlates with Mx expression

Rainbow trout of different sizes (10 and 100 g) were injected intramuscularly (i.m.) or intraperitoneally (i.p.) with different doses (range 10ng-10μg) of a viral haemorrhagic septicaemia (VHS)-DNA vaccine (pcDNA3vhsG). As controls, fish were injected with the pcDNA3 plasmid alone, or with inactivated VHS virus. Fish were challenged at different times post-vaccination (p.v.) to assess protection. At certain times p.v., serum samples were analysed for neutralising antibody and liver tissue was analysed for Mx mRNA expression. A DNA dose of 0.5 μg injected by the i.m. route induced protection in fish of all sizes in challenges performed either 1 or 4 weeks p.v. This dose also conferred effective protection up to 9 months p.v. in fish >100 g. With lower doses of DNA (0.1 and 0.01 μg) and challenge at 4 weeks p.v., 10 g fish were partially protected but protection was not observed in 100 g fish. Vaccination by the i.p. route induced no or lower levels of protection compared with the i.m. route. Fish vaccinated with 0.5 μg DNA i.m. had no detectable serum neutralising antibody (NAb) at 4 weeks p.v. (with the exception of a single 10 g fish) but antibody was detected at 8 weeks and 6 months p.v. but not at 9 months p.v. However, cohorts of these fish showed effective protection at all timepoints. Lack of detectable levels of NAb (at 9 weeks p.v.) despite partial protection in challenge at 4 weeks p.v. was also observed with 0.01 μg doses of DNA i.m. NAb was detected in sera of fish at 8 weeks after vaccination with 0.1 μg i.m. but not in fish
vaccinated with doses of 0.01-0.5 mug i.p. Early protection (1 week p.v.) correlated with elevated Mx gene expression.

**General information**

State: Published
Organisations: Department of Systems Biology, Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: McLauchlan, P. (Ekstern), Collet, B. (Ekstern), Ingerslev, E. (Intern), Secombes, C. (Ekstern), Lorenzen, N. (Intern), Ellis, A. (Ekstern)
Pages: 39-50
Publication date: 2003
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Fish & shellfish immunology
Volume: 15
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BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.36 SJR 1.114 SNIP 1.16
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.268 SNIP 1.171 CiteScore 3.19
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.138 SNIP 1.089 CiteScore 2.92
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.001 SNIP 1.149 CiteScore 3.11
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.151 SNIP 1.174 CiteScore 3.02
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.196 SNIP 1.265 CiteScore 3.52
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.131 SNIP 1.056
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.96 SNIP 1.101
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 0.952 SNIP 1.062
Scopus rating (2007): SJR 0.842 SNIP 1.378
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.954 SNIP 1.298
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.789 SNIP 0.861
Web of Science (2005): Indexed yes
DNA vaccination using porcine circovirus type 2 structural protein

**General information**

State: Published
Organisations: National Veterinary Institute, Sektion for Eksotiske Virussygdomme, Division of Virology
Authors: Kamstrup, S. (Intern), Barfoed, A. M. (Ekstern), Frimann, T. H. (Ekstern), Ladekjær-Mikkelsen, A. (Ekstern), Bøtner, A. (Intern)
Publication date: 2003
Event: Abstract from 6th International Congress of Veterinary Virology, St.Malo, France.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 22512
Publication: Research - peer-review › Journal article – Annual report year: 2003

**Abstract**

Experimental infection with the Paderborn isolate of classical swine fever virus in 10-week-old pigs: determination of viral replication kinetics by quantitative RT-PCR, virus isolation and antigen ELISA

We performed experimental infection in 10-week-old pigs with the Paderborn isolate of classical swine fever virus (CSFV). Despite being epidemiologically linked to the major CSFV outbreak in The Netherlands in 1997, the in vivo replication kinetics of this isolate have to our knowledge not been described in detail previously. We found that oronasal infection with 10^4.7 TCID50 produced mortality in three out of five pigs after 29-31 days, and severe clinical symptoms in one out of five pigs, while one out of five pigs exhibited no clinical symptoms. At this infection dose, pigs had viral RNA (monitored by quantitative reverse transcription (RT)-PCR) in serum as soon as 2 days post-infection, and excretion of infectious virus (monitored by sentinel pigs) appeared to be virtually concomitant with viremia onset. While virus RNA was cleared from the serum of most pigs after 1-2 weeks, some pigs had viral RNA in serum for more than 30 days, and exhibited only mild clinical symptoms. We observed an excellent correlation between clinical symptoms and viral RNA loads in serum, while serum antibody levels were low. Clinically affected pigs had up to 1000-fold higher serum viral RNA loads than did pigs without clinical symptoms. At this level of infection, and this age group, the Paderborn isolate exhibited a strikingly wide range of replication patterns, which might be relevant to the spread of the virus through susceptible pig populations, and the severity of the 1997-1998 outbreak.

**General information**

State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Technical University of Denmark
Authors: Uttenthal, Å. (Intern), Storgaard, T. (Ekstern), Oleksiewicz, M. (Ekstern), de Stricker, K. (Ekstern)
Pages: 197-212
Publication date: 2003
Main Research Area: Technical/natural sciences

**Publication information**
Journal: Veterinary Microbiology
Volume: 92
Issue number: 3
ISSN (Print): 0378-1135
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.326 SNIP 1.208
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.393 SNIP 1.21 CiteScore 2.56
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.281 SNIP 1.262 CiteScore 2.54
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.438 SNIP 1.484 CiteScore 3
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.437 SNIP 1.579 CiteScore 3.18
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.562 SNIP 1.738 CiteScore 3.27
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.371 SNIP 1.476
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.29 SNIP 1.472
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.169 SNIP 1.3
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.043 SNIP 1.322
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.022 SNIP 1.401
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.078 SNIP 1.262
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.869 SNIP 1.259
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.913 SNIP 1.186
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.84 SNIP 1.112
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.833 SNIP 1.058
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 0.82 SNIP 1.088
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 0.703 SNIP 1.078
Original language: English
meat juice, experimental infection, quantitative RT-PCR, diagnosis, hog cholera virus, Paderborn isolate, classical swine fever virus
Generation of an infectious clone of VR-2332, a highly virulent North American type isolate of porcine reproductive and respiratory syndrome virus

A full-length cDNA clone of the prototypical North American porcine reproductive and respiratory syndrome virus (PRRSV) isolate VR-2332 was assembled in the plasmid vector pOK(12). To rescue infectious virus, capped RNA was transcribed in vitro from the pOK(12) clone and transfected into BHK-21C cells. The supernatant from transfected monolayers were serially passaged on Marc-145 cells and porcine pulmonary alveolar macrophages. Infectious PRRSV was recovered on Marc-145 cells as well as porcine pulmonary macrophages; thus, the cloned virus exhibited the same cell tropism as the parental VR-2332 strain. However, the cloned virus was clearly distinguishable from the parental VR-2332 strain by an engineered marker, a BstZ171 restriction site. The full-length cDNA clone had 11 nucleotide changes, 2 of which affected coding, compared to the parental VR-2332 strain. Additionally, the transcribed RNA had an extra G at the 5’ end. To examine whether these changes influenced viral replication, we examined the growth kinetics of the cloned virus in vitro. In Marc-145 cells, the growth kinetics of the cloned virus reflected those of the parental isolate, even though the titers of the cloned virus were consistently slightly lower. In experimentally infected 5.5-week-old pigs, the cloned virus produced blue discoloration of the ears, a classical clinical symptom of PRRSV. Also, the seroconversion kinetics of pigs infected with the cloned virus and VR-2332 were very similar. Hence, virus derived from the full-length cDNA clone appeared to recapitulate the biological properties of the highly virulent parental VR-2332 strain. This is the first report of an infectious cDNA clone based on American-type PRRSV. The availability of this cDNA clone will allow examination of the molecular mechanisms behind PRRSV virulence and attenuation, which might in turn allow the production of second-generation, genetically engineered PRRSV vaccines.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Nielsen, H. (Ekstern), Liu, G. (Ekstern), Nielsen, J. (Intern), Oleksiewicz, M. (Ekstern), Bøtner, A. (Intern), Storgaard, T. (Ekstern), Faaberg, K. (Ekstern)
Pages: 3702-3711
Publication date: 2003
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Virology
Volume: 77
Issue number: 6
ISSN (Print): 0022-538X
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): SJR 3.052 SNIP 1.131 CiteScore 4.42
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 3.286 SNIP 1.138 CiteScore 4.42
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 3.168 SNIP 1.219 CiteScore 4.4
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 3.468 SNIP 1.26 CiteScore 4.92
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 3.154 SNIP 1.227 CiteScore 5.2
Immunohistochemical detection of SWC3, CD2, CD3, CD4 and CD8 antigens in paraformaldehyde fixed and paraffin embedded porcine lymphoid tissue

Identification of the different cell types of the immune system is important for in situ studies on the pathogenesis of infectious diseases in various animals, including the pig. Unfortunately, many monoclonal anti-leukocyte antibodies are only useful for staining frozen tissue sections with inherent poor tissue morphology, and are not readily adapted to formaldehyde fixed and paraffin embedded tissue with well preserved morphology. Seven well characterised monoclonal antibodies against porcine leukocyte antigens were tested on neutral buffered paraformaldehyde fixed and paraffin embedded porcine tissue sections using the highly sensitive tyramide signal amplification system. Combining this method with different antigen retrieval techniques enabled us to detect CD2, CD3, CD4, CD8 and SWC3 antigen expressing cells in porcine lymphoid tissue. Thus, we describe herein methods for the detection of several major cell types of the porcine immune system in fixed tissue with optimal preservation of histological details.

General information
State: Published
Organisations: Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research, National Veterinary Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, Technical University of Denmark
Authors: Tingstedt, J. E. (Ekstern), Tornehave, D. (Ekstern), Lind, P. (Intern), Nielsen, J. (Intern)
In utero infection with porcine reproductive and respiratory syndrome virus modulates leukocyte subpopulations in peripheral blood and bronchoalveolar fluid of surviving piglets

It is well known that piglets congenitally infected with porcine reproductive and respiratory syndrome virus (PRRSV) can be viremic at birth, and that preweaning mortality due to secondary infections often increases during acute outbreaks of PRRS. Therefore, an immunosuppressive effect of in utero infection has been suggested. The aim of the present study was to characterise the changes of leukocyte populations in piglets surviving in utero infection with PRRSV. A total of 27 liveborn uninfected control piglets and 22 piglets infected transplacently with a Danish strain of PRRSV were included. At 2 and 4 weeks of age, 21 of 22 (96%) and 7 of 14 (50%) examined infected piglets were still viremic, whereas PRRSV could not be detected in the six infected piglets examined at 6 weeks of age. Flow cytometry analysis was used to determine the phenotypic composition of leukocytes in peripheral blood and bronchoalveolar lavage fluid (BALF) of 2-, 4- and 6-week-old infected piglets and age-matched uninfected controls. The key observation in the present study is that high levels of CD8+ cells constitute a dominant feature in peripheral blood and BALF of piglets surviving in utero infection with PRRSV. In BALF, the average high level of CD8+ cells in 2-week-old infected piglets (33.4±12.6%) was followed by a decline to 7.3±3.0 and 11.1±3.0% at 4 and 6 weeks of age. BALF of control piglets contained 1.6±0.9, 2.3±1.8 and 1.9±0.5% CD8+ cells, only. In peripheral blood, however, the average number of CD8+ cells remained at high levels in the infected piglets throughout the post-natal experimental period (2.8±1.9, 2.9±1.8 and 3.2±1.7×10^6 CD8+ cells/ml at 2, 4 and 6 weeks, respectively). In the controls, the average levels of CD8+ cells were 0.9±0.2, 1.9±1.7 and 1.6±0.5×10^6/ml, respectively. Furthermore, the numbers of CD2+, CD4+CD8+ and SLA-classII+ cells, respectively, in peripheral blood, together with the levels of CD2+ and CD3+ cells in BALF were increased in the infected piglets infected in utero compared to the uninfected controls. The kinetic analyses carried out in the present study reflect that in utero infection with PRRSV modulates immune cell populations in peripheral blood and BALF of surviving piglets. The observed changes are characterised by high levels of CD8+ cells supporting an important role of these cells in PRRSV infection. The present results, however, do not support the existence of post-natal immunosuppression following in utero infection with PRRSV.

General information
State: Published
Organisations: Sektion for Ekstotske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Nielsen, J. (Ekstern), Bøtner, A. (Intern), Tingstedt, J. E. (Ekstern), Aasted, B. (Ekstern), Johnsen, C. K. (Ekstern), Riber, U. (Ekstern), Lind, P. (Ekstern)
Pages: 135-151
Publication date: 2003
Main Research Area: Technical/natural sciences

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Journal: Veterinary Immunology and Immunopathology
Volume: 93
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
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 1.63 SJR 0.73 SNIP 0.704
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 0.856 SNIP 0.752 CiteScore 1.67
In utero infection with PRRSV affects immune functions of surviving piglets

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Nielsen, J. (Ekstern), Bøtner, A. (Intern), Aasted, B. (Ekstern), Johnsen, C. (Ekstern), Riber, U. (Ekstern), Tingstedt, J. E. (Ekstern), Lind, P. (Ekstern)

Original language: English
DOIs: 10.1016/S0165-2427(03)00068-0
Source: orbit
Source-ID: 241333
Publication: Research - peer-review › Journal article – Annual report year: 2003

Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 0.768 SNIP 0.719 CiteScore 1.6
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 0.808 SNIP 0.805 CiteScore 1.89
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 0.837 SNIP 0.922 CiteScore 2.15
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 0.849 SNIP 0.996 CiteScore 2.16
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 0.77 SNIP 0.945
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 0.768 SNIP 0.852
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 0.69 SNIP 0.866
Scopus rating (2007): SJR 0.77 SNIP 0.925
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.784 SNIP 0.993
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.676 SNIP 0.937
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.742 SNIP 0.984
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.659 SNIP 0.757
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.64 SNIP 0.915
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.63 SNIP 0.84
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 0.569 SNIP 0.807
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 0.442 SNIP 0.654
Mercury decreases culturability of *Pseudomonas frederiksbergensis* JAJ 28 in soil microcosms

Mercury is a biologically potent heavy metal, which has been found to change the diversity of culturable bacteria. Therefore, we investigated whether Hg kills bacteria in soil or reduces culturability. Soil microcosms were inoculated with *Pseudomonas frederiksbergensis* JAJ 28 and were sampled regularly during 28 days. The total number of acridine orange-stained cells was relatively constant, and Hg reduced the number on only one sampling day. However, the fraction of culturable cells on 1/10 tryptic soy agar was lowered on days 6, 13, and 21. The number of microcolony forming units, which represents viable cells, was also affected by Hg, but this effect was delayed compared with the effects on CFUs. The amount of headspace CO2 per cell was overall increased by Hg, another indication of the toxic effects of Hg on the bacterial cells. Our results thus emphasize the need to take culturability into account when studying the effects of heavy metals on bacterial diversity.

General information

State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Technical University of Denmark
Authors: Johnsen, K. (Ekstern), Ekelund, F. (Ekstern), Binnerup, S. J. (Ekstern), Rasmussen, L. D. (Intern)
Molecular epidemiology of PRRSV

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Storgaard, T. (Ekstern), Oleksiewicz, M. (Ekstern), Stadejek, T. (Ekstern), Forsberg, R. (Ekstern), Nielsen, H. S. (Ekstern), Bøtner, A. (Intern)
Publication date: 2003
Event: Abstract from 4th International Symposium on Emerging and Re–emerging Pig Diseases, Rome, Italy.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 241711
Publication: Research › Conference abstract for conference – Annual report year: 2003

Phylogeography of infectious haematopoietic necrosis virus in North America
Infectious hematopoietic necrosis virus (IHNV) is a rhabdoviral pathogen that infects wild and cultured salmonid fish throughout the Pacific Northwest of North America. IHNV causes severe epidemics in young fish and can cause disease or occur asymptotically in adults. In a broad survey of 323 IHNV field isolates, sequence analysis of a 303 nucleotide variable region within the glycoprotein gene revealed a maximum nucleotide diversity of 8.6%, indicating low genetic diversity overall for this virus. Phylogenetic analysis revealed three major virus genogroups, designated U, M and L, which varied in topography and geographical range. Intragroup genetic diversity measures indicated that the M genogroup had three- to fourfold more diversity than the other genogroups and suggested relatively rapid evolution of the M genogroup and stasis within the U genogroup. We speculate that factors influencing IHNV evolution may have included ocean migration ranges of their salmonid host populations and anthropogenic effects associated with fish culture.

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Kurath, G. (Ekstern), Garver, K. (Ekstern), Troyer, R. (Ekstern), Emmenegger, E. (Ekstern), Einer-Jensen, K. (Intern), Anderson, E. (Ekstern)
Pages: 803-814
Publication date: 2003
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of General Virology
Volume: 84
Issue number: 4
ISSN (Print): 0022-1317
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 2.93 SJR 1.499 SNIP 0.886
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.729 SNIP 1.007 CiteScore 3.26
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.683 SNIP 1.059 CiteScore 3.25
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.749 SNIP 1.161 CiteScore 3.64
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.518 SNIP 1.038 CiteScore 3.28
ISI indexed (2012): ISI indexed yes
PMWS og PRRS - Opdatering og aktuelt nyt

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Bøtner, A. (Intern)
Publication date: 2003
Main Research Area: Technical/natural sciences

Publication information
Journal: DDD's årsmøde
Original language: English
Source: orbit
Source-ID: 229830
Publication: Research - peer-review › Journal article – Annual report year: 2003

PMWS - status over viden og forskning

General information
We investigated whether the prey-predator dynamics of bacteria and protozoa were affected by inorganic mercury at concentrations of 0, 3.5 and 15 mg Hg(II) kg soil(-1). The amount of bioavailable Hg was estimated using a biosensor-assay based on the mer-lux gene fusion. The numbers of bacterial CFUs on the general medium 1/100 tryptic soy agar (TSA) were significantly decreased when the soil had been amended with Hg. In contrast, no effect was seen on the number of CFUs on the Pseudomonas-specific medium Gould's S1 agar. Protozoan numbers estimated by the most probable number (MPN) method with 1/100 TSB as growth medium were also negatively affected by Hg. The different fractions of protozoa were affected to different degrees suggesting that amoebae were less sensitive than slow-growing flagellates, which again were less sensitive than the fast-growing flagellates. In contrast, Hg did not induce any detectable changes in the diversity of flagellate morphotypes. In the treatment with 15 mg Hg kg(-1) a transiently increased number of bacteria was seen at day 6 probably concomitant with a decrease in the numbers of protozoa. This might indicate that Hg affected the prey-predator dynamics in communities of culturable bacteria and protozoa in soil. Furthermore, we showed that the number of Pseudomonas spp. was not affected by Hg whereas the number of bacteria growing on a general medium was.
bioavailable mercury, microcosms, Pseudomonas, protozoa, prey-predator dynamics

DOIs:
10.1016/S0038-0717(03)00178-0
Proficiency testing of national reference laboratories in Europe – contributions to quality assurance? (O-78)

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Ariel, E. (Intern), Skall, H. F. (Intern), Andersen, J. (Ekstern), Olesen, N. J. (Intern)
Publication date: 2003
Event: Abstract from 11th International Conference on Diseases of Fish and Shellfish, St. Julians, Malta.
Main Research Area: Technical/natural sciences
Source: orbit
Publication: Research › Conference abstract for conference – Annual report year: 2003

Serological profiles in Danish PMWS case and control herds

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Ladekjær-Mikkelsen, A. (Ekstern), Bøtner, A. (Intern), Nielsen, J. (Ekstern), Hassing, A. (Ekstern), Bækbo, P. (Ekstern)
Publication date: 2003
Event: Abstract from 4th International Symposium on Emerging and Re–emerging Pig Diseases, Rome, Italy.
Main Research Area: Technical/natural sciences
Source: orbit
Publication ID: 241703
Publication: Research › Conference abstract for conference – Annual report year: 2003

Serologiske profiler for PCV2 og PPV i danske besætninger med og uden Postweaning Multisystemic Wasting Syndrome (PMWS)

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Hassing, A. (Ekstern), Bækbo, P. (Ekstern), Bøtner, A. (Intern), Ladekjær-Mikkelsen, A. (Ekstern)
Pages: 606
Publication date: 2003
Main Research Area: Technical/natural sciences
Publication information
Journal: VetInfo
Original language: Danish
Source: orbit
Publication ID: 241718
Publication: Research › Journal article – Annual report year: 2003

Serum Treatment to Prevent PMWS in Pigs Experimentally Infected with PCV2 and PRRSV

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research
Authors: Ladekjær-Mikkelsen, A. S. (Ekstern), Nielsen, J. (Intern), Bille-Hansen, V. (Intern), Bøtner, A. (Intern)
Publication date: 2003
Event: Abstract from 6th International Congress of Veterinary Virology, St.Malo, France, .
Main Research Area: Technical/natural sciences
Source: orbit
Publication ID: 241473
Publication: Research - peer-review › Conference abstract for conference – Annual report year: 2003
Sundhed og produktion hos svin i multisitesystemer

General information
State: Published
Organisations: Division of Microbiology and Risk Assessment, National Food Institute, Sektion for Eksotiske Virussejdlommene, Division of Virology, National Veterinary Institute, Secretariat, Division of Veterinary Diagnostics and Research
Authors: Busch, M. E. (Ekstern), Vigre, H. (Intern), Lohse, L. (Intern), Jensen, T. (Ekstern), Bækbo, P. (Ekstern), Bøtner, A. (Intern), Nielsen, J. (Intern), Nielsen, J. P. (Ekstern), Sørensen, V. (Intern)
Pages: 28-34
Publication date: 2003
Main Research Area: Technical/natural sciences

Publication information
Journal: Dansk Veterinaertidsskrift
Volume: 86
Issue number: 13
ISSN (Print): 0106-6854
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
ISI indexed (2013): ISI indexed no
BFI (2012): BFI-level 1
ISI indexed (2012): ISI indexed no
BFI (2011): BFI-level 1
ISI indexed (2011): ISI indexed no
BFI (2010): BFI-level 1
BFI (2009): BFI-level 1
BFI (2008): BFI-level 1
Original language: Danish
Source: orbit
Source-ID: 240271
Publication: Research - peer-review › Journal article – Annual report year: 2003

Sundhedstilstanden i dansk akvakultur

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute,
Fødevareregion Vejle, Dansk Dambrugerforening
Authors: Schyth, B. D. (Intern), Korsholm, H. (Ekstern), Henriksen, N. H. (Ekstern)
Pages: 22-27
Publication date: 2003
Main Research Area: Technical/natural sciences

Publication information
Journal: Fiskehelse
Volume: 5
Issue number: 1
Original language: Danish
Links:
https://www.tekna.no/arkiv/FHF/Bladet%20Fiskehelse/2003%20nr%201.pdf
Source: orbit
Source-ID: 250974
Publication: Communication › Journal article – Annual report year: 2003
**Vertical transfer of fish diseases**

**General information**
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Midtlyng, P. (Ekstern), Wolffrom, T. (Ekstern), Bovo, G. (Ekstern), Håstein, T. (Ekstern), Hill, B. (Ekstern), Landsverk, K. (Ekstern), Storset, A. (Ekstern), Michel, C. (Ekstern), Olesen, N. J. (Intern)
Publication date: 2003
Event: Abstract from 11th International Conference on Diseases of Fish and Shellfish, St. Julians, Malta.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 241716
Publication: Research › Conference abstract for conference – Annual report year: 2003

**Airborne transmission of A. pleuropneumoniae and PRRS virus between pig units**

**General information**
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, Secretariat, Division of Microbiology and Risk Assessment, National Food Institute
Authors: Kristensen, C. S. (Ekstern), Bøtner, A. (Intern), Angen, Ø. (Intern), Sørensen, V. (Intern), Jorsal, S. E. L. (Intern), Takai, H. (Ekstern), Barfod, K. (Intern), Nielsen, J. P. (Ekstern)
Pages: 272-272
Publication date: 2002

**Host publication information**
Title of host publication: Proceedings of the 17th International Pig Veterinary Society Congress
Article number: Paper 102
Main Research Area: Technical/natural sciences
Conference: 17th International Pig Veterinary Society Congress, Ames, Iowa, United States, 02/06/2002 - 02/06/2002
Electronic versions: SSUNDMFP6416033014200.pdf
Source: orbit
Source-ID: 240243
Publication: Research - peer-review › Article in proceedings – Annual report year: 2002

**A longitudinal study of cell-mediated immunity in pigs infected with porcine parvovirus**
Porcine parvovirus (PPV) is an ubiquitous pathogen causing reproductive failure in swine. Protection against reproductive failure caused by acute PPV infection has commonly been related to the presence of specific antibodies in the dam. However, the role of cell-mediated immunity during chronic PPV infection remains to be elucidated, and may be relevant to the pathogenesis of novel diseases such as postweaning multisystemic wasting syndrome (PMWS), which may be triggered by coinfection with PPV and porcine circovirus type 2 (PCV2). To investigate whether pigs infected with PPV generate a cell-mediated immune response, a longitudinal infection experiment was performed, using swine leukocyte antigens (SLA) class I characterized growing pigs (haplotype H7/H7). Pigs were intranasally inoculated with PPV at 0, 80, and 136 days. At predetermined time points, peripheral blood mononuclear cells (PBMC) were isolated, and virus-specific lymphoproliferative responses and the cytolytic activities of cytotoxic T-lymphocytes (CTL) and natural killer (NK) cells were examined. Cytolytic assays were performed by the chromium release method, using as targets a syngeneic porcine kidney cell line established for the purpose (CTL assays) and K562 cells (NK assays). A specific proliferative response of PBMC from virus-infected pigs to PPV was observed from day 101 onwards. In contrast, PBMC from mock-infected pigs did not proliferate in response to PPV. Flow cytometric analysis indicated that the CD4(+)CD8(+) T-cell subset of PBMC proliferated in response to virus antigen, in keeping with the assumed role for these cells in immunological memory. This is, to our knowledge, the first indication of a cellular immune response following PPV infection. A weak CTL activity, which peaked on days 80 and 87, was observed in PPV-infected pigs. In vitro restimulation of PBMC with live PPV did not induce further CTL activity. A pronounced NK cell activity was detected in both virus-infected and control pigs throughout the experiment, and may have negatively affected the sensitivity of the CTL assay. In conclusion, the findings of a late lymphoproliferative response together with weak CTL activity are in keeping with an effective control of acute PPV infection by humoral immunity, but open the possibility that cellular immunity may play a role in controlling PPV reinfection. Finally, we reind that the established experimental model using SLA characterized pigs may constitute a valuable tool for future studies of CTL activity in pigs.

**General information**
State: Published
A novel fish rhabdovirus from Sweden is closely related to the Finnish rhabdovirus 903/87

A novel rhabdovirus, preliminary designated as the Sea trout rhabdovirus 28/97 (STRV 28/97), was isolated from sea trout (Salmo trutta trutta) in Sweden in 1996. The fish showed central nervous symptoms, and at the autopsy petechial bleedings in the mesenteric fat were visible. STRV 28/97 was shown to be serologically related to the vesiculotype rhabdovirus 903/87 isolated from brown trout (Salmo trutta lacustris) in Finland [1,3]. The sequences for the nucleocapsid protein, phosphoprotein, matrix protein, glycoprotein and beginning of the polymerase protein of STRV 28/97 were determined. At the amino acid level the genes were over 97% similar to virus 903/87. The nucleocapsid proteins, glycoproteins and beginning of the polymerase protein of STRV 28/97 and virus 903/87 were clustered with the vesiculoviruses and the phosphoproteins close to the vesiculoviruses in protein parsimony analysis. The matrix proteins formed a distinct clade in protein parsimony analysis.

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Johansson, T. (Ekstern), Ostman-Myllyoja, L. (Ekstern), Hellstrom, A. (Ekstern), Martelius, S. (Ekstern), Olesen, N. J. (Intern), Bjorklund, H. (Ekstern)
Pages: 127-138
Publication date: 2002
Main Research Area: Technical/natural sciences

Publication Information
Journal: Virus Genes
Volume: 25
Issue number: 2
ISSN (Print): 0920-8569
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.635 SNIP 0.685 CiteScore 1.55
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.759 SNIP 0.773 CiteScore 1.55
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.729 SNIP 0.774 CiteScore 1.62
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.84 SNIP 0.934 CiteScore 1.94
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.755 SNIP 0.809 CiteScore 1.8
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.834 SNIP 0.996 CiteScore 1.92
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.742 SNIP 0.852
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.83 SNIP 0.757
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.642 SNIP 0.727
Scopus rating (2007): SJR 0.583 SNIP 0.682
Scopus rating (2006): SJR 0.64 SNIP 0.566
Scopus rating (2005): SJR 0.646 SNIP 0.622
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.58 SNIP 0.565
Cytokine mRNA profiles in bronchoalveolar cells of piglets experimentally infected in utero with porcine reproductive and respiratory syndrome virus: Association of sustained expression of IFN-gamma and IL-10 after viral clearance

An experimental model was used to investigate mRNA cytokine profiles in bronchoalveolar cells (BALC) from piglets, infected in utero with porcine reproductive and respiratory syndrome virus (PRRSV). The BALC’s were analyzed for the cytokines TNF-alpha, IFN-gamma, IL-8, IL-10, and IL-12(p40) by real-time TaqMan polymerase chain reaction in 2-, 4-, and 6-week-old piglets, respectively. High levels of IFN-gamma mRNA was detected in all piglets, while IL-10 was upregulated in 2-week-old piglets, was at normal levels in 4-week-old piglets, and elevated again in 6-week-old piglets. IL-12 was weakly elevated in all three age groups. Virus was reduced by 50% in 4-week-old piglets and cleared by 6 weeks.
of age. The sustained expression of IFNgamma and reduction of IL-10 production indicate an important role for these cytokines in immunity to PRRSV.
Cytokine mRNA profiles in bronchoalveolar cells of piglets experimentally infected in utero with with porcine reproductive and respiratory syndrome virus: Association of sustained expression of IFN-gamma and IL-10 after viral clearance

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research
Authors: Johnsen, C. (Ekstern), Bøtner, A. (Intern), Kamstrup, S. (Intern), Lind, P. (Intern), Nielsen, J. (Ekstern)
Pages: 549-556
Publication date: 2002
Main Research Area: Technical/natural sciences

Publication information
Journal: Viral Immunology
Volume: 15
Issue number: 4
ISSN (Print): 0882-8245
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 0.686 SNIP 0.392 CiteScore 1.26
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.75 SNIP 0.55 CiteScore 1.34
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.683 SNIP 0.583 CiteScore 1.47
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 0.941 SNIP 0.658 CiteScore 1.9
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.852 SNIP 0.58 CiteScore 1.67
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.879 SNIP 0.609 CiteScore 1.75
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 0.8 SNIP 0.603
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 0.859 SNIP 0.645
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 0.993 SNIP 0.661
Scopus rating (2007): SJR 0.909 SNIP 0.599
Scopus rating (2006): SJR 1.063 SNIP 0.785
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.09 SNIP 0.59
Scopus rating (2004): SJR 0.994 SNIP 0.599
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.742 SNIP 0.556
Cytokine mRNA profiles in the lungs of pigletsexperimentally infected in utero with porcine reproductive and respiratory syndrome virus (PRRSV): Evidence for sustained expression of IFN-G and IL-10 after viral clearance from the lungs

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research
Authors: Johnsen, C. K. (Ekstern), Bøtner, A. (Intern), Kamstrup, S. (Intern), Lind, P. (Intern), Nielsen, J. (Intern)
Publication date: 2002
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 241332
Publication: Research › Journal article – Annual report year: 2002

Cytokine profiles in peripheral blood mononuclear cells and lymph node cells from piglets infected in utero with porcine reproductive and respiratory syndrome virus (PRRSV)
The aim of the present study was to investigate at 2, 4, and 6 weeks after birth cytokine expression by peripheral blood mononuclear cells and bronchial lymph node cells from piglets infected in utero with porcine reproductive and respiratory syndrome virus (PRRSV). Technically, by flow cytometry we were able to measure gamma interferon (gamma-IFN), tumor necrosis factor alpha (TNF-alpha), interleukin-4 (IL-4), and IL-8 levels. In general, we found increases in the percentages of IL-4-, gamma-IFN-, and TNF-alpha-producing lymphocytes in the infected piglets compared to the percentages in the uninfected control animals, while there was a decrease in the percentage of IL-8-producing monocytes. We believe that these findings reflect a general lymphocyte activation stage that is created due to the infection and that occurs in combination with impairment of the monocyte function, possibly due to the ongoing viral replication in these cells. Single-cell bronchial lymph node preparations exhibited very much the same cytokine profiles as peripheral blood mononuclear cells except for a lack of IL-8 production. When the levels of the individual cytokines in the three groups of PRRSV-infected piglets were compared, the levels of cytokine expression at 4 weeks diverged from those at 2 and 6 weeks, in that there was a significant decrease in the numbers of lymphocytes producing gamma-IFN and TNF-alpha. This tendency was also observed among blood monocytes and lymph node macrophages. Possible reasons for this temporary immunosuppression in the piglets at 4 weeks are discussed.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Section for Veterinary Epidemiology and public sector consultancy, Division of Veterinary Diagnostics and Research
Authors: Aasted, B. (Ekstern), Bach, P. (Ekstern), Nielsen, J. (Intern), Lind, P. (Intern)
Pages: 1229-1234
Publication date: 2002
Main Research Area: Technical/natural sciences

Publication information
Journal: Clinical and Diagnostic Laboratory Immunology
Volume: 9
Issue number: 6
ISSN (Print): 1071-412X
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
Development of a rapid in vitro protein refolding assay which discriminates between peptide-bound and peptide-free forms of recombinant porcine major histocompatibility class I complex (SLA-I)

The extracellular domains of swine leukocyte antigen class I (SLA-I, major histocompatibility complex protein class 1) were cloned and sequenced for two haplotypes (114 and H7) which do not share any alleles based on serological typing, and which are the most important in Danish farmed pigs. The extracellular domain of SLA-I was connected to porcine beta2 microglobulin by glycine-rich linkers. The engineered sin.-le-chain proteins, consisting of fused SLA-I and beta2 microglobulin, were overexpressed as inclusion bodies in Escherichia coli. Also, variants were made of the single-chain proteins, by linking them through glycine-rich linkers to peptides representing T-cell epitopes from classical swine fever virus (CSFV) and foot-and-mouth disease virus (FMDV). An in vitro refold assay was developed, using a monoclonal anti-SLA antibody (PT85A) to gauge refolding. The single best-defined, SLA-I restricted porcine CD8(+) T-cell epitope currently known is a 9-residue peptide from the polyprotein of CSFV (J. Gen. Virol, 76 (1995) 3039). Based on results with the CSFV epitope and two porcine haplotypes (H4 and H7), the in vitro refold assay appeared able to discriminate between peptide-free and peptide-occupied forms of SLA-I. It remains to be seen whether the rapid and technically very simple in vitro refold assay described here will prove generally applicable for the screening of virus-derived peptides for SLA-I binding.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Technical University of Denmark
Authors: Oleksiewicz, M. (Ekster), Kristensen, B. (Ekster), Ladekjaer-Mikkelsen, A. (Ekster), Nielsen, J. (Intern)
Pages: 55-77
Publication date: 2002
Main Research Area: Technical/natural sciences

Publication information
Journal: Veterinary Immunology and Immunopathology
Volume: 86
Issue number: 1-2
ISSN (Print): 0165-2427
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 1.63 SJR 0.73 SNIP 0.704
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 0.856 SNIP 0.752 CiteScore 1.67
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 0.768 SNIP 0.719 CiteScore 1.6
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 0.808 SNIP 0.805 CiteScore 1.89
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 0.837 SNIP 0.922 CiteScore 2.15
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 0.849 SNIP 0.996 CiteScore 2.16
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 0.77 SNIP 0.945
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 0.768 SNIP 0.852
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 0.69 SNIP 0.866
Scopus rating (2007): SJR 0.77 SNIP 0.925
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 0.784 SNIP 0.993
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 0.676 SNIP 0.937
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.742 SNIP 0.984
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.659 SNIP 0.757
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.64 SNIP 0.915
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.63 SNIP 0.84
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 0.569 SNIP 0.807
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 0.442 SNIP 0.654

Original language: English
foot-and-mouth disease virus, cloning, swine beta 2 microglobulin, prokaryotic expression, in vitro protein refolding, MHC-I, major histocompatibility complex class I, peptide binding, classical swine fever virus, SLA-I, Swine leukocyte antigen class I
DOIs:
10.1016/S0165-2427(02)00015-6
Source: orbit
Source-ID: 229973
Publication: Research - peer-review › Journal article – Annual report year: 2002

Dyr som influenzareservoir

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Effect of heavy metal contamination on the microbial subsurface soil community

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Sørensen, S. J. (Ekstern), Rasmussen, L. D. (Intern), de Lipthay, J. R. (Ekstern)
Publication date: 2002
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 242394
Publication: Research - peer-review › Paper – Annual report year: 2002

Experimental inoculation of late term pregnant sows with a field isolate of porcine reproductive and respiratory syndrome vaccine-derived virus

The use of a live attenuated porcine reproductive and respiratory syndrome virus (PRRSV) vaccine in piglets has been associated with reproductive disorders in non-vaccinated sows. Vaccine-derived virus (VDV) has been isolated from foetuses, stillborn pigs, and dead piglets, indicating that the live vaccine spread from vaccinated piglets to non-vaccinated sows, and that the virus might be implicated in the severe reproductive problems observed. In the present study, one such VDV isolate was used to experimentally infect pregnant sows in the last trimester. The chosen isolate, which had more than 99.6% identity to the attenuated vaccine virus, originated from the lungs of a stillborn pig from a swine herd with a sudden high level of stillborn pigs and increased piglet mortality in the nursing period. Intranasal inoculation of sows with the virus isolate resulted in congenital infection, foetal death, and preweaning pig mortality. As such, the present study showed that vaccine-derived PRRSV can cause disease in swine consistent with PRRS.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research, Technical University of Denmark
Authors: Nielsen, J. (Intern), Bøtner, A. (Intern), Bille-Hansen, V. (Intern), Oleksiewicz, M. B. (Ekstern), Storgaard, T. (Ekstern)
Pages: 1-13
Publication date: 2002
Main Research Area: Technical/natural sciences
Publication information
Journal: Veterinary Microbiology
Volume: 84
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
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.326 SNIP 1.208
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.393 SNIP 1.21 CiteScore 2.56
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.281 SNIP 1.262 CiteScore 2.54
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.438 SNIP 1.484 CiteScore 3
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.437 SNIP 1.579 CiteScore 3.18
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.562 SNIP 1.738 CiteScore 3.27
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.371 SNIP 1.476
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.29 SNIP 1.472
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.169 SNIP 1.3
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.043 SNIP 1.322
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.022 SNIP 1.401
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.078 SNIP 1.262
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.869 SNIP 1.259
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.913 SNIP 1.186
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.84 SNIP 1.112
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.833 SNIP 1.058
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 0.82 SNIP 1.088
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 0.703 SNIP 1.078
Original language: English
pig-viruses, experimental infection, field isolated, attenuated vaccines, porcine reproductive and respiratory syndrome virus (PRRSV)
DOIs:
10.1016/S0378-1135(01)00450-3
Source: orbit
Source-ID: 230628
Publication: Research - peer-review › Journal article – Annual report year: 2002
Factors affecting the transfer of porcine parvovirus antibodies from sow to piglets

**General information**

State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Damm, B. I. (Ekstern), Friggens, N. C. (Ekstern), Nielsen, J. (Intern), Ingvartsen, K. L. (Ekstern), Pedersen, L. J. (Ekstern)
Pages: 487-495
Publication date: 2002
Main Research Area: Technical/natural sciences

**Publication information**

Journal: Transboundary and Emerging Diseases
Volume: 49
ISSN (Print): 1865-1674
Ratings:
- BFI (2018): BFI-level 1
- Web of Science (2018): Indexed yes
- BFI (2017): BFI-level 1
- Web of Science (2017): Indexed yes
- BFI (2016): BFI-level 1
- Scopus rating (2016): CiteScore 2.16 SJR 0.994 SNIP 1.096
- Web of Science (2016): Indexed yes
- BFI (2015): BFI-level 1
- Scopus rating (2015): SJR 1.258 SNIP 1.262 CiteScore 2.29
- Web of Science (2015): Indexed yes
- BFI (2014): BFI-level 1
- Scopus rating (2014): SJR 1.038 SNIP 1.19 CiteScore 2.23
- Web of Science (2014): Indexed yes
- BFI (2013): BFI-level 1
- Scopus rating (2013): SJR 0.953 SNIP 1.123 CiteScore 2.33
- ISI indexed (2013): ISI indexed yes
- Web of Science (2013): Indexed yes
- BFI (2012): BFI-level 1
- Scopus rating (2012): SJR 0.917 SNIP 1.149 CiteScore 2.04
- ISI indexed (2012): ISI indexed yes
- Web of Science (2012): Indexed yes
- BFI (2011): BFI-level 1
- Scopus rating (2011): SJR 0.941 SNIP 1.146 CiteScore 2.05
- ISI indexed (2011): ISI indexed yes
- BFI (2010): BFI-level 1
- Scopus rating (2010): SJR 0.747 SNIP 0.986
- Web of Science (2010): Indexed yes
- BFI (2009): BFI-level 1
- Scopus rating (2009): SJR 0.597 SNIP 0.899
- BFI (2008): BFI-level 1
- Scopus rating (2008): SJR 0.356 SNIP 0.7
- Web of Science (2008): Indexed yes
- Scopus rating (2007): SJR 0.449 SNIP 0.774
- Scopus rating (2006): SJR 0.419 SNIP 0.763
- Scopus rating (2005): SJR 0.388 SNIP 0.836
- Scopus rating (2004): SJR 0.293 SNIP 0.575
- Scopus rating (2003): SJR 0.295 SNIP 0.67
- Scopus rating (2002): SJR 0.233 SNIP 0.461
- Scopus rating (2001): SJR 0.265 SNIP 0.225
- Scopus rating (2000): SJR 0.252 SNIP 0.165
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
Authors: Larsen, L. E. (Intern), Tjørnehøj, K. (Intern), Riber, U. (Intern), Heegaard, P. M. H. (Intern), Røntved, C. (Ekstern), Viuff, B. (Ekstern)
Publication date: 2002
Event: Abstract from Buiatric Congres, Hannover, Germany
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 242414
Publication: Research - peer-review › Journal article – Annual report year: 2002

It was recently reported that DNA vaccination of rainbow trout fingerlings against viral hemorrhagic septicaemia virus (VHSV) induced protection within 8 days after intramuscular injection of plasmid DNA. In order to analyse the specificity of this early immunity, fish were vaccinated with plasmid DNA encoding the VHSV or the infectious haematopoietic necrosis virus (IHNV) glycoprotein genes and later challenged with homologous or heterologous pathogens. Challenge experiments revealed that immunity established shortly after vaccination was cross-protective between the two viral pathogens whereas no increased survival was found upon challenge with bacterial pathogens. Within two months after vaccination, the cross-protection disappeared while the specific immunity to homologous virus remained high. The early immunity induced by the DNA vaccines thus appeared to involve short-lived non-specific anti-viral defence mechanisms.

Immunity induced shortly after DNA vaccination of rainbow trout against rhabdoviruses protects against heterologous virus but not against bacterial pathogens

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute, Clear Springs Foods Inc.
Authors: Lorenzen, N. (Intern), Lorenzen, E. (Intern), Einer-Jensen, K. (Intern), LaPatra, S. E. (Ekstern)
Pages: 173-179
Publication date: 2002
Main Research Area: Technical/natural sciences

It was recently reported that DNA vaccination of rainbow trout fingerlings against viral hemorrhagic septicaemia virus (VHSV) induced protection within 8 days after intramuscular injection of plasmid DNA. In order to analyse the specificity of this early immunity, fish were vaccinated with plasmid DNA encoding the VHSV or the infectious haematopoietic necrosis virus (IHNV) glycoprotein genes and later challenged with homologous or heterologous pathogens. Challenge experiments revealed that immunity established shortly after vaccination was cross-protective between the two viral pathogens whereas no increased survival was found upon challenge with bacterial pathogens. Within two months after vaccination, the cross-protection disappeared while the specific immunity to homologous virus remained high. The early immunity induced by the DNA vaccines thus appeared to involve short-lived non-specific anti-viral defence mechanisms.
Influenza A virus i et zoonotisk perspektiv

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Dybkær, K. (Ekstern), Handberg, K. J. (Ekstern), Munch, H. (Ekstern), Bøtner, A. (Intern), Jørgensen, P. H. (Ekstern)
Pages: 6-10
Publication date: 2002
Main Research Area: Technical/natural sciences

Publication information
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Volume: 85
Issue number: 6
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BFI (2013): BFI-level 1

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Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Dybkær, K. (Ekstern), Handberg, K. J. (Ekstern), Munch, H. (Ekstern), Bøtner, A. (Intern), Jørgensen, P. H. (Ekstern)
Pages: 6-10
Publication date: 2002
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Publication information
Journal: Dansk Veterinærtidsskrift
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BFI (2013): BFI-level 1

Influenza A virus i et zoonotisk perspektiv

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Dybkær, K. (Ekstern), Handberg, K. J. (Ekstern), Munch, H. (Ekstern), Bøtner, A. (Intern), Jørgensen, P. H. (Ekstern)
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Publication information
Journal: Dansk Veterinærtidsskrift
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BFI (2013): BFI-level 1

Influenza A virus i et zoonotisk perspektiv

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Dybkær, K. (Ekstern), Handberg, K. J. (Ekstern), Munch, H. (Ekstern), Bøtner, A. (Intern), Jørgensen, P. H. (Ekstern)
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Journal: Dansk Veterinærtidsskrift
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BFI (2014): BFI-level 1
BFI (2013): BFI-level 1

Influenza A virus i et zoonotisk perspektiv

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Dybkær, K. (Ekstern), Handberg, K. J. (Ekstern), Munch, H. (Ekstern), Bøtner, A. (Intern), Jørgensen, P. H. (Ekstern)
Pages: 6-10
Publication date: 2002
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Publication information
Journal: Dansk Veterinærtidsskrift
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BFI (2013): BFI-level 1

Influenza A virus i et zoonotisk perspektiv

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Dybkær, K. (Ekstern), Handberg, K. J. (Ekstern), Munch, H. (Ekstern), Bøtner, A. (Intern), Jørgensen, P. H. (Ekstern)
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Journal: Dansk Veterinærtidsskrift
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Issue number: 6
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BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
BFI (2013): BFI-level 1
Investigation into the susceptibility of saithe Pollachius virens to infectious salmon anaemia virus (ISAV) and their potential role as a vector for viral transmission

Wild-caught saithe Pollachius virens were experimentally exposed to an isolate of infectious salmon anaemia virus (ISAV) of Norwegian origin. Mortality attributable to ISAV did not occur following exposure by intra-peritoneal (i.p.) injection of virus or by cohabitation with ISAV-infected Atlantic salmon Salmo salar. Despite the individual testing of 120 ISAV-exposed saithe, ISAV was not detectable using RT-PCR, the most sensitive ISAV diagnostic tool demonstrated to date. Furthermore, saithe exposed to ISAV-infected salmon were not capable of transmitting virus when transferred to tanks containing naive salmon. Thus saithe appear to be resistant to this Norwegian isolate of ISAV and incapable of supporting its replication. Saithe which co-exist with salmon in and around aquaculture facilities are considered unlikely to have a significant impact on the epizootiology of ISAV.
Måling af biotilgængeligt kviksølv med en bakteriel biosensor

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Rasmussen, L. D. (Intern), Sørensen, S. J. (Ekstern)
Publication date: 2002
Main Research Area: Technical/natural sciences

Publication information
Journal: Miljøforskning
Volume: 53
Original language: Danish
Source: orbit
Source-ID: 229930
Publication: Research - peer-review › Journal article – Annual report year: 2002

Mistanke om klassisk svinepest
Molecular methods for assessing and manipulating the diversity of microbial populations and processes

State: Published
Organisations: National Food Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Sørensen, S. J. (Ekstern), de Lipthay, J. R. (Ekstern), Müller, A. K. (Intern), Barkay, T. (Ekstern), Hansen, L. H. (Ekstern), Rasmussen, L. D. (Intern)
Number of pages: 640
Publication date: 2002

Host publication information
Title of host publication: Enzymes in the Environment
Publisher: C R C Press LLC
Edition: 1
ISBN (Print): 978-0824706142
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 242382
Publication: Research - peer-review › Book chapter – Annual report year: 2002

PCR detection of classical swine fever virus in meat juice

State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Uttenthal, Å. (Intern)
Publication date: 2002

Host publication information
Title of host publication: 5th ESVV Pestivirus symposium
Porcine B-cells recognize epitopes that are conserved between the structural proteins of American- and European-type porcine reproductive and respiratory syndrome virus

By selecting phage display libraries with immune sera from experimentally infected pigs, porcine B-cell epitopes in the open reading frame (ORF) 2, 3, 5 and 6 proteins of European-type porcine reproductive and respiratory syndrome virus (PRRSV) were identified. The sequences of all the epitopes were well conserved in European-type PRRSV and even between European- and American-type PRRSV. Accordingly, sera from pigs infected with American-type PRRSV cross-reacted with the European-type epitopes. Thus, this study showed, for the first time, the presence of highly conserved epitopes in the matrix protein and envelope glycoproteins of PRRSV. ORF5 and 6 epitopes localized to protein parts that are predicted to be hidden in PRRSV virions. In contrast, ORF2 and 3 epitopes localized to putative protein ectodomains. Due to the interesting localization, the sequence surrounding the ORF2 and 3 epitopes was subjected to closer scrutiny. A heptad motif, VSRRRIYQ, which is present in a single copy in ORF2 and 3 proteins, was identified; this arrangement is completely conserved in all European-type PRRSV sequences available. The VSRRRIYQ repeat motif colocalized closely...
with one of the ORF2 epitopes and secondary structure modelling showed that this segment of the ORF2 protein could form an amphipathic helix. Intriguingly, a mutation associated with virulence/attenuation of an American vaccine strain of PRRSV also localized to this ORF2 protein segment and affected the hydrophobic face of the predicted amphipathic helix. Further work is needed to determine whether these findings delineate a functional domain in the PRRSV ORF2 protein.

**General information**
- **State:** Published
- **Organisations:** Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Technical University of Denmark
- **Authors:** Oleksiewicz, M. B. (Ekstern), Bøtner, A. (Intern), Normann, P. (Intern)
- **Pages:** 1407-1418
- **Publication date:** 2002
- **Main Research Area:** Technical/natural sciences

**Publication information**
- **Journal:** Journal of General Virology
- **Volume:** 83
- **Issue number:** 6
- **ISSN (Print):** 0022-1317
- **Ratings:**
  - BFI (2018): BFI-level 1
  - Web of Science (2018): Indexed yes
  - BFI (2017): BFI-level 1
  - Web of Science (2017): Indexed yes
  - BFI (2016): BFI-level 1
  - Scopus rating (2016): CiteScore 2.93 SJR 1.499 SNIP 0.886
  - BFI (2015): BFI-level 1
  - Scopus rating (2015): SJR 1.729 SNIP 1.007 CiteScore 3.26
  - Web of Science (2015): Indexed yes
  - BFI (2014): BFI-level 1
  - Scopus rating (2014): SJR 1.683 SNIP 1.059 CiteScore 3.25
  - Web of Science (2014): Indexed yes
  - BFI (2013): BFI-level 1
  - Scopus rating (2013): SJR 1.749 SNIP 1.161 CiteScore 3.64
  - ISI indexed (2013): ISI indexed yes
  - Web of Science (2013): Indexed yes
  - BFI (2012): BFI-level 1
  - Scopus rating (2012): SJR 1.518 SNIP 1.038 CiteScore 3.28
  - ISI indexed (2012): ISI indexed yes
  - Web of Science (2012): Indexed yes
  - BFI (2011): BFI-level 1
  - Scopus rating (2011): SJR 1.675 SNIP 1.149 CiteScore 3.6
  - ISI indexed (2011): ISI indexed yes
  - Web of Science (2011): Indexed yes
  - BFI (2010): BFI-level 1
  - Scopus rating (2010): SJR 1.657 SNIP 1.058
  - Web of Science (2010): Indexed yes
  - BFI (2009): BFI-level 1
  - Scopus rating (2009): SJR 1.644 SNIP 1.13
  - Web of Science (2009): Indexed yes
  - BFI (2008): BFI-level 1
  - Scopus rating (2008): SJR 1.636 SNIP 1.068
  - Web of Science (2008): Indexed yes
  - Scopus rating (2007): SJR 1.581 SNIP 1.135
  - Web of Science (2007): Indexed yes
  - Scopus rating (2006): SJR 1.688 SNIP 1.127
  - Web of Science (2006): Indexed yes
Post Weaning Multisystemic Wasting Syndrome in Denmark

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research
Authors: Hassing, A. (Ekstern), Bøtner, A. (Intern), Ladekjær-Mikkelsen, A. (Ekstern), Bækbo, P. (Ekstern), Jorsal, S. E. L. (Intern), Bille-Hansen, V. (Intern)
Number of pages: 173
Publication date: 2002

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Title of host publication: Proceeding of the 17th International Pig Veterinary Congress
Main Research Area: Technical/natural sciences
Conference: The 17th International Pig Veterinary Congress, Iowa, 01/01/2002
Source: orbit
Source-ID: 241433
Publication: Research › Article in proceedings – Annual report year: 2002

Postweaning Multisystemic Wasting Syndrome in Denmark

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
Authors: Jorsal, S. E. L. (Intern), Bøtner, A. (Intern), Ladekjær-Mikkelsen, A. S. (Ekstern), Bækbo, P. (Ekstern), Jorsal, S. E. L. (Intern), Bille-Hansen, V. (Intern)
Pages: 4-7
Publication date: 2002

Post-weaning Multisystemic Wasting Syndrome (PMWS)

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
Authors: Jorsal, S. E. L. (Intern), Bøtner, A. (Intern), Ladekjær-Mikkelsen, A. (Ekstern), Bille-Hansen, V. (Intern)
Pages: 4-7
Publication date: 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.
Reproduction of postweaning multisystemic wasting syndrome (PMWS) in immunostimulated and non-immunostimulated 3-week-old piglets experimentally infected with porcine circovirus type 2 (PCV2)

Postweaning multisystemic wasting syndrome (PMWS) in swine is causally associated with the newly recognised pathogen, porcine circovirus type 2 (PCV2). In this study, 3-week-old SPF PCV2-seronegative piglets were inoculated intranasally with PCV2. The effect of immunostimulation on the induction of PMWS was investigated by immunisation with keyhole limpet hemocyanin (KLH) emulsified in incomplete Freunds adjuvant. The study was terminated 5 weeks after inoculation. While disease was not observed in the age-matched controls, two out of five non-immunised PCV2-infected piglets died on postinoculation day (PID) 21, and one was euthanized on PID 25 in moribund condition. These animals had appeared lethargic with persistent fever from PID 12 onwards. The euthanized pig appeared smaller than littermates and suffered from jaundice. At postmortem examination, gastric ulceration, icterus, and liver and thymus atrophy were observed. Furthermore, histological lesions of degenerating hepatocytes and hepatitis in combination with lymphoid depletion and syncytial cells in lymph nodes were consistent with the diagnosis of PMWS. One out of five immunostimulated PCV2-infected piglets was euthanized on PID 22 with convulsions after a period with wasting. This pig was lethargic from PID 14 onwards with persistent fever from PID 8 and transient dyspnoea. No differences in clinical signs, gross pathologic or histological findings were observed for the remaining non-immunostimulated and immunostimulated PCV2-infected piglets. All 10 PCV2-inoculated piglets seroconverted to PCV2 within 14 days after inoculation. By virus isolation, quantitative polymerase chain reaction (Q-PCR), and immunostaining of cryostat sections, it was demonstrated that lymphoid tissue contained abundant PCV2 antigen. Viral DNA load in serum samples was assessed by Q-PCR. All four PMWS-affected piglets had high levels of PCV2 DNA in serum, suggesting that there was a correlation between high levels of viral DNA in serum and the development of PMWS. In conclusion, infection with PCV2 caused PMWS in SPF piglets, however, the immunostimulation did not seem to play a critical role.
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 2.65 SJR 1.326 SNIP 1.208
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 1.393 SNIP 1.21 CiteScore 2.56
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 1.281 SNIP 1.262 CiteScore 2.54
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 1.438 SNIP 1.484 CiteScore 3
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 1.437 SNIP 1.579 CiteScore 3.18
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 1.562 SNIP 1.738 CiteScore 3.27
ISI indexed (2011): ISI indexed yes
Web of Science (2011): Indexed yes
BFI (2010): BFI-level 2
Scopus rating (2010): SJR 1.371 SNIP 1.476
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 2
Scopus rating (2009): SJR 1.29 SNIP 1.472
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 2
Scopus rating (2008): SJR 1.169 SNIP 1.3
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.043 SNIP 1.322
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.022 SNIP 1.401
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.078 SNIP 1.262
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 0.869 SNIP 1.259
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 0.913 SNIP 1.186
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 0.84 SNIP 1.112
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 0.833 SNIP 1.058
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 0.82 SNIP 1.088
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 0.703 SNIP 1.078
Original language: English
Freunds adjuvant, pig-viruses, postweaning multisystemic wasting syndrome (PMWS), immunostimulation, porcine circovirus type 2 (PCV2)
Status på PMWS situationen i Danmark

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State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Section for Veterinary Diagnostics, Division of Veterinary Diagnostics and Research
Authors: Ladekjær-Mikkelsen, A. (Ekstern), Bøtner, A. (Intern), Jorsal, S. E. L. (Intern), Bille-Hansen, V. (Intern), Hassing, A. (Ekstern), Bækbo, P. (Ekstern)
Pages: 22-23
Publication date: 2002
Main Research Area: Technical/natural sciences

The effect of heavy-metal pollution on the microbial community in subsurface soil

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, National Food Institute
Authors: Sørensen, S. J. (Ekstern), Rasmussen, L. D. (Intern), Müller, A. K. (Intern), de Lipthay, J. R. (Ekstern), Barkay, T. (Ekstern)
Publication date: 2002
Event: Poster session presented at DOE-NABIR PI workshop, Warrenton, VA, United States.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 242405
Publication: Research - peer-review › Poster – Annual report year: 2002

The genetic diversity of European type PRRSV is similar to that of the North American type but is geographically skewed within Europe

Porcine reproductive and respiratory syndrome virus (PRRSV) is a recently emerged pathogen. Two PRRSV genotypes exist, North American and European, which are only 55-70% identical at the nucleotide level. Previous studies have shown high nucleotide diversity in the North American genotype and low nucleotide diversity in the European genotype. Here, we analyzed the ORF5 and ORF7 genes for a large number of new European type PRRSV isolates in conjunction with existing database sequences. This new analysis showed that contrary to previous assumptions, genetic diversity is at least as high in the European genotype as in the North American genotype. Furthermore, we showed that genetic diversity of European type PRRSV has a marked geographical pattern, with exceptionally high genetic diversity among Italian sequences. The geographical pattern of diversity in relation to the epidemiology of PRRSV in Europe is discussed. Discrepancies between ORF5- and ORF7-based genealogies were observed, and further analysis of the data set confirmed the presence of recombination. We were therefore able to report the first observation of recombination in wild-type isolates of European genotype PRRSV

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Technical University of Denmark
Authors: Forsberg, R. (Ekstern), Storgaard, T. (Ekstern), Nielsen, H. S. (Ekstern), Oleksiewicz, M. B. (Ekstern), Cordioli, P. (Ekstern), Sala, G. (Ekstern), Hein, J. (Ekstern), Bætner, A. (Intern)
Pages: 38-47
Publication date: 2002
Main Research Area: Technical/natural sciences

Publication information
Journal: Virology
Volume: 299
Issue number: 1
ISSN (Print): 0042-6822
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Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): SJR 1.883 SNIP 0.96 CiteScore 3.47
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 1.789 SNIP 0.898 CiteScore 3.2
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 1.695 SNIP 0.919 CiteScore 3.14
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Scopus rating (2013): SJR 1.773 SNIP 0.959 CiteScore 3.37
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 1.751 SNIP 0.978 CiteScore 3.57
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 1.673 SNIP 0.93 CiteScore 3.32
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.712 SNIP 0.86
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.756 SNIP 0.906
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.983 SNIP 0.964
Scopus rating (2007): SJR 1.877 SNIP 0.987
Scopus rating (2006): SJR 1.802 SNIP 0.887
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.649 SNIP 0.899
Scopus rating (2004): SJR 1.58 SNIP 0.942
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 1.688 SNIP 0.961
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 1.616 SNIP 0.88
Web of Science (2002): Indexed yes
Scopus rating (2001): SJR 1.755 SNIP 0.906
Web of Science (2001): Indexed yes
Scopus rating (2000): SJR 1.806 SNIP 0.989
Web of Science (2000): Indexed yes
Scopus rating (1999): SJR 1.883 SNIP 0.995

Original language: English
European genotype, recombination, porcine reproductive and respiratory syndrome virus, PRRSV, genetic diversity, molecular epidemiology
Toxicity testing and chemical analyses of recycled fibre-based paper for food contact

Food-contact materials, including paper, have to comply with a basic set of criteria concerning safety. This means that paper for food contact should not give rise to migration of components, which can endanger human health. The objectives of this pilot study were, first, to compare paper of different qualities as food-contact materials and to perform a preliminary evaluation of their suitability from a safety point of view, and, second, to evaluate the use of different in vitro toxicity tests for screening of paper and board. Paper produced from three different categories of recycled fibres (B-D) and a raw material produced from virgin fibres (A) were obtained from industry, and extracts were examined by chemical analyses and diverse in vitro toxicity test systems. The products tested were either based on different raw materials or different treatments were applied. Paper category B was made from 40% virgin fibres, 40% unprinted cuttings from newspapers, and 20% de-inked newspapers and magazines. Paper categories C and D were based on newspapers and magazines. However, paper D was de-inked, whereas C was not. To identify constituents of the papers with a potential to migrate into foodstuff, samples of the paper products were extracted with either 99% ethanol or water. Potential migrants in the extracts were identified and semiquantified by GC-1R-MS or GC-HRMS. In parallel to the chemical analyses, a battery of four different in vitro toxicity tests with different endpoints were applied to the same extracts: (1) a cytotoxicity test using normal human skin fibroblasts. The test was based on measurements of the reduction of resazurin to resorufin by cellular redox processes and used as a screening test for acute or general toxicity; (2) a Salmonella/microsome assay (Ames test) as a screening test for mutagenic and potentially carcinogenic compounds; (3) a recombinant yeast cell bioassay as a screening test for compounds with oestrogenic activity; (4) an aryl hydrocarbon (Ah)-receptor assay (CALUX assay) as a screening test for compounds with dioxin-like activity. In addition, the papers were tested for microbial content and, in general, the microbiological load was quite low. The following microorganisms were counted and identified on both surface and homogenized pulp samples: the total number of aerobic bacteria, the number of aerobic and anaerobic spore formers, the number of Bacillus cereus/thuringiensis, and the number of yeast and moulds. The chemical analyses showed a significantly higher amount and different composition pattern of chemicals extracted with ethanol compared with water. Analyses of the ethanol extracts showed a distinctly smaller number and lower concentrations of chemicals in extracts prepared from sample A compared with extracts of samples B-D. The compounds identified in B-D were similar, but the amounts were lower in B compared with C and D. In accordance with the chemical analyses, the water extracts were less cytotoxic than the ethanol extracts. The extract prepared from virgin fibres was less cytotoxic than the extracts prepared from paper made from recycled fibres, and extracts prepared from C was the most cytotoxic. None of the extracts showed mutagenic activity. No conclusion about the oestrogenic activity could be made, because all extracts were cytotoxic to the test organism (yeast cells). Ethanol extracts of A and B showed a negligible positive response in the Ah-receptor assay at the highest nontoxic concentration, whereas C and D showed a more pronounced effect with C being the most potent. A comparable weak effect of water extracts of samples B-D was.

General information
State: Published
Organisations: Division of Toxicology and Risk Assessment, National Food Institute, Division of Food Chemistry, Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Division of Microbiology and Risk Assessment
Pages: 13-28
Publication date: 2002
Main Research Area: Technical/natural sciences

Publication information
Journal: Food Additives and Contaminants
Volume: 19
Issue number: Suppl. S
ISSN (Print): 0265-203X
Ratings:
BFI (2018): BFI-level 1
BFI (2017): BFI-level 1
BFI (2016): BFI-level 1
BFI (2015): BFI-level 1
BFI (2014): BFI-level 1
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 1
Udsætningsål og åleherpesvirus

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Olesen, N. J. (Intern)
Pages: 220
Publication date: 2002
Main Research Area: Technical/natural sciences

Publication information
Journal: Ferskvandsfiskeribladet
Volume: 100
Issue number: 10
ISSN (Print): 0015-0223
Vergleich von Methoden zum Nachweis einer Infektion mit verschiedenen Isolaten des Virus der Infektiösen Hämatopoetischen Nekrose (IHNV)

**General information**
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Bergmann, S. (Ekstern), Ariel, E. (Intern), Skall, H. F. (Intern), Fichtner, D. (Ekstern), Schlotfeldt, H. (Ekstern), Olesen, N. J. (Intern)
Pages: 385-389
Publication date: 2002
Main Research Area: Technical/natural sciences

**Publication information**
Journal: Berliner und Muenchener Tierarztliche Wochenschrift
Volume: 115
ISSN (Print): 0005-9366
Ratings:
- BFI (2018): BFI-level 1
- Web of Science (2018): Indexed yes
- BFI (2017): BFI-level 1
- Web of Science (2017): Indexed Yes
- BFI (2016): BFI-level 1
- Scopus rating (2016): SJR 0.308 SNIP 0.272 CiteScore 0.6
- BFI (2015): BFI-level 1
- Scopus rating (2015): SJR 0.438 SNIP 0.389 CiteScore 0.7
- BFI (2014): BFI-level 1
- Scopus rating (2014): SJR 0.391 SNIP 0.55 CiteScore 0.77
- BFI (2013): BFI-level 1
- Scopus rating (2013): SJR 0.366 SNIP 0.514 CiteScore 0.79
- ISI indexed (2013): ISI indexed yes
- BFI (2012): BFI-level 1
- Scopus rating (2012): SJR 0.362 SNIP 0.424 CiteScore 0.72
- ISI indexed (2012): ISI indexed yes
- BFI (2011): BFI-level 1
- Scopus rating (2011): SJR 0.386 SNIP 0.639 CiteScore 0.8
- ISI indexed (2011): ISI indexed yes
- BFI (2010): BFI-level 1
- Scopus rating (2010): SJR 0.344 SNIP 0.735
- BFI (2009): BFI-level 1
- Scopus rating (2009): SJR 0.471 SNIP 0.663
- BFI (2008): BFI-level 1
- Scopus rating (2008): SJR 0.385 SNIP 0.49
- Scopus rating (2007): SJR 0.313 SNIP 0.57
- Scopus rating (2006): SJR 0.276 SNIP 0.501
- Scopus rating (2005): SJR 0.317 SNIP 0.614
- Scopus rating (2004): SJR 0.406 SNIP 0.651
- Web of Science (2004): Indexed yes
- Scopus rating (2003): SJR 0.305 SNIP 0.626
Viral haemorrhagic septicaemia virus in the marine environment in Northern Europe

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Skall, H. F. (Intern), King, J. (Ekstern), Brudeseth, B. (Ekstern), Mellergaard, S. (Intern), Olesen, N. J. (Intern)
Publication date: 2002
Event: Abstract from Symposium on Viruses of Lower Vertebrates, Seattle, USA.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 241527
Publication: Research - peer-review › Journal article – Annual report year: 2002

Effects of mercury contamination on the culturable heterotrophic, functional and genetic diversity of the bacterial community in soil

This study investigates the effect of mercury contamination on the culturable heterotrophic, functional and genetic diversity of the bacterial community in soil. The changes in diversity were monitored in soil microcosms, enriched with 25 μg Hg(II) g(-1) soil, over a period of 3 months. The culturable heterotrophic diversity was investigated by colony morphology and colony appearance on solid LB medium. Functional diversity was analysed as sole carbon utilisation patterns in ECOplates. Genetic diversity was measured as bands on denaturing gradient gel electrophoresis (DGGE) gels obtained by purification of total soil DNA and amplification of bacterial 16S rDNA fragments by polymerase chain reaction. Concentrations of bioavailable and total mercury were measured throughout the experiment. The effect on the culturable heterotrophic and genetic diversity was very similar, showing an immediate decrease after mercury addition but then slowly increasing throughout the entire experimental period. Pre-exposure levels were not reached within the time span of this investigation. The DGGE band pattern indicated that a shift in the community structure was responsible for recovered diversity. When analysed by Shannon-Weaver indices, functional diversity was found to increase almost immediately after mercury addition and to remain at a level higher than the control soil for the rest of the experiment. The fraction of culturable heterotrophic bacteria increased from 1% to 10% of the total bacterial number as a result of mercury addition, and the mercury-resistant population increased to represent the entire heterotrophic population. (C) 2001 Federation of European Microbiological Societies. Published by Elsevier Science B.V.. All rights reserved.
Adaptation of the bacterial community to heavy metal contamination

General information
State: Published
Organisations: National Food Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Müller, A. K. (Intern), Rasmussen, L. D. (Intern), Sørensen, S. J. (Ekstern)
Pages: 49-53
Publication date: 2001
Main Research Area: Technical/natural sciences

Publication information
Journal: FEMS Microbiology Letters
Volume: 204
ISSN (Print): 0378-1097
Ratings:
BFI (2018): BFI-level 1

Original language: English
soil microcosm, microbial community, ECOplate, denaturing gradient gel electrophoresis, colony morphology

DOIs:
10.1016/S0168-6496(01)00111-8
Source: orbit
Source-ID: 242375
Publication: Research - peer-review › Journal article – Annual report year: 2001
### General information

**State:** Published  
**Organisations:** Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute  
**Authors:** Ladekjær-Mikkelsen, A. (Ekstern), Nielsen, J. (Ekstern), Storgaard, T. (Ekstern), Bøtner, A. (Intern), Allan, G. (Ekstern), McNeilly, F. (Ekstern)  
**Pages:** 759-760  
**Publication date:** 2001  
**Main Research Area:** Technical/natural sciences

### Publication information

**Journal:** Veterinary Record  
**Volume:** 148  
**ISSN (Print):** 0042-4900  
**Ratings:**  
- **BFI (2018):** BFI-level 1  
- **Web of Science (2018):** Indexed yes  
- **BFI (2017):** BFI-level 1  
- **Web of Science (2017):** Indexed Yes  
- **BFI (2016):** BFI-level 1  
- **Scopus rating (2016):** SJR 0.442 SNIP 0.692 CiteScore 0.3  
- **BFI (2015):** BFI-level 1  
- **Scopus rating (2015):** SJR 0.509 SNIP 0.794 CiteScore 0.39  
- **BFI (2014):** BFI-level 1  
- **Scopus rating (2014):** SJR 0.469 SNIP 0.839 CiteScore 0.41  
- **Web of Science (2014):** Indexed yes  
- **BFI (2013):** BFI-level 1  
- **Scopus rating (2013):** SJR 0.474 SNIP 0.821 CiteScore 0.5  
- **ISI indexed (2013):** ISI indexed yes  
- **Web of Science (2013):** Indexed yes  
- **BFI (2012):** BFI-level 1  
- **Scopus rating (2012):** SJR 0.491 SNIP 0.883 CiteScore 0.52  
- **ISI indexed (2012):** ISI indexed yes  
- **Web of Science (2012):** Indexed yes  
- **BFI (2011):** BFI-level 1  
- **Scopus rating (2011):** SJR 0.563 SNIP 0.9 CiteScore 0.62  
- **ISI indexed (2011):** ISI indexed yes  
- **Web of Science (2011):** Indexed yes  
- **BFI (2010):** BFI-level 1  
- **Scopus rating (2010):** SJR 0.574 SNIP 0.835  
- **Web of Science (2010):** Indexed yes  
- **BFI (2009):** BFI-level 1  
- **Scopus rating (2009):** SJR 0.642 SNIP 0.996  
- **Web of Science (2009):** Indexed yes  
- **BFI (2008):** BFI-level 2  
- **Scopus rating (2008):** SJR 0.553 SNIP 0.854  
- **Web of Science (2008):** Indexed yes  
- **Scopus rating (2007):** SJR 0.498 SNIP 0.814  
- **Web of Science (2007):** Indexed yes  
- **Scopus rating (2006):** SJR 0.64 SNIP 0.949  
- **Web of Science (2006):** Indexed yes  
- **Scopus rating (2005):** SJR 0.582 SNIP 0.923  
- **Web of Science (2005):** Indexed yes  
- **Scopus rating (2004):** SJR 0.618 SNIP 0.949  
- **Web of Science (2004):** Indexed yes
A molecular clock dates the common ancestor of European-type porcine reproductive and respiratory syndrome virus at more than 10 years before the emergence of disease

The disease caused by porcine reproductive and respiratory syndrome virus (PRRSV) emerged independently and almost simultaneously in Europe (1990) and North America (1987). The original reservoir of the virus and the date it entered the pig populations is not known. In this study, we demonstrate an accurate molecular clock for the European PRRSV ORF 3 gene, place the root in the genealogy, estimate the rate of nucleotide substitution, and date the most recent common viral ancestor of the data set to 1979; more than 10 years before the onset of the European epidemic. Based on these findings, we conclude that PRRSV virus most likely entered the pig population some time before the epidemic emergence of the virus, and hence, that emergence of European-type PRRSV is not the result of a recent species transmission event. Together, our results show that ORF3 sequencing is a valuable epidemiologic tool for examining the emergence and spread of PRRSV in Europe. As such, the panel of well-characterized and highly divergent ORF3 sequences described in this study provides a reference point for future molecular epidemiologic studies.
Assessment of a commercial kit collection for diagnosis of the fish viruses: IHNV, IPNV, SVCV and VHSV.

A commercial kit collection for the detection of the fish pathogenic viruses, VHSV, IHNV, IPNV, and SVCV, was assessed for its ability to detect isolates in selected panels of the respective viruses. The kit collection, which was based on fluorescence staining of infected cell cultures in tissue culture plates, fulfilled the promised requirements for the IHN kit only. The IPN, the SVC and especially the VHS kit were lacking in either specificity or sensitivity. The findings stress the need for commercial companies to carry out proper validation before market release.

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Ariel, E. (Intern), Olesen, N. J. (Intern)
Pages: 6-11
Publication date: 2001
Main Research Area: Technical/natural sciences

Publication information
Journal: European Association of Fish Pathologists. Bulletin
Volume: 21
Issue number: 1
ISSN (Print): 0108-0288
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): 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
Characterisation of European perch rhabdoviruses (P-267)

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Olesen, N. J. (Intern), Skall, H. F. (Intern), Kjær, T. E. (Intern), Johansson, T. (Ekstern), Björklund, H. (Ekstern)
Publication date: 2001
Event: Poster session presented at 10th International Conference on Diseases of Fish and Shellfish, Dublin, Ireland.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 242043
Publication: Research › Poster – Annual report year: 2001

Classical swine fever (CSF) marker vaccine - Trial I. Challenge studies in weaner pigs

Two commercial marker vaccines against classical swine fever virus (CSFV) and companion diagnostic tests were examined in 160 conventional pigs. To test the vaccines in a “worst case scenario”, group of 10 weaners were vaccinated using a single dose of an E2 (gp55) based vaccine at days -21, -14, -10 or -7, and subsequently challenged at day 0. The challenge virus was CSFV 277, originating from a recent outbreak of classical swine fever (CSF) in Germany. In all groups, only 5 out of 10 pigs were challenged; the remaining 5 pigs served as vaccinated contact controls. Also, three control groups, each consisting of 10 non-vaccinated pigs, were challenged in parallel to the vaccinated animals. CSFV could be isolated from all non-vaccinated pigs. Among these pigs 40% displayed a chronic course of the infection (virus positive for more than 10 days). Pigs vaccinated 21 or 14 days before challenge displayed no clinical signs of CSFV after challenge. However, they were still able to replicate CSFV when challenged, as measured by reisolation of CSFV from leukocytes of the directly challenged pigs. CSFV could be isolated from the leukocytes of 25% of the pigs vaccinated 21 days before challenge and 50% of the pigs vaccinated 14 days before challenge. Chronic infection was not observed, but transmission to one vaccinated contact pig occurred. From all pigs vaccinated 10 or 7 days before challenge, CSFV could be reisolated. We observed a chronic course of infection in 5% of pigs vaccinated 10 days before challenge and in 30% of pigs vaccinated 7 days before challenge. The mortality rate was 20% in the pigs vaccinated 10 days before challenge, and varied between 20 and 80% in pigs vaccinated 7 days prior to challenge. The contact animals had lower mortality (0-20%) than directly challenged pigs, probably mirroring the delayed time point of infection. There was thus some protection against clinical illness by both marker vaccines, but not a solid protection against infection and virus shedding. The efficacy of the vaccine was best if used 3 weeks before challenge and a clear correlation between time inter-Val from vaccination to challenge and the level of virus shedding was observed. Each vaccine had its own accompanying discriminatory ELISA, but 18% of the virus positive pigs never scroconverted in these tests.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Uttenthal, Å. (Intern), Le Potier, M. (Ekstern), Romero, L. (Ekstern), De Mia, G. (Ekstern), Floegel-Niesmann, G. (Ekstern)
Pages: 85-106
Publication date: 2001
Main Research Area: Technical/natural sciences
Publication information
Journal: Veterinary Microbiology
Volume: 83
Issue number: 2
ISSN (Print): 0378-1135
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed yes
Development of a functional test for estimating bacterial community adaptation to heavy metal contamination

**General information**
State: Published
Organisations: National Food Institute, Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Müller, A. K. (Intern), Rasmussen, L. D. (Intern), Sørensen, S. J. (Ekstern)
Publication date: 2001
Event: Poster session presented at SETAC, Copenhagen, Denmark.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 242404
Publication: Research - peer-review › Poster – 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 Eksotiske Virussygdomme, Division of Virology
Authors: Larsen, L. E. (Intern), Tjørnehøj, K. (Intern), Viuff, B. (Ekstern), Røntved, C. (Ekstern)
Publication date: 2001
Event: Abstract from RSV after 45 Years Symposium, Sergovia, Spanien.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 240797
Publication: Research › Conference abstract for conference – Annual report year: 2001

Effect of mercury on bacteria and flagellates in soil

**General information**
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Holtze, M. (Ekstern), Rasmussen, L. D. (Intern), Ekelund, F. (Ekstern), Johnsen, K. (Ekstern)
Publication date: 2001
Event: Poster session presented at 9th International Symposium on Microbial Ecology, Amsterdam, Netherlands.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 242403
Publication: Research - peer-review › Poster – Annual report year: 2001

Egtvedsyge i tre dambrug

**General information**
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Nylin, B. (Ekstern), Olesen, N. J. (Intern)
Pages: 126-132
Publication date: 2001
Main Research Area: Technical/natural sciences

**Publication information**
Journal: Ferskvandsfiskeribladet
Volume: 99
Issue number: 6
ISSN (Print): 0015-0223
Ratings:
ISI indexed (2013): ISI indexed no
ISI indexed (2012): ISI indexed no
ISI indexed (2011): ISI indexed no
Original language: Danish
Epitope mapping porcine reproductive and respiratory syndrome virus by phage display: the nsp2 fragment of the replicase polyprotein contains a cluster of B-cell epitopes

We screened phage display libraries of porcine reproductive and respiratory syndrome virus (PRRSV) protein fragments with sera from experimentally infected pigs to identify linear B-cell epitopes that are commonly recognized during infection in vivo. We identified 10 linear epitope sites (ES) 11 to 53 amino acids in length. In the replicase polyprotein, a total of eight ES were identified, six of which localized to the Nsp2 replicase polyprotein processing end product. In the structural proteins, a total of two ES were identified, in the ORF3 and ORF4 minor envelope glycoproteins. The ORF4 ES was previously identified by monoclonal antibody mapping (J. J. M. Meulenberg, A. P. van Nieuwstadt, A. van Essen-Zandenberg, and J. P. M. Langeveld, J. Virol, 71:6061-6067, 1997), but its immunogenicity had not been examined in pigs. We found that six experimentally PRRSV-infected pigs consistently had very high antibody titers against the ORF4 ES. In some animals, sera diluted 1:62,500 still gave weak positive enzyme immunoassay reactivity against the ORF4 ES. This hitherto unrecognized immunodominance likely caused phages displaying the ORF4 ES to outcompete phages displaying other ES during library screening with porcine sera and accounted for our failure to identify more than two ES in the structural genes of PRRSV. Genetic analysis showed that variable ES were also the most immunogenic in vivo. Serological analysis indicated differences in the immunoglobulin A responses between short-term and longer-term viremic pigs towards some ES. The implications of these findings for PRRSV diagnostics and immunopathogenesis are discussed.

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute, Stald/vægterservice
Authors: Oleksiewicz, M. (Ekstern), Bøtner, A. (Intern), Toft, P. (Ekstern), Normann, P. (Intern), Storgaard, T. (Ekstern)
Pages: 3277-3290
Publication date: 2001
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Virology
Volume: 75
Issue number: 7
ISSN (Print): 0022-538X
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): SJR 3.052 SNIP 1.131 CiteScore 4.42
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): SJR 3.286 SNIP 1.138 CiteScore 4.42
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): SJR 3.168 SNIP 1.219 CiteScore 4.4
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): SJR 3.468 SNIP 1.26 CiteScore 4.92
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): SJR 3.154 SNIP 1.227 CiteScore 5.2
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 2
Scopus rating (2011): SJR 3.399 SNIP 1.288 CiteScore 5.37
Epitope mapping Porcine Reproductive and Respiratory Syndrome Virus (PRRSV) by phage display: The nsp2 fragment of the replicase polyprotein contains a cluster of B-cell epitopes

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Oleksiewicz, M. B. (Ekstern), Bøtner, A. (Intern), Toft, P. (Ekstern), Normann, P. (Ekstern), Storgaard, T. (Ekstern)
Pages: 3277-3290
Publication date: 2001
Main Research Area: Technical/natural sciences

Publication information
Journal: Journal of Virology
Volume: 75
Issue number: 7
ISSN (Print): 0022-538X
Ratings:
BFI (2018): BFI-level 2
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 2
Scopus rating (2016): SJR 3.052 SNIP 1.131 CiteScore 4.42
Experimental infection of 3-week-old piglets with PCV2 altered the level of various peripheral blood leukocyte populations

General information
State: Published
Experimental susceptibility of Atlantic salmon Salmo salar and turbot Scophthalmus maximus to European freshwater and marine isolates of viral haemorrhagic septicaemia virus

A number of viral haemorrhagic septicaemia (VHS) virus isolates of European marine origin were shown to be of low pathogenicity or non-pathogenic to Atlantic salmon parr by waterborne infection. A reference freshwater VHS virus isolate known to be highly pathogenic to rainbow trout was also of low pathogenicity to Atlantic salmon. Virus was detected in some mortalities, however, demonstrating viral entry and replication. European marine VHS virus isolates do not appear to pose an imminent threat to the Atlantic salmon culture industry. Turbot were found to be refractive or of low susceptibility to marine VHS virus isolates of sprat origin and to a reference freshwater isolate, with mortalities of 0 to 13.5%. Conversely, turbot were susceptible by varying degrees to a number of VHS virus isolates taken from herring, with mortalities ranging from 16 to 68%. These results emphasise the vulnerability of turbot culture to the VHS virus isolates that are enzootic to the European marine environment.
Finfish in aquaculture and their diseases A retrospective view on the European Community.

General information
State: Published
Organisations: Section of Fish Diseases, Division of Poultry, Fish and Fur Animals, National Veterinary Institute
Authors: Ariel, E. (Intern), Olesen, N. J. (Intern)
Publication date: 2001
Event: Abstract from 10th International Conference on Diseases of Fish and Shellfish, Dublin, Ireland.
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 230627
Publication: Research › Journal article – 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
Authors: Larsen, L. E. (Intern)
Pages: 6-7
Publication date: 2001
Main Research Area: Technical/natural sciences

Publication information
Genetic diversity of Kinetoplastida (protozoa) in natural environments revealed by Denaturing Gradient Gel Electrophoresis

General information
State: Published
Organisations: Sektion for Eksotiske Virussygdomme, Division of Virology, National Veterinary Institute
Authors: Rasmussen, L. D. (Intern), Hansen, L. H. (Ekstern), Sørensen, S. J. (Ekstern)
Publication date: 2001
Main Research Area: Technical/natural sciences
Source: orbit
Source-ID: 242392
Publication: Research - peer-review › Paper – Annual report year: 2001

Projects:

AquaExcel II
National Veterinary Institute
Section for Virology
Period: 01/10/2015 → 01/10/2020
Number of participants: 1
Project participant: Mikkelsen, Susie Sommer (Intern)
Project

Investigation of transmission dynamics and virulence of new African Swine Fever Virus strains
National Veterinary Institute
Section for Virology
Section for Epidemiology
Period: 01/08/2015 → 31/07/2018
Number of participants: 4
Phd Student: Olesen, Ann Sofie (Intern)
Supervisor: Bøtner, Anette (Intern)
Boklund, Anette (Intern)
Main Supervisor: Rasmussen, Thomas Bruun (Intern)
Project

ParaFish Control
National Veterinary Institute
Section for Virology
Period: 01/04/2015 → 01/04/2020
Number of participants: 1
Project participant:
Mikkelsen, Susie Sommer (Intern)

Project

A plant-produced immunoenhanced pig vaccine against PRRS

National Veterinary Institute
Section for Immunology and Vaccinology
Section for Virology
Center for Electron Nanoscopy
Aarhus University
Boehringer Ingelheim Vetmedica, Inc.
Period: 01/01/2014 → 31/12/2018
Number of participants: 3
Acronym: Pigvac
Project participant:
Sørensen, Maria Rathmann (Intern)
Larsen, Lars Erik (Intern)
Approving authority:
Jungersen, Gregers (Intern)

Swine plasma immunoglobulins against post-weaning diarrhoea

National Veterinary Institute
Division of Veterinary Diagnostics and Research
Innate Immunology
Virology
Section for Immunology and Vaccinology
KiBif ApS

Videncenter for Svineproduktion, Landbrug & Fødevarer
Period: 01/10/2012 → 30/09/2015
Number of participants: 3
Project ID: 22619
Project participant:
Larsen, Lars Erik (Intern)
Hedegaard, Chris Juul (Intern)
Project applicant:
Heegaard, Peter Mikael Helweg (Intern)

Financing sources
Source: Public research council
Name of research programme: GUDP - Projekt. Udviklings- og demonstrationsprojekt med forskningsandel
Amount: 5,017,193.00 Danish Kroner
Year of approval: 2012

Relations
Activities:
5th European Veterinary Immunology Workshop
Mucosal Vaccines, Adjuvants & Delivery
15th International Conference on Production Diseases in Farm Animals
10th International Veterinary Immunology Symposium
10th Workshop in Protein.DTU
2nd international symposium on alternatives to antibiotics (ATA)
11th International Veterinary Immunology Symposium
Bayesian statistical analysis to assess serological testing strategies for avian influenza surveillance in Europe
Club 5 Joint Research 2012
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Virology
Animal Health and Veterinary Laboratories Agency
CVI Lelystad
SVA, Sweden
Period: 01/10/2012 → 31/10/2013
Number of participants: 1
Project ID: 22531
Project participant:
Larsen, Lars Erik (Intern)
Project

Akvakulturuddannelse
National Veterinary Institute
Section for Virology
National Institute of Aquatic Resources
Dansk Akvakultur
Danmarks Miljøundersøgelser
University of Copenhagen
Period: 01/05/2012 → 10/06/2014
Number of participants: 1
Project participant:
Boutrup, Torsten Snogdal (Intern)
Project

Molecular Tracing of Viral Pathogens in Aquaculture
National Veterinary Institute
Section for Virology
National Veterinary Institute
Agence nationale de la sécurité sanitaire, alimentation, environnement et travail
IFREMER
IRD
Friedrich Loeffler Institute
Period: 01/04/2012 → 31/03/2015
Number of participants: 1
Acronym: MOLTRAQ
Project participant:
Mikkelsen, Susie Sommer (Intern)
Project

Relations
Activities:
Workshop: Molecular tracing of viral diseases in aquaculture
MOLTRAQ Workshop
Project
Cooperative refining of the BioChip microarray into a routine investigative tool to address emerging viral diseases
Club 5 project

In two previous projects, UK BioChip and EU NoE project Epizone, we have established micro-array principles to detect rare or newly emerging viruses. In the UK BioChip project we established the technology and successfully provided evidence for its feasibility (Gurrala et al., 2009). In the latter, we extended the approach and adopted the technology to in situ synthesis printing for its punctuality, higher density and lower background.

The key aim of the proposes project is to refine the microarray probe coverage for transfer into a regular investigatative tool, particularly addressing avian diseases. The array will also be used to investigate several Diagnosis Not Reached (DNR) cases where multiple infections or emerging/novem viruses are suspected.

European Surveillance Network for Influenza in Pigs 3
This "European surveillance network for influenza in pigs 3 (ESNIP 3)" is in part a continuation of a surveillance network that was established during a previous EC concerted action (ESNIP 2, SSPE-022749). This second co-ordination action, which ran from 2005 until 2008, sought to achieve a better understanding of the epidemiology of swine influenza in Europe. Ten partners from eight different European countries (Belgium, The Netherlands, Italy, France, Germany, Spain, Bulgaria and UK) were involved including two industrial partners. Seven of these ESNIP 2 partners are members of the current ESNIP 3 consortium. ESNIP 3 will build upon the achievements of ESNIP 1 and 2 which were:
1) The standardisation of protocols for swine influenza (SI) virus (SIV) isolation, serology, antigenic and genetic typing of SIV isolates.
2) The selection and production of reference virus strains and (hyperimmune) sera. These were made available to all participants for preliminary sub typing of SIV isolates.
3) The establishment of a central SIV bank with a collection of recent isolates from various geographical areas in Europe.
4) The establishment of an electronic database with relevant information on the SIV isolates that were obtained in different countries during the life of the network.
5) The antigenic and genetic characterisation of a number of recent H1N1, H3N2 and H1N2 SIV isolates from different European countries.
6) The organisation of a serological survey to obtain preliminary data on the prevalence of different SIV subtypes in various European countries.

National Veterinary Institute
Division of Veterinary Diagnostics and Research
Virology
Period: 01/10/2010 → 31/10/2013
Number of participants: 1
ESNIP3
Acronym: ESNIP 3
Project ID: 22492
Project Manager, organisational:
Larsen, Lars Erik (Intern)
Documents:
ESNIP3_part_B.pdf

New tools and approaches to control Porcine Reproductive and Respiratory Syndrome in the EU and Asia
Virology
Division of Veterinary Diagnostics and Research
National Veterinary Institute
Ghent University
Consejo Superior de Investigaciones Cientificas
Centre de Recerca en Sanitat Animal
Parco Technologico Padano
Eidgenossiches Volkswirtschaftsdepartement
Panstwowy Instytut Weterynaryjny
University of Edinburgh
Secretary of State for Environment, Food and Rural Affairs
Stichting Dienst Landbouwkundig Onderzoek
Chinese Academy of Agricultural Sciences
Ministry of Agriculture and Rural Development
Boehringer Ingelheim Vetmedica, Inc.
Period: 01/01/2010 → 31/12/2014
Number of participants: 24
Contact person:
Rodrigo, Rafael (Ekstern)
Sanchez-Serrano, Jose Juan (Ekstern)
Domingo, Mariano (Ekstern)
Taranzi, Luigi (Ekstern)
Piaatti, Giancarlo (Ekstern)
Griot, Christian (Ekstern)
Summermatter, Kathrin (Ekstern)
Wijaszka, Tadeusz (Ekstern)
Kotelba, Barbara (Ekstern)
Waddell, Derek (Ekstern)
Campbell, Fiona (Ekstern)
Boriello, Peter (Ekstern)
Thorns, Christopher (Ekstern)
Bianchi, Andre (Ekstern)
Zoonotiske aspekter af Hepatitis E i Danmark

Virology
Division of Veterinary Diagnostics and Research
National Veterinary Institute
National Food Institute
FoodDTU
Statens Seruminstitute
Period: 01/01/2010 → 31/12/2012
Number of participants: 4
Project ID: 22442
Project participant:
Christensen, Laurids Siig (Intern)
Böttiger, Blenda (Ekstern)
Larsen, Hans Henrik (Ekstern)
Project Manager, organisational:
Larsen, Lars Erik (Intern)

Financing sources
Source: Forskningsprojekter - Fødevareministeriet
Name of research programme: Forskningsprojekter - Fødevareministeriet
Amount: 917,000.00 Danish Kroner

Inaktivering af virus i gødning på tørre overflader

Section of Swine fever etc.

Division of Virology
National Veterinary Institute
Period: 01/10/2009 → 30/09/2010
Number of participants: 2
Pig, classical swine fever, manure
Project ID: 22389
Project participant:
Elbrink, Heidi (Intern)
Project Manager, organisational:
Uttenthal, Åse (Intern)
The Network of Animal Disease Infectiology Research Facility
NADIR aims to facilitate the development of Europe's high level bio-containment facilities for which there is a strong demand from both the public and private sectors in the field of medical and veterinarian research, which have to respond to upgraded ethical and safety regulations whilst providing reliable answers in term of physiopathology for emerging infectious diseases (diagnosis, transmission conditions, risk analysis, therapeutic targets) or for vaccines and therapeutic trials.

National Veterinary Institute
Section for Virology
Period: 01/05/2009 → 30/04/2013
Number of participants: 1
Acronym: NADIR
Project participant:
Boutrup, Torsten Snogdal (Intern)

Improve tools and strategies for the prevention and control of classical swine fever
7th Framework programme
Research project aiming at the use of chimeric, live DIVA vaccines for practical use in wild boar and domestic pigs.

National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virusydomme
Centrum voor Onderzoek in Diergeneeskunde en Agrochemie
Agence Française de Sécurité Sanitaire des Aliments
CAO-DVMP
CVI Lelystad
Fort Dodge
Friedrich Loeffler Institute
ISZ
Institute of Virology and Immunology
ONCFS
SCU
SVA
Stiftung Tierärztliche Hochschule Hannover
Helmholtz Centre for Environmental Research
Period: 01/03/2009 → 28/02/2013
Number of participants: 2
DIVA vaccine, swine fever
Acronym: CSFV_goDIVA
Project ID: 22371
Number of related Ph.D. students: 1
Project participant:
Utenthal, Åse (Intern)
Rangelova, Desislava Yordanova (Intern)

Relations
Activities:
Dissemination on CSFV_goDIVA

Project

**Betydning af tidlig kontakt for kalvens velfærd**

Virology

Division of Veterinary Diagnostics and Research

National Veterinary Institute

Aarhus University

Period: 01/01/2009 → 31/12/2012

Number of participants: 2

Project ID: 22394

Project participant:

Larsen, Lars Erik (Intern)

Project Manager, organisational:
Jensen, Margit Bak (Ekstern)

**Financing sources**

Source: Forsk. Private danske - Fonde

Name of research programme: Forsk. Private danske - Fonde

Amount: 536,213.00 Danish Kroner

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**Indsættelsesstrategi, lungebetaændelse eller intensiv fodring som årsag til leverbylder**

Virology

Division of Veterinary Diagnostics and Research

National Veterinary Institute

AgroTech A/S

Period: 01/01/2009 → 12/07/2014

Number of participants: 3

Project ID: 22393

Project participant:

Larsen, Lars Erik (Intern)

Graumann, Anne Mette (Ekstern)

Project Manager, organisational:
Jungersen, Mogens Vestergaard (Intern)

**Financing sources**

Source: Forsk. Private danske - Fonde

Name of research programme: Forsk. Private danske - Fonde

Amount: 168,000.00 Danish Kroner

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**Improved vaccination strategies in marine aquaculture**

Section of Fish Diseases

Division of Poultry, Fish and Fur Animals

National Veterinary Institute

National Institute of Aquatic Resources

University of Copenhagen

Danish Aquaculture Association
Targeted Design of DIVA Vaccines Using Reverse Genetics

This project involves research to provide the tools needed for the establishment of genetically modified pestiviruses engineered specifically for the requirements of the Differentiate Infected from Vaccinated Animals (DIVA) principle. New innovative strategies are needed to facilitate construction of stable infectious pestivirus clones in order to obtain genetically modified pestiviruses from a wider range of pestiviral strains. The novel full-genome amplification strategy for pestiviruses, that our group has developed recently opens new ways for targeted design of chimeric pestiviruses specifically tailored for use as DIVA vaccines against classical swine fever (CSF). In this project, this novel generic strategy for amplification of pestiviruses will be combined with the innovative BAC (bacterial artificial chromosome) technology. This allows construction of stable infectious clones of large RNA viruses and facilitates specific genetic manipulation hence a new set of molecular tools can be established, which will give increased flexibility in design of new modified pestiviruses for the future generation of DIVA vaccines. Using this strategy, for targeted design of genetically modified pestiviruses, the work can be expedited and focused in principal on any pestiviral strain and hence is not limited to the availability of an existing infectious clone. The long RT-PCR strategy will significantly simplify and streamline the workflow and pave the way for in vitro characterisation and in vivo testing of new and improved DIVA vaccine candidates.
EPIZONE WP 4.1 : PCR diagnostics

PCR diagnostics is an important part of routine diagnostics as well as for research purposes

Virology
Division of Veterinary Diagnostics and Research
National Veterinary Institute
Period: 01/06/2006 → 01/06/2011
Number of participants: 2
classical swine fever, PCR, pig, diagnostics
Project ID: 22081_130597
Project participant:
Rasmussen, Thomas Bruun (Intern)
Uttenthal, Åse (Intern)

Financing sources
Source: Forskningsrådene - Andre
Name of research programme: Forskningsrådene - Andre
Amount: 2,200,000.00 Danish Kroner

EPIZONE WP 7.3 : Clinical Support systems for Classical swine fever

To analyse the clinical scoring system which is the base for the clinical suspicion for classical swine fever (CSFV). Using computer based comparison and weighed data sampling for both CSFV as other febrile diseases an international disease detection system is produced. The server based system is running in Wageningen University, The Netherlands.

Sektion for Eksotiske Virussygdomme
Division of Virology
National Veterinary Institute
Period: 01/06/2006 → 01/06/2011
Number of participants: 3
classical swine fever, clinical support system, diagnosis
Acronym: CSS-CSFV
Project ID: 22088_130607
Project participant:
Nielsen, Jens (Intern)
Lohse, Louise (Intern)

Project Manager, organisational:
Uttenthal, Åse (Intern)

Financing sources
Source: Forsk. EU - Rammeprogram
Name of research programme: Forsk. EU - Rammeprogram
Amount: 300,000.00 Danish Kroner

Activities:
Positive-Strand RNA Viruses (N1)
Period: 1 May 2016 → 5 May 2016
Camille Melissa Johnston (Participant)
National Veterinary Institute
Section for Virology

Related event
Positive-Strand RNA Viruses (N1)
01/05/2016 → 05/05/2016
Austin, Texas, United States
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

PhD Social committee (External organisation)
Period: Apr 2016 → …
Camille Melissa Johnston (Participant)
National Veterinary Institute
Section for Virology

Description
Social committee for PhD students at DTU Vet

Related external organisation
PhD Social committee
Activity: Membership › Membership of committees, commissions, boards, councils, associations, organisations, or similar

Virus Y-PRV2 A new piscine orthoreovirus in rainbow trout: establishment of challenge model and long term pathogenetic study
Period: 30 Nov 2015
Niccolò Vendramin (Speaker)
National Veterinary Institute
Section for Virology
Documents:
Virus Y final

Related event
DAFINET and ProFish Workshop
17/11/2015 → 18/11/2015
København, Denmark
Activity: Talks and presentations › Conference presentations

DAFINET and ProFish Workshop
Period: 17 Nov 2015 → 18 Nov 2015
Tine Moesgaard Iburg (Participant)
National Veterinary Institute
Section for Virology

Related event
DAFINET and ProFish Workshop
17/11/2015 → 18/11/2015
København, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.
Aquaexcel 2020: Kick off meeting 2015
Period: 1 Nov 2015 → 3 Nov 2015
Tine Moesgaard Iburg (Participant)
National Veterinary Institute
Section for Virology

Related event
Aquaexcel 2020: Kick off meeting 2015
01/11/2015 → 03/11/2015
Montpellier, France
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

EURL-Fish training course
Period: 12 Oct 2015
Tine Moesgaard Iburg (Organizer)
National Veterinary Institute
Section for Virology

Related event
EURL-Fish training course: Introduction to histopathology in fish diseases
12/10/2015 → 15/10/2015
Copenhagen, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

17th International Conference on Diseases of Fish and Shellfish
Period: 7 Sep 2015 → 11 Sep 2015
Niccolò Vendramin (Organizer)
National Veterinary Institute
Section for Virology

Description
Organization of a specific WS on "Fish health in Mediterranean Aquaculture, past mistakes and future challenges" within the 17th EAFP conference
Documents:
Fish health in Mediterranean Aquaculture leaflet

Related event
17th International Conference on Diseases of Fish and Shellfish
07/09/2015 → 11/09/2015
Las Palmas, Spain
Activity: Attending an event › Participating in or organising a conference

17th International Conference on Diseases of Fish and Shellfish
Period: 7 Sep 2015 → 11 Sep 2015
Tine Moesgaard Iburg (Participant)
National Veterinary Institute
Section for Virology

Related event
17th International Conference on Diseases of Fish and Shellfish
07/09/2015 → 11/09/2015
Las Palmas, Spain
Activity: Attending an event › Participating in or organising a conference
17th International Conference on Diseases of Fish and Shellfish
Period: 7 Sep 2015 → 11 Sep 2015
Susie Sommer Mikkelsen (Speaker)
National Veterinary Institute
Section for Virology

17th International Conference on Diseases of Fish and Shellfish
07/09/2015 → 11/09/2015
Las Palmas, Spain
Activity: Talks and presentations › Conference presentations

Related event

Workshop of the African and Classical Swine Fever National Reference Laboratories
09/06/2015 → 10/06/2015
Madrid, Spain
Activity: Talks and presentations › Conference presentations

Description
Next Generation Sequencing of Classical Swine Fever Virus

Related event

19th Annual Meeting of the National Reference Laboratories for Fish Diseases
Susie Sommer Mikkelsen (Speaker)
National Veterinary Institute
Section for Virology

19th Annual Meeting of the National Reference Laboratories for Fish Diseases
27/05/2015 → 28/05/2015
København, Denmark
Activity: Talks and presentations › Conference presentations

19th Annual Workshop for national reference laboratories for fish diseases
Niccolò Vendramin (Participant)
National Veterinary Institute
Section for Virology

Description
4 Scientific talks and 1 coauthorship at the Annual workshop for national reference laboratories for fish diseases
Documents:
3-Update Med disease 2014 Niven
3- Parafish Control Niven
1-Proficiency test 2015
2-Training courses 2015
1- Overview of the disease situation and surveillance in Europe in 2014

Related event

19th Annual Workshop for national reference laboratories for fish diseases
27/05/2015 → 28/05/2015
Copenhagen, Denmark
Activity: Attending an event › Participating in or organising a conference

19th Annual Workshop for national reference laboratories for fish diseases
Tine Moesgaard Iburg (Participant)
National Veterinary Institute
Section for Virology

Related event

19th Annual Workshop for national reference laboratories for fish diseases
27/05/2015 → 28/05/2015
Copenhagen, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Workshop: Molecular tracing of viral diseases in aquaculture
Period: 26 Jan 2015 → 30 Jan 2015
Susie Sommer Mikkelsen (Speaker)
National Veterinary Institute
Section for Virology

Description
Workshop: Molecular tracing of viral diseases in aquaculture
Documents:
Program of MOLTRAQ workshop in Montpellier Jan 2015 16.12.14

Related event

Workshop: Molecular tracing of viral diseases in aquaculture
26/01/2015 → 30/01/2015
Montpellier, France
Activity: Talks and presentations › Conference presentations

Carp Edema Virus Workshop
Period: 12 Jan 2015 → 13 Jan 2015
Susie Sommer Mikkelsen (Participant)
National Veterinary Institute
Section for Virology

Description
A total of 20 participants from 11 countries attended the meeting over the two days period. The workshop combined different single oral presentations and sessions with general discussions. The workshop was organized and held due to the increasing amount of diagnostic cases where CEV was detected in diseased cyprinids (both Koi and common carp). The primary aim of the workshop was to share knowledge, diagnostic protocols and material among participants and evaluate different strategies on how to tackle this issue.

Carp Edema Virus Workshop

Related event

Carp Edema Virus Workshop
12/01/2015 → 13/01/2015
København, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

**CEV Meeting**
**Period:** 12 Jan 2015 → 13 Jan 2015
**Niccolò Vendramin (Organizer)**
National Veterinary Institute
Section for Virology

**Description**
Organization of international 2 days workshop on Carp Edema Virus CEV
Documents:
Booklet final

**Related event**
**CEV Meeting: Carp Edema Virus - CEV Workshop**
12/01/2015 → 13/01/2015
Copenhagen, Denmark
Activity: Attending an event › Participating in or organising a conference

**Journal of General Virology (Journal)**
**Period:** 2014 → 2017
**Graham Belsham (Editor)**
National Veterinary Institute
Section for Virology

**Description**
as per title

**Related journal**

**Journal of General Virology**
0022-1317
BFI (2018): BFI-level 1, Scopus rating (2016): CiteScore 2.93 SJR 1.499 SNIP 0.886, ISI indexed (2013): ISI indexed yes,
Web of Science (2018): Indexed yes
Central database
Activity: Research › Journal editor

**Journal of General Virology (Journal)**
Graham Belsham (Editor)
National Veterinary Institute
Section for Virology

**Description**
Guest Editor

**Related journal**

**Journal of General Virology**
0022-1317
BFI (2018): BFI-level 1, Scopus rating (2016): CiteScore 2.93 SJR 1.499 SNIP 0.886, ISI indexed (2013): ISI indexed yes,
Web of Science (2018): Indexed yes
Central database
Activity: Research › Peer review of manuscripts
Dafinet 2014
Period: 11 Nov 2014 → 13 Nov 2014
Morten Sichlau Bruun (Participant)
National Veterinary Institute
Section for Virology

Related event
Dafinet 2014: Fish models in Research
Frederiksberg, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Antibiotics and Antibiotic Resistance in Aquaculture
Period: 27 Oct 2014
Morten Sichlau Bruun (Lecturer)
National Veterinary Institute
Section for Virology

Related event
24201 Diseases and Veterinary Aspects Related to Aquaculture
01/09/2014 → 01/12/2014
Frederiksberg, Denmark
Activity: Talks and presentations › Conference presentations

Molecular tracing of aquatic viruses - MOLTRAQ
Period: 14 Oct 2014
Susie Sommer Mikkelsen (Lecturer)
National Veterinary Institute
Section for Virology

Related event
9th International Symposium on Viruses of Lower Vertebrates
01/10/2014 → 04/10/2014
Malaga, Spain
Activity: Talks and presentations › Conference presentations

Description
Foredrag: MOLTRAQ - Tracing of VHSV in Denmark
Documents:
9th islvv abstract book

Related event
9th International Symposium on Viruses of Lower Vertebrates
01/10/2014 → 04/10/2014
Malaga, Spain
Activity: Talks and presentations › Conference presentations
Assessment of zoonotic potential of four European swine influenza viruses in the ferret model
Period: 17 Sep 2014 → 19 Sep 2014
Kristina Fobian (Lecturer)
National Veterinary Institute
Section for Virology
Section for Bacteriology, Pathology and Parasitology

Description
The reverse zoonotic events that introduced the 2009 pandemic influenza virus into swine herds have drastically increased the diversity of reassortants throughout Europe. The pandemic potential of these novel reassortments is unknown, hence necessitating enhanced surveillance of European swine herds and enhanced focus on risk assessment of these new viruses. In this study, four European swine influenza viruses were assessed for their zoonotic potential. Of the four viruses, two were enzootic viruses of subtype H1N2 (with avian-like H1) and H3N2 and two were new reassortants, one with avian-like H1 and human-like N2 and one with pandemic H1 and swine-like N2. All viruses replicated to high viral titers in nasal wash- and nasal turbinate samples from inoculated ferrets and transmitted efficiently by direct contact. Only the H3N2 virus transmitted to naïve ferrets via respiratory droplets. Growth kinetics using human bronchial cells showed that all four viruses were able to replicate to high titers. Further, the viruses revealed preferential binding to the α2,6-sialylated glycans and investigation of the antiviral susceptibility of the viruses revealed that they were all sensitive to neuraminidase inhibitors. These findings suggest that the investigated viruses have the potential to infect humans and further underline the need for continued surveillance as well as pandemic and zoonotic assessment of new influenza reassortants.

Related event
Influenza2014: One Influenza, One World, One Health: Bringing together veterinary and human influenza
09/09/2014 → 11/09/2014
Oxford, United Kingdom
Activity: Talks and presentations › Conference presentations

Real-time PCR for diagnostics and surveillance of Fish Diseases
Period: 15 Sep 2014 → 17 Sep 2014
Susie Sommer Mikkelsen (Organizer)
National Veterinary Institute
Section for Virology

Description
Afholdelse af og undervisning i Real-time PCR for diagnostics and surveillance of Fish Diseases for internationale deltagere fra 12 lande.
Documents:
Training course Report

Related event
Real-time PCR for diagnostics and surveillance of Fish Diseases
15/09/2014 → 17/09/2014
Frederiksberg C, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

EURL training course 2014
Period: 8 Sep 2014 → 12 Sep 2014
Morten Sichlau Bruun (Organizer)
National Veterinary Institute
Section for Virology

Related event
EURL training course 2014
08/09/2014 → 17/09/2014
Comparative analysis of sequences from PT 2013  
Period: 4 Jun 2014  
Susie Sommer Mikkelsen (Lecturer)  
National Veterinary Institute  
Section for Virology  

Related event  
18th Annual Workshop of the National Reference Laboratories for Fish Diseases  
03/06/2014 → 04/06/2014  
Frederiksberg C, Denmark  
Activity: Talks and presentations › Conference presentations  

Molecular tracing of aquatic viruses: Tracing of VHSV in Denmark  
Period: 4 Jun 2014  
Susie Sommer Mikkelsen (Lecturer)  
National Veterinary Institute  
Section for Virology  

Related event  
18th Annual Workshop of the National Reference Laboratories for Fish Diseases  
03/06/2014 → 04/06/2014  
Frederiksberg C, Denmark  
Activity: Talks and presentations › Conference presentations  

18th Annual Workshop of the National Reference Laboratories for Fish Diseases  
Period: 3 Jun 2014 → 4 Jun 2014  
Morten Sichlau Bruun (Participant)  
National Veterinary Institute  
Section for Virology  

Related event  
18th Annual Workshop of the National Reference Laboratories for Fish Diseases  
03/06/2014 → 04/06/2014  
Frederiksberg C, Denmark  
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.  

18th Annual Workshop of the National Reference Laboratories for Fish Diseases  
Period: 3 Jun 2014 → 4 Jun 2014  
Susie Sommer Mikkelsen (Speaker)  
National Veterinary Institute  
Section for Virology  

Related event  
18th Annual Workshop of the National Reference Laboratories for Fish Diseases  
03/06/2014 → 04/06/2014  
Frederiksberg C, Denmark  
Activity: Talks and presentations › Conference presentations
18th Annual Workshop of the National Reference Laboratories for Fish Diseases  
Period: 3 Jun 2014 → 4 Jun 2014  
Niccolò Vendramin (Participant)  
National Veterinary Institute  
Section for Virology  
Description  
Scientific talk at Annual Workshop for national reference lab for fish diseases  
Documents:  
3- update on Med. Niven Abstract  
3 - Training courses 2014  
4- PT 2013  
Related event  
18th Annual Workshop of the National Reference Laboratories for Fish Diseases  
03/06/2014 → 04/06/2014  
Copenhagen, Denmark  
Activity: Attending an event › Participating in or organising a conference

PMCV and PRV occurrence in wild and farmed fish in Denmark  
Period: 3 Jun 2014  
Susie Sommer Mikkelsen (Lecturer)  
National Veterinary Institute  
Section for Virology  
Related event  
18th Annual Workshop of the National Reference Laboratories for Fish Diseases  
03/06/2014 → 04/06/2014  
Frederiksberg C, Denmark  
Activity: Talks and presentations › Conference presentations

UPDATE ON FISH DISEASE SITUATION IN THE MEDITERRANEAN BASIN  
Period: 3 Jun 2014  
Niccolò Vendramin (Speaker)  
National Veterinary Institute  
Section for Virology  
Documents:  
3- update on Med. Niven Abstract  
Related event  
18th Annual Workshop of the National Reference Laboratories for Fish Diseases  
03/06/2014 → 04/06/2014  
Copenhagen, Denmark  
Activity: Talks and presentations › Conference presentations

MOLTRAQ Workshop  
Period: 19 May 2014 → 23 May 2014  
Susie Sommer Mikkelsen (Organizer)  
National Veterinary Institute  
Section for Virology  
Description  
Workshop for interne partnere m.h.p. at præsentere projekter og teknikker for samarbejdspartnere, efterfulgt af et progress meeeting.
Related event

MOLTRAQ Workshop
Period: 19 May 2014 → 23 May 2014
Morten Sichlau Bruun (Participant)
National Veterinary Institute
Section for Virology

Related event

MOLTRAQ Workshop
Period: 19/03/2014 → 23/03/2014
Berlin, Germany
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Related event

Workgroup for Sampling and Diagnostic Procedures for the Surveillance and Confirmation of KHV Disease
Period: 25 Feb 2014 → 26 Feb 2014
Susie Sommer Mikkelsen (Participant)
National Veterinary Institute
Section for Virology

Related event

Workgroup for Sampling and Diagnostic Procedures for the Surveillance and Confirmation of KHV Disease
Period: 25/02/2014 → 26/02/2014
Frederiksberg C, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Danish Fish Immunology Research Network (DAFINET) workshop
Period: 12 Nov 2013 → 14 Nov 2013
Morten Sichlau Bruun (Participant)
National Veterinary Institute
Section for Virology
National Institute of Aquatic Resources

Description
DAFINET Workshop, Fish Immunology: From Egg to Adult Fish

Related event

Danish Fish Immunology Research Network (DAFINET) workshop: Fish Immunology: From Egg to Adult Fish
Period: 12/11/2013 → 14/11/2013
Frederiksberg, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Dr Philos in Veterinary Sciences , 1. opponent (External organisation)
Period: 6 Nov 2013 → 7 Nov 2013
Åse Uttenthal (External examiner)
Section for Virology
National Veterinary Institute
Description
Dr Thesis Gelagay Ayelet Melasse: "Epidemiological investigation and molecular characterization of major viral diseases of livestock: Implication for disease control in Ethiopia"

1. opponent in Dr Philos Commitee. Veterinary University of Oslo

Body type: Evaluation comitee
Degree of recognition: International
Activity: Examinations and supervision › External examination

Aqua Excel
Period: 16 Oct 2013 → 18 Oct 2013
Susie Sommer Mikkelsen (Participant)

National Veterinary Institute

Section for Virology

Description
Main elements of the course:
The genome – introduction, sequencing, construction, annotation and comparative genome mapping. How genomic information can help to refine phenotyping. Identification and exploration of genomic regions associated with variation of aquaculture-related traits. Practical training.

Related event

Aqua Excel: Contribution of genomic approaches to the development of a sustainable aquaculture for temperate and Mediterranean fish
16/10/2013 → 18/12/2013
Rennes, France
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

EPIZONE Annual Meeting (External organisation)
Period: 2 Oct 2013 → 5 Oct 2013
Åse Uttenthal (Member)

National Veterinary Institute

Description
Member of Scientific Commitee, responsible for "Diagnostics"

Body type: Network of Excellence
Degree of recognition: International
Links:
http://www.epizone-eu.net/

Related external organisation

EPIZONE Annual Meeting
Activity: Membership › Membership in review committee

Dyreforsøgstilsynets mini-seminar
Period: 24 Sep 2013
Morten Sichlau Bruun (Participant)

National Veterinary Institute

Section for Virology

National Institute of Aquatic Resources

Related event
Dyreforsøgstilsynets mini-seminar: Vurdering af belastning af forsøgsdyr
24/09/2013 → 24/09/2013
Bagsværd, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

16th International Conference on Diseases of Fish and Shellfish
Period: 2 Sep 2013 → 5 Sep 2013
Susie Sommer Mikkelsen (Participant)
National Veterinary Institute
Section for Virology

Description
EAFP - 16th International Conference on Diseases of Fish and Shellfish.
Links:
http://eafp2013.fi/ (Congress website)

Related event
16th International Conference on Diseases of Fish and Shellfish
02/09/2013 → 06/09/2013
Tampere, Finland
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

16th International Conference on Diseases of Fish and Shellfish
Period: 2 Sep 2013
Torsten Snogdal Boutrup (Participant)
National Veterinary Institute
Section for Virology

Description
16th International Conference on Diseases of Fish and Shellfish.
Biannually Congress of the European Association of Fish Pathologists.

Related event
16th International Conference on Diseases of Fish and Shellfish
02/09/2013 → 06/09/2013
Tampere, Finland
Activity: Attending an event › Participating in or organising a conference

16th International Conference on Diseases of Fish and Shellfish
Period: 2 Sep 2013 → 6 Sep 2013
Morten Sichlau Bruun (Participant)
National Veterinary Institute
Section for Virology
National Institute of Aquatic Resources

Description
16th International Conference on Diseases of Fish and Shellfish.

Related event
16th International Conference on Diseases of Fish and Shellfish
02/09/2013 → 06/09/2013
Tampere, Finland
Activity: Attending an event › Participating in or organising a conference
Whole inactivated virus vaccine prototype protects against viral encephalopathy and retinopathy in european sea bass (D. labrax)
Period: 2 Sep 2013 → 6 Sep 2013
Niccolò Vendramin (Speaker)
National Veterinary Institute
Section for Virology

Description
Oral presentation at EAFP Conference semptember 2013 Tampere.
Documents:
C:\Users\Niven\Desktop\0101_001

Related event

16th International Conference on Diseases of Fish and Shellfish
02/09/2013 → 06/09/2013
Tampere, Finland
Activity: Talks and presentations › Conference presentations

16th International Symposium of the World Association for Veterinary Laboratory Diagnosticians
Period: 7 Jun 2013
Åse Uttenthal (Chairman)
National Veterinary Institute
Section for Virology

Description
Session 4, oral 7, Miscellaneous

Related event

16th International Symposium of the World Association for Veterinary Laboratory Diagnosticians
05/06/2013 → 08/06/2013
Berlin, Germany
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Concentrating antibodies towards BVDV from milk
Period: 6 Jun 2013
Åse Uttenthal (Lecturer)
National Veterinary Institute
Section for Virology

Description
Oral presentation

Related event

16th International Symposium of the World Association for Veterinary Laboratory Diagnosticians
05/06/2013 → 08/06/2013
Berlin, Germany
Activity: Talks and presentations › Conference presentations

Dyreforsøgstilsynets mini-seminar om fisk som forsøgsdyr
Period: 4 Jun 2013
Morten Sichlau Bruun (Participant)
National Veterinary Institute
Section for Virology
National Institute of Aquatic Resources

**Description**
Dyreforsøgstilsynets mini-seminar om fisk som forsøgsdyr

**Related event**
**Dyreforsøgstilsynets mini-seminar om fisk som forsøgsdyr**
04/06/2013 → 04/06/2013
Kastrup, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

**EURL Training courses. Report and topics for future courses.**
Period: 30 May 2013
Susie Sommer Mikkelsen (Lecturer)
National Veterinary Institute
Section for Virology
Documents:
17th Annual Meeting of the National Reference Laboratories for Fish Diseases

**Related event**
**17th Annual Workshop of the National Reference Laboratories for Fish Diseases**
29/05/2013 → 30/05/2013
Copenhagen, Denmark
Activity: Talks and presentations › Conference presentations

**MOLTRAQ - molecular epidemiology for fish diseases**
Period: 30 May 2013
Susie Sommer Mikkelsen (Lecturer)
National Veterinary Institute
Section for Virology

**Description**
Oral presentation.
Documents:
17th Annual Meeting of the National Reference Laboratories for Fish Diseases

**Related event**
**17th Annual Workshop of the National Reference Laboratories for Fish Diseases**
29/05/2013 → 30/05/2013
Frederiksberg, Denmark
Activity: Talks and presentations › Conference presentations

**17th Annual Workshop of the National Reference Laboratories for Fish Diseases**
Period: 29 May 2013 → 30 May 2013
Morten Sichlau Bruun (Participant)
National Veterinary Institute
Section for Virology
National Institute of Aquatic Resources

**Description**
17th Annual Workshop of the National Reference Laboratories for Fish Diseases.

**Related event**
**17th Annual Workshop of the National Reference Laboratories for Fish Diseases**
17th Annual Workshop of the National Reference Laboratories for Fish Diseases
Period: 29 May 2013 – 30 May 2013
Susie Sommer Mikkelsen (Speaker)
National Veterinary Institute
Section for Virology

Description
Oral presentation: MOLTRAQ - molecular epidemiology for fish diseases Oral presentation: EURL training courses. Report and topics for future courses

17th Annual Workshop of the National Reference Laboratories for Fish Diseases.

Related event

17th Annual Workshop of the National Reference Laboratories for Fish Diseases
29/05/2013 → 30/05/2013
Copenhagen, Denmark
Activity: Talks and presentations › Conference presentations

17th Annual Workshop of the National Reference Laboratories for Fish Diseases
Period: 29 May 2013 – 30 May 2013
Torsten Snogdal Boutrup (Speaker)
National Veterinary Institute
Section for Virology

Description
Årligt møde for de Europæiske referencelaboratorier for fiskesygdomme, med opdatering på diagnostik, forskning og sygdomssituation i Europa.

17th annual Workshop of the National Reference Laboratories for Fish Diseases. Copenhagen, Denmark, May 29-30, 2013.

Related event

17th Annual Workshop of the National Reference Laboratories for Fish Diseases
29/05/2013 → 30/05/2013
Copenhagen, Denmark
Activity: Talks and presentations › Conference presentations

Overlevelse af virus i miljøet
Period: 29 May 2013
Åse Uttenthal (Lecturer)
National Veterinary Institute
Section for Virology

Description
Lecturing veterinarians in the Veterinary Administration

Fødevarestyrelsens aktualitetskursus, Vejle, Danmark

Related external organisation

Unknown external organisation
Det er en virus! hvorfor bliver man syg?
Period: 3 May 2013
Åse Uttenthal (Lecturer)
National Veterinary Institute
Section for Virology

Description
Vilvorde laborantskole, dyrepasser klasse

Related event
Bestil en forsker: Forskningens døgn
02/05/2013 → 04/05/2013
Denmark
Activity: Talks and presentations › Conference presentations

Det er en virus! Hvorfor bliver man syg?
Period: 2 May 2013
Åse Uttenthal (Lecturer)
National Veterinary Institute
Section for Virology

Description
Ørestadens Gymnasium, København S

Related event
Bestil en forsker: Forskningens døgn
02/05/2013 → 04/05/2013
Denmark
Activity: Talks and presentations › Conference presentations

5th Meeting on Global Microbial Identifier
Period: 27 Feb 2013 → 28 Feb 2013
Susie Sommer Mikkelsen (Participant)
National Food Institute
National Veterinary Institute
Section for Virology

Description
GMI focuses on the use of genome sequencing techniques in a global system for microbiological identification and epidemiological surveillance

Links:
http://www.food.dtu.dk/english/News/2012/12/Invitation_5th_Meeting_on_Global_Microbial_Identifier (Link to invitation)

Related event
5th Meeting on Global Microbial Identifier
27/02/2013 → 28/02/2013
København, Denmark
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

Dissemination on CSFV_goDIVA
Period: 30 Jan 2013 → 31 Jan 2013
Åse Uttenthal (Organizer)
National Veterinary Institute
Section for Virology

Description
Dissemination meeting for stake holders, CODA-CERVA Ukkels, Brussels, Belgium

CSFV_goDIVA dissemination meeting
Links:
http://www.csfvaccine.org/ (CSFV_goDIVA project)

Related event
Dissemination on CSFV_goDIVA: Improve tools and strategies for the prevention and control of classical swine fever. 
31/01/2013 → …
Brussels, Belgium
Activity: Attending an event › Participating in or organising a conference

Svinepest i en globaliseret verden
Period: 29 Jan 2013
Åse Uttenthal (Invited speaker)
National Veterinary Institute
Section for Virology

Description
Talk on swine fevers for a group of pig farmers

Related event
Ø-Vet årsmøde
29/01/2013 → …
Ringsted, Denmark
Activity: Talks and presentations › Conference presentations

EUURL training course 2013
Period: 28 Jan 2013 → 31 Jan 2013
Susie Sommer Mikkelsen (Organizer)
National Veterinary Institute
Section for Virology

Description
Course responsible and teacher
Documents:
Training Course Report 2013

Related event
EUURL training course 2013: Advanced Bio-Molecular techniques and bio-informatics
28/01/2013 → 31/07/2013
Aarhus, Denmark
Activity: Attending an event › Participating in or organising a conference

Expert groups in Denmark with special reference to Classical and African swine fever
Period: 3 Dec 2012
Åse Uttenthal (Invited speaker)
National Veterinary Institute
Section for Virology
Related event

**Nordic-Baltic Veterinary Contingency Group: Expert group Ad hoc meeting**

03/12/2012 → 04/12/2012
Copenhagen, Denmark
Activity: Talks and presentations › Conference presentations

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**CoVetLab**

Period: 27 Nov 2012 → 28 Nov 2012
Susie Sommer Mikkelsen (Participant)
National Veterinary Institute
Section for Virology

**Description**
The aim of the workshop will be for CoVetLab members to share information (previous experiences/ current best practice, etc) about the use of microarrays and next generation sequencing for detection and characterization of diseases of unknown aetiology

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**CoVetLab: Emerging Approaches to Novel Pathogen Discovery**

27/11/2012 → 28/11/2012
Weybridge, United Kingdom
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

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**Workshop on ASFV**

Åse Uttenthal (Participant)
National Veterinary Institute
Section for Virology

**Description**
ASFV laboratory expert

ASFV workshop in Latvia

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**Workshop on ASFV: EU - Russian collaboration**

29/10/2012 → 31/10/2012
Sigunda, Latvia
Activity: Attending an event › Participating in or organising workshops, courses, seminars etc.

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**Svinepest - faglig dag for svinedyrlæger på Lindholm: Vesikulaere sygdomme hos gris**

Period: 28 Sep 2012
Louise Lohse (Speaker)
National Veterinary Institute
Section for Virology

**Description**
Foredrag for svinedyrlæger

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**Svinepest - faglig dag for svinedyrlæger på Lindholm: Vesikulaere sygdomme hos gris**

28/09/2012 → …
Denmark
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations
**9th International Congress of Veterinary Virology**

**Period:** 6 Sep 2012  
Åse Uttenthal (Speaker)  
National Veterinary Institute  
Section for Virology

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**Related event**

**9th International Congress of Veterinary Virology**  
04/09/2012 → 07/09/2012  
Madrid, Spain  
Activity: Talks and presentations › Conference presentations

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**Schmallenberg virus - et nyt virus hos drøvtyggere: Forekomst, spredning, klinik og diagnostik**

**Period:** 5 Sep 2012  
Louise Lohse (Lecturer)  
National Veterinary Institute  
Division of Virology  
Sektion for Eksotiske Virussygdomme

**Description**

Indlæg på Kvægkonference 2012  
Documents:  
Schmallenberg_virus_Kv._konference_05092012.docx

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**Related event**

**Kvægkonference 2012: Sikring af sunde og sygdomsfri dyr i kvægbruget**

04/09/2012 → …  
Bredsten, Denmark  
Activity: Talks and presentations › Conference presentations

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**Hvad er vigtigt for et stærkt beredskab - set fra en laboratoriedyrlæges indfaldsvinkel?**

**Period:** 26 Jul 2012  
Jens Nielsen (Speaker)  
National Veterinary Institute  
Section for Virology

**Description**

Mundtlig præsentation ved “Åben høring om det danske veterinære beredskab” arrangeret af Folketingets Udvalg for Fødeværer, Landbrug og Fiskeri. Høringen fandt sted i Landstingssalen på Christiansborg.

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**Unknown external organisation**  
Activity: Talks and presentations › Conference presentations

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**Studies of Classical Swine Fever in pigs based on experimental infections**

**Period:** 24 Jul 2012  
Åse Uttenthal (Lecturer)  
National Veterinary Institute  
Division of Virology  
Sektion for Eksotiske Virussygdomme
Description
Lecture given at Sichuan University, Chengdu, China

Invited lecture at Sichuan University
Links:
http://www.csfvaccine.org/ (project homepage)

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

Studies of Classical Swine Fever in pigs based on experimental infections
Period: 24 Jul 2012
Åse Uttenthal (Lecturer)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Lecture at Sichuan University, Chengdu, China

Lecturer for Phd students during a research stay at Sichuan University
Links:
http://www.csfvaccine.org/ (CSFV_goDIVA EU project)

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

6th Annual Meeting EPIZONE
Period: 13 Jun 2012
Åse Uttenthal (Participant)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
EPIZONE, 6th annual meeting "Viruses on the move"
Chairman of the session "Epidemiology and emerging diseases"
Links:
http://www.epizone-eu.net/ (EU Network of Excellence)

Related event

6th Annual Meeting EPIZONE
13/06/2012 → 14/06/2012
Brighton, United Kingdom
Activity: Attending an event › Participating in or organising a conference

National reference laboratories swine fevers
Period: 6 Jun 2012
Åse Uttenthal (Speaker)
National Veterinary Institute
Section for Virology
**Description**
The efficacy of CP7_E2alf: an animal study involving piglets from C-strain vaccinated sows. Rangelova, Nielsen, Strandbygaard, Blome, Uttenthal.

**Workshop for ASFV and CSFV laboratories**

**Related event**

**National reference laboratories swine fevers**
05/06/2012 → 08/12/2012
Hannover, Germany
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

**Virus og vaccination, hvorfor bliver man syg?**
Period: 19 Apr 2012
Åse Uttenthal (Lecturer)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Description**
"Bestil en forsker", populærvidenskabelig formidling. Foredrag for 270 elever fra 7-9 klasse, Lille Næstved skole, april 2012
Links:
http://forsk.dk/

**Related external organisation**

**Unknown external organisation**
Activity: Talks and presentations › Conference presentations

**Controlling CSFV without vaccination: CSFV control from an EU perspective**
Period: 18 Dec 2011
Åse Uttenthal (Lecturer)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Description**
Lecture at Shaoguan University, Guangdong, China

**Related external organisation**

**Unknown external organisation**
Activity: Talks and presentations › Conference presentations

**African Swine Fever experiments within NADIR (Event)**
Period: 6 Nov 2011
Jens Nielsen (Reviewer)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Related event**

**African Swine Fever experiments within NADIR: Interest, prospects, contributions and practical feasibilities at DTU Vet, Denmark**
**Improve tools and strategies for the prevention and control of classical swine fever (CSFV_goDIVA)**

*Period: 7 Jun 2010 → 10 Jun 2010*

Åse Uttenthal (Speaker)

National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Description**

During a "project fair" the CSFVgo_DIVA project was presented by an oral presentation. The project coordinator Frank Koenen was unable to participate in the meeting so as the deputy coordinator I gave the presentation of this EU Strep FP7 project.

**Place:** EPIZONE 4. annual meeting. Saint Malo, France

**Related external organisation**

Unknown external organisation

**Activity:** Talks and presentations › Conference presentations

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**Comparison of clinical and paraclinical parameters as tools for early diagnosis of classical swine fever**

*Period: 19 May 2010 → 20 May 2010*

Louise Lohse (Speaker)

National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Description**

Presentation of results achieved in animal experimental studies including CSFV in a current national research project.

**Place:** CSF annual meeting, Poland

**Related external organisation**

Unknown external organisation

**Activity:** Talks and presentations › Conference presentations

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**Evaluation of the influence of lyophilisation on ASF diagnostic tests – studies in Denmark**

*Period: 17 Jun 2009*

Thomas Bruun Rasmussen (Speaker)

National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Related event**

**Annual Meeting of the National African Swine Fever Laboratories**

17/06/2009 → 17/06/2009
Madrid, Spain

**Activity:** Talks and presentations › Talks and presentations in private or public companies and organisations

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**Comparison of early pathogenesis of CSFV-Glietorf and CSFV-Romania in Danish pigs**

*Period: 14 Jun 2009 → 15 Jun 2009*

Louise Lohse (Speaker)

National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Presentation of results achieved in a animal experimental study including CSFV in a current 3-year National research project.
Place: CSF annual meeting, Spain

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Genetic stability of pestivirus genomes cloned into BACs (EPIZONE): 3rd EPIZONE Annual Meeting "Crossing Borders"
Period: 13 May 2009
Thomas Bruun Rasmussen (Speaker)
Division of Virology
Sektion for Eksotiske Virussygdomme
National Veterinary Institute

Description
Genetic stability of pestivirus genomes cloned into BACs Thomas Bruun Rasmussen, DTU Vet Ilona Reimann, FLI Åse Uttenthal, DTU Vet Martin Beer, FLI Infectious cDNA clones are a prerequisite for directed genetic manipulations of pestivirus genomes to obtain attenuated pestiviruses designed as new modified live DIVA vaccine candidates against classical swine fever. However, the construction of new infectious pestivirus cDNA clones has been hampered due to the large size of the pestivirus genome and due to genetic instability of the cloned cDNA, which in combination with plasmid vectors tend to be unstable and deleterious in the bacterial host. Therefore, new strategies are needed to facilitate construction of stable infectious cDNA clones of pestivirus strains. In a collaborative research project, between DTU Vet and FLI, on the establishment of genetically modified pestiviruses engineered specifically for the DIVA principle, we cloned a series of complete pestivirus genomes, obtained by full-length RT-PCR, directly into the bacterial artificial chromosome (BAC) vector "pBeloBAC11". This BAC vector provides a markedly higher stability of cloned sequences in E. coli compared to plasmids that form the basis for the existing pestivirus cDNA clones. In this study, two of the newly constructed BAC clones were analysed for genetic stability of the cloned pestivirus genomes to demonstrate the suitability of the BAC vector for harbouring pestivirus genomes. Two BAC clones, comprising the complete genomes of BDV Gifhorn (pBeloGif3) and CSFV Paderborn (pBeloPader10) were passaged 15 times in E.coli representing at least 360 bacteria generations. From 15th passage of the BAC clones, the entire 5' and 3' ends of the cloned genomes and parts of the open reading frame were sequenced and compared to the sequences of the parent BAC clones. The sequenced areas represent approximately 20 % of the cloned genome. No mutations were observed after the extensive passaging of the cDNA clones in the bacterial host, indicating a highly stable system for cloning and maintenance of complete pestivirus genomes. This work was supported by the by the Danish Research Council for Technology and Production Sciences (DRCITPS grant 274-07-0198) and the EU Network of Excellence, EPIZONE (Contract No FOOD-CT-2006-016236).
Place: Antalya, Turkey
Degree of recognition: International

Related event
3rd Annual Meeting of EPIZONE
12/05/2009 → 15/05/2009
Antalya, Turkey
Activity: Talks and presentations › Conference presentations

Hepatitis E Virus - en ny zoonose?
Period: 8 May 2009 → 9 May 2009
Solvej Østergaard Breum (Speaker)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Virology

Description
Biomedicine

Period: 16 Feb 2009
Tanya von Rosen (Lecturer)
Division of Virology
Sektion for Eksotiske Virussygdomme
National Veterinary Institute

Description
Modul 2a: DIVA Diagnostic

Related external organisation

University of Copenhagen
Bülowsvej 17, 1780, Copenhagen, Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

Patobiologisk basiskursus - Virologi: RT-PCR påvisning af hundesygevirus nukleinsyre
Period: 9 Feb 2009 → 20 Feb 2009
Tanya von Rosen (Lecturer)
Division of Virology
Sektion for Eksotiske Virussygdomme
National Veterinary Institute

Related external organisation

University of Copenhagen
Bülowsvej 17, 1780, Copenhagen, Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

Organisation of rabies control and rabies prevention in Denmark: CRL Rabies Workshop
Period: 16 Dec 2008
Thomas Bruun Rasmussen (Speaker)
Division of Virology
Sektion for Eksotiske Virussygdomme
National Veterinary Institute

Description
Place: Nancy, France

Related event

CRL Rabies Workshop
01/01/2008 → …
Nancy, France
Activity: Talks and presentations › Conference presentations

Hepatitis E Virus is prevalent in the Danish pig population
Period: 31 Oct 2008
Solvej Østergaard Breum (Speaker)
7th ESVV Pestivirus Symposium: Generation of recombinant pestiviruses using a full genome amplification strategy.
Period: 16 Sep 2008 → 19 Sep 2008
Thomas Bruun Rasmussen (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Dyreforsøg på Lindholm 2008
Period: 10 Sep 2008
Louise Lohse (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Diagnosis of PRRSV – a review
Period: 24 Jul 2008 → 25 Jul 2008
Lars Erik Larsen (Speaker)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Virology

Related event
Diagnosis of PRRSV – a review: EuroPRRSnet workshop
24/07/2008 → 25/07/2008
Brussels
Activity: Talks and presentations › Conference presentations

Building Bridges: Workshop on Swine Diseases
Åse Uttenthal (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
CSF- The global situation. How to obtain information on the current CSFV situation globally and measures in Denmark to assure freedom from CSFV.
Place: Shanghai, China

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Hepatitis E Virus (HEV) - en ny zoonose?
Period: 27 May 2008
Solvej Østergaard Breum (Speaker)
National Veterinary Institute
Division of Veterinary Diagnostics and Research
Virology

Description
Place: FOOD DTU - Aftagerkonference

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Bluetongue
Period: 1 Mar 2008
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Foredrag om Bluetongue for veterinærstuderende på kurset Biomedicin

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Bluetongue i Europa med fokus på introduktion af bluetongue virus serotype 8 i nordvest Europa
Period: 1 Jan 2008
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Place: Regionalforening for dyrlæger i Nordjylland, Ålborg

Related external organisation
Bluetongue situationen
Period: 1 Nov 2007
Anette Bøtner (Speaker)

National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virusssygdomme

Description
Note: Dialogmøde imellem Veterinærinstituttet og Fødevarestyrelsen. Veterinærinstituttet

Related external organisation
National Veterinary Institute
Denmark
Activity: Other

Bluetongue: The virus, clinical signs, transmission and diagnosis, Dansk Selskab for Veterinær Patologi og Hygiejne
Period: 1 Oct 2007
Anette Bøtner (Speaker)

National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virusssygdomme

Description
Note: KU-Life
Activity: Other

European Association of Fish Pathologists (EAFP) (External organisation)
Period: 1 Sep 2007 → 1 Sep 2015
Lone Madsen (Secretary)

National Veterinary Institute
Section for Bacteriology, Pathology and Parasitology
Section for Virology

Description
General secretary of the EAFP council (the council having 6 members: president, vice-president, treasurer, general secretary, publications officer, meetings secretary)

Body type: Council of the association
Degree of recognition: International

Related external organisation
European Association of Fish Pathologists (EAFP)
Activity: Membership › Board duties in companies, associations, or public organisations

IPC for CSFV real-time assay
Period: 1 Sep 2007
Thomas Bruun Rasmussen (Speaker)

National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Note: Real-time PCR Workshop* EPIZONE WP4.1
Place: Insel Riems, Germany

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

IPC for CSFV real-time assay
Period: 1 Sep 2007
Åse Uttenthal (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Note: Real-time PCR Workshop* EPIZONE WP4.1
Place: Insel Riems, Germany

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Cattle Consultancy Days
Anette Bøtner (Participant)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Bluetongue in Europe with focus on the recent introduction of bluetongue virus in north-western Europe

Note: Cattle Consultancy Days

Related event

Cattle Consultancy Days
29/08/2007 → 30/08/2007
Nyborg, Denmark
Activity: Attending an event › Participating in or organising a conference

Internal positive control for CSFV real-time assay: novel approach to control reverse transcription.
Period: 1 Jan 2007 → …
Thomas Bruun Rasmussen (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Note: Annual Meeting of National Classical Swine Fever Laboratories
Place: Hannover, Germany
Internal positive control for CSFV real-time assay: novel approach to control reverse transcription.

Period: 1 Jan 2007 → …
Åse Uttenthal (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Note: Annual Meeting of National Classical Swine Fever Laboratories
Place: Hannover, Germany

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Marker properties of the chimeric pestivirus CP7_E2gif.

Period: 1 Jan 2007 → …
Thomas Bruun Rasmussen (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Note: Oral presentation at the EPIZONE WP4.3 DIVA meeting
Place: Copenhagen, Denmark

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Multicenter comparison of nucleic acid extraction robots using quantitative RT-PCR.: Stratagene Regional QPCR Meeting

Period: 1 Jan 2007 → …
Thomas Bruun Rasmussen (Speaker)
Multicenter comparison of nucleic acid extraction robots using quantitative RT-PCR.: Stratagene Regional QPCR Meeting
Period: 1 Jan 2007 → …
Åse Uttenthal (Speaker)

Dialogmøde imellem Danmarks Fødevareforskning og Fødevarestyrelsen
Period: 1 Nov 2006
Anette Bøtner (Participant)

PMWS in Denmark: Epidemiology, Diagnosis and Control
Period: 1 Jul 2006
Anette Bøtner (Speaker)
Related event

19th International Pig Veterinary Society Congress
16/07/2006 → 19/07/2006
Copenhagen, Denmark
Activity: Talks and presentations › Conference presentations

**Biosafety forhold på Lindholm herunder bygning af nye mund- og klovesyge faciliteter**
Period: 1 Jun 2006
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Related event

**Biosafety forhold på Lindholm herunder bygning af nye mund- og klovesyge faciliteter**
01/06/2006 → 01/06/2006
Activity: Talks and presentations › Conference presentations

**DIVA vaccines to pigs based on genetically modified pestiviruses: Oral presentation at Virology meeting**
Period: 1 Jan 2006 → …
Thomas Bruun Rasmussen (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Place: Hjalet

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

**DIVA vaccines to pigs based on genetically modified pestiviruses: Oral presentation at Virology meeting**
Period: 1 Jan 2006 → …
Åse Uttenthal (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Place: Hjalet

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

**Establishment and characterisation of chimeric pestivirus: Oral presentation at Virusdag 2006**
Period: 1 Jan 2006 → …
Thomas Bruun Rasmussen (Speaker)
National Veterinary Institute
Division of Virology
Establishment and characterisation of chimeric pestivirus: Oral presentation at Virusdag 2006
Period: 1 Jan 2006 → ...
Åse Uttenthal (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

DFVF's rolle i det veterinære beredskab og service
Period: 1 Nov 2005
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

6th International Pestivirus Symposium of the European Society of Veterinary Virology
Period: 13 Sep 2005 → 16 Sep 2005
Thomas Bruun Rasmussen (Participant)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Uniform extraction of RNA and DNA for quantitative multiplex PCR detection of classical and African swine fevers in blood or meat juice.
Place: Thun, Switzerland
**6th International Pestivirus Symposium of the European Society of Veterinary Virology**

Period: 13 Sep 2005 → 16 Sep 2005

**ESVV Pestivirus Symposium; 6**

**Period:** 13 Sep 2005 → 16 Sep 2005

Åse Uttenthal (Speaker)

National Veterinary Institute

Division of Virology

Sektion for Eksotiske Virussygdomme

**Description**

Uniform extraction of RNA and DNA for quantitative multiplex PCR detection of classical and African swine fevers in blood or meat juice.

**Place:** Thun, Switzerland

**Related external organisation**

**Tåstrup**

**Activity:** Talks and presentations › Talks and presentations in private or public companies and organisations

**Mund- klovesyge**

**Period:** 1 May 2005

Anette Bøtner (Guest lecturer)

Division of Virology

Sektion for Eksotiske Virussygdomme

National Veterinary Institute

**Description**

Note: Beredskabskursus for dyrlæger i fødevareafdelingerne samt kødkontrollen

**Related external organisation**

**Vejle**

**Activity:** Talks and presentations › Guest lectures, external teaching and course activities at other universities

**Epidemiologiske undersøgelser og prøveudtagelse. MKS, SP, ND, AI.**

**Period:** 1 Apr 2005

Anette Bøtner (Lecturer)

Division of Virology
The standardisation, quality control and validation of molecular diagnostic tests (OIE/WAVLD); 7: Seminar on Application of Biotechnology to Zoonotic Disease Diagnosis
Period: 1 Jan 2005 → …
Åse Uttenthal (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Place: Montevideo, Uruguay

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Thomas Bruun Rasmussen (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Place: Montevideo, Uruguay

Related external organisation
Unknown external organisation
Activity: Talks and presentations › Conference presentations

Mund- klovesyge
Period: 1 Nov 2004
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Note: Beredskabskursus for dyrlæger i fødevareafdelingerne samt kødkontrollen

Related event
Beredskabskursus for dyrlæger i fødevareafdelingerne samt kødkontrollen
01/11/2004 → 01/11/2004
Vejle, Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

Serumbehandling af PMWS. Resultater af afprøvning af serum mod PMWS
Period: 1 Nov 2004
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Description**
Note: DVHS efterårs møde
Activity: Other

**Mund- klovesyge**
Period: 1 Oct 2004
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Description**
Note: Beredskabskursus for regionsdyrlæger

**Related event**
**Beredskabskursus for regionsdyrlæger**
01/10/2004 → 01/10/2004
Aarhus, Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

**Mund- klovesyge**
Period: 1 Feb 2004
Anette Bøtner (Guest lecturer)
Division of Virology
Sektion for Eksotiske Virussygdomme
National Veterinary Institute

**Related external organisation**
**Vejle**
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

**PRRS, PMWS/PDNS, Svineinfluenza**
Period: 1 Feb 2004
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Related external organisation**
**Århus**
Activity: Other

**Mund- klovesyge**
Period: 1 Jan 2004
Anette Bøtner (Guest lecturer)
Experiences with eradication of PRRS in Danish swine herds
Period: 1 Dec 2003
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

PMWS – Status over viden og forskning
Period: 1 Oct 2003
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

PMWS og PRRS – Opdatering og aktuelt nyt
Period: 1 Sep 2003
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

PMWS og circovirus hos grise
Period: 1 Mar 2003
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Gæsteforelæsning ved KVL ved uddeling af Intervets legat for unge veterinærvitenskabelige forskere

Related external organisation
Royal Veterinary and Agricultural University
Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

PMWS – status: Grundforskning og langsigtede løsninger – diagnostik, x-virus, serumudvikling og vaccineudvikling
Period: 1 Mar 2003
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Note: Møde med formænd og ledende konsulenter. Landsudvalget

Related external organisation
Kolding Fjord Hotel, Kolding
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

PMWS status i Danmark
Period: 1 Sep 2002
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Note: DDD's årsmøde

Related event

DDD's årsmøde
01/09/2002 → …
Denmark
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

Reproduction of PMWS in immunostimulated and non-immunostimulated conventional 3-week-old piglets experimentally infected with PCV2
Period: 1 Sep 2001
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Conference on ssDNA Viruses of Plants and Birds, Pigs and Primates, PMWS
Related event

Reproduction of PMWS in immunostimulated and non-immunostimulated conventional 3-week-old piglets experimentally infected with PCV2
01/09/2001 → 01/09/2001
St. Malo, France
Activity: Talks and presentations › Conference presentations

Post-weaning Multisystemic Wasting Syndrome (PMWS) og circovirus type 2
Period: 1 Feb 2001
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
DSVPH på KVL

Related external organisation

Royal Veterinary and Agricultural University
Denmark
Activity: Other

Circovirus og PMWS – hvor står vi
Period: 1 Nov 2000
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme
Activity: Other

Post-weaning Multisystemic Wasting Syndrome (PMWS) og circovirus type 2
Period: 1 Oct 2000
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Related external organisation

Hotel Kolding Fjord
Activity: Other

Post-weaning Multisystemic Wasting Syndrome (PMWS) og circovirus type 2
Period: 1 Sep 2000
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Note: DDD's årsmøde Hotel Nyborg Strand
Related external organisation

Den Danske Dyr lægeforening
Peter Bangs Vej 30, DK-2000, Frederiksberg, Denmark
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

PRRS
Period: 1 Jul 2000
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Place: Kina

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

PRRSV diversitet: Immunologisk problem eller epidemiologisk værktøj
Period: 4 May 2000 → 5 May 2000
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
DVHS møde 4.-5. maj 2000

Related event

DVHS Møde
04/05/2000 → 05/05/2000
Denmark
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

Field experiences with Porcine Reproductive and Respiratory Syndrome (PRRS) and with the use of a live PRRS-vaccine in Denmark
Period: 1 Jan 2000
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Related event

Field experiences with Porcine Reproductive and Respiratory Syndrome (PRRS) and with the use of a live PRRS-vaccine in Denmark
01/01/2000 → 01/01/2000
China
Activity: Talks and presentations › Conference presentations

Virussygdomme hos svin. PPV, svineinfluenza, PRRS samt porcint circovirus (PMWS)
Period: 25 Nov 1999
Anette Bøtner (Lecturer)
Division of Virology
Sektion for Eksotiske Virussygdomme
National Veterinary Institute

Description
Note: Fagdyrlægekursus vedrørende svin

Related event
Fagdyrlægekursus vedrørende svin
01/01/1999 → …
Slagelse
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

PMWS – en ny svinesygdom
Period: 27 Oct 1999
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Conference

Related event
PMWS – en ny svinesygdom
27/10/1999 → 27/10/1999
Herning
Activity: Talks and presentations › Conference presentations

Diagnosing vaccine induced PRRS. Distinction between infections with European and American/vaccine type PRRS virus after vaccination with a modified-live PRRS vaccine
Period: 22 Jun 1999
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
3rd International Symposium on PRRS

Related event
Diagnosing vaccine induced PRRS. Distinction between infections with European and American/vaccine type PRRS virus after vaccination with a modified-live PRRS vaccine
22/06/1999 → 22/06/1999
Ploufragan
Activity: Talks and presentations › Conference presentations

Status vedrørende circovirus infektioner i Danmark
Period: 7 May 1999
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Swine Disease Conference for Swine Practitioners, Iowa State University

**Field experiences with PRRS and with the use of a live vaccine in Denmark**

- **Period:** 12 Nov 1998
- **Anette Bøtner** (Speaker)
- **National Veterinary Institute**
- **Division of Virology**
- **Sektion for Eksotiske Virussygdomme**

**Description**

Swine Disease Conference for Swine Practitioners, Iowa State University

**Place:** Iowa State University

**Related external organisation**
**Unknown external organisation**
Activity: Talks and presentations › Conference presentations

**PCR til påvisning og typning af PRRS-virus**
Period: 6 Nov 1998
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Description**
Note: Efterårsmede i Dansk Veterinaer Hyologisk Selskab

**Related event**

**DVHS efterårsmede**
06/11/1998 → …
Denmark
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

**PRRS - The Danish experience**
Period: 6 Aug 1998
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Description**
XVIII Nordic Veterinary Congress, 4.- 7. August 1998
Place: Helsinki, Finland

**Related external organisation**

**Unknown external organisation**
Activity: Talks and presentations › Conference presentations

**Challenge of previously PRRS infected pigs with PRRS vaccine virus**
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Description**
Note: International Pig veterinary Society
Place: Birmingham, U.K.

**Related external organisation**

**Unknown external organisation**
Activity: Talks and presentations › Conference presentations

**PRRS - "der Dänische Fall" aus dänischer Sicht**
Period: 24 Apr 1998
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
3rd Munich Symposium - Diseases of pig

Related event

PRRS - "der Dänische Fall" aus dänischer Sicht
Munich
Activity: Talks and presentations › Conference presentations

Epidemiology and control of PRRS: The Danish experience with use of a live modified PRRS vaccine in a PRRS control programme
Period: 27 Mar 1998
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
S.I.P.A.S. 1998 annual meeting "Epidemiology and control of PRRS"
Place: Parma, Italy

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

Appearance of acute PRRS-like symptoms in sow herds after vaccination with modified-live PRRS vaccine
Period: 18 Sep 1997
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Related event

Appearance of acute PRRS-like symptoms in sow herds after vaccination with modified-live PRRS vaccine
18/09/1997 → 18/09/1997
Iowa State University
Activity: Talks and presentations › Conference presentations

SeroLOGiske besætningsprofiler: PRRS, influenza: Kontrol af luftvejsslideer hos svin i fremtidens produktionssystemer
Period: 13 Mar 1997
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Note: Pfizer symposium

Related external organisation
**Unknown external organisation**  
Activity: Talks and presentations › Conference presentations

**PRRS-serologi**  
Period: 20 Nov 1996  
Anette Bøtner (Speaker)  
National Veterinary Institute  
Division of Virology  
Sektion for Eksotiske Virussygdomme  
Activity: Other

**SeroLOGI, epidemiologi og produktionsresultater i danske besætninger med PRRS**  
Period: 8 Nov 1996  
Anette Bøtner (Speaker)  
National Veterinary Institute  
Division of Virology  
Sektion for Eksotiske Virussygdomme

**Description**  
Place: Kolding

**Related external organisation**  
**Unknown external organisation**  
Activity: Talks and presentations › Conference presentations

**On the risk of transfer of PRRS-virus between herds and the Danish strategy of control**  
Anette Bøtner (Speaker)  
National Veterinary Institute  
Division of Virology  
Sektion for Eksotiske Virussygdomme

**Description**  
Eight European A.I. Vets Meeting 7-9 October 1996

**Related external organisation**  
**Billund, Denmark**  
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

**PRRS vaccination of boars**  
Anette Bøtner (Speaker)  
National Veterinary Institute  
Division of Virology  
Sektion for Eksotiske Virussygdomme

**Description**  
Eight European A.I. Vets Meeting

**Related external organisation**  
**Billund, Denmark**  
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations
PRRS - Sygdommen og vaccinen
Period: 11 Apr 1996
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Place: Ringsted

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

PRRS - Sygdommen og vaccinen
Period: 28 Mar 1996
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Place: Aalborg

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

PRRS - Sygdommen og vaccinen
Period: 27 Mar 1996
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Note: Veterinaerfagligt debatmøde om PRRS

Related external organisation

Kolding
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

PRRS, Porcin Reproduktions- og Respirationssygdom: "Ætiologi og klinik" samt "Vaccineafprøvning incl.serologiske undersøgelser for PRRS"
Period: 20 Mar 1996
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme
Description
Note: Dansk Selskab for Veterinær patologi og hygiejne

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

PRRS: Sygdommen og vaccinen
Period: 19 Feb 1996
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
PRRS-møde for svineproducenter

Related external organisation

Åbenrå
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

PRRS: Sygdommen og vaccinen
Period: 13 Feb 1996
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
PRRS-møde for svineproducenter

Related external organisation

Ringsted
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

PRRS: Sygdommen og vaccinen
Period: 9 Feb 1996
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
PRRS-møde for svineproducenter

Related external organisation

Brædstrup
Activity: Talks and presentations › Conference presentations

PRRS: Sygdommen og vaccinen
Period: 8 Feb 1996
Anette Bøtner (Participant)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Description**
Note: PRRS-møder for svineproducenter

**Related event**

**Sygdommen og vaccinen: PRRS-møde for svineproducenter**
08/02/1996 → 08/02/1996
Aalborg, Denmark
Activity: Other

**Diagnosis of PRRS**
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Description**
2nd International Symposium on Porcine Reproductive and Respiratory Syndrome (PRRS)

**Related event**

**Diagnosis of PRRS: 2nd International Symposium on Porcine Reproductive and Respiratory Syndrome (PRRS)**
09/08/1995 → 10/08/1995
Copenhagen
Activity: Talks and presentations » Conference presentations

**Foreløbige resultater fra PRRSV podningsforsøg på orner fremlagt for Landsudvalget for svin**
Period: 9 May 1995
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Description**
Bestyrelsesmøde

**Related external organisation**

**Axelborg**
Activity: Talks and presentations » Talks and presentations in private or public companies and organisations

**Danske erfaringer med serologiske undersøgelser for PRRS og nyt vedr. PRRS vacciner**
Period: 1 Dec 1994
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

**Description**
Note: Dansk Veterinær Hyologisk Selskab's efterårsmøde
Related event

DVHS' efterårsmøde
01/12/1994 → …
Denmark
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

Virologiske risici ved anvendelse af husdyrgødning og affald
Period: 23 Jun 1994
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Related event

Virologiske risici ved anvendelse af husdyrgødning og affald
23/06/1994 → 23/06/1994
Kolding
Activity: Talks and presentations › Conference presentations

PRRS-virologi, diagnostik
Period: 21 Jun 1994
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Møde med svinerådgivere om PRRS

Related external organisation

Åbenrå
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

PPV, PRRS, Svineinfluenza
Period: 17 Jan 1994
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Afholdt for Svinefagdyrlæge-kursister

Related external organisation

Unknown external organisation
Activity: Talks and presentations › Conference presentations

Virusinfektioner som årsag til reproduktionsforstyrrelser hos svin – herunder serologiske aspekter
Period: 29 Oct 1993
Anette Bøtner (Speaker)
National Veterinary Institute
Related event

Virusinfektioner som årsag til reproduktionsforstyrrelser hos svin – herunder serologiske aspekter: Immunologi og Reproduktion
20/12/1993 → …
Ålborg, Denmark
Activity: Talks and presentations › Conference presentations

Virusinfektioner som årsag til reproduktionsforstyrrelser hos svin – herunder serologiske aspekter
Period: 12 Oct 1993
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Related event

Virusinfektioner som årsag til reproduktionsforstyrrelser hos svin – herunder serologiske aspekter: Immunologi og Reproduktion
12/10/1993 → …
Næstved, Denmark
Activity: Talks and presentations › Conference presentations

Status vedrørende porcin reproduktions- og respirationssygdom
Period: 27 Aug 1992
Anette Bøtner (Lecturer)
Division of Virology
Sektion for Eksotiske Virussygdomme
National Veterinary Institute

Description
Præstø amts dyrlægeforening på besøg på Lindholm

Related external organisation

Lindholm
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations
Status vedrørende porcin reproduktions- og respirationssygdom
Period: 7 May 1992
Anette Bøtner (Speaker)
Division of Virology
Sektion for Eksotiske Virussygdomme
National Veterinary Institute

Description
Dansk Veterinær Hyologisk Selskab

Related external organisation
Dansk Veterinær Hyologisk Selskab, Kolding, Danmark
Activity: Talks and presentations › Talks and presentations in private or public companies and organisations

Virus og diagnostik af virusinfektioner
Period: 7 May 1992
Anette Bøtner (Lecturer)
Division of Virology
Sektion for Eksotiske Virussygdomme
National Veterinary Institute

Description
Dansk Veterinær Hyologisk Selskab

Related external organisation
Dansk Veterinær Hyologisk Selskab
Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

Mave-tarm-sygdomme hos svin "TGE, svinepest"
Period: 12 Dec 1991
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Description
Den danske Dyrlægeforenings efteruddannelseskursus

Related external organisation
Den Danske Dyrlægeforening
Peter Bangs Vej 30, DK-2000, Frederiksberg, Denmark
Activity: Talks and presentations › Guest lectures, external teaching and course activities at other universities

Svineinfluenza
Period: 20 Oct 1991
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme
Evidence of spread of derivatives of attenuated vaccine strains of suid herpesvirus 1 (pseudorabies virus)
Period: 1 Jan 1991 → …
Bertel Strandbygaard (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Svineinfluenza
Period: 5 Nov 1990
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Svineinfluenza - Ny subtype i Danmark
Anette Bøtner (Speaker)
National Veterinary Institute
Division of Virology
Sektion for Eksotiske Virussygdomme

Total immunoglobulin hos regnbueørred: Vurdering af IgM-koncentration i sera fra regnbueørredere fra forskellige miljøer
Period: 1 Jan 1985
Niels Jørgen Olesen (Participant)
Division of Poultry, Fish and Fur Animals
Section of Fish Diseases
National Veterinary Institute

Description
Head: Niels Jørgen Olesen

Related external organisation
SVS, Statens Veterinære Seruminstitut, Århus
Activity: Other

Fiskesygdomme på EDB
Period: 1 Jan 1984
Niels Jørgen Olesen (Participant)
Division of Poultry, Fish and Fur Animals
Section of Fish Diseases
National Veterinary Institute

Description
Head: Niels Jørgen Olesen

Related external organisation
Den Kongelige Veterinær og Landbohøjskole
Activity: Other

Prizes:

IUIS VIC Keystone rejse legat
Simon Welner (Recipient)
National Veterinary Institute, Center for Biological Sequence Analysis, Section for Immunology and Vaccinology, Section for Virology

Description
Fondsmidler til at hjælpe PhD/DVM studerende med at deltage i Keystone symposiet ad 20.-25.01.2015: "Immunity to veterinary pathogens: Informing vaccine development"

Modtog et legat på 1000 USD. Dog skal jeg betale nogle af pengene tilbage, da jeg også modtog et andet legat udbudt af Keystone, så jeg i alt har modtaget flere penge end mine rejseomkostninger er budgetteret til.

Details
Awarded date: 20 Jan 2015
Granting Organisations: IUIS VIC: International Union of Immunological Societies - Veterinary Immunology Commitee
Prize: Prizes, scholarships, distinctions

Keystone symposia future of science fund scholarship
Simon Welner (Recipient)
National Veterinary Institute, Center for Biological Sequence Analysis, Section for Immunology and Vaccinology, Section for Virology

Description
Fik bevilget 1200 USD

Details
Awarded date: 20 Jan 2015
Prize: Prizes, scholarships, distinctions

Press clippings:
Beskidte lastbiler kan bringe svinepest til Danmark
Åse Uttenthal
17/09/2010
National Veterinary Institute, Division of Virology, Sektion for Eksotiske Virussygdomme

Media contribution (1)

Beskidte lastbiler kan bringe svinepest til Danmark
17/09/2010
Landbrugsavisen, Print
Åse Uttenthal
National Veterinary Institute, Division of Virology, Sektion for Eksotiske Virussygdomme
Press / Media

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

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

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

PMWS
Anette Bøtner
19/04/2003
National Veterinary Institute, Division of Virology, Sektion for Eksotiske Virussygdomme

Media contribution (1)

PMWS
19/04/2003
Television
Anette Bøtner
National Veterinary Institute, Division of Virology, Sektion for Eksotiske Virussygdomme
Press / Media

PMWS - serumbehandling: Interview, Landsbiadet, februar, 2003
Anette Bøtner
01/01/2003
National Veterinary Institute, Division of Virology, Sektion for Eksotiske Virussygdomme
PMWS - serumbehandling: Interview, Landsbladet, februar, 2003
01/01/2003
Print
Anette Bøtner
National Veterinary Institute, Division of Virology, Sektion for Eksotiske Virussygdomme
Press / Media

PMWS: Interview, Landsbladet September 2003
Anette Bøtner
01/01/2003
National Veterinary Institute, Division of Virology, Sektion for Eksotiske Virussygdomme
Press / Media

Rabies hos får
Anette Bøtner
20/08/1998
National Veterinary Institute, Division of Virology, Sektion for Eksotiske Virussygdomme
Press / Media

PRRS
Anette Bøtner
06/05/1994
National Veterinary Institute, Division of Virology, Sektion for Eksotiske Virussygdomme
Press / Media
PRRS
Anette Bøtner
02/05/1994
National Veterinary Institute, Division of Virology, Sektion for Eksotiske Virussygdomme

Media contribution (1)

PRRS
02/05/1994
Television
Anette Bøtner
National Veterinary Institute, Division of Virology, Sektion for Eksotiske Virussygdomme
Press / Media