First report of Taenia ovis infection in Danish sheep (Ovis aries)

We report Taenia ovis infection in Danish sheep for the first time. In spring 2016, the metocestode stage of T. ovis was at slaughter observed in heart muscles, diaphragm and skeletal muscles from approx. a third of all sheep from one specific farm localised in South Jutland. The diagnosis was confirmed by molecular typing of the mitochondrial cytochrome c oxidase I (cox1) gene. Three newly imported dogs were suspected but the definitive host was unidentifiable. The finding is not regulated in the meat control procedures. However, infected meat is usually condemned due to aesthetic reasons causing economic losses. Thus, finding of T. ovis is of concern to sheep meat producers in the area, as the infection could have spread further on to other farms.
A cross-sectional field study on potential associations between feed quality measures and usage of antimicrobials in commercial mink (Neovison vison)

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

**General information**

State: Published
Organisations: National Veterinary Institute, Epidemiology, Department of Applied Mathematics and Computer Science, Diagnostic & Development, Kopenhagen Fur
Authors: Jensen, V. F. (Intern), Sommer, H. M. (Intern), Struve, T. (Ekstern), Clausen, J. (Ekstern), Chriél, M. (Intern)

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A cross-sectional study of oral antibacterial treatment patterns in relation to specific diarrhoeal pathogens in weaner pigs

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

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Organisations: National Veterinary Institute, Epidemiology, Diagnostic & Development
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Animal prevalence of livestock-associated methicillin-resistant Staphylococcus aureus in five Danish mink farms

General information
State: Published
Organisations: National Veterinary Institute, Bacteriology & Parasitology, Diagnostic & Development
Authors: Fertner, M. E. (Intern), Pedersen, K. (Intern), Hansen, J. E. (Intern), Larsen, G. (Intern), Chriél, M. (Intern)
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Animal prevalence of livestock-associated methicillin-resistant Staphylococcus aureus in five Danish mink (Neovison vison) farms

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

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Antimicrobial resistance among pathogenic bacteria from mink (Neovison vison) in Denmark

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

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

Although Danish farmed mink are frequently infected with Coccidia, knowledge of factors affecting the infection is scarce. Thus, we studied age, geographical and season-related factors affecting coccidia prevalence. Unsporulated oocysts excretion was quantified microscopically (n=4142) every 7-14th day (April-October 2016) from bitches and cups on 30 farms (n=335 mink) from South- or North Jutland, or Zealand. Minimum once, 60.9% (n=204) mink excreted Eimeria, 56.7% (n=190) Isospora and 20.9% (n=70) excreted both coccidia. Positive mink were identified on all farms. Eimeria prevalence was higher on the Zealand farms (25.4±2.2%, P<0.0001) compared to South- and North Jutland farms (5.4±2.9%; 7.5±4.1%). Isospora prevalence was similar regardless of farm locality (12.2±2.9%, 11.8±3.5%, 9.2±7.1%). Eimeria prevalence peaked in June-July (12.6%-24.9%), while Isospora prevalence peaked in July-August (12.1%-27.6%).
More cups (19.5%) than bitches (4.6%) were *Isospora* positive, while *Eimeria* prevalence was similar for cups (15.7%) and bitches (10.5%). For cups, *Eimeria* prevalence peaked when cups were 7-11 weeks old and again when 18-24 weeks old. *Isospora* prevalence peaked in cups 13-15 weeks old. Three *Eimeria* types were characterized by size and wall thickness (unverified by PCR); A, B and C. Types B and C (40.9%, 39.8%) were more prevalent than A (19.3%). Bitches were primarily infected with type B (50.4%), while type C (48.0%) predominated in cups. Type B infections dominated in mink from Zealand (56.5±13.7%), while mink from Jutland were primarily infected with type C (55.6±28.6%; 81.9±19.4%). Farmed mink showed high coccidia prevalence with seasonal- and age-related *Isospora* prevalence, and seasonal- and geographical-related *Eimeria* prevalence.

**Coccidia infections in Danish farmed mink**

**General information**
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Authors: Petersen, H. H. (Intern), Chriél, M. (Intern), Hansen, M. S. (Intern)
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Main Research Area: Technical/natural sciences
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**Coccidie-infektion hos danske farmmink – et overset problem?**

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Authors: Petersen, H. H. (Intern), Hansen, M. S. (Intern), Chriél, M. (Intern), Holm, T. (Ekstern)
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Comparison of antimicrobial resistance in E. coli isolated from rectal and floor samples in pens with diarrhoeic nursery pigs in Denmark

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

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Organisations: National Veterinary Institute, Diagnostic & Development, University of Copenhagen, Pig Research Centre
Authors: Weber, N. R. (Ekstern), Nielsen, J. P. (Ekstern), Jorsal, S. E. L. (Intern), Haugegaard, S. (Intern), Denwood, M. (Ekstern), Pedersen, K. S. (Ekstern)
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Comparison of bacterial culture and qPCR testing of rectal and pen floor samples as diagnostic approaches to detect enterotoxigenic E. coli in nursery pigs

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

General information
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Authors: Weber, N. R. (Ekstern), Nielsen, J. P. (Ekstern), Hjulsager, C. K. (Intern), Jorsal, S. E. L. (Intern), Haugegaard, S. (Ekstern), Hansen, C. F. (Ekstern), Pedersen, K. S. (Ekstern)
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Evaluation of a commercial competitive enzyme-linked immunosorbent assay for detection of avian influenza virus subtype H5 antibodies in zoo birds

The hemagglutination inhibition (HI) test is the current gold standard for detecting antibodies to avian influenza virus (AIV). Enzyme-linked immunosorbent assays (ELISAs) have been explored for use in poultry and certain wild bird species because of high efficiency and lower cost. This study compared a commercial ELISA for detection of AIV subtype H5 antibodies with HI test of 572 serum samples from zoo birds. There was no significant difference between the results of the two tests when statistically compared by a McNemar χ² test (P = 0.86) and assessment of κ (κ = 0.87). With a specificity of 94.2% (95% confidence interval [CI], 0.92-0.97), a sensitivity of 93.9% (95% CI, 0.91-0.97), and an excellent correlation between the two tests, this ELISA can be recommended as an alternative to the HI test for preliminary screening of zoo bird sera for antibodies to AIV subtype H5.

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Authors: Jensen, T. H. (Intern), Andersen, J. H. (Ekstern), Hjulsager, C. K. (Intern), Chriél, M. (Intern), Bertelsen, M. F. (Ekstern)
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Scopus rating (2014): SJR 0.34 SNIP 0.505 CiteScore 0.57
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Scopus rating (2013): SJR 0.305 SNIP 0.523 CiteScore 0.57
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): SJR 0.311 SNIP 0.602 CiteScore 0.53
ISI indexed (2012): ISI indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): SJR 0.303 SNIP 0.457 CiteScore 0.54
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BFI (2010): BFI-level 1
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Experimental Vaccine Against Mink Astrovirus Infection Reduces the Incidence of Brain Lesions

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Authors: Hansen, M. S. (Intern), Baule, C. (Ekstern), Ullman, K. (Ekstern), Jensen, T. H. (Ekstern), Larsen, G. (Ekstern), Chriél, M. (Intern)
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Scopus rating (2014): SJR 0.562 SNIP 0.775 CiteScore 1.17
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Foreskøn af antibiotikaresistens i bakterieisolater fra danske mink

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Authors: Chriél, M. (Intern), Corvera Kløve Lassen, D. (Ekstern), Larsen, G. (Intern), Jensen, V. F. (Intern), Pedersen, K. (Intern)
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Organisations: National Veterinary Institute, Virology, Department of Bio and Health Informatics, Disease Intelligence and Molecular Evolution, Diagnostic & Development, Department of Biotechnology and Biomedicine, Kopenhagen Fur
Genome analysis of Clostridium perfringens isolates from healthy and necrotic enteritis infected chickens and turkeys

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

General information
State: Published
Organisations: National Veterinary Institute, Virology, Diagnostic & Development, Department of Biotechnology and Biomedicine, Department of Bio and Health Informatics, Disease Intelligence and Molecular Evolution, Kopenhagen Fur
Pages: 169-172
Publication date: 2017

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Place of publication: Aarhus N
Publisher: Kopenhagen Fur
Main Research Area: Technical/natural sciences
Electronic versions: DTU6.pdf
Publication: Research - peer-review › Book chapter – Annual report year: 2017

Global phylogenetic analysis of contemporary aleutian mink disease viruses (AMDVs)
Aleutian mink disease has major economic consequences on the mink farming industry worldwide, as it causes a disease that affects both the fur quality and the health and welfare of the mink. The virus causing this disease is a single-stranded DNA virus of the genus Amdoparvovirus belonging to the family of Paroviridae. In Denmark, infection with AMDV has largely been restricted to a region in the northern part of the country since 2001, affecting only 5% of the total Danish mink farms. However, in 2015 outbreaks of AMDV were diagnosed in all parts of the country. Initial analyses revealed that the outbreaks were caused by two different strains of AMDV that were significant different from the circulating Danish strains. To track the source of these outbreaks, a major investigation of global AMDV strains was initiated. Samples from 13 different countries were collected and partial NS1 gene was sequenced and subjected to phylogenetic analyses. The analyses revealed that AMDV exhibited substantial genetic diversity. No clear country wise clustering was evident, but exchange of viruses between countries was revealed. One of the Danish outbreaks was caused by a strain of AMDV that closely resembled a strain originating from Sweden. In contrast, we did not identify any potential source for the other and more widespread outbreak strain. To the authors knowledge this is the first major global phylogenetic study of contemporary AMDV partial NS1 sequences. The study proved that partial NS1 sequencing can be used to distinguish virus strains belonging to major clusters. The partial NS1 sequencing can therefore be a helpful tool in combination with epidemiological data, in relation to outbreak tracking. However detailed information on farm to farm transmission requires full genome sequencing.

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

Publication information
Journal: Virology Journal
Identification of Dermacentor reticulatus Ticks Carrying Rickettsia raoultii on Migrating Jackal, Denmark

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

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

General information

State: Published

Organisations: National Veterinary Institute, Bacteriology & Parasitology, Diagnostic & Development, Statens Serum Institut, Technical University of Denmark

Authors: Hansen, J. E. (Intern), Rhod Larsen, A. (Ekstern), Skov, R. L. (Ekstern), Chriél, M. (Intern), Larsen, G. (Intern), Angen, Ø. (Ekstern), Larsen, J. (Ekstern), Corvera Kløve Lassen, D. (Ekstern), Pedersen, K. (Intern)
Lungebetændelse hos mink med ansamlinger af mononukleære inflammationsceller

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

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

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

General information
State: Published
Organisations: National Veterinary Institute, Diagnostic & Development
Authors: Pagh, S. (Ekstern), Chriél, M. (Intern)
Number of pages: 77
Publication date: 2017

Publication information
Publisher: DTU Veterinaerinstituttet
Original language: Danish
Main Research Area: Technical/natural sciences
Publication: Research - peer-review › Report – Annual report year: 2017

MRSA i mink (Neovison vison) indsendt til diagnostik

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

Host publication information
Title of host publication: Faglig årsberetning 2016 : Kopenhagen Fur
Place of publication: Aarhus N
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.
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
Web of Science (2006): Indexed yes
Original language: English
Diarrhoea, NNPDS, Neonatal piglets, Virus
Electronic versions:
s12917_017_1239_5.pdf
DOIs:
10.1186/s12917-017-1239-5
Source: FindIt
Source-ID: 2392840751
Publication: Research - peer-review › Journal article – Annual report year: 2017

Outbreak tracking of Aleutian mink disease virus (AMDV) using partial NS1 gene sequencing

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

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

Publication information
Journal: Virology Journal
Volume: 14
Issue number: 119
ISSN (Print): 1743-422X
Population genomics of the raccoon dog (Nyctereutes procyonoides) in Denmark: insights into invasion history and population development

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

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

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

General information

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

Publication information

Journal: Journal of Veterinary Diagnostic Investigation
Volume: 29
Issue number: 6
ISSN (Print): 1040-6387
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Web of Science (2017): Indexed Yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 1.27 SJR 0.634 SNIP 0.864
BFI (2015): BFI-level 1
Scopus rating (2015): SJR 0.699 SNIP 0.894 CiteScore 1.44
BFI (2014): BFI-level 1
Scopus rating (2014): SJR 0.781 SNIP 0.902 CiteScore 1.36
Web of Science (2014): Indexed yes
Spirocerca-parasit: En tropisk/subtropisk hundeparasit, som medfører kræftlignende svelster, er nu påvist i tre danske ræve fra Thy-området


**General information**

**State:** Published

**Organisations:** National Veterinary Institute, Bacteriology & Parasitology, Diagnostic & Development

**Authors:** Petersen, H. H. (Intern), Larsen, G. (Intern), Chriél, M. (Intern)

**Pages:** 30-33

**Publication date:** 2017
Spread of avian pathogenic Escherichia coli ST117 O78:H4 in Nordic broiler production

Escherichia coli infections known as colibacillosis constitute a considerable challenge to poultry farmers worldwide, in terms of decreased animal welfare and production economy. Colibacillosis is caused by avian pathogenic E. coli (APEC). APEC strains are extraintestinal pathogenic E. coli and have in general been characterized as being a genetically diverse population. In the Nordic countries, poultry farmers depend on import of Swedish broiler breeders which are part of a breeding pyramid. During 2014 to 2016, an increased occurrence of colibacillosis on Nordic broiler chicken farms was reported. The aim of this study was to investigate the genetic diversity among E. coli isolates collected on poultry farms with colibacillosis issues, using whole genome sequencing. Hundred and fourteen bacterial isolates from both broilers and broiler breeders were whole genome sequenced. The majority of isolates were collected from poultry with colibacillosis on Nordic farms. Subsequently, comparative genomic analyses were carried out. This included in silico typing (sero- and multi-locus sequence typing), identification of virulence and resistance genes and phylogenetic analyses based on single nucleotide polymorphisms. In general, the characterized poultry isolates constituted a genetically diverse population. However, the phylogenetic analyses revealed a major clade of 47 closely related ST117 O78:H4 isolates. The isolates in this clade were collected from broiler chickens and breeders with colibacillosis in multiple Nordic countries. They clustered together with a human ST117 isolate and all carried virulence genes that previously have been associated with human uropathogenic E. coli. The investigation revealed a lineage of ST117 O78:H4 isolates collected in different Nordic countries from diseased broilers and breeders. The data indicate that the closely related ST117 O78:H4 strains have been transferred vertically through the broiler breeding pyramid into distantly located farms across the Nordic countries.
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
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 2.181 SNIP 1.015
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 2.067 SNIP 1.005
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.846 SNIP 1.04
Web of Science (2007): Indexed yes
Scopus rating (2006): SJR 1.431 SNIP 0.895
Web of Science (2006): Indexed yes
Scopus rating (2005): SJR 1.994 SNIP 0.894
Web of Science (2005): Indexed yes
Scopus rating (2004): SJR 1.852 SNIP 0.617
Web of Science (2004): Indexed yes
Scopus rating (2003): SJR 1.909 SNIP 0.561
Web of Science (2003): Indexed yes
Scopus rating (2002): SJR 1.342 SNIP 0.532
Scopus rating (2001): SJR 0.132 SNIP 0.016
Original language: English
APEC, Colibacillosis, Comparative genomics, Phylogenetic analysis, Virulence factors
Electronic versions:
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Links:
Udvikling af en sandwich-ELISA til måling af immunglobulin G i minkblod

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

Host publication information
Title of host publication: Faglig årsberetning 2016 : Kopenhagen Fur
Place of publication: Aarhus N
Publisher: Kopenhagen Fur
Main Research Area: Technical/natural sciences

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

General information
State: Accepted/In press
Organisations: National Veterinary Institute, Pathology, Diagnostic & Development, Aalborg Zoo
Authors: Pagh, S. (Ekstern), Hansen, M. S. (Intern), Jensen, B. (Ekstern), Pertoldi, C. (Ekstern), Chriél, M. (Intern)
Number of pages: 9
Publication date: 2017
Main Research Area: Technical/natural sciences

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Journal: Zoology and Ecology
ISSN (Print): 2165-8005
Ratings:
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Scopus rating (2016): CiteScore 0.56
Scopus rating (2015): CiteScore 0.52
Scopus rating (2014): CiteScore 0.39
Scopus rating (2013): CiteScore 0
Original language: English
Body size, Body weight, Fat, Mating strategies, Mating behaviour, Fox, Population structure
Electronic versions:
IN PRESS
DOIs:
10.1080/21658005.2017.1409997

Bibliographical note
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Beskrivelse af dyreværnsmæssig korrekt aflivning af dyr på EU-listen

General information
State: Published
Organisations: National Veterinary Institute, Diagnostic & Development, Pathology
Number of pages: 15
Publication date: 2016

Publication information
Place of publication: Frederiksberg C
Publisher: Veterinærinstituttet, Danmarks Tekniske Universitet
Original language: Danish
Main Research Area: Technical/natural sciences

Bibliographical note
Rapporten er ikke offentlig tilgængelig
Publication: Commissioned › Report – Annual report year: 2017

Beskrivelse af dyreværnsmæssig korrekt aflivning af dyr på EU-listen - anbefalinger

General information
State: Published
Organisations: National Veterinary Institute, Diagnostic & Development, Pathology
Number of pages: 3
Publication date: 2016

Publication information
Place of publication: Frederiksberg C
Publisher: Veterinærinstituttet, Danmarks Tekniske Universitet
Original language: Danish
Main Research Area: Technical/natural sciences

Bibliographical note
Rapporten er ikke offentlig tilgængelig
Publication: Commissioned › Report – Annual report year: 2017

Buevåbnets effektivitet

General information
State: Published
Organisations: National Veterinary Institute, Pathology, Diagnostic & Development
Authors: Jensen, T. K. (Intern), Hansen, M. S. (Intern), Wolf-Jäckel, G. (Intern), Chriél, M. (Intern)
Number of pages: 16
Publication date: 2016

Publication information
Place of publication: Frederiksberg C
Publisher: DTU Veterinærinstituttet
Original language: Danish
Main Research Area: Technical/natural sciences

Bibliographical note
Notat er ikke offentligt tilgængeligt
Publication: Commissioned › Report – Annual report year: 2017

Diagnostiske undersøgelser af pelsdyr ved DTU Veterinærinstituttet - november 2015 - oktober 2016

General information
Diagnostiske undersøgelser af pelsdyr ved DTU Veterinærinstituttet - november 2014 - oktober 2015

General information
State: Published
Organisations: National Veterinary Institute, Diagnostic & Development, Bacteriology & Parasitology, Virology, Pathology
Authors: Chriél, M. (Intern), Larsen, G. (Intern), Holm, E. (Intern), Hjulsager, C. K. (Intern), Pedersen, K. (Intern), Jensen, V. F. (Intern), Jensen, T. K. (Intern), Hansen, M. S. (Intern)
Number of pages: 26
Publication date: 2015

Publication information
Place of publication: Frederiksberg C
Publisher: DTU Veterinærinstituttet
Original language: Danish
Main Research Area: Technical/natural sciences

Bibliographical note
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Publication: Commissioned › Report – Annual report year: 2017

Projects:

Reservoirværters mulige rolle for persistens af rådyrsyge
National Veterinary Institute
Bacteriology & Parasitology
Diagnostic & Development
Period: 01/10/2017 → 01/07/2018
Number of participants: 2
Project applicant:
Chriél, Mariann (Intern)
Project Coordinator:
Petersen, Heidi Huus (Intern)
Project

Optimeret sygdomsforebyggelse i slagtesvinebesætninger
National Veterinary Institute
Diagnostic & Development
Virology
Innate Immunology
SEGES Pig Research Center
Period: 01/01/2015 → 31/12/2017
Number of participants: 5
Number of related Ph.D. students: 1
Project participant:
Larsen, Lars Erik (Intern)
Hjulsager, Charlotte Kristiane (Intern)
Skovgaard, Kerstin (Intern)
Phd Student:
Goecke, Nicole Bakkegård (Intern)
Project Manager, academic:
Jorsal, Sven Erik Lind (Intern)

Financing sources
Source: Private funding (private)
Name of research programme: Svineafgiftsfonden
Amount: 1,776,000.00 Danish Kroner
Year of approval: 2014
Documents:
Optimeret sygdomsforebyggelse i slægtesvinebesætninger
Project