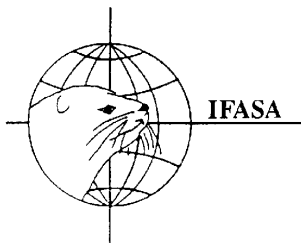
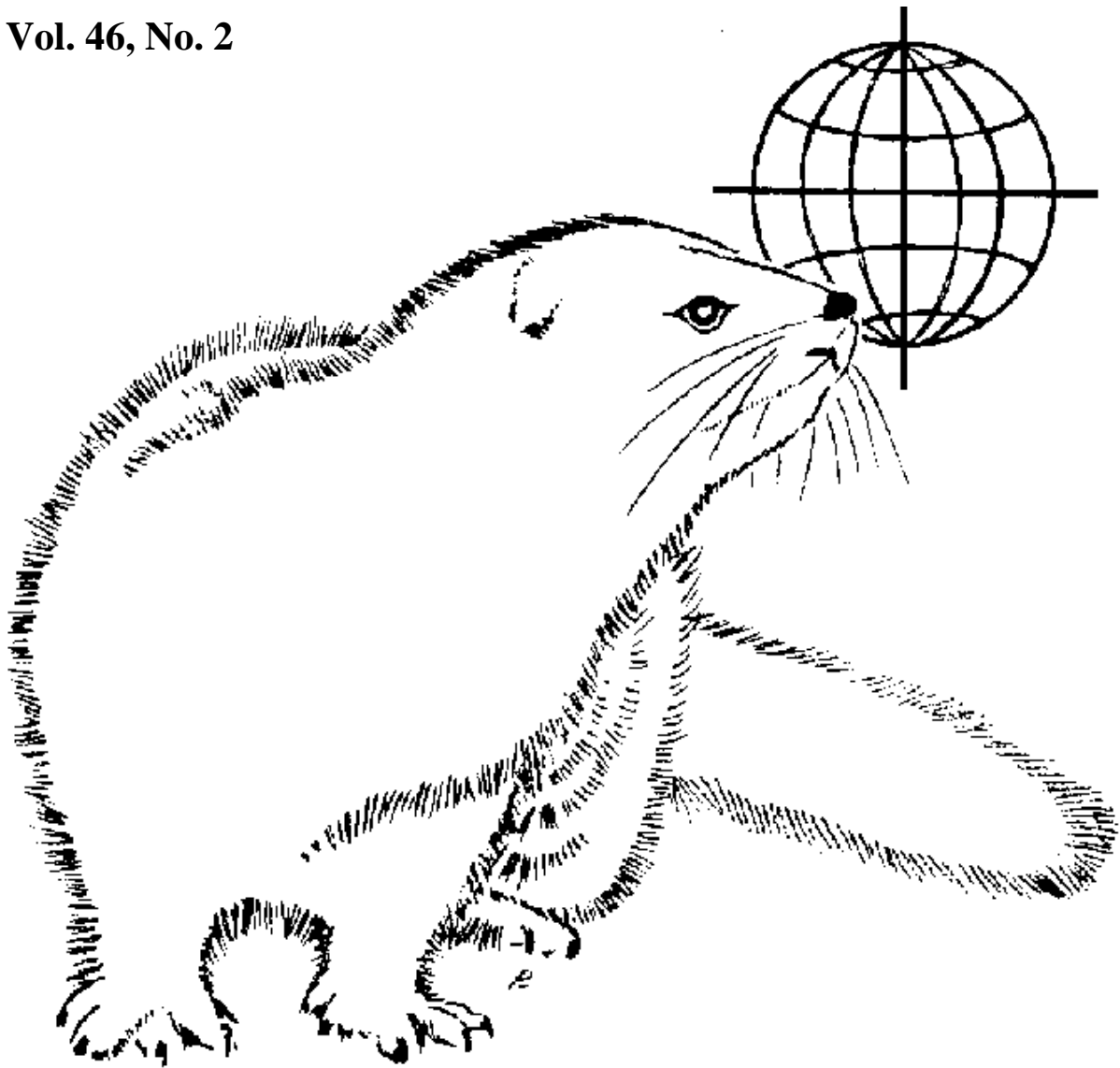


# SCIENTIFUR

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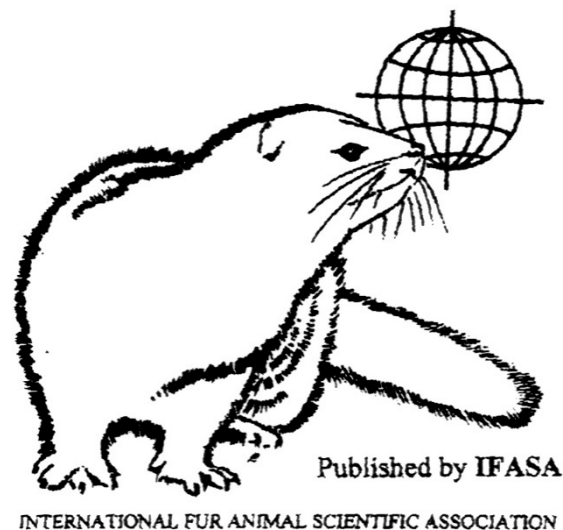
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## Notes from the Editor

The COVID-19 pandemic has had fatal consequences for the mink production in Europe. In the Netherlands, the production was phased out in 2021 instead of in 2024 as originally planned. In Denmark, all mink were culled in the autumn 2020, and a ban on mink production is maintained until the end of 2022. Latest, by December 21, 2021 Italy adopted a ban on breeding of fur-bearing animals including mink, foxes, raccoon dogs and chinchillas, and closure of all active fur farms in Italy by June 30, 2022.

Another issue for European fur animal production is a recent - 16 March 2022 - European Citizens' Initiative "Fur Free Europe", which is forwarded to the European Commission. The organisers of the initiative call furthermore on the Commission to introduce an EU-wide ban on keeping and killing animals for the purpose of fur production. They also ask for a ban of fur and fur products in the EU market.

European Citizens' Initiatives were introduced in the Lisbon Treaty officially launched in April

2012. The "Fur Free Europe" Initiative is judged to fulfill the formal conditions and is as such considered legally admissible. However, at time of writing the Commission has not analysed the substance of the proposal. A prerequisite for a further step is collection of one million statements of support within one year from at least seven different member states. The Commission could decide either to take the request forward or not, but will be required to explain its reasoning.

Publications in this issue of *Scientifur* show that SARS-CoV-2 infections in mink can be linked to human infections. Zoonotic spill-over of SARS-CoV-2 can also occur from mink to human but a study points at that mink-adapted viruses are unlikely to pose an increased threat to humans. However, overall the studies conclude that continuous surveillance of mink farms is needed.

Vivi Hunnicke Nielsen

Editor *Scientifur*





**BREEDING, GENETICS AND REPRODUCTION****Characterisation of the Complete Mitochondrial Genome of Critically Endangered *Mustela lutreola* (Carnivora: Mustelidae) and Its Phylogenetic and Conservation Implications**Skorupski J<sup>1,2,3</sup><sup>1</sup>*Institute of Marine and Environmental Sciences, University of Szczecin, Adama Mickiewicza 16 St., 70-383 Szczecin, Poland.*<sup>2</sup>*Polish Society for Conservation Genetics LUTREOLA, Maciejkowa 21 St., 71-784 Szczecin, Poland.*<sup>3</sup>*The European Mink Centre, 71-415 Szczecin, Poland.*

In this paper, a complete mitochondrial genome of the critically endangered European mink *Mustela lutreola* L., 1761 is reported. The mitogenome was 16,504 bp in length and encoded the typical 13 protein-coding genes, two ribosomal RNA genes and 22 transfer RNA genes, and harboured a putative control region. The A+T content of the entire genome was 60.06% (A > T > C > G), and the AT-skew and GC-skew were 0.093 and -0.308, respectively. The encoding-strand identity of genes and their order were consistent with a collinear gene order characteristic for vertebrate mitogenomes. The start codons of all protein-coding genes were the typical ATN. In eight cases, they were ended by complete stop codons, while five had incomplete termination codons (TA or T). All tRNAs had a typical cloverleaf secondary structure, except tRNA<sup>Ser(AGC)</sup> and tRNA<sup>Lys</sup>, which lacked the DHU stem and had reduced DHU loop, respectively. Both rRNAs were capable of folding into complex secondary structures, containing unmatched base pairs. Eighty-one single nucleotide variants (substitutions and indels) were identified. Comparative interspecies analyses confirmed the close phylogenetic relationship of the European mink to the so-called ferret group, clustering the European polecat, the steppe polecat and the black-footed ferret. The obtained results are expected to provide useful molecular data, informing and supporting effective conservation measures to save *M. lutreola*.

*Genes (Basel). 2022 Jan 10; 13 (1):125.**Doi: 10.3390/genes13010125.***NUTRITION, FEEDING AND MANAGEMENT****Urinary and plasma metabolome of farm mink (*Neovison vison*) after an intervention with raw or cooked poultry offal: a <sup>1</sup>H NMR investigation**Trimigno A<sup>1</sup>, Khakimov B<sup>1</sup>, Quaade ML<sup>2</sup>, Honoré OL<sup>2</sup>, Clausen T<sup>3</sup>, Blaabjerg K<sup>3</sup>, Engelsen SB<sup>1</sup>, Hammer ASV<sup>2</sup><sup>1</sup>*Department of Food Science, University of Copenhagen, Frederiksberg, Denmark.*<sup>2</sup>*Department of Veterinary and Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Copenhagen, Denmark.*<sup>3</sup>*Danish Fur Breeders Research Centre, Holstebro, Denmark.*

The introduction of high amounts of cooked poultry offal in mink feed has been associated with health problems in growing mink. Cooking mink feed is a convenient way of reducing microbiological activity, but it may have a negative effect on raw material quality and animal welfare. This study investigates growth and health of mink fed raw or cooked poultry offal and describes urinary and blood plasma metabolic changes related to the feeding. A total of 65 male mink were divided in three feeding groups, two fed cooked offal and one group fed raw offal, and the plasma and urine samples were collected at 3 time points during the growth. Both bio-fluids and feed samples were measured by <sup>1</sup>H NMR spectroscopy and resulted metabolomics data were analysed using univariate and multivariate statistical methods that revealed dominating effect of the mink growth stages and to a less extent the feeding regime. Metabolome differences in relation to low body mass index (BMI) and kidney lesions were observed in plasma. Disease and decrease in BMI was associated with high creatinine and dimethylglycine content in plasma. These molecules were also particularly indicative of the cooked feeds. Moreover, low urinary taurine levels were also associated with disease and low BMI. Individual mink appeared to show negative effects of the cooked feed diet, including impaired growth and gross pathological lesions involving the kidneys. This may be related to the absorption of essential metabolites such as amino acids and fats, necessary for mink growth, that are negatively impacted by the cooking process.

*Arch Anim Nutr. 2022 Mar 15; 1-18.**Doi: 10.1080/1745039X.2021.2003682.*

### **A three-dimensional reconstructive study of pelvic cavity in the red fox (*Vulpes vulpes*)**

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*Anat Histol Embryol.* 2022 Mar; 51(2):215-220.

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## **BEHAVIOUR AND WELFARE**

### **Computer Vision for Detection of Body Posture and Behavior of Red Foxes**

Schütz AK<sup>1</sup>, Krause ET<sup>2</sup>, Fischer M<sup>3</sup>, Müller T<sup>4</sup>, Freuling CM<sup>5</sup>, Conraths FJ<sup>1</sup>, Homeier-Bachmann T<sup>1</sup>, Lentz HHK<sup>1</sup>

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The behavior of animals is related to their health and welfare status. The latter plays a particular role in animal experiments, where continuous monitoring is essential for animal welfare. In this study, we focus on red foxes in an experimental setting and study their behavior. Although animal behavior is a complex concept, it can be described as a combination of body posture and activity. To measure body posture

and activity, video monitoring can be used as a non-invasive and cost-efficient tool. While it is possible to analyze the video data resulting from the experiment manually, this method is time consuming and costly. We therefore use computer vision to detect and track the animals over several days. The detector is based on a neural network architecture. It is trained to detect red foxes and their body postures, i.e., 'lying', 'sitting', and 'standing'. The trained algorithm has a mean average precision of 99.91%. The combination of activity and posture results in nearly continuous monitoring of animal behavior. Furthermore, the detector is suitable for real-time evaluation. In conclusion, evaluating the behavior of foxes in an experimental setting using computer vision is a powerful tool for cost-efficient real-time monitoring.

*Animals (Basel).* 2022 Jan 19; 12 (3):233.

Doi: 10.3390/ani12030233.

## **HEALTH AND DISEASE**

### **Immunogenicity of an Inactivated Canine Adenovirus Type 1 Vaccine for Foxes**

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Canine adenovirus type 1 (CAV-1) is the etiologic agent of fox encephalitis. As with most viral agents, the best method of prevention is vaccination. In this study, the CAV-1 strain F1301 strain was used to construct a new type 1 canine adenovirus inactivated vaccine candidate, and its safety and immunogenicity were evaluated in silver foxes. Next, animals were challenged and survival rates of animals vaccinated with either the commercially available or the current candidate vaccine were examined. The results confirmed that the inactivated CAV-1 vaccine prepared in this study can effectively protect against challenge with virulent CAV-1 in silver foxes, and the safety

profile was improved relative to that of the commercial vaccine. This study confirmed that the fox CAdV-1 F1301 strain can be used as a platform for an inactivated CAdV-1 vaccine.

*Front Vet Sci.* 2022 Feb 15; 9: 678671.  
Doi: 10.3389/fvets.2022.678671. eCollection 2022.

### Zoonotic spill-over of SARS-CoV-2: mink-adapted virus in humans

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*Clin Microbiol Infect.* 2022 Mar; 28 (3): 451.e1-451.e4.

Doi: 10.1016/j.cmi.2021.12.001. Epub 2021 Dec 15.

### SARS-CoV-2 outbreaks on Danish mink farms and mitigating public health interventions

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### Background

First severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infections on Danish mink farms were reported in June 2020 and thereupon spread geographically. We provide population-level evidence on excess human incidence rates in Danish municipalities affected by disease outbreaks on mink farms and evaluate the effectiveness of two non-pharmaceutical interventions, i.e. culling of infected mink and local lockdowns.

### Methods

We use information on SARS-CoV-2 outbreaks on mink farms in 94 Danish municipalities together with data on human SARS-CoV-2 cases and tested persons in Weeks 24-51 of 2020. Difference-in-difference estimation and panel event studies for weekly human incidence rates are applied to (i) identify epidemiological trends of human SARS-CoV-2 infections associated with disease outbreaks on mink farms, and (ii) quantify the mitigating effects from the two non-pharmaceutical interventions.

### Results

SARS-CoV-2 outbreaks on mink farms in a municipality associate with an increase in weekly human incidence rates by about 75%; spatial spillover effects to neighbouring municipalities are also observed. Local lockdowns reduce human incidence rates, while culling of mink appears to be more effective in combination with a lockdown. The temporal lag between an outbreak on a mink farm and a significant increase in human incidence rates is estimated to be 1-3 weeks; lockdowns and culling of mink neutralize this effect 4-8 weeks after the initial outbreak.

### Conclusions

SARS-CoV-2 infections among farmed mink in Denmark significantly link to local human infection trends. Strict animal and human disease surveillance in regions with mink farming should be pursued internationally to mitigate future epidemic developments.

*Eur J Public Health.* 2022 Feb 1; 32 (1): 151-157.

Doi: 10.1093/eurpub/ckab182.

### Mutations that adapt SARS-CoV-2 to mink or ferret do not increase fitness in the human airway

Zhou J<sup>1</sup>, Peacock TP<sup>1</sup>, Brown JC<sup>1</sup>, Goldhill DH<sup>1</sup>, Elrefaey AME<sup>2</sup>, Penrice-Randal R<sup>3</sup>, Cowton VM<sup>4</sup>, De Lorenzo G<sup>4</sup>, Furnon W<sup>4</sup>, Harvey WT<sup>4</sup>, Kugathasan R<sup>1</sup>, Frise R<sup>1</sup>, Baillon L<sup>1</sup>, Lassaunière R<sup>5</sup>, Thakur N<sup>6</sup>, Gallo G<sup>2</sup>, Goldswain H<sup>3</sup>, Donovan-Banfield F<sup>3</sup>, Dong X<sup>3</sup>, Randle NP<sup>3</sup>, Sweeney F<sup>1</sup>, Glynn MC<sup>1</sup>, Quantrill JL<sup>1</sup>, McKay PF<sup>1</sup>, Patel AH<sup>4</sup>, Palmarini M<sup>4</sup>, Hiscox JA<sup>7</sup>, Bailey D<sup>2</sup>, Barclay WS<sup>8</sup>

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### **SARS-CoV-2 Outbreak on a Spanish Mink Farm: Epidemiological, Molecular, and Pathological Studies**

*Badiola JJ<sup>1</sup>, Otero A<sup>1</sup>, Sevilla E<sup>1</sup>, Marín B<sup>1</sup>, Martínez MG<sup>1</sup>, Betancor M<sup>1</sup>, Sola D<sup>1</sup>, Lázaro SP<sup>1</sup>, Lozada J<sup>1</sup>, Velez C<sup>2</sup>, Chiner-Oms A<sup>3</sup>, Comas I<sup>4</sup>, Cancino-Muñoz I<sup>3</sup>, Monleón E<sup>1</sup>, Monzón M<sup>1</sup>, Acín C<sup>1</sup>, Bolea R<sup>1</sup>, Moreno B<sup>1</sup>*

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Farmed minks have been reported to be highly susceptible to severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and may represent a risk to humans. In this study, we describe the first outbreak of SARS-CoV-2 occurred on a mink farm in Spain,

between June and July 2020, involving 92,700 animals. The outbreak started shortly after some farm workers became seropositive for SARS-CoV-2. Minks showed no clinical signs compatible with SARS-CoV-2 infection throughout the outbreak. Samples from 98 minks were collected for histopathological, serological, and molecular studies. Twenty out of 98 (20.4%) minks were positive by RT-qPCR and 82 out of 92 (89%) seroconverted. This finding may reflect a rapid spread of the virus at the farm with most of the animals overcoming the infection. Additionally, SARS-CoV-2 was detected by RT-qPCR in 30% of brain samples from positive minks. Sequencing analysis showed that the mink sequences were not closely related with the other mink SARS-CoV-2 sequences available, and that this mink outbreak has its probable origin in one of the genetic variants that were prevalent in Spain during the first COVID-19 epidemic wave. Histological studies revealed bronchointerstitial pneumonia in some animals. Immunostaining of viral nucleocapsid was also observed in nasal turbinate tissue. Farmed minks could therefore constitute an important SARS-CoV-2 reservoir, contributing to virus spread among minks and humans. Consequently, continuous surveillance of mink farms is needed.

*Front Vet Sci. 2022 Jan 21; 8: 805004.*

*Doi: 10.3389/fvets.2021.805004. eCollection 2021.*

### **Histopathology and localization of SARS-CoV-2 and its host cell entry receptor ACE2 in tissues from naturally infected US-farmed mink (Ostaneovison vison)**

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Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) causes respiratory disease in mink similar to human COVID-19. We characterized the pathological findings in 72 mink from US farms with SARS-CoV-2 outbreaks, localized SARS-CoV-2 and its host cellular receptor angiotensin-converting enzyme 2 (ACE2) in mink respiratory tissues, and evaluated the utility of various test methods and specimens for SARS-CoV-2 detection in necropsy tissues. Of SARS-CoV-2-positive animals found dead, 74% had bronchiolitis and diffuse alveolar damage (DAD). Of euthanized SARS-CoV-2-positive animals, 72% had only mild interstitial pneumonia or minimal nonspecific lung changes (congestion, edema, macrophages); similar findings were seen in SARS-CoV-2-negative animals. Suppurative rhinitis, lymphocytic perivascular inflammation in the lungs, and lymphocytic infiltrates in other tissues were common in both SARS-CoV-2-positive and SARS-CoV-2-negative animals. In formalin-fixed paraffin-embedded (FFPE) upper respiratory tract (URT) specimens, conventional reverse transcription-polymerase chain reaction (cRT-PCR) was more sensitive than in situ hybridization (ISH) or immunohistochemistry (IHC) for detection of SARS-CoV-2. FFPE lung specimens yielded less detection of virus than FFPE URT specimens by all test methods. By IHC and ISH, virus localized extensively to epithelial cells in the nasal turbinates, and prominently within intact epithelium; olfactory mucosa was mostly spared. The SARS-CoV-2 receptor ACE2 was extensively detected by IHC within turbinate epithelium, with decreased detection in lower respiratory tract epithelium and alveolar macrophages. This study expands on the knowledge of the pathology and pathogenesis of natural SARS-CoV-2 infection in mink and supports their further investigation as a potential animal model of SARS-CoV-2 infection in humans.

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**Integrated histopathological, lipidomic, and metabolomic profiles reveal mink is a useful animal model to mimic the pathogenicity of severe COVID-19 patients**

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Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is transmitted on mink farms between minks and humans in many countries. However, the systemic pathological features of SARS-CoV-2-infected minks are mostly unknown. Here, we demonstrated that minks were largely permissive to SARS-CoV-2, characterized by severe and diffuse alveolar damage, and lasted at least 14 days post inoculation (dpi). We first reported that infected minks displayed multiple organ-system lesions accompanied by an increased inflammatory response and widespread viral distribution in the cardiovascular, hepatobiliary, urinary, endocrine, digestive, and immune systems. The viral protein partially co-localized with activated Mac-2<sup>+</sup> macrophages throughout the body. Moreover, we first found that the alterations in lipids and metabolites were correlated with the histological lesions in infected minks, especially at 6 dpi, and were similar to that of patients with severe and fatal COVID-19. Particularly, altered metabolic pathways, abnormal digestion, and absorption of vitamins, lipids, cholesterol, steroids, amino acids, and proteins, consistent with hepatic dysfunction, highlight metabolic and immune dysregulation. Enriched kynurenine in infected minks contributed to significant activation of the kynurenine pathway and was related to macrophage activation. Melatonin, which has significant anti-inflammatory and immunomodulating effects, was significantly downregulated at 6 dpi and displayed potential as a targeted medicine. Our data first illustrate systematic analyses of infected minks to recapitulate those observations

in severe and fetal COVID-19 patients, delineating a useful animal model to mimic SARS-CoV-2-induced systematic and severe pathophysiological features and provide a reliable tool for the development of effective and targeted treatment strategies, vaccine research, and potential biomarkers.

*Signal Transduct Target Ther.* 2022 Jan 28; 7(1): 29.  
Doi: 10.1038/s41392-022-00891-6.

### **Ferrets are valuable models for SARS-CoV-2 research**

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Coronavirus disease 2019 (COVID-19), caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), resulted in an ongoing pandemic with millions of deaths worldwide. Infection of humans can be asymptomatic or result in fever, fatigue, dry cough, dyspnea, and acute respiratory distress syndrome with multiorgan failure in severe cases. The pathogenesis of COVID-19 is not fully understood, and various models employing different species are currently applied. Ferrets can be infected with SARS-CoV-2 and efficiently transmit the virus to contact animals. In contrast to hamsters, ferrets usually show mild disease and viral replication restricted to the upper airways. Most reports have used the intranasal inoculation route, while the intratracheal infection model is not well characterized. Herein, we present clinical, virological, and pathological data from young ferrets intratracheally inoculated with SARS-CoV-2. Infected animals showed no significant clinical signs, and had transient infection with peak viral RNA loads at 4 days postinfection, mild to moderate rhinitis, and pulmonary endothelialitis/vasculitis. Viral antigen was exclusively found in the respiratory epithelium of the nasal cavity, indicating a particular tropism for cells in this location. Viral antigen was associated with epithelial damage and influx of inflammatory cells, including activated neutrophils releasing neutrophil extracellular traps.

Scanning electron microscopy of the nasal respiratory mucosa revealed loss of cilia, shedding, and rupture of epithelial cells. The currently established ferret SARS-CoV-2 infection models are comparatively discussed with SARS-CoV-2 pathogenesis in mink, and the advantages and disadvantages of both species as research models for zoonotic betacoronaviruses are highlighted.

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### **Complete genomic sequencing of canine distemper virus with nanopore technology during an epizootic event**

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Canine distemper virus (CDV) endangers a wide range of wild animal populations, can cross species barriers and therefore representing a significant conservation and animal health risk around the globe. During spring to autumn 2021, according to our current estimates a minimum of 50 red foxes (*Vulpes vulpes*) died of CDV in Hungary, with CDV lesions. Oral, nasal and rectal swab samples were RT-PCR screened for Canine Distemper Virus from red fox carcasses. To investigate in more detail the origins of these CDV strains, 19 complete genomes were sequenced with a pan-genotype CDV-specific amplicon-based sequencing method developed by our laboratory and optimized for the Oxford Nanopore Technologies platform. Phylogenetic analysis of the complete genomic sequences and separately the hemagglutinin gene sequences revealed the role of the Europe lineage of CDV as a causative agent for the

current epizootic. Here we highlight the growing importance of fast developing rapid sequencing technologies to aid rapid response activities during epidemics or epizootic events. We also emphasize the urgent need for improved surveillance of CDV, considering the epizootic capability of enzootic strains as reported in the current study. For such future efforts, we provide a novel NGS protocol to facilitate future genomic surveillance studies.

*Sci Rep.* 2022 Mar 8; 12 (1): 4116.  
Doi: 10.1038/s41598-022-08183-3.

### Identification and primary application of hybridomas cell secreting monoclonal antibodies against mink (*Neovison vison*) interferon-gamma

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### Experimental Infection of Captive Red Foxes (*Vulpes vulpes*) with *Mycobacterium bovis*

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In Europe, animal tuberculosis (TB) due to *Mycobacterium bovis* involves multi-host communities that include cattle and wildlife species, such as wild boar (*Sus scrofa*), badgers (*Meles meles*) and red deer (*Cervus elaphus*). Red fox (*Vulpes vulpes*) infections have also been recently reported in some TB endemic regions in the Iberian Peninsula and France, with some of the infected animals shedding *M. bovis* in urine and feces. In order to understand the pathogenesis of *M. bovis* infection in foxes and the associated risk of transmission, 12 captive foxes (6 females and 6 males) were inoculated orally with  $2 \times 10^7$  colony-forming units of a French field isolate of *M. bovis*. Clinical samples (urine, feces and oropharyngeal swabs) were collected every four weeks and tested for molecular diagnosis and bacteriology. Serological responses were measured by IDEXX *M. bovis* Ab Test and Multi Antigen Print Immunoassay (MAPIA). At a post-mortem examination performed 12 weeks post infection (wpi), tissues were tested for the presence of *M. bovis* and associated gross and microscopic TB-like lesions. *M. bovis* was detected by PCR in bladder swabs of 3 animals at 12 wpi. It was also detected pre-mortem at different time points of the experiment in the oropharyngeal mucus of three individuals and in the feces of nine foxes, with two of them confirmed by bacteriology. All 12 foxes had at least 4 PCR positive samples (out of the 23 tested), and all but 1 fox had at least 1 culture positive sample. The culture negative fox was PCR positive in both retropharyngeal and mesenteric lymph nodes, in line with the results of the other animals. Seroconversion was observed in all foxes except one during the

experiment, and in nine at the final time point. No gross visible lesions were found in any animal at the post-mortem examination. The histology showed small granulomas within the lymph nodes, tonsils, liver and lungs from eight animals, with the presence of few acid-fast bacilli. These results confirmed that all orally-infected foxes developed mild TB lesions but they were able to shed mycobacteria in about 75% of cases, 1 month post-infection (9 out of 12 foxes). These results show that it is possible to induce typical TB infection experimentally in captive foxes, with measurable *M. bovis* excretion; such an experimental system could be useful for future evaluations of diagnostics and vaccines in this species.

*Microorganisms*. 2022 Feb 6; 10 (2): 380.  
Doi: 10.3390/microorganisms10020380.

### Isolation and Genetic Characterization of Parvoviruses From Dogs, Cats, Minks, and Raccoon Dogs in the Eastern Region of Shandong Province, China

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The eastern region of Shandong province, China, is an intensive economic mink and raccoon dog breeding area. To investigate the molecular variations of parvovirus in cats, dogs, minks, and raccoon dogs from this region, feline panleukopenia virus (FPV), canine parvovirus 2 (CPV-2), mink enteritis virus (MEV), and raccoon dog parvovirus (RDPV) were separately isolated and characterized from the respective animals with gastroenteritis. PCR amplification showed that there were 15/18 (83.3%), 9/13 (69.2%), 8/11 (72.7%), and 3/7 (42.9%) samples from the diseased animals separately positive for FPV, CPV-2, MEV, and RDPV. Of these, a total of six FPV, six MEV, four CPV-2, and three RDPV strains were successfully isolated using F81 cells. Next, the near-complete genomes of 19 parvovirus isolates were

amplified and analyzed. The viral particle 2 (VP2) sequence alignment showed that they shared 97.2-100% nucleotide similarity. Phylogenetic analysis showed that the five FPV isolates were in the same branch, and an FPV isolate was closely related with MEV and RDPV isolates obtained in this study. These suggested that cross-species infection occurred in the Shandong region between the FPV, MEV, and RDPV. For the four CPV-2 isolates, three were antigenic variant strains CPV-2a, and the other was antigenic variant strain CPV-2c. Additionally, the mutations that had emerged in the VP2 amino acids of CPV-2 also occurred in the VP2 from the FPV, MEV, and RDPV isolates. This study suggested that the continuous evolution of the parvovirus may be accelerated in areas with a high density of economic animal trading/breeding, and controlling parvovirus infection in these animals remains a challenge.

*Front Microbiol*. 2022 Feb 28; 13: 862352.  
Doi: 10.3389/fmicb.2022.862352. eCollection 2022.

### Detection of Carbapenem Resistance of *Proteus mirabilis* Strains Isolated from Foxes, Raccoons and Minks in China

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*Proteus mirabilis*, an opportunistic pathogen, is found to be an emerging threat to both animals and humans for a variety of infections. However, the characteristics of *P. mirabilis* infections from foxes, raccoons and minks remain unclear. In this context, we identified the antibiotic resistance genes and virulence genes of *P. mirabilis* isolates from foxes, raccoons and minks in China. Most isolates showed resistance to florfenicol (90.57%), trimethoprim-sulfamethoxazole (73.58%), and imipenem (71.70%). A total of 73.58% of isolates were resistant to antibiotics from at least three or more classes, and were categorized as multi-drug resistant. A total of 33.33% of the isolates were resistant to antibiotics from seven classes. The most prevalent resistant were *sulI* (94.34%), followed by *floR*, *bla<sub>TEM</sub>*, *aac(6')Ib-cr* and *bla<sub>OXA-1</sub>* with the detection rate of 88.68%, 83.02%, 71.70% and 60.38%, respectively. Among the 51 *P.*



*mirabilis* isolates that were resistant to beta-lactam antibiotics, all isolates carried at least one beta-lactam gene. In addition, *bla*<sub>NDM</sub> and *bla*<sub>OXA-24</sub> genes were firstly reported in carbapenem-resistant *P. mirabilis* isolates from foxes, raccoons and minks. All isolates exhibited the virulence genes *ureC*, *zapA*, *pmfA*, *atfA* and *mrpA*. *P. mirabilis* isolates carrying all detected 10 virulence genes from different animal species showed different lethal abilities in a *G. mellonella* larvae model. More importantly, the profiles of antibiotic resistance genes of isolates from fur animals and the environment were generally similar, and phylogenetic analysis showed that the *P. mirabilis* isolates from farm environment samples may have close relatedness with that from animals.

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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.