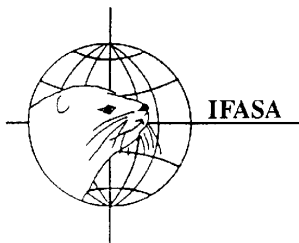
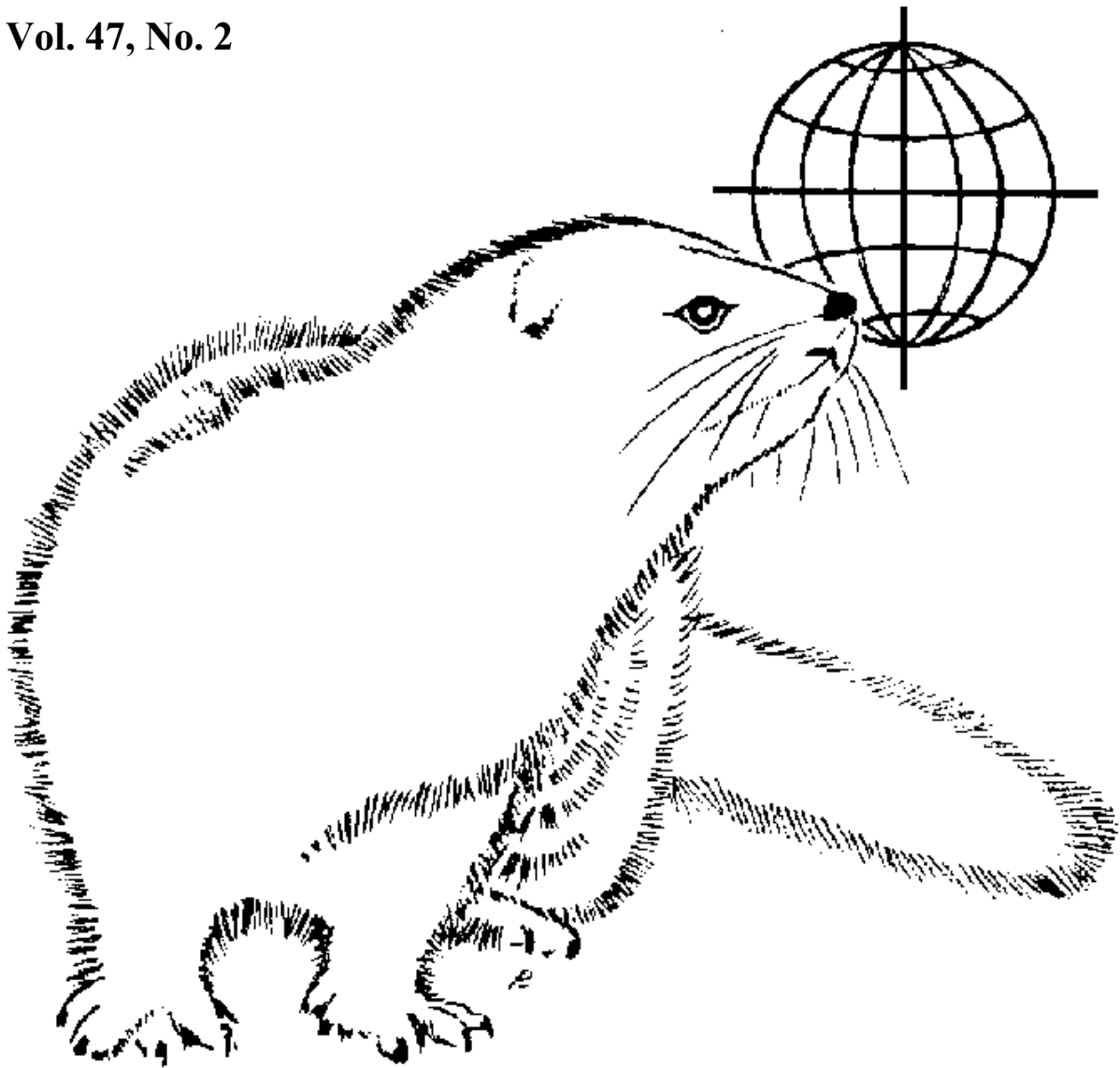


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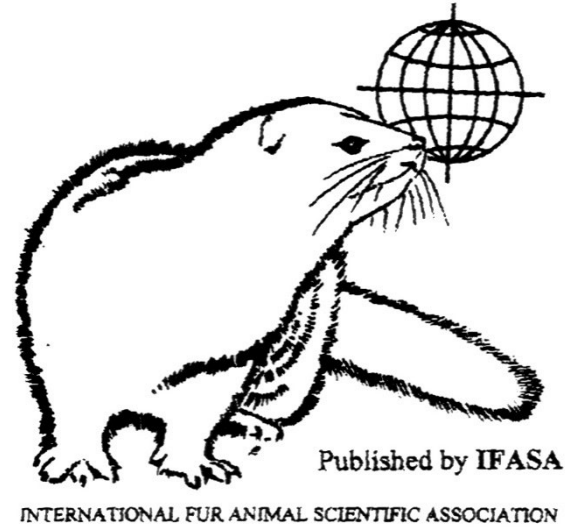
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Notes from the Editor

The Covid-19 pandemic had serious consequences for mink production. The susceptibility of mink to infection with SARS-CoV-2 and the possibility of many and serious mutations in an infected population and subsequent mink to human transmission, led to shutdown of mink production in several countries.

An outbreak in Europe in northwestern Spain of highly pathogenic avian influenza in intensively farmed mink similarly highlights the need for constant attention to infection transmission in connection with fur animal production.

Other issues regarding fur animal production are experienced in Europe, where there are groups that oppose the production. The opponents express criticism of the behavior and welfare of fur animals when they are kept in cages. More than 60 animal welfare organizations have joined forces not only to ban fur animal production in the European Union, but also to ban imports of fur from third countries. In total, there

are collected more than 1.7 million signatures against fur animal production per 1st March 2023 through a European citizens' initiative - Fur Free Europe. When more than 1 million signatures have been collected, the EU Commission must decide which initiatives should potentially be taken to meet the citizens' initiative. The first step is for the member states to validate the collected signatures. The European Commission then has 6 months to deal with the initiative.

In research, studies are carried out to assess the behavior of fur animals under production conditions. In this issue of *Scientifur*, the results of a study of mink reproductive behavior are given. The results indicate that mink can express natural reproductive behavior under breeding conditions.

Vivi Hunnicke Nielsen

Editor *Scientifur*

BREEDING, GENETICS AND REPRODUCTION**Isolation and characterization of the mink interferon-epsilon gene and its antiviral activity**

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The interferon (IFN) response is the first line of defense against viral invasion and thus plays a central role in the regulation of the immune response. IFN-epsilon (IFN-ε) is a newly discovered type I IFN that does not require viral induction, unlike other type I IFNs. IFN-ε is constitutively expressed in epithelial cells and plays an important role in mucosal immunity. In this study, we evaluated the biological activity of the mink-IFN (MiIFN)-ε gene in prokaryotic cells. Quantitative reverse transcription-polymerase chain reaction (qRT-PCR) was used to evaluate IFN-ε expression in different mink tissues. MiIFN-ε was highly expressed in brain, lung, tracheal, kidney, intestinal, bladder, ovarian, and testis tissues. There was no significant difference in MiIFN-ε expression between female and male minks, except in the reproductive system. Expression of the small ubiquitin-like modifier (SUMO3)-MiIFN-ε fusion gene was induced by isopropylβ-d-thiogalactoside, and MiIFN-ε was collected after SUMO-specific protease digestion. We tested the antiviral activity of MiIFN-ε against vesicular stomatitis virus (VSV) in epithelial cells of feline kidney 81 (F81). We used qRT-PCR to analyze the expression of several IFN-stimulated genes (ISGs), including ISG15, 2'-5' oligoadenylate synthetase (2'-5'OAS1), and myxovirus resistance protein 1 (Mx1). Recombinant IFN-ε induced high ISG expression in F81 cells. Compared with those in the cell control group, expressions of ISG15, Mx1, and 2'-5' OAS1 in the VSV-GFP control, IFN-ε, and MiIFN-ε-inhibited VSV-GFP groups were significantly increased. Compared with those in the VSV-

GFP control group, expressions of ISG15 and 2'-5' OAS1 in the IFN-ε and MiIFN-ε-inhibited VSV-GFP groups were significantly increased, and the differences were highly significant ($p < 0.0001$). IFN-ε played an indirect antiviral role. These findings lay the foundation for detailed investigation of IFN-ε in the future.

Front Vet Sci. 2023 Jan 27; 9:972433.

Doi: 10.3389/fvets.2022.972433. eCollection 2022.

A Novel Universal Primer Multiplex Real-Time PCR (UP-M-rtPCR) Approach for Specific Identification and Quantitation of Cat, Dog, Fox, and Mink Fractions Using Nuclear DNA Sequences

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Adulteration of meat with carnivorous animals (such as cats, dogs, foxes, and minks) can cause ethical problems and lead to disease transmission; however, DNA quantitative methods for four carnivorous species in one tube reaction are still rare. In this study, a carnivore-specific nuclear DNA sequence that is conserved in carnivorous animals but has base differences within the sequence was used to design universal primers for its conserved region and corresponding species-specific probes for the hypervariable region. A novel universal primer multiplex real-time PCR (UP-M-rtPCR) approach was developed for the specific identification and quantitation of cat, dog, fox, and mink fractions in a single reaction, with a 0.05 ng absolute limit of detection (LOD) and 0.05% relative LOD. This approach simplifies the PCR system and improves the efficiency of simultaneous identification of multiple animal-derived ingredients in meat. UP-M-rtPCR showed good accuracy (0.48-7.04% relative deviation) and precision (1.42-13.78% relative standard deviation) for quantitative analysis of cat, dog, fox, and mink DNA as well as

excellent applicability for the evaluation of meat samples.

Foods. 2023 Jan 31; 12 (3):594.
Doi: 10.3390/foods12030594.

How was genetic diversity transferred with translocations from ex situ to in situ? A case study of the European mink translocation to Hiiumaa Island in Estonia

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³Institute of Veterinary Medicine and Animal Sciences, Estonian University of Life Sciences, Tartu, Estonia.

Zoo Biol. 2023 Mar 15.

Doi: 10.1002/zoo.21763. Online ahead of print.

Bayesian analysis of genetic and environmental effects on litter traits in a red fox (*Vulpes vulpes*) herd under long-term selection

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Anim Sci J. 2023; 94 (1): e13807.

Doi: 10.1111/asj.13807.

Microsatellite profiling of hosts from parasite-extracted DNA illustrated with raccoons (*Procyon lotor*) and their *Baylisascaris procyonis* roundworms

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Background

Important information on movement pathways and introduction routes of invasive parasites can be obtained by comparing the genetic makeup of an invader with its spatial genetic structure in other distribution areas. Sometimes, the population genetic structure of the host might be more informative than that of the parasite itself, and it is important to collect tissue samples of both host and parasite. However, host tissue samples are frequently not available for analysis. We aimed to test whether it is possible to generate reliable microsatellite profiles of host individuals by amplifying DNA extracted from a nematode parasite, using the raccoon (*Procyon lotor*) and the raccoon roundworm (*Baylisascaris procyonis*) as a test case.

Methods

Between 2020 and 2021, we collected tissue as well as a single roundworm each from 12 raccoons from central Germany. Both the raccoon and the roundworm DNA extracts were genotyped using 17 raccoon-specific microsatellite loci. For each roundworm DNA extract, we performed at least eight amplification reactions per microsatellite locus.

Results

We extracted amplifiable raccoon DNA from all 12 roundworms. We obtained at least two amplification products for 186 of the 204 possible genotypes. Altogether 1077 of the 1106 genotypes (97.4%) matched the host-DNA derived reference genotypes and thus did not contain genotyping errors. Nine of the 12 roundworm-derived genetic profiles matched the reference profiles from the raccoon hosts, with one additional genetic profile containing genotyping errors at a single locus. The remaining two genetic profiles were deemed unsuitable for downstream analysis because of genotyping errors and/or a high proportion of missing data.

Conclusions

We showed that reliable microsatellite-based genetic profiles of host individuals can be obtained by amplifying DNA extracted from a parasitic nematode. Specifically, the approach can be applied to reconstruct invasion pathways of roundworms when samples of the raccoon hosts are lacking. Further research should

assess whether this method can be replicated in smaller species of parasitic nematodes and other phyla of parasites more generally.

Parasit Vectors. 2023 Feb 25; 16 (1):76.
Doi: 10.1186/s13071-023-05703-6.

NUTRITION, FEEDING AND MANAGEMENT

Diet of Free Ranging American Mink (*Neovison vison*) in Denmark

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Non-native American mink (*Neovison vison*) is a widely spread predator in Denmark. The feral population in mainland Denmark consists of captive-born mink that escaped from fur farms and wild mink born in nature, whereas the population on Bornholm is almost all wild-born mink. In this study, the diets of feral mink in mainland Denmark and on the island of Bornholm are analyzed. The aim of this study was to examine (1) whether the diet of the larger captive-born mink differs from that of the smaller wild-born mink, (2) assess the regional variations between the diets of mink in mainland Denmark and on Bornholm, and (3) investigate the seasonal variation in the diet composition of mink. The stomach contents of 364 mink (243 wild-born and 114 captive-born) culled in the years 2019-2022 were analyzed. Of these, 203 mink were from mainland Denmark, and 154 were from Bornholm. No significant differences were found between the diets of captive-born mink and wild-born mink or the mink found in mainland Denmark and on the island of Bornholm. Significantly more empty stomachs were found during spring than during the summer and autumn, suggesting a bottleneck in the diet during spring.

Animals (Basel). 2023 Jan 28; 13 (3):461.
Doi: 10.3390/ani13030461.

Effects of Dietary Supplementation of *Spirulina platensis* on the Immune System, Intestinal Bacterial Microbiome and Skin Traits of Mink

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The impact of dietary inclusion of *Spirulina platensis* on the immune system, intestinal microbiome and skin of mink was investigated. Forty-eight animals were equally separated into four groups. Groups B and D were control animals, while groups A and C had their feed supplemented daily with 100 mg/kg of body weight *Spirulina*. Mink in groups A and B were descended from dams supplemented with spirulina during their reproductive period, while those in groups C and D were descended from dams fed the control diets. Fur growth rate and quality were graded semi-quantitatively. Fecal microbiome analysis, skin thickness histomorphometry, immunohistochemical labeling and counts of immune cells in the colon, mesenteric lymph nodes and spleen and quantitative gene expression analysis of cytokines in the colon were performed. Skin thickness, fur growth rate and skin quality were similar among groups ($p > 0.05$). However, differences were observed among groups concerning the relative and differential abundance of bacterial species. Tgf- β expression was lower in group A, whereas IL- β 1 was lower in group C compared to group B ($p < 0.05$). Group D had significantly lower numbers of inflammatory cells in the colon and mesenteric lymph nodes. The results revealed

that *Spirulina* decreased indices of subclinical inflammation in mink gut, while differences in the bacterial communities among groups were observed.

Animals (Basel). 2023 Jan 4; 13 (2):190.
Doi: 10.3390/ani13020190.

BEHAVIOUR AND WELFARE

An Ethogram of the Reproductive Behaviour of the American Mink (*Neovison vison*) in Farmed Conditions

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Ethograms can serve as benchmarks against which abnormal animal behaviour can be identified, and then normal behaviour can be restored by appropriately modifying the environment in which an individual resides. The aim of the present study was to create an ethogram of the reproductive behaviour of American mink kept in farmed conditions. The research material consisted of 12 one-year-old male American mink, pearl coloured, selected randomly from among the varieties of coloured mink on the farm, and 60 two-year-old females. The animals participating in the study were grouped into two breeding sets, each consisting of 30 females and 6 males. Reproductive rituals included chasing the female, grasping her neck with the teeth, marking the local area, mounting the partner, and sniffing the neck, anal and genital areas. The copulation times recorded in this study varied greatly, ranging from several minutes to over two hours. The obtained results indicate that the American mink can express some natural reproductive behaviour in breeding conditions, which may also be an indicator of the welfare of these animals.

Animals (Basel). 2023 Jan 28; 13 (3): 443.
Doi: 10.3390/ani13030443.

HEALTH AND DISEASE

Highly pathogenic avian influenza A(H5N1) virus infection in farmed minks, Spain, October 2022

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In October 2022, an outbreak in Europe of highly pathogenic avian influenza (HPAI) A(H5N1) in intensively farmed minks occurred in northwest Spain. A single mink farm hosting more than 50,000 minks was involved. The identified viruses belong to clade 2.3.4.4b, which is responsible of the ongoing epizootic in Europe. An uncommon mutation (T271A) in the PB2 gene with potential public health implications was found. Our investigations indicate onward mink transmission of the virus may have occurred in the affected farm.

Euro Surveill. 2023 Jan; 28 (3):2 300001.

Doi: 10.2807/1560-7917.ES.2023.28.3.2300001.

Letter to the editor: Highly pathogenic influenza A(H5N1) viruses in farmed mink outbreak contain a disrupted second sialic acid binding site in neuraminidase, similar to human influenza A Viruses

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We read with much interest the article by Agüero et al. [1], reporting a highly pathogenic influenza A(H5N1) virus outbreak in farmed minks in north-west Spain in October 2022. Genetic characterisation of the viruses showed that they resembled the A/gull/France/22P015977/2022-like genotype within clade 2.3.4.4b. Considering efficient airborne transmission of human viruses among ferrets (reviewed in [2]), the concern is raised that adaptation of avian viruses to mink may provide a first step towards potential human-to-human transmission.

The authors focused on the amino acid substitution T271A in polymerase subunit PB2, which is known to enhance polymerase activity of influenza A virus (IAV) in mammalian host cells similar to the seminal PB2 E627K mutation. They also show that the only substitution in haemagglutinin (HA) in comparison with closely related avian strains is I390M. This mutation is in the stem region of HA and might be associated with altered HA stability and transmissibility but as of yet has no known biological relevance. Mutations previously associated with increased human-type alpha 2,6-linked sialic acid receptor binding and/or airborne transmission in ferrets [2] were still limited to the lack of a glycosylation site at position 158. Substitutions F74S and V163L in neuraminidase (NA), which are located at sites of unknown functional importance, also distinguished the viruses in minks from closely related avian viruses. Remarkably, all four viruses from minks contained a methionine at position 396 located in the second sialic acid binding site (2SBS) in NA (for a review on the 2SBS, see [3]). Influenza A(H5N1) viruses predominantly carry an isoleucine at this position, which is critical for efficient binding of sialic acid to the 2SBS [3,4].

Phylogenetic analysis using Nextstrain (<https://nextstrain.org>, accessed: 1 Feb 2023 [5]) indicated that the I396M substitution, seldom observed in other H5N1 viruses, was acquired in an avian host immediately before emergence of the H5N1 virus in mink. The analysis moreover showed that substitution S369I, which is at the position of a sialic acid contact residue in the 2SBS, was obtained immediately before the acquisition of I396M. Substitution of residues at positions 369 and 396 has been shown to negatively affect NA activity [3,4], herein referred to as residues 372 and 400. A functional 2SBS promotes

NA activity, presumably by bringing multivalent sialic acid substrates in closer proximity of the catalytic site. A functional 2SBS, which specifically binds to alpha 2,3-linked sialic acid receptors, has been lost in all human (pandemic) viruses and in several other viruses adapted to mammalian host species. Notably, whereas a 2SBS is conserved in nearly all avian IAVs [3], it is disrupted in some avian influenza A(H7N9) and A(H9N2) isolates. This preceded the acquisition of mutations in HA that decreased binding to avian-type alpha 2,3-linked sialic acid receptors. It is possible that this concerted evolution of NA and HA is driven by the need to preserve an optimal HA-NA balance. At the same time, such compensatory mutations may also increase binding to human-type receptors [3], as was recently demonstrated for H5N1 viruses [6].

Disruption of the 2SBS in H5N1 viruses in minks is thus far an unreported feature that they have in common with human-adapted influenza A viruses. Loss of the 2SBS may drive selection for changes in the receptor binding properties of HA, possibly resulting in increased binding to human-type receptors. Such changes in HA are expected to promote replication and transmission in mammalian hosts, including humans. Preservation or loss of the 2SBS is likely a viral host range determinant and could be an early adaptation signal that should be included in analysis of the pandemic potential of emerging IAVs.

Eurosurveillance, Volume 28, Issue 7, 16/Feb/2023

Authors' response: Highly pathogenic influenza A(H5N1) viruses in farmed mink outbreak contain a disrupted second sialic acid binding site in neuraminidase, similar to human influenza A Viruses

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To the editor: We would like to thank the authors of the letter for their valuable contributions to our article describing a highly pathogenic avian influenza (HPAI) virus outbreak in farmed minks in Spain in October 2022 [1].

de Vries et al. highlighted that the HPAI A(H5N1) viruses identified in Spain in minks contain a disrupted second sialic acid binding site (2SBS) in neuraminidase, similar to human influenza A viruses [2,3]. In addition, they also pointed out that the mutations at position S369I and I396M of neuraminidase (NA) implicated in the loss of the 2SBS had already been acquired in avian hosts before the emergence of the outbreak in minks. We agree with the authors that the evolution of NA in avian viruses in relation to altered receptor-binding properties is an aspect that should not be overlooked. Based on the currently available genetic data, at the time of writing of the article, among the HPAI H5 viruses sequenced in Europe since autumn 2020, mutations S369I and I396M of the NA had already been identified in combination in six H5N1 viruses identified in gulls in the Netherlands and Belgium between June and October 2022. In particular, in Europe, these mutations were detected only in viruses belonging to the A/gull/France/22P015977/2022-like genotype [1]. This genotype emerged from reassortment events with viruses of the gull-adapted A(H13) subtype from which it acquired the NP, PA and NS genes [4].

Since its first identification in May 2022, the genotype has been extensively detected in colony-breeding seabird species, mainly European herring gulls (83.3% of the available sequences of this genotype from birds are seabird species). What has caused these two mutations to appear in the generally conserved 2SBS in NA of this genotype is a matter of speculation. Considering that the H13 and H16 subtype viruses, which are particularly adapted to gulls, differ from avian viruses of other species by their receptor-binding properties [5], it cannot be excluded that the NA mutations might be related to adaptation of these viruses to this specific avian host. However,

a founder effect also needs to be considered. Whatever the origin of these mutations might be, additional in vitro and in vivo studies are needed to evaluate the biological impact of the 2SBS disruption in the specific genome constellation of the A/gull/France/22P015977/2022-like genotype, identified in both the avian and mammalian hosts.

This applies also to other mutations shown to alter the receptor binding specificity in vitro, and which have been described in viruses of clade 2.3.4.4b A(H5) identified in the avian host in Europe since 2020 [6]. These have not been described in our rapid communication, as our focus was to highlight the mutations detected in the viruses identified in minks in Spain compared with the most closely related H5N1 viruses characterised in the avian population. Their actual effect on the biological characteristics of these circulating viruses still remains unexplored.

The sequence data available indicate that the A/gull/France/22P015977/2022-like genotype is not prevalent in Europe and represents 9.1% of all the sequences available since its emergence in May 2022 (up to 10 February 2023). However, bias exists between publicly accessible sequences and the number of outbreaks reported in the avian and mammal populations. The mutations described by de Vries remind us about the importance of carefully analysing whole genome sequences and vigilantly monitoring virus evolution in each host, whether domestic or wild. Any country that notifies an outbreak should ideally have access to sequencing and data sharing mechanisms. Genomic surveillance is crucial to quickly identify any virus with zoonotic potential that could pose a threat to animal and public health.

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SARS-CoV-2 in animals: susceptibility of animal species, risk for animal and public health, monitoring, prevention and control

EFSA Panel on Animal Health and Welfare (AHAW); Søren Saxmose Nielsen, Julio Alvarez, Dominique Joseph Bicout, Paolo Calistri, Elisabetta Canali, Julian Ashley Drewe, Bruno Garin-Bastuji, José Luis Gonzales Rojas, Christian Gortázar, Mette Herskin, Virginie Michel, Miguel Ángel Miranda Chueca, Barbara Padalino, Paolo Pasquali, Helen Clare Roberts, Hans Spoolder, An-

tonio Velarde, Arvo Viltrop, Christoph Winckler, Cornelia Adlhoch, Inmaculada Aznar, Francesca Baldinelli, Anette Boklund, Alessandro Brogna, Nora Gerhards, Lina Mur, Priyanka Nanapaneni, Karl Ståhl

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SARS-CoV-2 Monitoring on Mink Farms in Poland

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Introduction

Many countries have reported severe acute respiratory syndrome-coronavirus 2 (SARS-CoV-2) infections in mink, and transmission back to humans has raised the concern of novel variants emerging in these animals. The monitoring system on Polish mink farms detected SARS-CoV-2 infection first in January 2021 and has been kept in place since then.

Material and methods

Oral swab samples collected between February 2021 and March 2022 from 11,853 mink from 594 farms in different regions of Poland were screened molecularly for SARS-CoV-2. Isolates from those with the highest loads of viral genetic material from positive farms were sequenced and phylogenetically analysed. Serological studies were also carried out for one positive farm in order to follow the antibody response after infection.

Results

SARS-CoV-2 RNA was detected in mink on 11 farms in 8 out of 16 Polish administrative regions. Whole genome sequences were obtained for 19 SARS-CoV-2 strains from 10 out of 11 positive farms. These genomes belonged to four different variants of concern (VOC) - VOC-Gamma (20B), VOC-Delta (21J), VOC-Alpha (20I) and VOC-Omicron (21L) - and seven different Pango lineages - B.1.1.464, B.1.1.7, AY.43, AY.122, AY.126, B.1.617.2 and BA.2. One of the nucleotide and amino acid mutations specific for persistent strains found in the analysed samples was the Y453F host adaptation mutation. Serological testing of blood samples revealed a high rate of seroprevalence on the single mink farm studied.

Conclusion

Farmed mink are highly susceptible to infection with SARS-CoV-2 of different lineages, including Omicron BA.2 VOC. As these infections were asymptomatic, mink may become an unnoticeable virus reservoir generating new variants potentially threatening human health. Therefore, real-time monitoring of mink is extremely important in the context of the One Health approach.

J Vet Res. 2022 Dec 3; 66 (4): 449-458.

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One Health Investigation of SARS-CoV-2 in People and Animals on Multiple Mink Farms in Utah

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From July–November 2020, mink (*Neogale vison*) on 12 Utah farms experienced an increase in mortality rates due to confirmed SARS-CoV-2 infection. We conducted epidemiologic investigations on six farms to identify the source of virus introduction, track cross-species transmission, and assess viral evolution. Interviews were conducted and specimens were collected from persons living or working on participating farms and from multiple animal species. Swabs and sera were tested by SARS-CoV-2 real-time reverse transcription polymerase chain reaction (rRT-PCR) and serological assays, respectively. Whole genome sequencing was attempted for specimens with cycle threshold values <30. Evidence of SARS-CoV-2 infection was detected by rRT-PCR or serology in ≥1 person, farmed mink, dog, and/or feral cat on each farm. Sequence analysis showed high similarity between mink and human sequences on corresponding farms. On farms sampled at multiple time points, mink tested rRT-PCR positive up to 16 weeks post-onset of increased mortality. Workers likely introduced SARS-CoV-2 to mink, and mink transmitted SARS-CoV-2 to other animal species; mink-to-human transmission was not identified. Our findings provide critical evidence to support interventions to prevent and manage SARS-CoV-2 in people and animals on mink farms and emphasizes the importance of a One Health approach to address emerging zoonoses.

Viruses. 2022 Dec 29; 15 (1):96.

Doi: 10.3390/v15010096.

Hands off the Mink! Using Environmental Sampling for SARS-CoV-2 Surveillance in American Mink

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Throughout the COVID-19 pandemic, numerous non-human species were shown to be susceptible to natural infection by SARS-CoV-2, including farmed American mink. Once infected, American mink can transfer the virus from mink to human and mink to mink, resulting in a high rate of viral mutation. Therefore, outbreak surveillance on American mink farms is imperative for both mink and human health. Historically, disease surveillance on mink farms has consisted of a combination of mortality and live animal sampling; however, these methodologies have significant limitations. This study compared PCR testing of both deceased and live animal samples to environmental samples on an active outbreak premise, to determine the utility of environmental sampling. Environmental sampling mirrored trends in both deceased and live animal sampling in terms of percent positivity and appeared more sensitive in some low-prevalence instances. PCR CT values of environmental samples were significantly different from live animal samples' CT values and were consistently high (mean CT = 36.2), likely indicating a low amount of viral RNA in the samples. There is compelling evidence in favour of environmental sampling for the purpose of disease surveillance, specifically as an early warning tool for SARS-CoV-2; however, further work is needed to ultimately determine whether environmental samples are viable sources for molecular epidemiology investigations.

Int J Environ Res Public Health. 2023 Jan 10; 20 (2): 1248.

Doi: 10.3390/ijerph20021248.

Evolutionary rate of SARS-CoV-2 increases during zoonotic infection of farmed mink

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To investigate genetic signatures of adaptation to the mink host, we characterised the evolutionary rate heterogeneity in mink-associated severe acute respiratory syndrome coronaviruses (SARS-CoV-2). In 2020, the first detected anthropozoonotic spillover event of SARS-CoV-2 occurred in mink farms throughout Europe and North America. Both spillback of mink-associated lineages into the human population and the spread into the surrounding wildlife were reported, highlighting the potential formation of a zoonotic reservoir. Our findings suggest that the evolutionary rate of SARS-CoV-2 underwent an episodic increase upon introduction into the mink host before returning to the normal range observed in humans. Furthermore, SARS-CoV-2 lineages could have circulated in the mink population for a month before detection, and during this period, evolutionary rate estimates were between 3×10^{-3} and 1.05×10^{-2} (95 per cent HPD, with a mean rate of 6.59×10^{-3}) a four- to thirteen-fold increase compared to that in humans. As there is evidence for unique mutational patterns within mink-associated lineages, we explored the emergence of four mink-specific Spike protein amino acid substitutions Y453F, S1147L, F486L, and Q314K. We found that mutation Y453F emerged early in multiple mink outbreaks and that mutations F486L and Q314K may co-occur. We suggest that SARS-CoV-2 undergoes a brief, but considerable, increase in evolutionary rate in response to greater selective pressures during species jumps, which may lead to the occurrence of mink-specific mutations. These findings emphasise the necessity of ongoing surveillance of zoonotic SARS-CoV-2 infections in the future.

Virus Evol. 2023 Jan 10; 9 (1): vead002.
Doi: 10.1093/ve/vead002. eCollection 2023.

Diversity of viral communities in faecal samples of farmed red foxes

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Emerging and existing viruses from various human and animal samples have been studied and analyzed using viral metagenomics, which has proven to be an effective technique. Foxes, as a kind of significant economic animal, are widely raised in China. Viruses carried by foxes may potentially infect humans or other animals. There are currently very few studies of faecal virome in farmed foxes. Using viral metagenomics, we evaluated the faecal virome of twenty-four foxes collected from the same farm in Jilin Province, China. Some sequences more closely related to the families *Parvoviridae*, *Picornaviridae*, *Smacoviridae*, *Anelloviridae*, and *Herpesviridae* were detected in the faecal sample. The main animal viruses that infect farmed red foxes were parvovirus and picornavirus. Five smacovirus strains were found and provided evidence for genetic diversity in the genus *Smacoviridae*. In addition, some viruses infecting avian species or rats were detected in this study. The study helped us better understand faecal virome in farmed red foxes and assisted in the surveillance and prevention of viral diseases in these animals.

FrHeliyon. 2023 Jan 5; 9 (1): e12826.
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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.