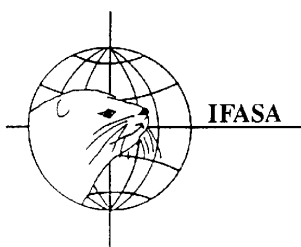
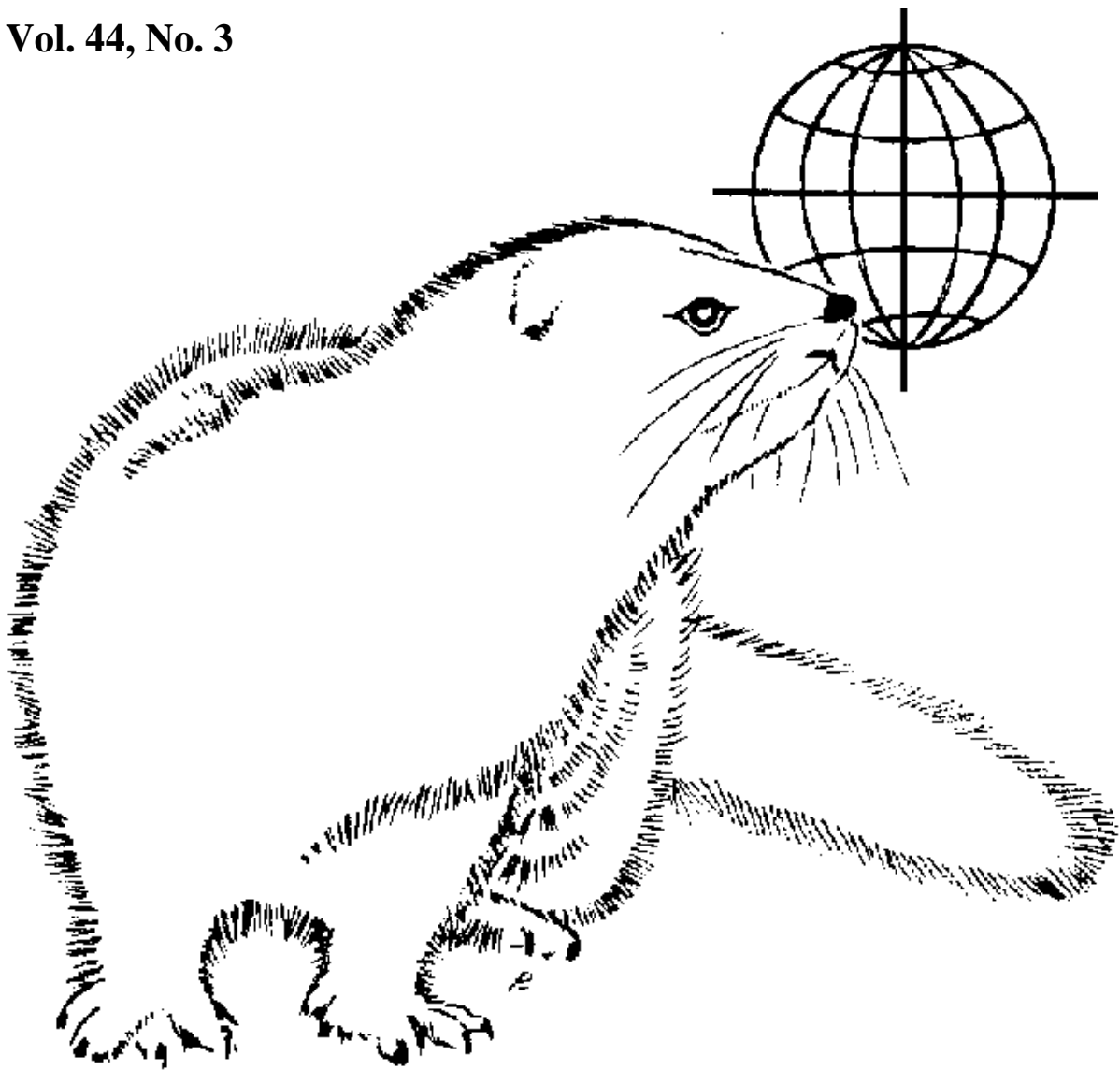


SCIENTIFUR

SCIENTIFIC INFORMATION IN FUR ANIMAL PRODUCTION

Vol. 44, No. 3



INTERNATIONAL FUR ANIMAL SCIENTIFIC ASSOCIATION

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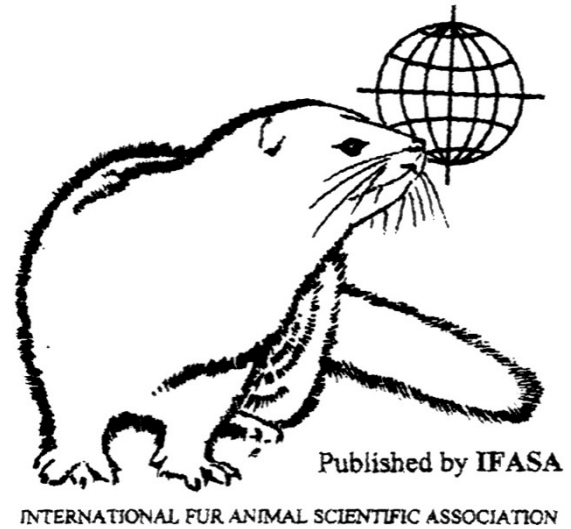
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Notes from the Editor

The Corona virus leading to COVID-19 originated most likely in bats, from where it was transmitted to another mammal, and from there to humans. Similar zoonotic patterns were observed for the Corona virus that led to SARS in 2003 in China, and MERS in 2012 in the Middle East. Historically, many infectious diseases (zoonosis) in humans similarly originated in animals including domestic livestock.

Mink have become a part of the COVID-19 pandemic issue. Outbreaks, first observed in mink farms in the Netherlands in April 2020, are caused by zoonosis in reverse with the transmission of virus from humans to mink. The infection has then spread from mink back to humans and two farm workers in the Netherlands have been infected. On mink farms, infections seem to spread among mink through droplets, feed, bedding or dust. Study of the virus as it spreads through the populations reveals many new mutations, but these mutations seem not to result in increased virulence. It was also shown that the virus can infect other animals including cats and dogs. Feral cats were found to be infected probably through the feed.

In Denmark, three farms have been infected. Mink on these farms have been killed on precautionary principle. Subsequently, mink on 125 farms have been tested for COVID-19. None of these farms were infected. Precautions such as frequent screening of the farms, orders to farm workers to use protective equipment and guidelines for hygiene for everyone who comes to mink farms will be introduced to keep

COVID-19 in mink herds at a minimum. These precautions mean that mink on infected farms are no longer required to be killed.

The experience with COVID-19 emphasizes the importance of extreme caution in livestock production. Extensive precautions have to be taken to limit the possibility of infections of herds, e.g. from wild animals. Conditions on farms need to ensure a limited spread of possible infections, and working conditions for farm workers have to minimize the risk of infections from both animals to humans and from humans to animals.

The XII International Scientific Congress in Fur Animal Production should have been held in Warsaw in Poland from 25 to 27 August 2020 in collaboration between the International Fur Animal Scientific Association (IFASA) and the Polish Society of Animal Production (PSAP). However, due to the COVID-19 pandemic the congress has been postponed to 24-26 August 2021. For further information, please consult: <https://ifasa2020.pl/>. The IFASA Congress is an important forum for researchers in fur animal production to gather to present and discuss recent research and outline research to address future challenges. An interesting and well-attended congress is foreseen in 2021.

Vivi Hunnicke Nielsen

Editor Scientifur

BREEDING, GENETICS AND REPRODUCTION**Combined analysis of group recorded feed intake and individually recorded body weight and litter size in mink**

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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 Apr 23; 1-9.

Doi: 10.1017/S1751731120000762.

Online ahead of print.

Linkage Disequilibrium, Effective Population Size and Genomic Inbreeding Rates in American Mink Using Genotyping-by-Sequencing Data

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Front Genet. 2020 Mar 13; 11:223.

Doi: 10.3389/fgene.2020.00223. eCollection 2020.

Pantothenic Acid Promotes Dermal Papilla Cell Proliferation in Hair Follicles of American Minks via Inhibitor of DNA Binding 3/Notch Signaling Pathway

Wang Z¹, Nan W¹, Si H¹, Wang S², Zhang H³, Li G⁴

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Life Sci. 2020 Jul 1; 252: 117667.

Doi: 10.1016/j.lfs.2020.117667. Epub 2020 Apr 15.

Estradiol and Progesterone Affect Enzymes but Not Glucose Consumption in a Mink Uterine Cell Line (GMMe)

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Biosci Rep. 2020 Apr 30; 40 (4):BSR20193512.

Doi: 10.1042/BSR20193512.

First Assessment of Hoary Fox (*Lycalopex vetulus*) Seasonal Ovarian Cyclicity by Non-Invasive Hormonal Monitoring Technique

Zanini das Candeias I^{1,2}, da Motta Lima CF^{1,3}, Gemesio Lemos F^{1,4}, Spencoski KM⁵, Alvarenga de Oliveira C², Nucharin Songsasen⁶, de Barros Vaz Guimarães MA²

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Conserv Physiol. 2020 May 8; 8 (1): coaa039.

Doi: 10.1093/conphys/coaa039. eCollection 2020.

Administration of Aromatase Inhibitor MPV-2213ad to Blue Fox Vixens (*Vulpes Lagopus*) as a Model for Contraception in Female Dogs

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Theriogenology. 2020 Aug; 152: 53-63.

Doi: 10.1016/j.theriogenology.2020.04.009.

Epub 2020 Apr 15.

BEHAVIOUR AND WELFARE

Machine Learning Goes Wild: Using Data From Captive Individuals to Infer Wildlife Behaviours

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1. Remotely tracking distinct behaviours of animals using acceleration data and machine learning has been carried out successfully in several species in captive settings. In order to study the ecology of animals in natural habitats, such behaviour classification models need to be transferred to wild individuals.

However, at present, the development of those models usually requires direct observation of the target animals.

2. The goal of this study was to infer the behaviour of wild, free-roaming animals from acceleration data by training behaviour classification models on captive individuals, without the necessity to observe their wild conspecifics. We further sought to develop methods to validate the credibility of the resulting behaviour extrapolations.

3. We trained two machine learning algorithms proposed by the literature, Random Forest (RF) and Support Vector Machine (SVM), on data from captive red foxes (*Vulpes vulpes*) and later applied them to data from wild foxes. We also tested a new advance for behaviour classification, by applying a moving window to an Artificial Neural Network (ANN). Finally, we investigated four strategies to validate our classification output.

4. While all three machine learning algorithms performed well under training conditions (Kappa values: RF (0.82), SVM (0.78), ANN (0.85)), the established methods, RF and SVM, failed in classifying distinct behaviours when transferred from captive to wild foxes. Behaviour classification with the ANN and a moving window, in contrast, inferred distinct behaviours and showed consistent results for most individuals.

5. Our approach is a substantial improvement over the methods previously proposed in the literature as it generated plausible results for wild fox behaviour. We were able to infer the behaviour of wild animals that have never been observed in the wild and to further illustrate the credibility of the output. This framework is not restricted to foxes but can be applied to infer the behaviour of many other species and thus empowers new advances in behavioural ecology.



Fig. 1. Camera trap picture of a wild red fox (“Gerlinde”), collared in Berlin in 2016. The arrows symbolize the X-, Y- and Z-axis (corresponding to sway-, surge- and heave motion).

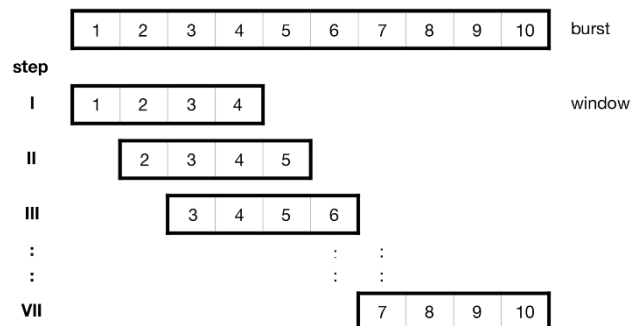


Fig 2. Schematic representation of the moving window approach: Starting at the beginning of a data set (“burst”, here $n = 10$), a fixed number of consecutive data (“window”, here $n = 4$) is taken out and analyzed. In the further step-by-step analysis, the window is shifted by one data set until the window has reached the end of the complete data set (7 steps in the schematic example).

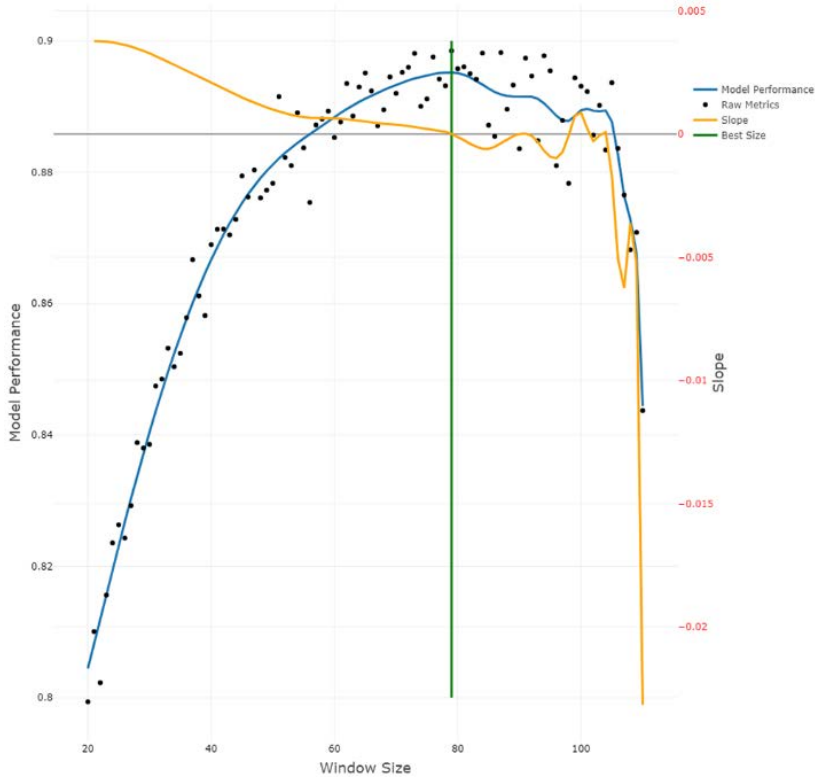


Fig. 3. ANN model performance in relation to window size. Black dots show the computed performance values. The blue line is the result of a General Additive Model, $k = 40$ [37] fit. The y-axis on the left side labelled “Model Performance” corresponds to the Model Performance line (blue) and Raw Metrics points (black). The orange line is the calculated slope of the model performance, which corresponds to the y-axis on the right side labelled “Slope”. The green vertical line represents the best window size of 79.

(a)

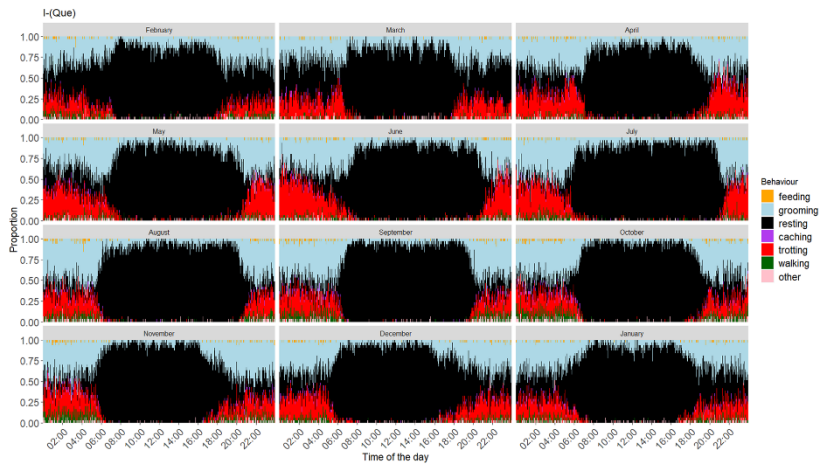
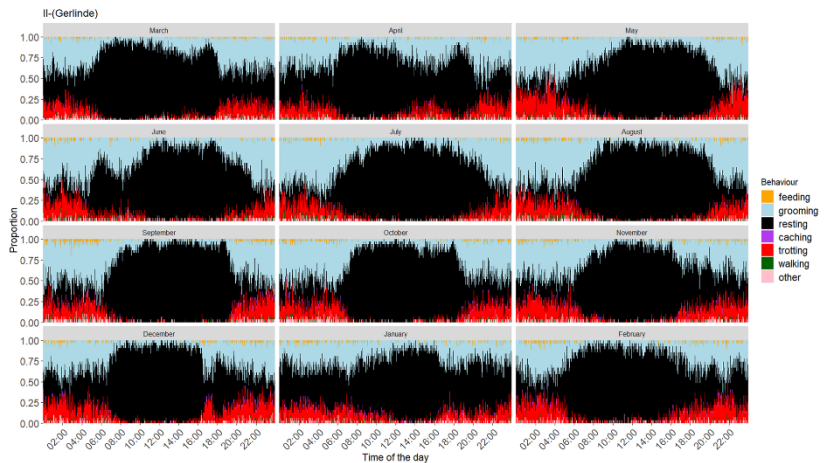


Fig. 4. Time-dependent composition of behaviours of Que (I) and Gerlinde (II). Stacked bars represent the proportion of each behavior at a given time of day, in each month. The data showed here span from February 2018 to January 2019 for Que and from March 2016 to February 2017 for Gerlinde.

(b)



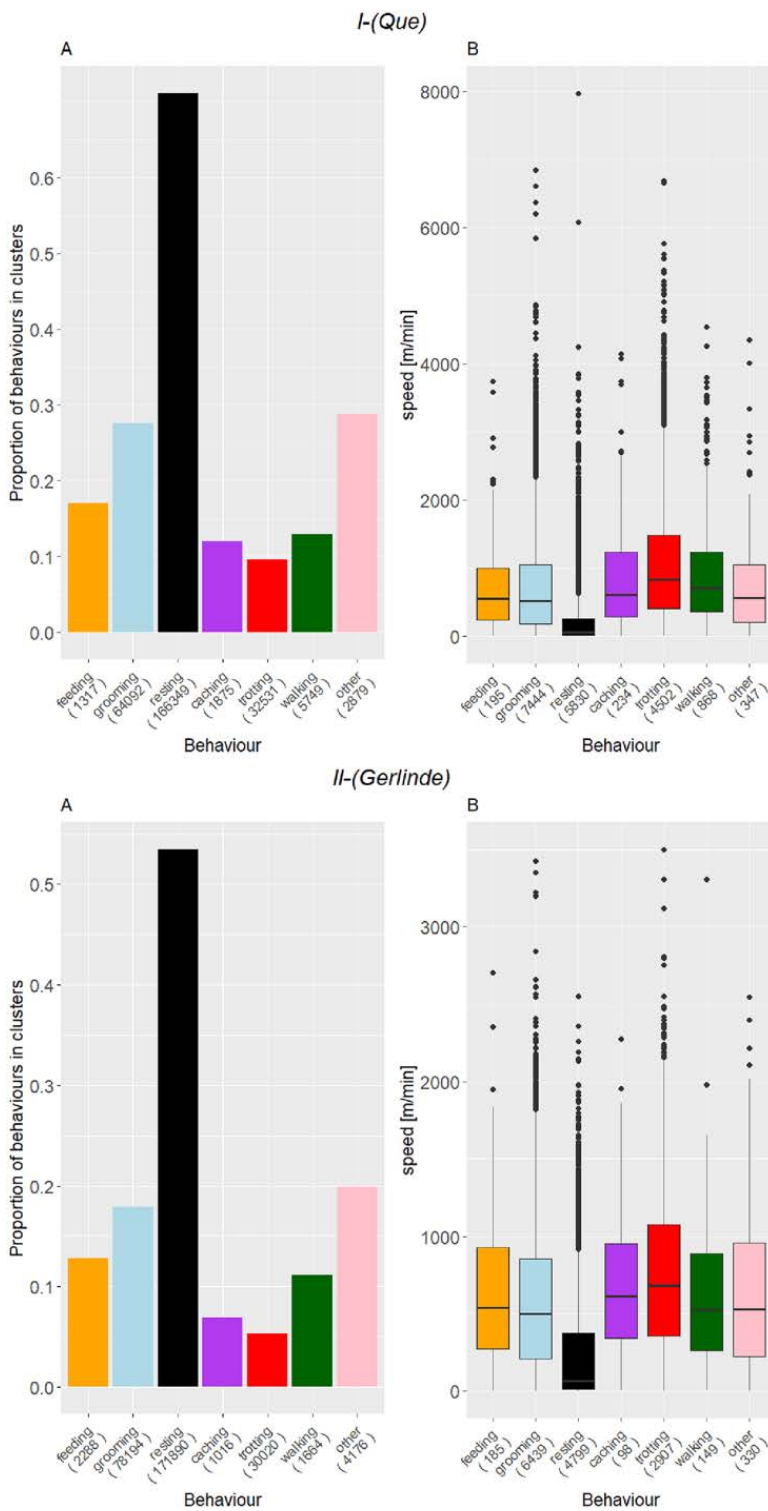


Fig. 5. Behaviour assessments of Que (I) and Gerlinde (II) in relation to GPS clusters (A) and speed (B).

The numbers in the brackets indicate the sample size of each behavior class (I).

Resting shows the highest association with GPS clusters (71 %) and trotting the lowest (9 %). Resting events are associated with significantly lower speed than trotting events (Wilcoxon rank sum test, $W = 3024826$, $p < 0.001$). (II) Resting shows the highest association with GPS clusters (53 %) and trotting the lowest (5 %). Resting events are associated with significantly lower speed than trotting events (Wilcoxon rank sum test, $W = 2286090$, $p < 0.001$).

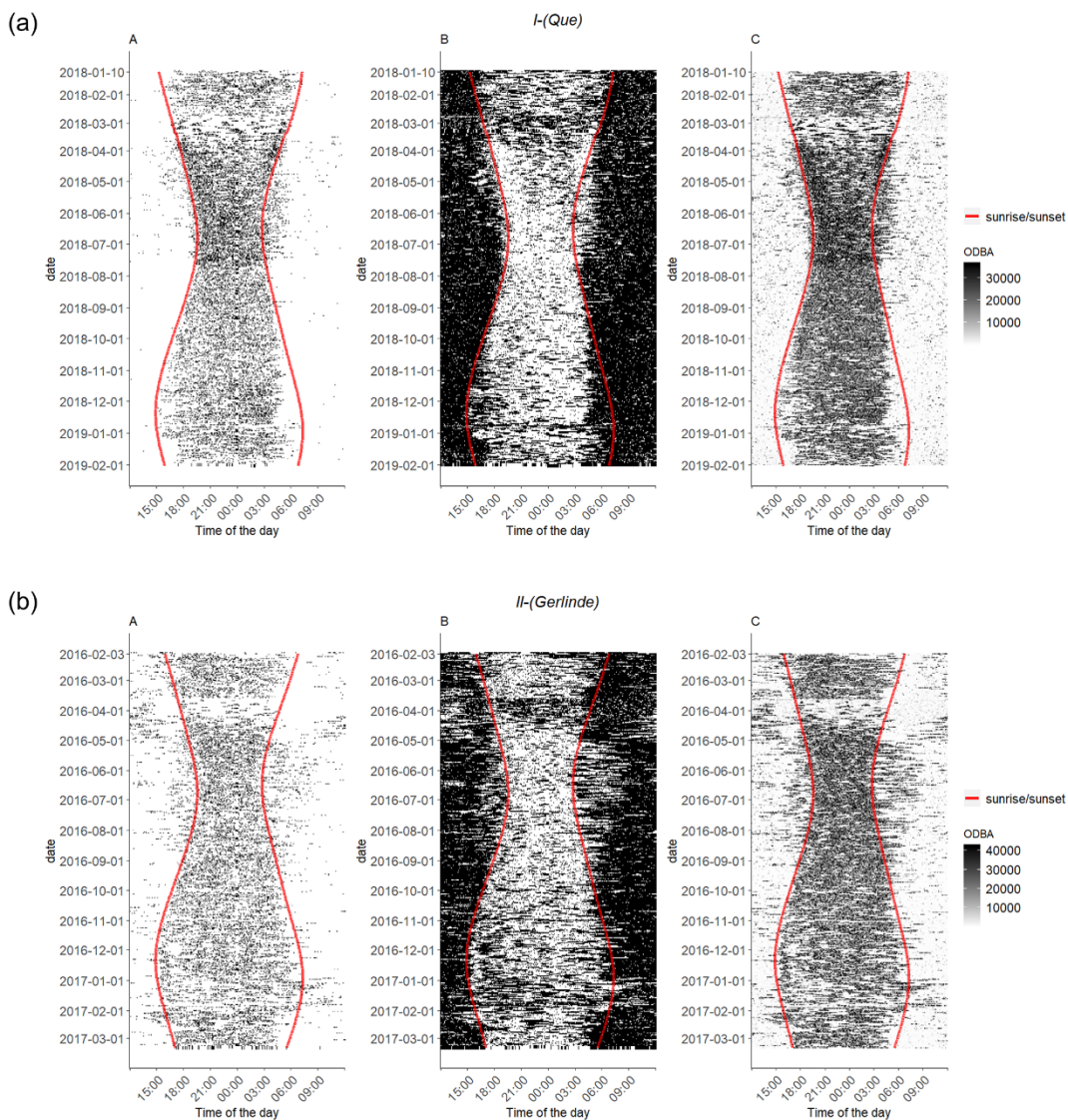


Fig. 6. Temporal distribution of trotting (A), resting (B) and ODBA values (C) for Que (I) and Gerlinde (II). The red lines indicate sunset and sunrise. (A) Black spaces indicate times at which trotting behaviour was classified, whereas white spaces indicate the classification of all other behaviours. (B) Black spaces indicate times at which resting behaviour was classified, whereas white spaces indicate classifications of all other behaviours. (C) Higher ODBA values are indicated by darker spaces.

PLoS One. 2020 May 5; 15(5): e0227317.

Doi: 10.1371/journal.pone.0227317.

eCollection 2020.

Are There Metacognitivist in the Fox Hole? A Preliminary Test of Information Seeking in an Arctic Fox (*Vulpes lagopus*)

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Over the last two decades, evidence has accrued that at least some nonhuman animals possess metacognitive abilities. However, of the carnivores, only domestic dogs have been tested. Although rarely represented in the psychological literature, foxes are good candidates for metacognition given that they cache their food. Two experiments assessed metacognition in one male arctic fox (*Vulpes lagopus*) for the first time. An information-seeking paradigm was used, in which the subject had the opportunity to discover which compartment was baited before making a choice by looking through a transparent window in the apparatus. In the first experiment, choice accuracy during seen trials was equal to choice accuracy on unseen trials. Importantly, there was no significant difference between the subject's looking behavior on seen versus unseen trials. In the second experiment, with chance probabilities reduced, the subject's choice accuracy on both seen and unseen trials was below chance. The subject did not exhibit looking behavior in any of the trials. Latencies to choose were not influenced by whether he witnessed baiting. Although we did not obtain evidence of metacognition in our tests of a single subject, we maintain that foxes may be good candidates for further tests using similar methodologies to those introduced here.

Behav Sci (Basel). 2020 Apr 26; 10 (5): 81.
Doi: 10.3390/bs10050081.

NUTRITION, FEEDING AND MANAGEMENT

The Vomeronasal Organ of Wild Canids: The Fox (*Vulpes Vulpes*) as a Model

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J Anat . 2020 Jun 25. Doi: 10.1111/joa.13254.
Online ahead of print.

Computed Tomography and Cross-Sectional Anatomy of the Head in the Red Fox (*Vulpes Vulpes*)

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Anat Histol Embryol. 2020 Apr 29.
Doi: 10.1111/ahel.12565. Online ahead of print.

HEALTH AND DISEASE

Coronavirus Rips Through Dutch Mink Farms, Triggering Culls

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Science. 2020 Jun 12; 368(6496):1169.
Doi: 10.1126/science.368.6496.1169.

SARS-CoV-2 Infection in Farmed Minks, the Netherlands, April and May 2020

Oreshkova N¹, Molenaar RJ², Vreman S¹, Harders F¹, Oude Munnink BB³, Hakze-van der Honing RW¹, Gerhards N¹, Tolsma P⁴, Bouwstra R², Sikkema RS³, Tacken MG¹, de Rooij MM⁵, Weesendorp E¹, Engelsma MY¹, Brusckhe CJ⁶, Am Smit L⁵, Koopmans M³, van der Poel WH¹, Stegeman A⁷

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Respiratory disease and increased mortality occurred in minks on two farms in the Netherlands, with interstitial pneumonia and SARS-CoV-2 RNA in organ and swab samples. On both farms, at least one worker had coronavirus disease-associated symptoms before the outbreak. Variations in mink-derived viral genomes showed between-mink transmission and no infection link between the farms. Inhalable dust contained viral RNA, indicating possible exposure of workers. One worker is assumed to have attracted the virus from mink.

Euro Surveill. 2020 Jun; 25 (23).

Doi: 10.2807/1560-7917.ES.2020.25.23.2001005.

Epidemiological Analysis of Arcanobacterium Phocae Isolated From Cases of Mink Dermatitis of a Single Farm

Alssahen M¹, Hassan AA¹, Sammra O¹, Lämmler C², Saarnisto MR³, Borowiak M⁴, Malorny B⁴, Rau J⁵, Prenger-Berninghoff E¹, Plötz M⁶, Abdulmawjood A⁶

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Molecular Evidence for Vaccine-Induced Canine Distemper Virus and Canine Adenovirus 2 Coinfection in a Fennec Fox

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A 61-d-old fennec fox (*Vulpes zerda*), 11 d after receiving a multivalent, modified-live virus vaccine containing canine distemper virus (CDV), canine adenovirus 2 (CAV-2), parainfluenza virus, parvovirus, and canine coronavirus, developed oculonasal discharge, and subsequently convulsions, and hemoptysis, and died. Microscopic changes in the cerebrum were evident, including neuronal degeneration and necrosis; intracytoplasmic eosinophilic inclusion bodies were observed in astrocytes. CDV was detected in the brain tissue by immunohistochemistry. Pulmonary lesions of multifocal necrotizing bronchopneumonia had Cowdry type A intranuclear inclusions in the bronchial epithelial cells. Electron microscopy revealed crystalline arrays of adenovirus-like particles within the intranuclear inclusions. Additionally, the hemagglutinin gene of CDV and the CAV-2 DNA polymerase gene were detected in the fennec fox; sequence analysis showed 100% identity with those of the vaccine strain viruses. To our knowledge, vaccine-induced CDV and CAV-2 coinfections using molecular analysis have not been reported previously. Therefore, vaccine strains should be considered prior to CDV vaccination in nondomestic carnivores.

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Spread of LA-MRSA CC398 in Danish Mink (Neovison Vison) and Mink Farm Workers

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

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A lytic *Pseudomonas aeruginosa* phage vB_PaeP_LP14 belonging to the family Podoviridae was isolated from infected mink. The microbiological characterization revealed that LP14 was stable at 40 to 50 °C and stable over a broad range of pH (5 to 12). The latent period was 5 min, and the burst size was 785 pfu/infected cell. The whole-genome sequencing showed that LP14 was a dsDNA virus and has a genome of 73,080 bp. The genome contained 93 predicted open reading frames (ORFs), 17 of which have known functions including DNA replication and modification, transcriptional regulation, structural and packaging proteins, and host cell lysis. No tRNA genes were identified. BLASTn analysis revealed that phage LP14 had a high-sequence identity (96%) with *P. aeruginosa* phage YH6. Both morphological characterization and genome annotation indicate that phage LP14 is a member of the family Podoviridae genus Litunavirus. The study of phage LP14 will provide basic information for further research on treatment of *P. aeruginosa* infections.

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Comparison of Streptococcus Halichoeri Isolates From Canine and Fur Animal Infections: Biochemical Patterns, Molecular Characteristics and Genetic Relatedness

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Background

Streptococcus halichoeri infections have been reported in grey seals, a European badger, a Stellar sea lion and humans, but its presence in companion and fur animals is unknown. Since 2010, *S. halichoeri*-like bacteria (SHL) have been isolated from fur animals and dogs in Finland. Our aim was to retrospectively investigate laboratory records for SHL from canine and fur animal infections, characterize the isolates and compare their genetic relatedness in relation to three reference strains: CCUG 48324^T, originating from a grey seal, and strains 67100 and 61265, originally isolated from humans.

Results

A total of 138 and 36 SHLs from canine and fur animal infections, respectively, were identified in the laboratory records. SHL was commonly associated with skin infections, but rarely as the only species. A

set of 49 canine and 23 fur animal SHLs were further characterized. MALDI-TOF confirmed them as being *S. halichoeri*. The growth characteristics were consistent with the original findings, but isolates were catalase positive. In total, 17 distinct API 20 Strep patterns were recorded among all 75 isolates tested, of which pattern 5563100 was the most common ($n = 30$). Antimicrobial resistance to erythromycin and clindamycin was common in canine isolates, but rare in fur animal isolates. Three clusters were observed by PFGE, and 16S rRNA sequencing revealed 98.1-100% similarities with the human strains and 98.1-99.5% with the seal strain. A phylogenetic tree of concatenated 16S rRNA and rpoB revealed closely related isolates with two clades. Fifteen canine isolates were identical to the human strains based on concatenated 16S rRNA and rpoB sequencing.

Conclusions

Streptococcus halichoeri appears to be quite a common bacterial species in the skin of dogs and fur animals. The clinical significance of *S. halichoeri* is uncertain, as it was rarely isolated as a monoculture. No apparent temporal or spatial clustering was detected, but isolates from different sources were genetically very similar. Because many canine isolates were genetically similar to the human reference strains, transmission between dogs and humans may be possible. WGS sequencing of strains from different sources is needed to further investigate the epidemiology and virulence of *S. halichoeri*.

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Urolithiasis and Cystitis Associated With *Staphylococcus Delphini* Group A and Mortality in Post-Weaning Mink Kits (*Neovison Vison*)

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Update on Diseases in Chinchillas: 2013-2019

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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.