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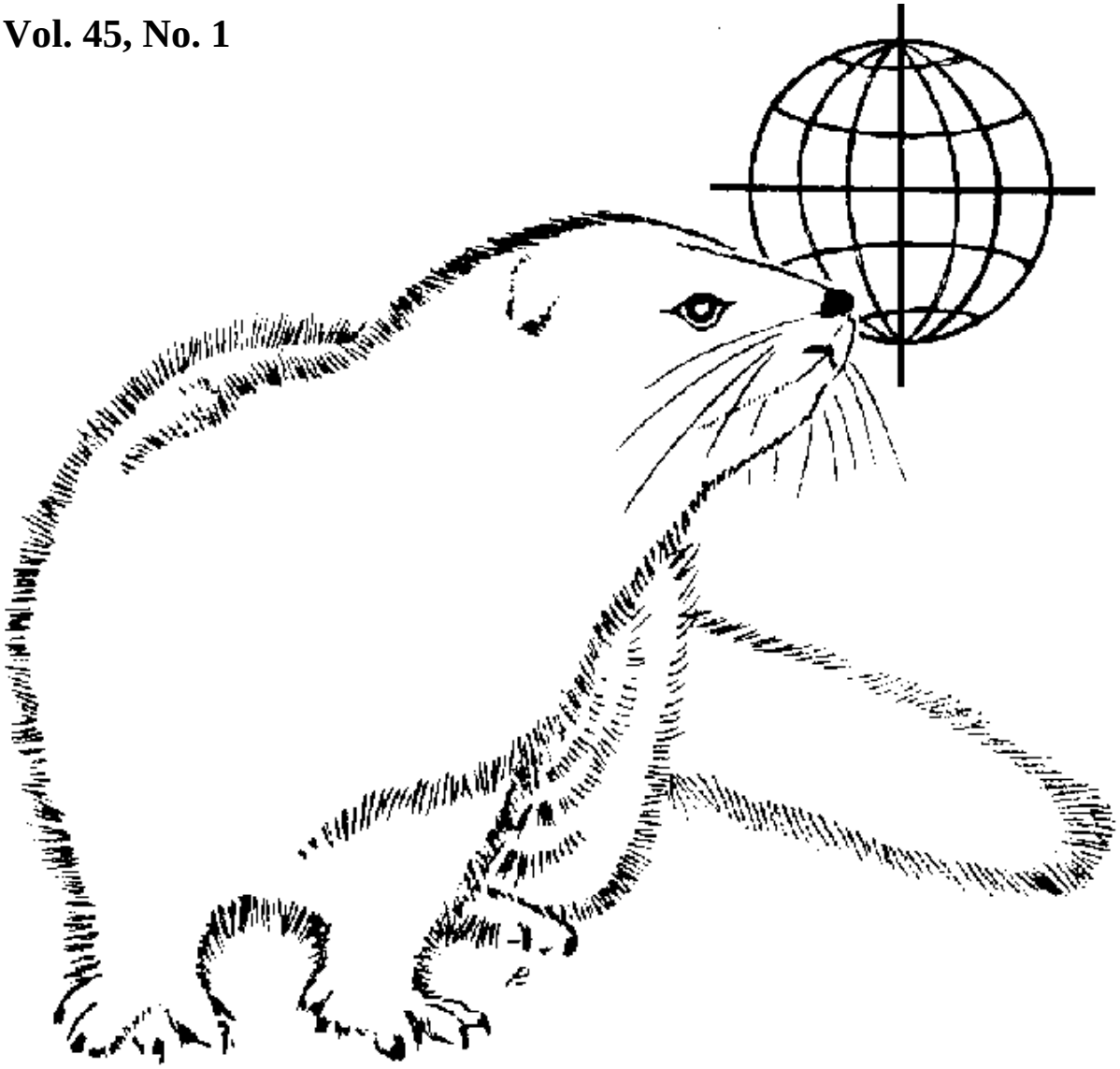

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Vivi Hunnicke Nielsen
SCIENTIFUR
P.O Box 14
DK-8830 Tjele, Denmark

Tel: **+45 2219 1351**
E-mail: Scientifur@dca.au.dk

SUBSCRIPTION: Free of charge: http://www.ifasanet.org

TREASURER'S ADDRESS. Correspondence to the Treasurer should be addressed to:

Steen H. Møller
IFASA
P.O. Box 14
DK-8830 Tjele, Denmark

Tel: **+45 8715 7926**
Fax: **+45 8715 4249**
E-mail: IFASA@anis.au.dk

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Kai-Rune Johannessen: E-mail: k.r.johannessen@norpels.no
Dr. Marian Brzozowski: E-mail: brzozowskim@delta.sggw.waw.pl

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Notes from the Editor

Mink production has become part of the COVID-19 pandemic with a concern that the production may affect the pandemic and the fight against it. At the same time, the production itself is strongly affected by the pandemic.

Coronavirus outbreaks are now reported on mink farms in Canada, Denmark, Greece, Italy, Lithuania, the Netherlands, Russia, Spain, Sweden and the United States. The infection originates from humans. The virus is then observed to spread rapidly on the infected farms and potentially to other farms.

Danish researchers have attempted to reveal how the virus infection can potentially spread from farm to farm, but so far without success. Samples from wild animals, cats and domestic animals such as rabbits and poultry have been investigated but no infections with Coronavirus were shown. Besides, high fences made of concrete, make wild animals an unlikely source of infection. Results of analyses of several feed samples did not show the presence of Coronavirus either. Airborne transmission between farms is assumed unlikely, as Coronavirus is a fragile RNA virus. In addition, no viruses were found in 100 air samples taken inside or outside the farm fences. Although Coronavirus was detected on the foot of a single gull, its spread by birds is also considered unlikely. In addition, preventive measures such as the creation of zones, isolation, protective equipment and testing have not stopped the infection. Infections from humans to mink have been detected but have not been documented as the only source of infection.

Crucial and with potential consequences for mink production, however, is that the infection can also be transmitted from mink to humans. The concern is the generation of several mutations in Coronavirus in the large number of mink on the farms, and that these mutations may reduce or eliminate the effect of vaccines.

This concern led the Danish government to order the culling of all mink in Denmark in early November 2020. This included breeding animals. Subsequently, about 15 million mink were culled. In addition, a temporary ban on mink farming was introduced until the end of 2021. These dramatic decisions also have serious consequences for the associated industries that manufacture and sell technical equipment such as feeding and pelting machines and feed kitchens, as they will have to close as well.

An urgent question is whether the crisis in the mink production could have been handled in a different way. Thus, what is the learning from the COVID-19 pandemic. Attention is drawn to the fact, that the normal model where authorities, the industry and the scientific communities collaborate and find constructive forward-looking solutions has not been used in this context. A timely effort including all relevant parties and their experience and knowledge should form the basis for viable solutions. Furthermore, the closure of all farms and related industries in the autumn of 2020 will challenge re-establishment of Danish mink production in 2022.

Many studies have been performed to investigate coronavirus infection in animals and the transmission of the virus from humans to animals and vice versa to understand the human-animal interface and the dynamics in the spread of the disease. Several of these studies are reported in this issue of Scientifur.

Aleutian Disease caused by Aleutian Disease Virus has been a problem for the mink production for a long time. Results from an article published in this issue of Scientifur indicate that heating of equipment, such as nest boxes, to 80 °C for at least 1 hour will remedy the problem by rendering the virus inactive.

For information of the XII International Scientific Congress in Fur Animal Production (the IFASA Congress 2021), planned to be held in Warsaw, Poland on 24-26 August 2021, please consult the conference webpage: https://ifasa2020.pl/ .

Vivi Hunnicke Nielsen

Editor Scientifur

Effect of Heat-Treated Aleutian Disease Virus in Mink

M. Sokacz[1], J. S. Easley[2], J. Link[1], S. Bursian[1], T. M. Taxis[1]
[1]Department Of Animal Science, Michigan State University, East Lansing, Michigan 48824, USA
[2]Mink Veterinary Consulting and Research Service, Glenbeulah, Wisconsin 53023, USA
Corresponding author: T. M. Taxis (taxistas@msu.edu)

Abstract
The mink industry has been affected by Aleutian disease virus (ADV) for decades. As such, ADV has been one of the leading causes of the mink industry's economic decline. The aim of this study was to examine the effectiveness of heat treatment to inactivate ADV as a method to decontaminate mink farm equipment. Thirty-six mink were obtained from an established ADV-negative farm to test the virulence of isolated virus heated at two different temperatures for two different time periods. Upon arrival at Michigan State University, animals were randomly assigned to one of the six treatment groups: negative control, positive control (unheated virus), virus heated at 70℃ for 1 or 2 hours and virus heated at 80℃ for 1 or 2 hours. Each animal was inoculated with ADV at a concentration of 10 x 10^{10} viral copies/mL. Animals weighing less than 1.0 Kg received 0.3 mL of the virus while animals weighing greater than 1.0 kg received 0.6 mL. Twenty-eight days later, blood and tissues samples were collected from euthanized mink, and ADV was detected via quantitative polymerase chain reaction (qPCR). Aleutian disease virus heated to 70℃ for 1 and 2 hours was detected via PCR and therefore considered virulent. However, ADV heated to 80℃ for 1 and 2 hours, was undetected via PCR and therefore considered inactive. These results suggest that heating equipment, such as nest boxes, to 80℃ for at least 1 hour is adequate to render ADV inactive

Introduction

Aleutian disease virus (ADV) is a persistent parvovirus that is considered to be the most important infectious disease influencing the economic losses of an already struggling commercial mink industry (Reichert et al., 2014). In 2019, the United States had a $25.1 million decrease in value of pelts produced compared to 2018 (USDA, 2020). The predominant effect of ADV is the suppression of the immune system in those animals infected (Porter et al., 1980). Commercial mink farms with ADV-positive herds can experience a decrease in fertility, spontaneous abortions, lower pelt quality, and death of animals due to secondary infections (Nituch et al., 2012).

Animals infected with ADV may be infectious before showing any signs of the disease. Since mink are housed in close quarters, this allows ADV to spread quickly between animals. When the virus is present on a farm, it is common practice for the farm to depopulate the herd and decontaminate the facility before repopulation. This process can take up to several months with no revenue. The present study investigates the use of viral heat inactivation as a decontamination method. The use of heat to inactivate the virus on nest boxes and various portable equipment may help prevent the reoccurrence of ADV after repopulation.

Methods and Materials

Ethics Statement

All research procedures for this trial were approved by the Michigan State University (MSU) Institutional Animal Care and Use Committee (PROTO 201900146).

Animals and housing

Thirty-six natural dark female mink were obtained from an established ADV-negative commercial mink farm and transported to MSU's University Research Containment Facility. The trial was conducted in two phases. Phase one included 18 mink that were 12 ± 0.18 weeks old, and phase two included 18 mink at 23 ± 0.14 weeks of age. Twelve- and 23-week-old mink are considered juveniles, therefore age should not be considered an experimental variable. Mink in each phase were randomly assigned to one of six treatment groups with each group having a designated room. Animals were acclimated for one week prior to the beginning of each phase.

Mink were individually housed in stainless-steel mesh cages 76.2 cm long x 30.5 cm wide x 45.7 cm high elevated approximately 1 m above the floor. Each cage contained a resting platform. Water was provided *ad libitum* by a nipple drinker. Animals

were provided feed once daily. The 12-week-old animals were fed Purina Friskies Liver and Chicken cat food and the 23-week-old mink were provided a diet of chopped liver, egg, and instant oatmeal to mimic the wet diet they were accustomed to eating on the commercial farm.

Virus preparation
The ADV administered to mink was prepared by the Wisconsin Veterinary Diagnostic Laboratory (WVDL; Madison, WI). Samples of purified virus were heated at 70℃ or 80℃ for 1 or 2 hours. The negative control was the virus vehicle (phosphate-buffered saline) and the positive control was unheated purified virus. The virus samples were stored at -80℃ until the day of administration.

Virus Injection
The 12-week-old mink were anesthetized with 0.3 mL of a 10:1 ketamine (100 mg/mL):xylazine (20 mg/mL) cocktail administered intramuscularly (IM) and 23-week-old mink were administered 0.6 mL of the cocktail. While anesthetized, each mink was weighed and a 1 mL blood sample taken from the jugular vein. Following blood collection, mink were administered by intraperitoneal injection 0.5 mL of the appropriate virus preparation. Phase one mink were injected with virus heated at 80℃ for 1 or 2 hours (6 animals per group) as well as the positive and negative control preparations (3 animals per group). Phase two mink were injected with the virus heated at 70℃ for 1 or 2 hours (6 animals per group), positive (3 animals) or negative (3 animals) control preparations.

Observations
Mink were monitored daily for signs of illness (rough fur coats, nose and/or eye discharge) and weighed weekly during the 28-day trial. Mink that died or were euthanized prior to the end of the trial because of clinical signs including loss of body weight were frozen for subsequent necropsy.

Necropsies
At the end of the 28-day trial, mink were injected intramuscularly with the ketamine/xylazine cocktail. Once unconscious, mink were individually euthanized by carbon dioxide and necropsied with the spleen, liver, blood, and mesenteric lymph node being collected for subsequent quantitative polymerase chain reaction (qPCR) detection of the virus by the WVDL. A cycle threshold (CT) value was recorded with each qPCR assay. A CT value, as defined by the WVDL, is the number of cycles required for the fluorescent signal to exceed background. Values of less than or equal to 36 are considered positive. Values that range from 37-40 indicate minimal amounts of target nucleic acid and may represent environmental contamination.

Results and Discussion
Clinical signs
Phase one animals, those injected with virus heated to 80°C, showed no clinical signs indicative of ADV infection. However, one animal in the negative control group refused to eat and was subsequently euthanized due to loss of body weight. One animal in the 70℃ 1-hour group was unable to recover from the initial injection of the ketamine/xylazine cocktail, and two animals in the same group died during the 28-day observation period without showing any clinical signs. Two animals, one each in the 70℃ 1-hour and 70℃ 2-hour groups, were euthanized when they showed signs indicative of ADV infection.

qPCR
Heating of ADV affected the ability to detect the virus by qPCR in mink tissues 28 days after being administered. Results presented in Table 1 indicate that virus heated to 80℃ for either 1 or 2 hours inactivated the virus, preventing infection. However, virus heated to 70℃ for 1 or 2 hours was infectious as CT values were below 40. There was one negative control animal that had a CT value of 39.1, which was attributed to sample contamination rather than infection.

The present study demonstrated that heat treatment of ADV can be an effective method for inactivating ADV. All of the mink in the 80℃ group tested negative for infective ADV. Therefore, heating the virus for 2 hours was no more effective than heating for 1 hour. Furthermore, CT values for the mink injected with the virus heated at 70℃ for 1 hour were similar to those mink administered virus heated to 70℃ for 2 hours.

Currently, the method to deal with an ADV outbreak is continuous decontamination and repopulation. A previous study indicated that removal of organic material and chemical disinfection of cages is a 120-day process (Prieto et al., 2014). Using an 80℃ heat treatment for 1 hour as a decontamination method would allow for decreased time required for repopulation on a farm. Denmark has experienced an 85% decrease in

the number of ADV positive farms by the use of continuous eradication (Aasted et al., 1998). Farmers who are in countries not as successful as Denmark may be able to utilize heat treatment to aid in their ADV decontamination process. A quicker sanitation period will allow for less down time and economic losses.

Heat inactivation of ADV is a useful tool for decontamination of equipment. We found the temperature that the virus is subjected to is more critical than the time the virus is heated. The effective temperature and duration of heating for ADV inactivation was 80℃, for at least 1 hour.

Table 1
The effect of injecting mink with Aleutian disease virus (ADV) heated at 70℃ or 80º C for 1 or 2 hours on quantitative polymerase chain reaction (qPCR) detection of virus in tissues.

Animal Number	Virus Preparation Injected	ADV qPCR Result	CT Value[1]
401	Vehicle	Negative	-
402	Vehicle	Negative	-
501	Vehicle	Negative	-
502	Vehicle	Negative	-
503	Vehicle	Positive	39.1
101	Unheated virus	Positive	14.5
102	Unheated virus	Positive	14.2
103	Unheated virus	Positive	13.9
801	Unheated virus	Positive	18.4
802	Unheated virus	Positive	18.5
803	Unheated virus	Positive	18.0
201	80º C – 1 hour	Negative	-
202	80º C – 1 hour	Negative	-
203	80º C – 1 hour	Negative	-
204	80º C – 1 hour	Negative	-
205	80º C – 1 hour	Negative	-
206	80º C – 1 hour	Negative	-
301	80º C – 2 hour	Negative	-
302	80º C – 2 hour	Negative	-
303	80º C – 2 hour	Negative	-
304	80º C – 2 hour	Negative	-
305	80º C – 2 hour	Negative	-
306	80º C – 2 hour	Negative	-
601	70º C – 1 hour	Positive	19.9
603	70º C – 1 hour	Positive	15.9
604	70º C – 1 hour	Positive	15.9
606	70º C – 1 hour	Positive	18.7
701	70º C – 2 hour	Positive	20.4
702	70º C – 2 hour	Positive	20.3
703	70º C – 2 hour	Positive	19.5
704	70º C – 2 hour	Positive	15.8
705	70º C – 2 hour	Positive	17.3
706	70º C – 2 hour	Positive	17.5

[1]Cycle threshold (CT) values ≥ 40 were considered a negative result and are designated as a dash.

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BREEDING, GENETICS AND REPRODUCTION

Combined analysis of group recorded feed intake and individually recorded body weight and litter size in mink

Madsen MD[1], Villumsen TM[1], Hansen BK[2], Møller SH[3], Jensen J[1], Shirali M[1]

[1]Department of Molecular Biology and Genetics, Aarhus University, 8830Tjele, Denmark.
[2]KopenhagenFur Consulting, Agro Foodpark 15, 8200Aarhus, Denmark.
[3]Department of Animal Science, Aarhus University, 8830Tjele, Denmark.

In the mink industry, feed costs are the largest variable expense and breeding for feed efficient animals is warranted. Implementation of selection for feed efficiency must consider the relationships between feed efficiency and the current selection traits BW and litter size. Often, feed intake (FI) is recorded on a cage with a male and a female and there is sexual dimorphism that needs to be accounted for. Study aims were to (1) model group recorded FI accounting for sexual dimorphism, (2) derive genetic residual feed intake (RFI) as a measure of feed efficiency, (3) examine the relationship between feed efficiency and BW in males (BWM) and females (BWF) and litter size at day 21 after whelping (LS21) in Danish brown mink and (4) investigate direct and correlated response to selection on each trait of interest. Feed intake records from 9574 cages, BW records on 16 782 males and 16 875 females and LS21 records on 6446 yearling females were used for analysis. Genetic parameters for FI, BWM, BWF and LS21 were obtained using a multivariate animal model, yielding sex-specific additive genetic variances for FI and BW to account for sexual dimorphism. The analysis was performed in a Bayesian setting using Gibbs sampling, and genetic RFI was obtained from the conditional distribution of FI given BW using genetic regression coefficients. Responses to single trait selection were defined as the posterior distribution of genetic superiority of the top 10% of animals after conditioning on the genetic trends. The heritabilities ranged from 0.13 for RFI in females and LS21 to 0.59 for BWF. Genetic correlations between BW in both sexes and LS21 and FI in both sexes were unfavorable, and single trait selection on BW in either sex showed increased FI in both sexes and reduced litter size. Due to the definition of RFI and high genetic correlation between BWM and BWF, selection on RFI did not significantly alter BW. In addition, selection on RFI in either sex did not affect LS21. Genetic correlation between sexes for FI and BW was high but significantly lower than unity. The high correlations across sex allowed for selection on standardized averages of animals' breeding values (BVs) for RFI, FI and BW, which yielded selection responses approximately equal to the responses obtained using the sex-specific BVs. The results illustrate the possibility of selecting against RFI in mink with no negative effects on BW and litter size.

Animal. 2020 Sep; 14(9): 1793-1801.
Doi: 10.1017/S1751731120000762.
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Familial disease history and fur color type are associated with urinary tract disease in farmed mink *(Neovison vison)*

Mundbjerg K[1], Tolver A[2], Sebbelov I[3], Clausen T[4], Lundfold J[5], Hammer AS[3]

[1]Department of Veterinary and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Ridebanevej 3, 1870 Frederiksberg C, Denmark; LVK Dyrlægerne A/S, Fynsvej 8, 9500 Hobro, Denmark.
[2]Data Science Lab, Department of Mathematical Sciences, University of Copenhagen, Universitetsparken 5, 2100 København Ø, Denmark.
[3]Department of Veterinary and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Ridebanevej 3, 1870 Frederiksberg C, Denmark.
[4]Danish Fur Breeders Research Centre, Herningvej 112, 7500 Holstebro, Denmark.
[5]Kopenhagen Fur a.m.b.a., Langagervej 60, 2600 Glostrup, Denmark.

Mink urinary tract disease (MUTD) and mink fatty liver disease (MFLD) constitute two important disease entities in the mink production associated with sudden mortality and economic loss. Genetic factors or heritability of the diseases have not previously been investigated. Since mortality associated with MUTD and MFLD mainly occurs in the young immature mink, a potential genetic predisposition would rarely be passed on by the mink itself but potentially by relatives. This study aimed to investigate familial aggregation of MUTD and MFLD based on data from four generations of mink on a research

farm. The study included a total of 27,511 mink of brown and black color type with a post mortem prevalence of 0.8% for MUTD (n = 221) and 0.5% for MFLD (n = 138) within a year from birth. The prevalence in the color types brown and black were 0.6% and 1.6% for MUTD and 0.5% and 0.7% for MFLD. Family history of MUTD in breeding animals was found to be associated with a significantly higher probability of MUTD leading to mortality in offspring (p = 0.012, RR = 1.7; CI [1.1-2.4]), however this association was not significant for MFLD (p = 0.163, RR = 1.5; CI [0.9-2.7]). Mink of the color type black showed significantly higher risk of MUTD (RR = 2.6; CI [2.0-3.3]) and MFLD (R = 1.6; CI [1.1-2.2]) compared to brown mink. The results indicate that genetic factors may play a role in understanding MUTD and that selective breeding may contribute to reduce mortalities associated with this disease.

Research in Veterinary Science .
2020 Dec; 133:326-331.
Doi: 10.1016/j.rvsc.2020.10.026.
Epub 2020 Nov 1.

Genome analysis of American minks reveals link of mutations in Ras-related protein-38 gene to Moyle brown coat phenotype

Manakhov AD[1,2,3], Mintseva MY[1,2], Andreev IA[2], Uralsky LI[1], Andreeva TV[1,2], Trapezov OV[4,5], Rogaev EI[6,7,8,9]

[1]Department of Genomics and Human Genetics, Vavilov Institute of General Genetics, Russian Academy of Sciences, Moscow, Russia, 119333.
[2]Center for Genetics and Genetic Technologies, Faculty of Biology, Lomonosov Moscow State University, Moscow, Russia, 119192.
[3]Sirius University of Science and Technology, Sochi, Russia, 354340.
[4]Department of Animals and Human Genetics, Institute of Cytology and Genetics, Siberian Branch of the Russian Academy of Sciences, Novosibirsk, Russia, 630090.
[5]Novosibirsk State University, Novosibirsk, Russia, 630090.
[6]Department of Genomics and Human Genetics, Vavilov Institute of General Genetics, Russian Academy of Sciences, Moscow, Russia, 119333.
[7]Center for Genetics and Genetic Technologies, Faculty of Biology, Lomonosov Moscow State University, Moscow, Russia, 119192.
[8]Sirius University of Science and Technology, Sochi, Russia, 354340.
[9]Department of Psychiatry, University of Massachusetts Medical School, Worcester, MA, 01604, USA.

Over 35 fur colours have been described in American mink (Neovison vison), only six of which have been previously linked to specific genes. Moyle fur colour belongs to a wide group of brownish colours that are highly similar to each other, which complicates selection and breeding procedures. We performed whole genome sequencing for two American minks with Moyle (m/m) and Violet (a/a m/m /p/p) phenotypes. We identified two frame-shift mutations in the gene encoding Ras-related protein-38 (RAB38), which regulates the trafficking of tyrosinase-containing vesicles to maturing melanosomes. The results highlight the role of RAB38 in the biogenesis of melanosomes and melanin and the genetic mechanism contributing to hair colour variety and intensity. These data are also useful for tracking economically valuable fur traits in mink breeding programmes.

Scientific Reports. 2020 Sep 28; 10 (1): 15876.
Doi: 10.1038/s41598-020-72239-5.

Complex intragene deletion leads to oculocutaneous albinism in tanuki *(Japanese raccoon dog)*

Mae Y[1], Nagara K[1], Miyazaki M[2], Katsura Y[3], Enomoto Y[3], Koga A[3]

[1]Iida City Zoo, Iida, Nagano 395-0046, Japan.
[2]Manabu Miyazaki Photography Office, Iijima, Nagano 399-3705, Japan.
[3]Primate Research Institute, Kyoto University, Inuyama, Aichi 484-8506, Japan.

Genome. 2020 Oct; 63 (10): 517-523.
Doi: 10.1139/gen-2020-0049. Epub 2020 Aug 12.

Fifty Years of Research on European Mink *Mustela lutreola* L., 1761 Genetics: Where Are We Now in Studies on One of the Most Endangered Mammals?

Skorupski J[1,2]

[1]Institute of Marine and Environmental Sciences, University of Szczecin, Adama Mickiewicza 16 St., 70-383 Szczecin, Poland.

[2]*Polish Society for Conservation Genetics LUTREOLA, Maciejkowa 21 St., 71-784 Szczecin, Poland.*

The purpose of this review is to present the current state of knowledge about the genetics of European mink *Mustela lutreola* L., 1761, which is one of the most endangered mammalian species in the world. This article provides a comprehensive description of the studies undertaken over the last 50 years in terms of cytogenetics, molecular genetics, genomics (including mitogenomics), population genetics of wild populations and captive stocks, phylogenetics, phylogeography, and applied genetics (including identification by genetic methods, molecular ecology, and conservation genetics). An extensive and up-to-date review and critical analysis of the available specialist literature on the topic is provided, with special reference to conservation genetics. Unresolved issues are also described, such as the standard karyotype, systematic position, and whole-genome sequencing, and hotly debated issues are addressed, like the origin of the Southwestern population of the European mink and management approaches of the most distinct populations of the species. Finally, the most urgent directions of future research, based on the research questions arising from completed studies and the implementation of conservation measures to save and restore *M. lutreola* populations, are outlined. The importance of the popularization of research topics related to European mink genetics among scientists is highlighted.

Genes (Basel). 2020 Nov 11; 11(11): 1332.
Doi: 10.3390/genes11111332.

Phylogenetic relationships between different raccoon dog *(Nyctereutes procyonoides)* populations based on four nuclear and Y genes

Hong YE[1,2], Lee H[1], Kim KS[3], Min MS[4]

[1]*Conservation Genome Resource Bank for Korean Wildlife (CGRB), Research Institute for Veterinary Science and College of Veterinary Medicine, Seoul National University, Seoul, 08826, Republic of Korea.*
[2]*Environmental Health Research Department, National Institute of Environmental Research, Incheon, 22689, Republic of Korea.*
[3]*Department of Natural Resource Ecology and Management, Iowa State University, Ames, IA, 50011, USA.*
[4]*Conservation Genome Resource Bank for Korean Wildlife (CGRB), Research Institute for Veterinary Science and College of Veterinary Medicine, Seoul National University, Seoul, 08826, Republic of Korea.*

Genes and Genomics. 2020 Sep; 42 (9): 1075-1085.
Doi: 10.1007/s13258-020-00972-2.
Epub 2020 Jul 28.

A comparative phylogenomic analysis of SARS-CoV-2 strains reported from non-human mammalian species and environmental samples

Ul-Rahman A[1,2,3], Shabbir MAB[4], Aziz MW[4], Yaqub S[4], Mehmood A[5], Raza MA[6], Shabbir MZ[7]

[1]*Faculty of Veterinary and Animal Sciences, Muhammad Nawaz Shareef University of Agriculture, Multan, 66000, Pakistan.*
[2]*Institute of Microbiology, University of Veterinary and Animal Sciences, Lahore, 54600, Pakistan.*
[3]*Quality Operations Laboratory, University of Veterinary and Animal Sciences, Outfall road, Lahore, 54600, Pakistan.*
[4]*Institute of Microbiology, University of Veterinary and Animal Sciences, Lahore, 54600, Pakistan.*
[5]*Veterinary Research Institute, Zarar Shaheed road, Lahore, 54000, Pakistan.*
[6]*Faculty of Veterinary and Animal Sciences, Muhammad Nawaz Shareef University of Agriculture, Multan, 66000, Pakistan.*
[7]*Quality Operations Laboratory, University of Veterinary and Animal Sciences, Outfall road, Lahore, 54600, Pakistan.*

Coronaviruses (CoVs) infect a wide range of domestic and wild mammals. These viruses have a potential and tendency to cross-species barriers and infect humans. Novel human coronavirus 2019-nCoV (hCoV-19) emerged from Wuhan, China, and has caused a global pandemic. Genomic features of SARS-CoV-2 may attribute inter-species transmission and adaptation to a novel host, and therefore is imperative to explicate the evolutionary dynamics of the viral genome and its propensity for differential host selection. We conducted an in silico analysis of all the coding gene sequences of SARS-CoV-2 strains (n = 39) originating from a range of non-human mammalian species, including pangolin, bat, dog, cat, tiger, mink, mouse, and the environmental samples such as wastewater, air and surface samples from the door

handle and seafood market. Compared to the reference SARS-CoV-2 strain (MN908947; Wuhan-Hu-1), phylogenetic and comparative residue analysis revealed the circulation of three variants, including hCoV-19 virus from humans and two hCoV-19-related precursors from bats and pangolins. A lack of obvious differences as well as a maximum genetic homology among dog-, cat-, tiger-, mink-, mouse-, bat- and pangolin-derived SARS-CoV-2 sequences suggested a likely evolution of these strains from a common ancestor. Several residue substitutions were observed in the receptor-binding domain (RBD) of the spike protein, concluding a promiscuous nature of the virus for host species where genomic alternations may be required for the adaptation to novel host/s. However, such speculation needs in vitro investigations to unleash the influence of substitutions towards species-jump and disease pathogenesis.

Molecular Biology Reports. 2020 Nov; 47 (11): 9207-9217.
Doi: 10.1007/s11033-020-05879-5.
Epub 2020 Oct 26.

Human coronavirus spike protein-host receptor recognition

Guruprasad L[1]

[1]School of Chemistry, University of Hyderabad, Hyderabad, 500046, India.

A variety of coronaviruses (CoVs) have infected humans and caused mild to severe respiratory diseases that could result in mortality. The human CoVs (HCoVs) belong to the genera of α- and β-CoVs that originate in rodents and bats and are transmitted to humans via zoonotic contacts. The binding of viral spike proteins to the host cell receptors is essential for mediating fusion of viral and host cell membranes to cause infection. The SARS-CoV-2 originated in bats (RaTG13 SARS-CoV) and is transmitted to humans via pangolins. The presence of 'PRRA' sequence motif in SARS-CoV-2 spike proteins from human, dog, cat, mink, tiger and lion suggests a common viral entry mechanism into host cells. In this review, we discuss structural features of HCoV spike proteins and recognition of host protein and carbohydrate receptors.

Progress in Biophysics and Molecular Biolology. 2020 Oct 31; S0079-6107 (20) 30110-3.
Doi: 10.1016/j.pbiomolbio.2020.10.006.
Online ahead of print.

A role for Msx genes in mammalian embryonic diapause

Cha J[1,2], Fenelon JC[3], Murphy BD[4], Shaw G[3], Renfree MB[3], Dey SK[1]

[1]Division of Reproductive Sciences, Cincinnati Children's Hospital Medical Center, USA.
[2]Present address: Division of Diabetes, Endocrinology, and Metabolism, Department of Medicine, Vanderbilt University Medical Center, USA.
[3]School of Biosciences, University of Melbourne, Melbourne, Australia.
[4]Centre de recherche en reproduction et fertilité, Université de Montréal, Québec, Canada.

Mammalian embryonic diapause is a reproductive phenomenon defined by the reversible arrest in blastocyst development and metabolic activity within the uterus which synchronously becomes quiescent to implantation. This natural strategy, evident in over 130 species across eight orders, can temporally uncouple conception from delivery until conditions are favorable for the survival of the mother and newborn. While the maternal endocrine milieu has been shown to be important for this process, the local molecular mechanisms by which the uterus and embryo achieve quiescence, maintain blastocyst survival and then resumes blastocyst activation with subsequent implantation in response to endocrine cues remains unclear. Here we review the first evidence that the proximal molecular control of embryonic diapause is conserved in three unrelated mammalian species which employ different endocrine programs to initiate diapause. In particular, uterine expression of muscle segment homeobox (*Msx*) genes *Msx1* or *Msx2* persists during diapause, followed by downregulation with blastocyst reactivation and implantation. Mice *(Mus musculus)* with conditional inactivation of *Msx1* and *Msx2* in the uterus fail to achieve diapause and reactivation. Remarkably, the mink *(Neovison vison)* and tammar wallaby *(Macropus eugenii)* share this pattern of *MSX1* or *MSX2* expression as in mice during delay - it persists during diapause and is rapidly downregulated upon implantation. Therefore, these findings were the first to provide evidence that there are common conserved molecular regulators in the uterus of unrelated mammals during embryonic diapause.

Bioscientifica Proceedings. 2020; 10: 44-51.
Doi: 10.1530/biosciprocs.10.002.

Morphometric Characteristics of the Spermatozoa of Blue Fox (*Alopex lagopus*) and Silver Fox (*Vulpes vulpes*)

Andraszek K[1], Banaszewska D[1], Szeleszczuk O[2], Kuchta-Gładysz M[2], Grzesiakowska A[2]

[1]Institute of Animal Science and Fisheries, Faculty of Agrobioengineering and Animal Husbandry, Siedlce University of Natural Sciences and Humanities, Prusa 14 Str, 08-110 Siedlce, Poland.
[2]Department of Animal Reproduction, Anatomy and Genomics, Faculty of Animal Sciences, University of Agriculture in Krakow, Mickiewicza 24/28 Str, 30-059 Kraków, Poland.

The results presented in this study are the first such extensive characterization of the sperm morphometry of the blue fox (*Alopex lagopus*) and silver fox (*Vulpes vulpes*), as representatives of the family Canidae. Canine spermatozoa, especially the sperm of farmed foxes, are not often described in studies on reproduction. The aim of the study was a detailed comparison of the morphometric dimensions and shape of the sperm of two fox species: silver fox and blue fox. Semen collected from 10 silver foxes and 10 blue foxes was used for the study. The specimens were stained with silver nitrate. Measurements were performed of the length, width, perimeter, and area of the head; the area of the acrosome and its coverage; the length of the midpiece and its coverage; the length of the tail; and the length of the end piece of the tail. In addition, four head shape indices were calculated: ellipticity, elongation, roughness and regularity. The following values for the morphometric parameters and shape indices were obtained for blue fox and silver fox, respectively: head length-6.72 µm and 6.33 µm; head width-4.54.µm and 4.21 µm; head perimeter-18.11 µm and 17.37 µm; head area-21.94 μm^2 and 21.11 μm^2; acrosome area-11.50 μm^2 and 10.92 μm^2; midpiece length-12.85 µm and 12.79 µm; tail end piece length-3.44 µm and 3.28 µm; tail length-65.23 µm and 65.09 µm; acrosome coverage-52.43% and 52.83%; midpiece coverage-19.71% and 19.65%; sperm length-71.95 µm and 71.42 µm; ellipticity-1.49 and 1.52; elongation-0.19 and 0.20; roughness-0.84 and 1.88; regularity-1.09 and 0.99. The significance of differences between species was verified by Tukey's test at $p \leq 0.05$. Statistically significant differences between species were found for the following parameters: head length, width, perimeter and area; acrosome area; tail, end piece, and total sperm length; roughness and regularity. The differences in the size and shape of sperm can be used to establish reference patterns for fox sperm enabling more accurate species identification.

Animals (Basel). 2020 Oct 20; 10 (10): 1927.
Doi: 10.3390/ani10101927.

NUTRITION, FEEDING AND MANAGEMENT

Comparative analysis of the gut microbiota of the blue fox *(Alopex lagopus)* and raccoon dog *(Nyctereutes procyonoides)*

Liu H[1], Li Z[1], Si H[1], Zhong W[1], Fan Z[1], Li G[2]

[1]Institute of Special Animal and Plant Sciences, Chinese Academy of Agricultural Sciences, 4899 Juye Street, Changchun, 130112, Jilin, China.
[2]Institute of Special Animal and Plant Sciences, Chinese Academy of Agricultural Sciences, 4899 Juye Street, Changchun, 130112, Jilin, China.

Archives of Microbiology. 2020 Jan; 202 (1): 135-142.
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All-trans-retinoic acid inhibits mink hair follicle growth via inhibiting proliferation and inducing apoptosis of dermal papilla cells through TGF-β2/Smad2/3 pathway

Nan W[1], Li G[2], Si H[1], Lou Y[3], Wang D[4], Guo R[4], Zhang H[5]

[1]College of Animal Science and Technology, Jilin Agricultural University, Changchun, Jilin, 130118, People's Republic of China; State Key Laboratory of Special Economic Animal Molecular Biology, Institute of Special Animal and Plant Sciences, Chinese Academy of Agricultural Sciences, Changchun, Jilin, 130112, People's Republic of China.
[2]State Key Laboratory of Special Economic Animal Molecular Biology, Institute of Special Animal and Plant Sciences, Chinese Academy of Agricultural

Sciences, Changchun, Jilin, 130112, People's Republic of China.
[3]College of Animal Science and Technology, Jilin Agricultural University, Changchun, Jilin, 130118, People's Republic of China.
[4]Changli Animal Disease Prevention and Control Center, Changli, Hebei, 066600, People's Republic of China.
[5]College of Animal Science and Technology, Hebei Normal University of Science and Technology, Qinhuangdao, Hebei, 066004, People's Republic of China; State Key Laboratory of Special Economic Animal Molecular Biology, Institute of Special Animal and Plant Sciences, Chinese Academy of Agricultural Sciences, Changchun, Jilin, 130112, People's Republic of China.

Acta Histochemica. 2020 Oct; 122 (7): 151603.
Doi: 10.1016/j.acthis.2020.151603.
Epub 2020 Aug 17.

Dietary supplementation of Ascophylum nodosum improved kidney function of mink challenged with Aleutian mink disease virus

Farid AH[1], Smith NJ[2,3]

[1]Department of Animal Science and Aquaculture, Faculty of Agriculture, Dalhousie University, Truro, Nova Scotia, B2N 5E3, Canada.
[2]Perennia Food and Agriculture, Bible Hill, Nova Scotia, B4N 1J5, Canada.
[3]Present Address: Farm Credit Canada, 332 Willow St, Truro, Nova Scotia, B2N 5A5, Canada.

Background
Feed additives which can ease the negative effects of infection by the Aleutian mink disease virus (AMDV) are of interest to mink farmers. The effects of kelp meal (Ascophylum nodosum) supplementation on immune response, virus replication and blood parameters of mink inoculated with AMDV were assessed. AMDV-free black mink (n = 75) were intranasally inoculated with a local strain of AMDV and fed a commercial pellet supplemented with kelp meal at the rates of 1.5% or 0.75% of the feed or were kept as controls (no kelp) for 451 days. Blood was collected on days 0 (pre-inoculation), 31, 56, 99, 155, 366 and 451 post-inoculation (dpi).

Results
No significant difference was observed among the treatments for the proportion of animals positive for antibodies against the virus measured by the counter-immunoelectrophoresis (CIEP), viremia measured by PCR, antibody titer measured by quantitative ELISA, total serum protein measured by a refractometer or elevated levels of gamma globulin measured by iodine agglutination test at the sampling occasions. At the termination of the experiment on 451 dpi, there were no differences among treatments for antibody titer measured by CIEP, total serum protein, albumin, globulins, albumin:globulin ratio, alkaline phosphatase, gamma-glutamyl transferase, and proportions of PCR positive spleen, lymph node or bone marrow samples, but blood urea nitrogen and creatine levels were significantly lower in the 1.5% kelp supplemented group than in the controls.

Conclusion
Kelp supplementation improved kidney function of mink infected with AMDV with no effect on liver function, immune response to infection by AMDV or virus replication.

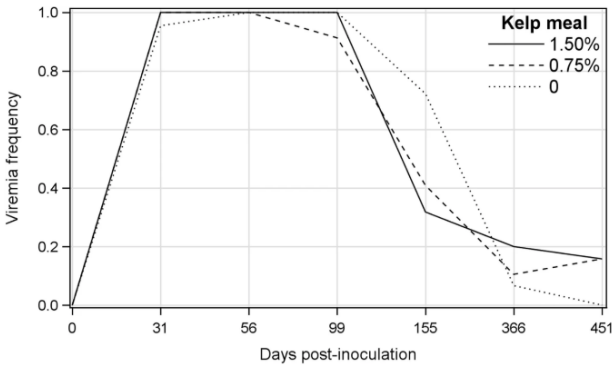

Fig. 1. Frequency of viremic mink of the kelp-supplemented and control groups on different post-inoculation days.

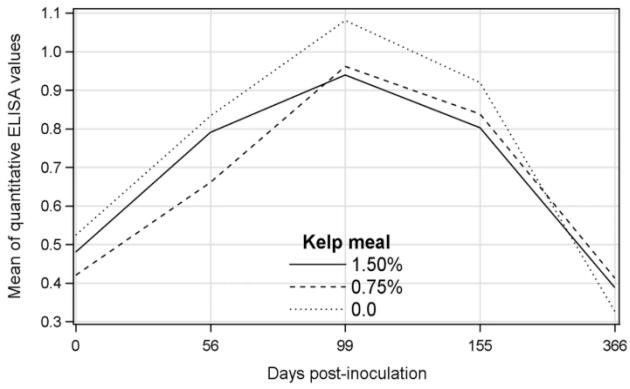

Fig. 2. Frequency of seropositive kelp-supplemented and control groups on different post-inoculation days.

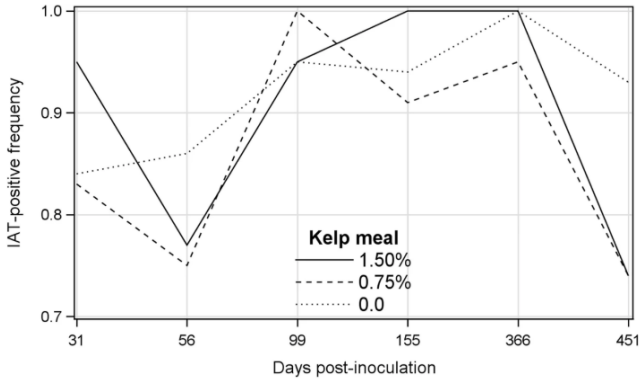

Fig. 3. Frequency of positive iodine agglutination test results of the kelp-supplemented and control mink on different post-inoculation days.

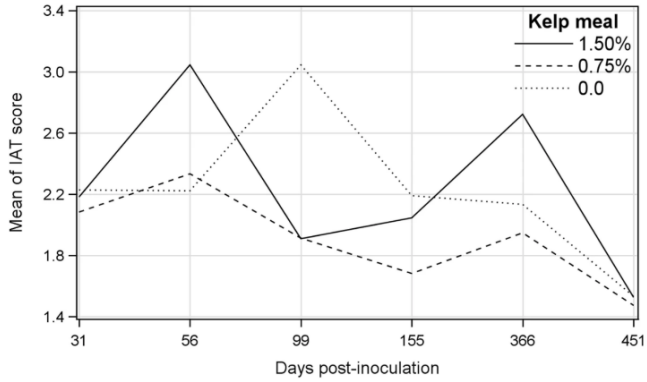

Fig. 4. Mean of iodine agglutination test scores (ranged from 0 to 4) of the kelp-supplemented and control mink on different post-inoculation days.

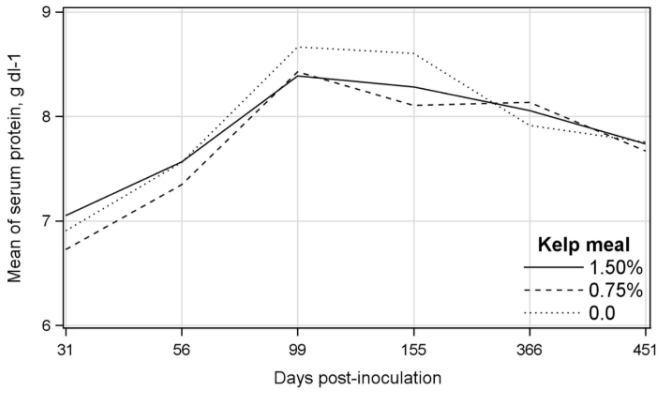

Fig. 5. Mean of serum protein measured by a refractometer of the kelp-supplemented and control mink on different post-inoculation days.

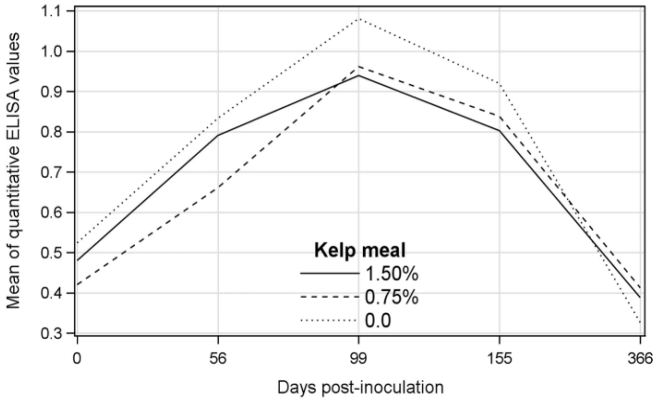

Fig. 6. Mean of quantitative ELISA results (unadjusted OD_{450}) of kelp-supplemented and control mink on different post-inoculation days.

BMC Veterinary Research. 2020 Nov 30; 16 (1): 465.
Doi: 10.1186/s12917-020-02685-w.

Discrimination of meat from fur-producing and food-providing animals using mass spectrometry-based proteomics

Qiu W[1], Zhang X[2], Zhang H[3], Liang C[2], Xu J[1], Gao H[2], Ai L[4], Zhao S[2], Wang Y[1], Yang Y[1], Zhao X[5]

[1]College of Food Science and Technology, Ocean University of China, No. 5 Yu Shan Road, Qingdao, Shandong Province 266003, PR China.
[2]Technology Center of Qingdao Customs District, No.70 Qutangxia Road, Qingdao, Shandong Province 266002, PR China.
[3]Technology Center of Qingdao Customs District, No.70 Qutangxia Road, Qingdao, Shandong Province 266002, PR China.
[4]Technology Center of Shijiazhuang Customs, Shijiazhuang, Hebei Province 050051, PR China.
[5]College of Food Science and Technology, Ocean University of China, No. 5 Yu Shan Road, Qingdao, Shandong Province 266003, PR China.

Food Research International. 2020 Nov; 137: 109446.
Doi: 10.1016/j.foodres.2020.109446.
Epub 2020 Jun 14.

Pandemic dooms Danish mink-and mink research

Lesté-Lasserre C[1]

[1]Christa Lesté-Lasserre is a freelance journalist in Paris.

Science. 2020 Nov 13; 370 (6518): 754.
Doi: 10.1126/science.370.6518.754.

Mass culling of minks to protect the COVID-19 vaccines: is it rational?

Frutos R[1,2], Devaux CA[3]

[1]Cirad, UMR 17, Intertryp, Montpellier, France.
[2]IES, UMR 5214 Université Montpellier-CNRS, Montpellier, France.
[3]IHU-Méditerranée Infection and CNRS, Marseille, France.

The Danish Government announced the culling of 17 million minks in rearing after the report of mink-specific mutations of severe acute respiratory syndrome coronavirus 2 in humans. The rationale behind this decision is that these mutations might negatively impact the deployment of anti-coronavirus disease 2019 vaccines. Is it a precautionary attitude or a panic-driven overreaction?

New Microbes and New Infections. 2020 Nov; 38: 100816.
Doi: 10.1016/j.nmni.2020.100816.
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Ban unsustainable mink production

Xia C[1], Lam SS[2,1], Sonne C[3,1]

[1]Nanjing Forestry University, Nanjing, China.
[2]Universiti Malaysia Terengganu, Terengganu, Malaysia.
[3]Aarhus University, Roskilde, Denmark.

Science. 2020 Oct 30; 370 (6516): 539.
Doi: 10.1126/science.abf0461.

BEHAVIOUR AND WELFARE

Infrared Thermography as an Indicator of Heat Loss in Fur-Chewing Chinchillas (*Chinchilla Lanigera*)

Łapiński S[1], Orel J[2], Niedbała P[1], Kucharska W[2], Jakubowska M[2], Lisowska-Lis A[3], Tombarkiewicz B[2], Lis MW[2]

[1]Department of Swine and Small Animal Breeding, University of Agriculture in Kraków, Kraków, Poland.
[2]Department of Veterinary, Reproduction and Animal Welfare, Faculty of Animal Science, University of Agriculture in Kraków, Kraków, Poland.
[3]State Higher Vocational School in Tarnów, Polytechnic Institute, Tarnów, Poland.

Journal of Applied Animal Welfare Science. Jul-Sep 2020; 23 (3): 338-347.
Doi: 10.1080/10888705.2019.1614924.
Epub 2019 May 16.

HEALTH AND DISEASE

Aleutian mink disease: spatio-temporal variation of prevalence and influence on the feral American mink

Zalewski A[1], Virtanen JME[2,3], Brzeziński M[4], Kołodziej-Sobocińska M[1], Jankow W[1], Sironen T[2,3]

[1]Mammal Research Institute, Polish Academy of Sciences, 17-230, Białowieża, Poland.
[2]Department of Veterinary Biosciences Faculty of Veterinary Medicine, University of Helsinki, Agnes Sjöbergin katu 2, 00790, Helsinki, Finland.
[3]Department of Virology Faculty of Medicine, University of Helsinki, Haartmaninkatu 3, 00290, Helsinki, Finland.
[4]Faculty of Biology, University of Warsaw, Żwirki i Wigury 101, 02-089, Warszawa, Poland.

Pathogens are one of the factors driving wildlife population dynamics. The spread of pathogens in wildlife is currently highly related to the transmission of pathogens from farmed animals, which has increased with the constant development of farming. Here, we analysed the spatio-temporal variation in the prevalence of Aleutian mink disease virus (AMDV) antibodies

in feral American mink (Neovison vison) populations in Poland (1153 individuals from 9 sites) in relation to mink farming intensity. AMDV was detected in feral mink at all study sites and the prevalence ranged from 0.461 in the northern region to 0.826 in the western region. Mink males and adults were infected more often than females and subadults; the infection was also more frequent during the mink breeding season than during non-breeding. The prevalence of AMDV changed nonlinearly in consecutive years and the peak of prevalence was every 3-4 years. The predicted AMDV prevalence was low at sites where the number of farmed mink was also low and increased linearly with the increase in the number of mink kept on farms. The predicted AMDV prevalence at sites with low mink farming intensity strongly varied between years, whereas at sites with high mink farming intensity, the predicted prevalence did not change significantly. AMDV infection affected the mink's body condition and caused an increase in the size of the spleen, liver, and kidneys. This study shows that Aleutian mink disease strongly affects feral mink but the spatio-temporal variation of its prevalence is complex and partly related to the transmission of the virus from farmed mink to feral populations. The study highlights the complexity of AMDV circulation in feral mink populations and implicates a potential spillover of the virus to native species.

Transboundary and Emerging Diseases. 2020 Nov 16.
Doi: 10.1111/tbed.13928. Online ahead of print.

Development of an antigen-capture enzyme-linked immunosorbent assay for diagnosis of Aleutian mink disease virus

Lu T[1], Wang Y[2], Wu Y[1], Zhao L[2], Wu S[1], Chen H[3]

1Institute for Laboratory Animal Research, Guizhou University of Traditional Chinese Medicine, Guiyang, 550025, China.
[2]State Key Laboratory of Veterinary Biotechnology, Harbin Veterinary Research Institute, Chinese Academy of Agricultural Sciences, 678 Haping Road, Harbin, 150069, China.
[3]State Key Laboratory of Veterinary Biotechnology, Harbin Veterinary Research Institute, Chinese Academy of Agricultural Sciences, 678 Haping Road, Harbin, 150069, China.

Archives of Virology. 2020 Oct 17.
Doi: 10.1007/s00705-020-04850-w.
Online ahead of print.

Employing MIC Data for Mink Pathogens to Propose Tentative Epidemiological Cut-Off Values: A Step Toward Rationalizing Antimicrobial Use in Mink

Nikolaisen NK[1,2], Ronaghinia AA[2,3], Kløve Lassen DC[4], Chehabi CN[1], Lindegaard M[1], Struve T[2], Chriél M[4], Damborg P[3], Kahlmeter G[5], Jensen LB[1], Pedersen K[6]

[1]National Food Institute, Research Group for Microbiology and Hygiene, Technical University of Denmark, Kongens Lyngby, Denmark.
[2]Department of Health and Diagnostics, Kopenhagen Fur A.M.B.A., Glostrup, Denmark.
[3]Department of Veterinary and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Copenhagen, Denmark.
[4]Centre for Diagnostics, Technical University of Denmark, Kongens Lyngby, Denmark.
[5]Klinisk Mikrobiologi, Växjö, Sweden.
[6]National Veterinary Institute, Uppsala, Sweden.

Optimizing antimicrobial dosage regimens and development of breakpoints for antimicrobial susceptibility testing are important prerequisites for rational antimicrobial use. The objectives of the study were (1) to produce MIC data for four mink pathogens and (2) to employ these MIC data to support the development of tentative epidemiological cut-off values (TECOFFs), which may be used for future development of mink-specific antimicrobial dosages and breakpoints. Broth microdilution was used to establish MIC distributions for 322 mink bacterial isolates of clinical origin from six European mink-producing countries. The included species were *E. coli* (n = 162), *S. delphini* (n = 63), *S. canis* (n = 42), and *P. aeruginosa* (n = 55). Sixty-four *E. coli* isolates and 34 *S. delphini* isolates were whole-genome sequenced and analyzed for antimicrobial resistance genes. No EUCAST MIC data are available on *S. delphini* and *S. canis*, hence tentative ECOFFs were suggested for the majority of the tested antimicrobials. For *E. coli* and *P. aeruginosa*, the wildtype distributions were in accordance with EUCAST data. Overall, the genotypes of the sequenced isolates were in concordance with the phenotypes. These data constitute an important piece in the puzzle of developing antimicrobial dosages and clinical breakpoints for

mink. Until pharmacokinetic and clinical data become available, the (tentative) ECOFFs can be used for monitoring resistance development and as surrogates for clinical breakpoints.

Frontiers in Veterinary Science. 2020 Oct 21; 7: 44594.
Doi: 10.3389/fvets.2020.544594. eCollection 2020.

Clinical and Pathological Findings in SARS-CoV-2 Disease Outbreaks in Farmed Mink (*Neovison vison*)

Molenaar RJ[1,2], Vreman S[3,2], Hakze-van der Honing RW[3], Zwart R[3], de Rond J[1], Weesendorp E[3], Smit LAM[4], Koopmans M[5], Bouwstra R[1], Stegeman A[4], van der Poel WHM[3]

[1]84762GD Animal Health, Deventer, Netherlands.
[2]Robert-Jan Molenaar and Sandra Vreman contributed equally to this work.
[3]Wageningen Bioveterinary Research, Lelystad, Netherlands.
[4]Utrecht University, Utrecht, Netherlands.
[5]Erasmus University, Rotterdam, Netherlands.

Veterinary Pathology, p. 2020 Sep; 57 (5): 653-657.
Doi: 10.1177/0300985820943535.
Epub 2020 Jul 14.

Transmission of SARS-CoV-2 on mink farms between humans and mink and back to humans

Munnink BBO[1], Sikkema RS[2], Nieuwenhuijse DF[2], Molenaar RJ[3], Munger E[2], Molenkamp R[2], van der Spek A[4], Tolsma P[5], Rietveld A[6], Brouwer M[6], Bouwmeester-Vincken N[7], Harders F[8], Hakze-van der Honing R[8], Wegdam-Blans MCA[9], Bouwstra RJ[3], Geurts van Kessel C[2], van der Eijk AA[2], Velkers FC[10], Smit LAM[11], Stegeman A[10], van der Poel WHM[8], Koopmans MPG[2]

[1]Erasmus MC, Department of Viroscience, WHO collaborating centre for arbovirus and viral hemorrhagic fever Reference and Research, Rotterdam, Netherlands. b.oudemunnink@erasmusmc.nl.
[2]Erasmus MC, Department of Viroscience, WHO collaborating centre for arbovirus and viral hemorrhagic fever Reference and Research, Rotterdam, Netherlands.
[3]Royal GD, Deventer, Netherlands.
[4]Netherlands Food and Consumer Product Safety Authority (NVWA), Utrecht, Netherlands.
[5]Municipal health Services GGD Brabant-Zuidoost, Eindhoven, Netherlands.
[6]Municipal health Services GGD Hart voor Brabant, 's-Hertogenbosch, Netherlands.
[7]Municipal health Services GGD Limburg-Noord, Venlo, Netherlands.
[8]Wageningen Bioveterinary Research, Lelystad, Netherlands.
[9]Stichting PAMM, Veldhoven, Netherlands.
[10]Farm Animal Health, Utrecht University, Utrecht, Netherlands.
[11]Institute for Risk Assessment Sciences (IRAS), Utrecht University, Utrecht, Netherlands.

Science. 2020 Nov 10; eabe5901.
Doi: 10.1126/science.abe5901.
Online ahead of print.

SARS-CoV-2 Transmission between Mink *(Neovison vison)* and Humans, Denmark

Hammer AS[1], Quaade ML[1], Rasmussen TB[2], Fonager J[2], Rasmussen M[2], Mundbjerg K[1], Lohse L[2], Strandbygaard B[2], Jørgensen CS[2], Alfaro-Núñez A[2], Rosenstierne MW[2], Boklund A[1], Halasa T[1], Fomsgaard A[2], Belsham GJ[2], Bøtner A[1,2]

[1]University of Copenhagen, Copenhagen, Denmark.
[2]Statens Serum Institut, Copenhagen, Denmark.

Severe acute respiratory syndrome coronavirus 2 has caused a pandemic in humans. Farmed mink (Neovison vison) are also susceptible. In Denmark, this virus has spread rapidly among farmed mink, resulting in some respiratory disease. Full-length virus genome sequencing revealed novel virus variants in mink. These variants subsequently appeared within the local human community.

Emerging Infectious Diseases. 2020 Nov 18; 27 (2).
Doi: 10.3201/eid2702.203794.
Online ahead of print.

SARS-CoV-2 and the human-animal interface: outbreaks on mink farms

Koopmans M[1]

[1]Department of Viroscience, Erasmus MC, 3015 GD Rotterdam, Netherlands.

Lancet Infectious Diseases. 2020 Nov 20; S1473-3099(20)30912-9.
Doi: 10.1016/S1473-3099(20)30912-9.
Online ahead of print.

COVID mink analysis shows mutations are not dangerous – yet

Mallapaty S

Nature. 2020 Nov; 587 (7834): 340-341.
Doi: 10.1038/d41586-020-03218-z.

Could Mustelids spur COVID-19 into a panzootic?

Manes C[1], Gollakner R[2], Capua I[3]

[1]One Health Center of Excellence, University of Florida Gainesville, Florida, USA.
[2]One Health Center of Excellence, University of Florida Gainesville, Florida, USA.
[3]One Health Center of Excellence, University of Florida,1604 McCarty Drive, room G047, Gainesville, FL 32603, United States.

Veterinaria Italiana. 2020 Sep 9.
Doi: 10.12834/VetIt.2375.13627.1.
Online ahead of print.

Susceptibility of Raccoon Dogs for Experimental SARS-CoV-2 Infection

Freuling CM[1], Breithaupt A[1], Müller T[1], Sehl J[1], Balkema-Buschmann A[1], Rissmann M[1], Klein A[1], Wylezich C[1], Höper D[1], Wernike K[1], Aebischer A[1], Hoffmann D[1], Friedrichs V[1], Dorhoi A[1], Groschup MH[1], Beer M[1], Mettenleiter TC[1]

[1]Friedrich-Loeffler-Institut, Greifswald-Insel Riems, Germany.

Raccoon dogs might have been intermediate hosts for severe acute respiratory syndrome-associated coronavirus in 2002-2004. We demonstrated susceptibility of raccoon dogs to severe acute respiratory syndrome coronavirus 2 infection and transmission to incontact animals. Infected animals had no signs of illness. Virus replication and tissue lesions occurred in the nasal conchae.

Emerging Infectious Diseases. 2020 Dec; 26 (12): 2982-2985.
Doi: 10.3201/eid2612.203733. Epub 2020 Oct 22.

Transmission of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) to animals: an updated review

Tazerji SS[1,2], Duarte PM[3], Rahimi P[4], Shahabinejad F[5], Dhakal S[6], Malik YS[7], Shehata AA[8,9], Lama J[10], Klein J[11], Safdar M[12], Rahman MT[13], Filipiak KJ[14], Rodríguez-Morales AJ[15], Sobur MA[13], Kabir F[16], Vazir B[17], Mboera L[18], Caporale M[19], Islam MS[13], Amuasi JH[20], Gharieb R[21], Roncada P[22], Musaad S[23], Tilocca B[22], Koohi MK[24], Taghipour A[25], Sait A[26], Subbaram K[27], Jahandideh A[16], Mortazavi P[28], Abedini MA[4], Hokey DA[29], Hogan U[30], Shaheen MNF[31], Elaswad A[32], Elhaig MM[33], Fawzy M[34]

[1]Young Researchers and Elites Club, Science and Research Branch, Islamic Azad University, Tehran, Iran.
[2]Faculty of Veterinary Medicine, Science and Research Branch, Islamic Azad University, Tehran, Iran.
[3]Faculty of Biological and Health Sciences, Universidade de Cuiabá (UNIC), Primavera Do Leste, MT, Brazil.
[4]Faculty of Veterinary Medicine, Science and Research Branch, Islamic Azad University, Tehran, Iran.
[5]Kerman University of Medical Sciences, Kerman, Iran.
[6]W. Harry Feinstone Department of Molecular Microbiology and Immunology, The Johns Hopkins Bloomberg School of Public Health, Baltimore, MD, USA.
[7]Division of Biological Standardization, ICAR-Indian Veterinary Research Institute, Izatnagar, Bareilly, Uttar Pradesh, India.
[8]Research and Development Section, PerNaturam GmbH, 56290, Gödenroth, Germany.
[9]Avian and Rabbit Diseases Department, Faculty of Veterinary Medicine, University of Sadat City, Sadat City, Egypt.
[10]RetroVirox, Inc., San Diego, CA, USA.

[11]*Faculty of Health and Social Sciences, University of South-Eastern Norway, Kongsberg, Norway.*
[12]*Department of Breeding and Genetics, Cholistan University of Veterinary & Animal Sciences, Bahawalpur, Pakistan.*
[13]*Department of Microbiology and Hygiene, Faculty of Veterinary Science, Bangladesh Agricultural University, Mymensingh, 2202, Bangladesh.*
[14]*Department of Cardiology, Medical University of Warsaw, Warsaw, Poland.*
[15]*Grupo de Investigacion Biomedicina, Faculty of Medicine, Fundacion Universitaria Autonoma de las Americas, Pereira, Risaralda, Colombia.*
[16]*Department of Clinical Science, Faculty of Specialized Veterinary Sciences, Science and Research Branch, Islamic Azad University, Tehran, Iran.*
[17]*Department of Physiology, Faculty of Specialized Veterinary Sciences, Science and Research Branch, Islamic Azad University, Tehran, Iran.*
[18]*Emerging and Vector-borne Diseases Program, SACIDS Foundation for One Health, Sokoine University of Agriculture, Morogoro, Tanzania.*
[19]*Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise "G. Caporale", Teramo, Italy.*
[20]*Global Health, and Infectious Diseases Research Group, Kumasi Collaborative Center for Research in Tropical Medicine, Kumasi, Ghana.*
[21]*Department of Zoonoses, Faculty of Veterinary Medicine, Zagazig University, Zagazig, Sharkia Province, Egypt.*
[22]*Department of Health Sciences, University "Magna Græcia" of Catanzaro, Catanzaro, Italy.*
[23]*Kanad Hospital, Alain, P.O. Box 1016, Abu Dhabi, UAE.*
[24]*Department of Comparative Biosciences, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran.*
[25]*Department of Clinical Science, Faculty of Veterinary Medicine, Karaj Branch, Islamic Azad University, Karaj, Iran.*
[26]*Virology Department, Pendik Veterinary Control Institute, Ministry of Food and Forestry, 34890, Pendik-Istanbul, Turkey.*
[27]*Department of Preparatory (Biology), Al-Ghad International Colleges for Applied Medical Sciences, Riyadh, Saudi Arabia.*
[28]*Pathobiology Department, Faculty of Veterinary Medicine, Science and Research Branch, Islamic Azad University, Tehran, Iran.*
[29]*Aeras, Rockville, MD, USA.*
[30]*Infection Prevention and Control, Technical Unit, Americares, Stamford, UK.*
[31]*Environmental Virology Laboratory, Water Pollution Research Department, National Research Division, National Research Center, Dokki, Giza, 12622, Egypt.*
[32]*Department of Animal Wealth Development, Faculty of Veterinary Medicine, Suez Canal University, Ismailia, 41522, Egypt.*
[33]*Department of Animal Medicine (Infectious Diseases), Faculty of Veterinary Medicine, Suez Canal University, Ismailia, 41522, Egypt.*
[34]*Department of Virology, Faculty of Veterinary Medicine, Suez Canal University, Ismailia, 41522, Egypt.*

COVID-19 caused by a novel severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) originated in Wuhan (Hubei province, China) during late 2019. It has spread across the globe affecting nearly 21 million people with a toll of 0.75 million deaths and restricting the movement of most of the world population during the past 6 months. COVID-19 became the leading health, economic, and humanitarian challenge of the twenty-first century. In addition to the considerable COVID-19 cases, hospitalizations, and deaths in humans, several cases of SARS-CoV-2 infections in animal hosts (dog, cat, tiger, lion, and mink) have been reported. Thus, the concern of pet owners is increasing. Moreover, the dynamics of the disease requires further explanation, mainly concerning the transmission of the virus from humans to animals and vice versa. Therefore, this study aimed to gather information about the reported cases of COVID-19 transmission in animals through a literary review of works published in scientific journals and perform genomic and phylogenetic analyses of SARS-CoV-2 isolated from animal hosts. Although many instances of transmission of the SARS-CoV-2 have been reported, caution and further studies are necessary to avoid the occurrence of maltreatment in animals, and to achieve a better understanding of the dynamics of the disease in the environment, humans, and animals. Future research in the animal-human interface can help formulate and implement preventive measures to combat the further transmission of COVID-19.

Journal of Translational Medicine.
2020 Sep 21; 18 (1): 358.
Doi: 10.1186/s12967-020-02534-2.

Potential zoonotic sources of SARS-CoV-2 infections

Jo WK[1], de Oliveira-Filho EF[1], Rasche A[1,2], Greenwood [AD]3,4, Osterrieder K[4], Drexler JF[1,2,5]

[1]Institute of Virology, Charité-Universitätsmedizin Berlin, Corporate Member of Freie Universität Berlin, Humboldt-Universität zu Berlin, and Berlin Institute of Health, Berlin, Germany.
[2]German Centre for Infection Research (DZIF), Associated Partner Charité-Universitätsmedizin Berlin, Berlin, Germany.
[3]Leibniz Institute for Zoo and Wildlife Research, Berlin, Germany.
[4]Institut für Virologie, Freie Universität Berlin, Berlin, Germany.
[5]Martsinovsky Institute of Medical Parasitology, Tropical and Vector-Borne Diseases, Sechenov University, Moscow, Russia.

The severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) causing coronavirus disease-2019 (COVID-19) likely has evolutionary origins in other animals than humans based on genetically related viruses existing in rhinolophid bats and pangolins. Similar to other animal coronaviruses, SARS-CoV-2 contains a functional furin cleavage site in its spike protein, which may broaden the SARS-CoV-2 host range and affect pathogenesis. Whether ongoing zoonotic infections are possible in addition to efficient human-to-human transmission remains unclear. In contrast, human-to-animal transmission can occur based on evidence provided from natural and experimental settings. Carnivores, including domestic cats, ferrets and minks, appear to be particularly susceptible to SARS-CoV-2 in contrast to poultry and other animals reared as livestock such as cattle and swine. Epidemiologic evidence supported by genomic sequencing corroborated mink-to-human transmission events in farm settings. Airborne transmission of SARS-CoV-2 between experimentally infected cats additionally substantiates the possibility of cat-to-human transmission. To evaluate the COVID-19 risk represented by domestic and farmed carnivores, experimental assessments should include surveillance and health assessment of domestic and farmed carnivores, characterization of the immune interplay between SARS-CoV-2 and carnivore coronaviruses, determination of the SARS-CoV-2 host range beyond carnivores and identification of human risk groups such as veterinarians and farm workers. Strategies to mitigate the risk of zoonotic SARS-CoV-2 infections may have to be developed in a One Health framework and non-pharmaceutical interventions may have to consider free-roaming animals and the animal farming industry.

Transboundary Emerging Diseases. 2020 Oct 9; Doi: 10.1111/tbed.13872. Online ahead of print.

Animals and SARS-CoV-2: Species susceptibility and viral transmission in experimental and natural conditions, and the potential implications for community transmission

Hobbs EC[1], Reid TJ[1]

[1]Australian Centre for Disease Preparedness (ACDP), Commonwealth Scientific and Industrial Research Organisation (CSIRO), East Geelong, VIC, Australia.

The current COVID-19 global pandemic, caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) of probable bat origin, has highlighted the ongoing need for a One Health response to emerging zoonotic disease events. Understanding the human-animal interface and its relevance to disease transmission remains a critical control point for many emerging zoonoses. Determination of the susceptibility of various animal species to infection with SARS-CoV-2 and the role of animals in the epidemiology of the disease will be critical to informing appropriate human and veterinary public health responses to this pandemic. A scoping literature review was conducted to collect, evaluate and present the available research evidence regarding SARS-CoV-2 infections in animals. Experimental studies have successfully demonstrated SARS-CoV-2 infection and transmission in cats, ferrets, hamsters, bats and non-human primates under experimental settings. Dogs appear to have limited susceptibility to SARS-CoV-2, while other domestic species including pigs and poultry do not appear susceptible. Naturally occurring SARS-CoV-2 infections in animals appear uncommon, with 14 pets, 8 captive big cats and an unreported number of farmed mink testing positive at the time of writing (early July 2020). Infections typically appear asymptomatic in dogs, while clinical signs of respiratory and/or gastrointestinal disease tend to be mild to moderate in felines, and severe to fatal in mink. Most animals are presumed to have been infected by close contact with COVID-19 patients. In domestic settings, viral transmission is self-

limiting; however in high-density animal environments, there can be sustained between-animal transmission. To date, two potential cases of animal-to-human transmission are being investigated, on infected mink farms. Given the millions of COVID-19 cases worldwide and ongoing potential for further zoonotic and anthroponotic viral transmission, further research and surveillance activities are needed to definitively determine the role of animals in community transmission of SARS-CoV-2.

Transboundary and Emerging Diseases. 2020 Oct 22.
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COVID-19-Zoonosis or Emerging Infectious Disease?

Haider N[1], Rothman-Ostrow P[2], Osman AY[1], Arruda LB[3], Macfarlane-Berry L[4], Elton L[3], Thomason MJ[3], Yeboah-Manu D[5], Ansumana R[6], Kapata N[7], Mboera L[8], Rushton J[2], McHugh TD[3], Heymann DL[9], Zumla A[3,10], Kock RA[1]

[1]The Royal Veterinary College, University of London, Hertfordshire, United Kingdom.
[2]Department of Epidemiology and Population Health, Institute of Infection, Veterinary and Ecological Sciences, University of Liverpool, Liverpool, United Kingdom.
[3]Division of Infection and Immunity, Department of Infection, Centre for Clinical Microbiology, University College London, London, United Kingdom.
[4]Epidemiology and One Health, Animal Health Policy Branch, Department of Agriculture, Water and the Environment, Canberra, ACT, Australia.
[5]Bacteriology Department, Noguchi Memorial Institute for Medical Research, University of Ghana, Accra, Ghana.
[6]Department of Community Medicine, Njala University, Bo, Sierra Leone.
[7]Zambia National Public Health Institute, Ministry of Health, Lusaka, Zambia.
[8]South African Centre for Infectious Diseases Surveillance (SACIDS) Foundation for One Health, Sokoine University of Agriculture, Morogoro, Tanzania.
[9]Infectious Disease Epidemiology, London School of Hygiene & Tropical Medicine, London, United Kingdom.
[10]National Institute of Health Research, Biomedical Research Centre, University College London Hospitals, National Health Service Foundation Trust, London, United Kingdom.

The World Health Organization defines a zoonosis as any infection naturally transmissible from vertebrate animals to humans. The pandemic of Coronavirus disease (COVID-19) caused by SARS-CoV-2 has been classified as a zoonotic disease, however, no animal reservoir has yet been found, so this classification is premature. We propose that COVID-19 should instead be classified an "*emerging infectious disease (EID) of probable animal origin*." To explore if COVID-19 infection fits our proposed re-categorization vs. the contemporary definitions of zoonoses, we reviewed current evidence of infection origin and transmission routes of SARS-CoV-2 virus and described this in the context of known zoonoses, EIDs and "spill-over" events. Although the initial one hundred COVID-19 patients were presumably exposed to the virus at a seafood Market in China, and despite the fact that 33 of 585 swab samples collected from surfaces and cages in the market tested positive for SARS-CoV-2, no virus was isolated directly from animals and no animal reservoir was detected. Elsewhere, SARS-CoV-2 has been detected in animals including domesticated cats, dogs, and ferrets, as well as captive-managed mink, lions, tigers, deer, and mice confirming zooanthroponosis. Other than circumstantial evidence of zoonotic cases in mink farms in the Netherlands, no cases of natural transmission from wild or domesticated animals have been confirmed. More than 40 million human COVID-19 infections reported appear to be exclusively through human-human transmission. SARS-CoV-2 virus and COVID-19 do not meet the WHO definition of zoonoses. We suggest SARS-CoV-2 should be re-classified as an EID of probable animal origin.

Frontiers in Public Health . 2020 Nov 26; 8: 596944.
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Severe acute respiratory syndrome coronavirus-2 natural animal reservoirs and experimental models: systematic review

Younes S[1], Younes N[1], Shurrab F[1], Nasrallah GK[1,2]

[1]Biomedical Research Center, Member of QU Health, Qatar University, Doha, Qatar.

[2]*Department of Biomedical Science, College of Health Sciences, Member of QU Health, Qatar University, Doha, Qatar.*

The current severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) outbreak has been rapidly spreading worldwide, causing serious global concern. The role that animal hosts play in disease transmission is still understudied and researchers wish to find suitable animal models for fundamental research and drug discovery. In this systematic review, we aimed to compile and discuss all articles that describe experimental or natural infections with SARS-CoV-2, from the initial discovery of the virus in December 2019 through to October 2020. We systematically searched four databases (Scopus, PubMed, Science Direct and Web of Science). The following data were extracted from the included studies: type of infection (natural or experimental), age, sample numbers, dose, route of inoculation, viral replication, detection method, clinical symptoms and transmission. Fifty-four studies were included, of which 34 were conducted on animal reservoirs (naturally or experimentally infected), and 20 involved models for testing vaccines and therapeutics. Our search revealed that Rousettus aegyptiacus (fruit bats), pangolins, felines, mink, ferrets and rabbits were all susceptible to SARS-CoV-2, while dogs were weakly susceptible and pigs, poultry, and tree shrews were not. In addition, virus replication in mice, mink, hamsters and ferrets resembled subclinical human infection, so these animals might serve as useful models for future studies to evaluate vaccines or antiviral agents and to study host-pathogen interactions. Our review comprehensively summarized current evidence on SARS-CoV-2 infection in animals and their usefulness as models for studying vaccines and antiviral drugs. Our findings may direct future studies for vaccine development, antiviral drugs and therapeutic agents to manage SARS-CoV-2-caused diseases.

Review in Medical Virology. 2020 Nov 18; e2196. Doi: 10.1002/rmv.2196. Online ahead of print.

Taking a lesson from the COVID-19 pandemic: Preventing the future outbreaks of viral zoonoses through a multi-faceted approach

Halabowski D[1], Rzymski P[2]

[1]*Institute of Biology, Biotechnology and Environmental Protection, Faculty of Natural Sciences, University of Silesia in Katowice, 40-007 Katowice, Poland.*
[2]*Department of Environmental Medicine, Poznan University of Medical Sciences, 60-806 Poznań, Poland; Integrated Science Association (ISA), Universal Scientific Education and Research Network (USERN), 60-806 Poznań, Poland.*

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Online ahead of print.

Highly conserved binding region of ACE2 as a receptor for SARS-CoV-2 between humans and mammals

Hayashi T[1,2], Abiko K[1], Mandai M[3], Yaegashi N[4], Konishi I[1,3,5]

[1]*National Hospital Organization Kyoto Medical Center, Kyoto, Japan.*
[2]*START, Japan Science and Technology Agency (JST), Tokyo, Japan.*
[3]*Department of Obstetrics and Gynecology, Kyoto University School of Medicine, Kyoto, Japan.*
[4]*Department of Obstetrics and Gynecology, Tohoku University School of Medicine, Miyagi, Japan.*
[5]*Immediate Past President of Asian Society of Gynecologic Oncology, Tokyo, Japan.*

Several cases of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection transmitted from human owners to their dogs have recently been reported. The first ever case of SARS-CoV-2 transmission from a human owner to a domestic cat was confirmed on March 27, 2020. A tiger from a zoo in New York, USA, was also reportedly infected with SARS-CoV-2. It is believed that SARS-CoV-2 was transmitted to tigers from their caretakers, who were previously infected with this virus. On May 25, 2020, the Dutch Minister of Agriculture, Nature and Food Quality reported that two employees were infected with SARS-CoV-2 transmitted from minks. These reports have influenced us to perform a comparative analysis among angiotensin-converting enzyme 2 (ACE2) homologous proteins for verifying the conservation of specific protein regions. One of the most conserved peptides is represented by the peptide "353-KGDFR-357 (*H. sapiens* ACE2 residue numbering), which is located on the surface of the ACE2 molecule and participates in the binding of SARS-

CoV-2 spike receptor binding domain (RBD). Multiple sequence alignments of the ACE2 proteins by ClustalW, whereas the three-dimensional structure of its binding region for the spike glycoprotein of SARS-CoV-2 was assessed by means of Spanner, a structural homology modeling pipeline method. In addition, evolutionary phylogenetic tree analysis by ETE3 was used. ACE2 works as a receptor for the SARS-CoV-2 spike glycoprotein between humans, dogs, cats, tigers, minks, and other animals, except for snakes. The three-dimensional structure of the KGDFR hosting protein region involved in direct interactions with SARS-CoV-2 spike RBD of the mink ACE2 appears to form a loop structurally related to the human ACE2 corresponding protein loop, despite of the reduced available protein length (401 residues of the mink ACE2 available sequence vs 805 residues of the human ACE2). The multiple sequence alignments of the ACE2 proteins shows high homology and complete conservation of the five amino acid residues: 353-KGDFR-357 with humans, dogs, cats, tigers, minks, and other animals, except for snakes. Where the information revealed from our examinations can support precision vaccine design and the discovery of antiviral therapeutics, which will accelerate the development of medical countermeasures, the World Health Organization recently reported on the possible risks of reciprocal infections regarding SARS-CoV-2 transmission from animals to humans.

Veterinary Quaterly. 2020 Dec; 40 (1): 243-249.
Doi: 10.1080/01652176.2020.1823522.

Emergence and Reemergence of Human Coronaviruses: Spike Protein as the Potential Molecular Switch and Pharmaceutical Target

Ahmad F[1], Kamal MA[2], Tekwani BL[1]

[1]Department of Infectious Diseases, Division of Drug Discovery, Southern Research, Birmingham Alabama 35205. United States.
[2]King Fahd Medical Research Center, King Abdulaziz University, P. O. Box 80216, Jeddah 21589. Saudi Arabia.

Current Pharmaceutical Design. 2020 Dec 15.
Doi: 0.2174/1381612826666201216113146.
Online ahead of print.

Spillover of SARS-CoV-2 into novel wild hosts in North America: A conceptual model for perpetuation of the pathogen

Franklin AB[1], Bevins SN[2]

[1]USDA National Wildlife Research Center, Fort Collins, CO, United States of America.
[2]USDA National Wildlife Research Center, Fort Collins, CO, United States of America.

There is evidence that the current outbreak of the novel coronavirus SARS-CoV-2, which causes COVID-19, is of animal origin. As with a number of zoonotic pathogens, there is a risk of spillover into novel hosts. Here, we propose a hypothesized conceptual model that illustrates the mechanism whereby the SARS-CoV-2 could spillover from infected humans to naive wildlife hosts in North America. This proposed model is premised on transmission of SARS-CoV-2 from human feces through municipal waste water treatment plants into the natural aquatic environment where potential wildlife hosts become infected. We use the existing literature on human coronaviruses, including SARS CoV, to support the potential pathways and mechanisms in the conceptual model. Although we focus on North America, our conceptual model could apply to other parts of the globe as well.

Science of The Total Environment. 2020 Sep 1; 733: 139358.
Doi: 10.1016/j.scitotenv.2020.139358.
Epub 2020 May 12.

Multi-species ELISA for the detection of antibodies against SARS-CoV-2 in animals

Wernike K[1], Aebischer A[1], Michelitsch A[1], Hoffmann D[1], Freuling C[1], Balkema-Buschmann A[1], Graaf A[1], Müller T[1], Osterrieder N[2,3], Rissmann M[1], Rubbenstroth D[1], Schön J[1], Schulz C[4], Trimpert J[2], Ulrich L[1], Volz A[4], Mettenleiter T[1], Beer M[1]

[1]Friedrich-Loeffler-Institut, Greifswald - Insel Riems, Germany.
[2]Institut für Virologie, Freie Universität Berlin, Berlin, Germany.
[3]Jockey Club College of Veterinary Medicine and Life Sciences, City University of Hong Kong, Kowloon Tong, Hong Kong.

[4]*University of Veterinary Medicine Hannover, Hanover, Germany.*

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has caused a pandemic with millions of infected humans and hundreds of thousands of fatalities. As the novel disease - referred to as COVID-19 - unfolded, occasional anthropozoonotic infections of animals by owners or caretakers were reported in dogs, felid species and farmed mink. Further species were shown to be susceptible under experimental conditions. The extent of natural infections of animals, however, is still largely unknown. Serological methods will be useful tools for tracing SARS-CoV-2 infections in animals once test systems are evaluated for use in different species. Here, we developed an indirect multi-species ELISA based on the receptor-binding domain (RBD) of SARS-CoV-2. The newly established ELISA was evaluated using 59 sera of infected or vaccinated animals, including ferrets, raccoon dogs, hamsters, rabbits, chickens, cattle and a cat, and a total of 220 antibody-negative sera of the same animal species. Overall, a diagnostic specificity of 100.0% and sensitivity of 98.31% were achieved, and the functionality with every species included in this study could be demonstrated. Hence, a versatile and reliable ELISA protocol was established that enables high-throughput antibody detection in a broad range of animal species, which may be used for outbreak investigations, to assess the seroprevalence in susceptible species or to screen for reservoir or intermediate hosts.

Transboundary Emerging Diseases. 2020 Nov 15.
Doi: 10.1111/tbed.13926. Online ahead of print.

Molecular characterization of Cryptosporidium spp. in minks *(Neovison vison)*, blue foxes *(Vulpes lagopus)*, and raccoon dogs *(Nyctereutes procyonoides)* in farms from Xinjiang, Northwest China

Qian W [1,2], Zhang Y[2], Jiang Y[2], Zhao A[2], Lv C[1], Qi M[3]

[1]*College of Animal Science and Technology, Henan University of Science and Technology, Luoyang, 471003, China.*
[2]*College of Animal Science, Tarim University, Tarim Road 1487, Alar, 843300, Xinjiang, China.*
[3]*College of Animal Science, Tarim University, Tarim Road 1487, Alar, 843300, Xinjiang, China.*

Parasitology Research. 2020 Nov; 119 (11): 3923-3927.
Doi: 10.1007/s00436-020-06909-8.
Epub 2020 Oct 3.

Morphological and molecular characterization of Cystoisospora laidlawi oocysts *(Apicomplexa: Eimeriidae)* in farmed American mink *(Neovison vison)* in Denmark

Petersen HH[1], Yang R[2], Chriel M[3,4], Liu D[5], Hansen MS[3,6], Ryan UM[2]

[1]*Centre for Diagnostics, Technical University of Denmark, Kemitorvet, 2800, Kgs. Lyngby, Denmark.*
[2]*School of Veterinary and Life Sciences, Murdoch University, Murdoch, Western Australia, 6150, Australia.*
[3]*Centre for Diagnostics, Technical University of Denmark, Kemitorvet, 2800, Kgs. Lyngby, Denmark.*
[4]*Centre for Rich Nature, The Danish Environmental Protection Agency, Tolderlundsvej 5, DK-5000, Odense C, Denmark.*
[5]*Jiangsu Co-innovation Center for Prevention and Control of Important Animal Infectious Diseases and Zoonoses, Yangzhou University, Yangzhou, 225009, Jiangsu, People's Republic of China.*
[6]*Department of Veterinary and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Grønnegårdsvej 15, 1870, Frederiksberg C, Denmark.*

Parasitology Research. 2020 Oct; 119 (10): 3549-3553.
Doi: 10.1007/s00436-020-06846-6.
Epub 2020 Aug 12.

Molecular characteristics of a canine distemper virus isolated from mink *(Neovison vison)* in Shandong, China, 2013

Liu F, Zhang H, Shan H

Acta Virologica. 2020; 64 (4): 501-505.
Doi: 10.4149/av_2020_410.

Generation and immunogenicity of virus-like particles based on mink enteritis virus capsid protein VP2 expressed in Sf9 cells

Wu H[1], Jin H[2], Wang L[1], Huo N[1], Liu D[2], Ding H[1], Cao Y[1], Liu C[1], Xi X[1], Jiao C[2], Spibey N[1], Shi J[2], Liu Y[3], Tian K[4]

[1]National Research Center for Veterinary Medicine, No. 3 Cuiwei Road, High-Tech District, Luoyang, 471003, Henan, China.
[2]Changchun SR Biological Technology Co., LTD, Changchun, 130012, Jilin, China.
[3]National Research Center for Veterinary Medicine, No. 3 Cuiwei Road, High-Tech District, Luoyang, 471003, Henan, China.
[4]National Research Center for Veterinary Medicine, No. 3 Cuiwei Road, High-Tech District, Luoyang, 471003, Henan, China.

Archives of Virology. 2020 Sep; 165 (9): 2065-2071. Doi: 10.1007/s00705-020-04703-6. Epub 2020 Jul 1.

Validating an empiric sulfadiazine-trimethoprim dosage regimen for treatment of Escherichia coli and Staphylococcus delphini infections in mink *(Neovison vison)*

Ronaghinia AA[1,2], Nikolaisen NK[2,3], Hansen SG[2], Poulsen HH[4], Frandsen HL[5], Struve T[2], Toutain PL[6,7], Damborg P[1]

[1]Department of Veterinary and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Frederiksberg, Denmark.
[2]Kopenhagen Diagnostics, Department of Health and Diagnostics, Kopenhagen Fur a.m.b.a, Glostrup, Denmark.
[3]National Food Institute, Research Group for Microbiology and Hygiene, Technical University of Denmark, Kongens Lyngby, Denmark.
[4]Department of Veterinary Clinical Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Frederiksberg, Denmark.
[5]National Food Institute, Technical University of Denmark, Kongens Lyngby, Denmark.
[6]Royal Veterinary College, University of London, London, UK.
[7]INTHERES, Université de Toulouse, INRA, ENVT, Toulouse, France.

J Veterinary Pharmacology and Therapeutics 2020 Sep 13.
Doi: 10.1111/jvp.12894. Online ahead of print.

Third-Generation Cephalosporin- and Tetracycline-Resistant *Escherichia coli* and Antimicrobial Resistance Genes from Metagenomes of Mink Feces and Feed

Agga GE[1], Silva PJ[1], Martin RS[2]

[1]Food Animal Environmental Systems Research Unit, Agricultural Research Service, U.S. Department of Agriculture, Bowling Green, Kentucky, USA.
[2]Utah Water Research Laboratory, Department of Civil and Environmental Engineering, Utah State University, Logan, Utah, USA.

Foodborne Pathogenes and Disease. 2020 Oct 20. Doi: 10.1089/fpd.2020.2851. Online ahead of print.

Molecular characteristics of H9N2 influenza viruses isolated from farmed raccoon dogs and arctic foxes in China

Qian Z[1], Shou-Yu G[2], Feng-Xia Z[2], Peng Y[1], Wen-Jian S[1], Jian-Liang L[1], Jiang S[1], Zhi-Jing X[3]

[1]Shandong Provincial Key Laboratory of Animal Biotechnology and Disease Control and Prevention, Shandong Agricultural University, Taian, Shandong Province, 271018, China; College of Veterinary Medicine, Shandong Agricultural University, Taian, Shandong Province 271018, China; Shandong Provincial Engineering Technology Research Center of Animal Disease Control and Prevention, Shandong Agricultural University, Taian, Shandong Province 271018, China.
[2]Shandong Provincial Key Laboratory of Animal Biotechnology and Disease Control and Prevention, Shandong Agricultural University, Taian, Shandong Province, 271018, China; College of Veterinary Medicine, Shandong Agricultural University, Taian, Shandong Province 271018, China.
[3]Shandong Provincial Key Laboratory of Animal Biotechnology and Disease Control and Prevention, Shandong Agricultural University, Taian, Shandong Province, 271018, China; College of Veterinary Medicine, Shandong Agricultural University, Taian,

Shandong Province 271018, China; Shandong Provincial Engineering Technology Research Center of Animal Disease Control and Prevention, Shandong Agricultural University, Taian, Shandong Province 271018, China.

Research in Veterinary Science. 2020 Nov 14; S0034-5288 (20) 31073-0.
Doi: 10.1016/j.rvsc.2020.11.006.
Online ahead of print.

Serological evidence of the infection of H7 virus and the co-infection of H7 and H9 viruses in farmed fur-bearing animals in eastern China

Yu Z[1,2,3], Cheng K[4], Wu J[5,6,7]

[1]Poultry Institute, Shandong Academy of Agricultural Sciences, Jinan, 250023, China.
[2]Shandong Provincial Key Laboratory of Poultry Diseases Diagnosis and Immunology, Jinan, 250023, China.
[3]Poultry Breeding Engineering Technology Center of Shandong Province, Jinan, 250023, China.
[4]Dairy Cattle Research Center, Shandong Academy of Agricultural Sciences, Jinan, 250132, China.
[5]Poultry Institute, Shandong Academy of Agricultural Sciences, Jinan, 250023, China.
[6]Shandong Provincial Key Laboratory of Poultry Diseases Diagnosis and Immunology, Jinan, 250023, China.
[7]Poultry Breeding Engineering Technology Center of Shandong Province, Jinan, 250023, China.

Brazilian Journal of Microbiology. 2020 Dec; 51 (4): 2163-2167.
Doi: 10.1007/s42770-020-00338-6.
Epub 2020 Jul 20.

New insights on the infection of pathogenic Leptospira species in American mink *(Neovison vison)* in southern Chile

Alfaro MAS[1], Raffo E[2], Bustos MI[3], Tomckowiack C[3], Tejeda C[3], Collado L[4], Medina-Vogel G[5]

[1]Instituto de Medicina Preventiva Veterinaria, Facultad de Ciencias Veterinarias, Universidad Austral de Chile, Valdivia, Chile.
[2]Servicio Agrícola Ganadero; Región de los Ríos, Valdivia, Chile.
[3]Instituto de Medicina Preventiva Veterinaria, Facultad de Ciencias Veterinarias, Universidad Austral de Chile, Valdivia, Chile.
[4]Instituto de Bioquímica y Microbiología, Facultad de Ciencias, Universidad Austral de Chile, Valdivia, Chile.
[5]Centro de Investigación para la Sustentabilidad, Universidad Andrés Bello, Santiago, Chile.

Tropical Animal Health and Production. 2020 Nov 16; 53 (1): 2.
Doi: 10.1007/s11250-020-02469-2.

The microbiota of farmed mink *(Neovison vison)* follows a successional development and is affected by early life antibiotic exposure

Bahl MI[1], Honoré AL[2], Skønager ST[2], Honoré OL[2], Clausen T[3], Andresen L[2], Hammer AS[2]

[1]National Food Institute, Technical University of Denmark, Kgs. Lyngby, Denmark.
[2]Department of Veterinary Clinical and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Frederiksberg C, Denmark.
[3]Danish Fur Breeders Research Centre, Holstebro, Denmark.

On many mink farms, antibiotics are used extensively during the lactation period to reduce the prevalence and severity of pre-weaning diarrhoea (PWD) in mink kits (also referred to as greasy kit syndrome). Concerns have been raised, that routine treatment of PWD with antibiotics could affect the natural successional development of the gut microbiota, which may have long lasting consequences. Here we investigated the effects of early life antibiotic treatment administered for 1 week (postnatal days 13-20). Two routes of antibiotic administration were compared to a non-treated control group (CTR, n = 24). Routes of administration included indirect treatment, through the milk from dams receiving antibiotics by intramuscular administration (ABX_D, n = 24) and direct treatment by intramuscular administration to the kits (ABX_K, n = 24). A tendency for slightly increased weight at termination (Day 205) was observed in the ABX_K group. The gut microbiota composition was profiled by 16S rRNA gene sequencing at eight time points between Day 7 and Day 205. A clear succes-

sional development of the gut microbiota composition was observed and both treatment regimens caused detectable changes in the gut microbiota until at least eight days after treatment ceased. At termination, a significant positive correlation was identified between microbial diversity and animal weight.

Scientific Reports. 2020 Nov 24; 10 (1): 20434. Doi: 10.1038/s41598-020-77417-z.

Translocation of intestinal bacteria as a cause of subcutaneous abscesses of the neck and head in American mink (Neovison vison) - a case report

Wlazło L[1], Łopuszyński W[2], Nowakowicz-Dębek B[3], Ossowski M[1], Bis-Wencel H[1]

[1]Department of Animal Hygiene and Environmental Hazards, University of Life Sciences in Lublin, Akademicka 13, 20-950, Lublin, Poland.
[2]Sub-Department of Pathomorphology and Forensic Veterinary Medicine, Department and Clinic of Animal Internal Diseases, University of Life Sciences in Lublin, Głęboka 30, 20-612, Lublin, Poland.
[3]Department of Animal Hygiene and Environmental Hazards, University of Life Sciences in Lublin, Akademicka 13, 20-950, Lublin, Poland.

Background
The problem of transmission of intestinal microorganisms to tissues occurs when intestinal epithelial cells do not adhere tightly (tight junction), which is caused by improper nutrition, usually associated with poor mucosal status. The impact on maintaining its proper condition in the case of animals also depends on the proper preparation and fragmentation of the ingredients of the feed. Intestinal microbiota disorders are increasingly indicated as one of the causes of many autoimmune, neurodevelopmental and metabolic diseases. However, there are no studies indicating damage to the intestinal barrier of animals resulting in the penetration of microorganisms from the gastrointestinal tract directly into the bloodstream which may result in the development of chronic inflammation.

Case presentation
On a mink *(Neovison vison)* farm with a foundation stock of 4,000 females, abscesses were observed in the head, followed by progressive deaths. Antibiotic treatment with amoxicillin and clavulanic acid added to the animals' feed was not successful. Macroscopic and microscopic changes indicated local suppurative inflammation of the skin and subcutaneous tissue with the presence of purulent fistulas. Microbiological analysis showed a significant increase in Escherichia coli in all samples taken from the abscesses. The results indicate the migration of intestinal bacteria through disturbance of the permeability of the intestinal barrier and their transfer to the blood. Symptoms were alleviated in all animals following changes in the feed components and in feed particle size.

Conclusions
It is necessary to take into account the possibility of transmission of intestinal bacteria in the etiology of inflammatory diseases in animals. Conducting more research in this field will improve the understanding of the relationship between intestinal microbes and the health of the body as a whole.

BMC Veterinary Research. 2020 Nov 10; 16 (1): 434. Doi: 10.1186/s12917-020-02654-3.

First molecular detection of Pneumocystis spp. in red foxes *(Vulpes vulpeslinnaeus, 1758)* and raccoon dogs *(Nyctereutes procyonoidesgray, 1834)*

Riebold D[1], Lubig J[2], Wolf P[3], Wolf C[3], Russow K[4], Loebermann M[4], Slevogt H[5], Mohr E[6], Feldhusen F[3], Reisinger EM[4]

[1]Host Septomics Group, Centre for Innovation Competence (ZIK) Septomics, University Hospital Jena, Jena, Germany; Division of Tropical Medicine and Infectious Diseases, Department of Medicine, University of Rostock, Germany.
[2]Division of Tropical Medicine and Infectious Diseases, Department of Medicine, University of Rostock, Germany; Chair for Animal Health and Animal Welfare, Faculty of Agriculture and Environmental Sciences, University of Rostock, Germany.
[3]State Office for Agriculture, Food Safety and Fishery Mecklenburg-Western Pomerania (LALLF-MV), Rostock, Germany.
[4]Division of Tropical Medicine and Infectious Diseases, Department of Medicine, University of Rostock, Germany.
[5]Host Septomics Group, Centre for Innovation Competence (ZIK) Septomics, University Hospital Jena, Jena, Germany.
[6]Chair for Animal Health and Animal Welfare, Faculty of Agriculture and Environmental Sciences, University of Rostock, Germany.

Comparative Immunology, Microbiology and Infectious Diseases. 2020 Dec; 73: 101531.
Doi: 10.1016/j.cimid.2020.101531.
Epub 2020 Aug 14.

Characterization and Complete Genome Analysis of Pseudomonas aeruginosa Bacteriophage vB_PaeP_LP14 Belonging to Genus Litunavirus

Shi X[1], Zhao F[1], Sun H[2], Yu X[1], Zhang C[1], Liu W[1], Pan Q[2], Ren H[3]

[1]College of Veterinary Medicine, Qingdao Agricultural University, Qingdao, Shandong, China.
[2]Qingdao Phagepharm Bio-tech Co, Ltd, Qingdao, Shandong, China.
[3]College of Veterinary Medicine, Qingdao Agricultural University, Qingdao, Shandong, China.

Current Microbiology . 2020 Sep; 77 (9): 2465-2474.
Doi: 10.1007/s00284-020-02011-5.
Epub 2020 May 4.

Association between Fur Animal Necrotizing Pyoderma in breeding farm mink *(Neovison vison)* and reduced fertility

Honoré OL[1], Sebbelov I[2], Wallin A[2], Petersen AM[2], Clausen T[3], Larsen PF[3], Hammer AS[2]

[1]Department of Veterinary and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Ridebanevej 3, 1870, Frederiksberg C, Denmark.
[2]Department of Veterinary and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Ridebanevej 3, 1870, Frederiksberg C, Denmark.
[3]Kopenhagen Forsking, Agro Food Park 15, 8200, Aarhus N, Denmark.

Background
The disease Fur Animal Necrotizing Pyoderma (FNP) has since 2000 been reported in many fur producing countries including Canada, Finland and Denmark. Development of FNP is characterised by rapidly forming treatment-resistant wounds on paws and in the head region. Economic losses related to FNP have been associated with mortality and decreased fur quality as well as increased veterinary costs. Also it has been suggested that FNP may be associated with reduced production results for breeding mink. The aim of this study was to evaluate if there is an association between FNP lesions in breeding animals and reduced production results based on a retrospective cohort study.

Results
1465 breeding animals (244 males and 1221 females) were followed during the breeding season 2019 on five Danish mink farms. Two farms were removed from the analysis since no occurrence of FNP appeared in the observation group. After exclusion, 846 breeding animals (148 males and 698 females) remained in the analysis and were divided into two groups: exposed (EXP) or non-exposed (N-EXP) depending on the disease history of the males during mating. Females exposed to FNP positive males during breeding in average produce 14% fewer kits ($P = 0.032$) and these females were also more than double as likely to produce small litters ($N \geq 3$) than N-EXP females. Female's from the EXP group were introduced more times to males than females in the N-EXP group ($P = 0.0001$, 2.5 more times in average). Females in the EXP group did not have a statistically higher risk of becoming barren ($P = 0.138$) though the relative risk of becoming barren was 77% higher after encountering a FNP male.

Conclusions
This study shows that FNP has more economic losses for the farms than direct loss of animals. Females in contact with males with FNP lesion during breeding have a higher risk of becoming barren, and produce significantly fewer kits compared to females whom haven't been in contact with a FNP positive male.

Acta Veterinaria Scandinavica. 2020 Dec 3; 62 (1): 66.
Doi: 10.1186/s13028-020-00564-w.

Outbreak of a novel disease caused by Staphylococcus pseudintermedius in raccoon dogs *(Nyctereutes procyonoides)*

Zhu Y[1], Junhong Liu[1], Guo K[1], Qiu J[1], Cheng Z[1], Liu F[1], Zhao Y[1], Zhang D[1], Guo H[1], Li H[1]

[1]Shandong Provincial Key Laboratory of Animal Biotechnology and Disease Control and Prevention, College of Animal Science and Veterinary Medicine, Shandong Agricultural University, Tai'an, China.

Transbound Emerg Dis. 2020; 00: 1–10.

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Nielsen, 1992; Hansen & Berg, 1993; Bakken *et al*., 1999.

The list of references should be arranged in alphabetic order according to the name of the first author and the year of publication within the names. The year of publication should be written between the name(s) and the title:

Nielsen, V.H., Møller, S.H., Hansen, B.K. & Berg, P. (2007). Genotype - environment interaction in mink. *Scientifur*, 31 (3), 89.

Shirali, M., Nielsen, V.H., Møller S.H. & Jensen, J. (2015). Longitudinal analysis of residual feed intake and BW in mink using random regression with heterogeneous residual variance. *Animal*, 8 (10), 1597-1604.