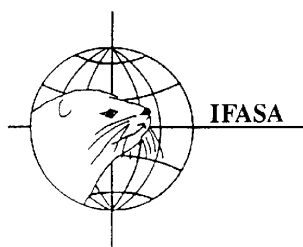
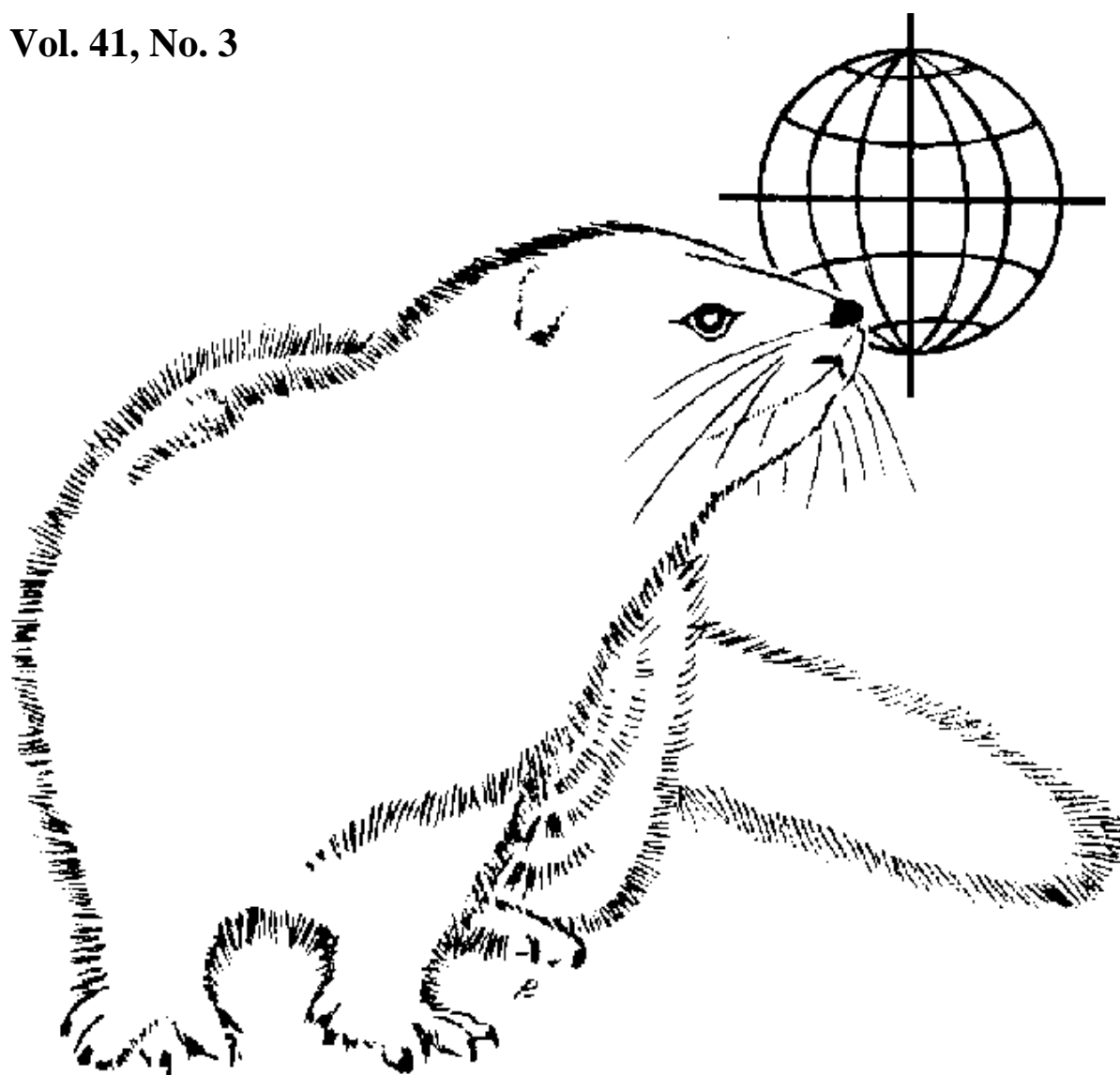


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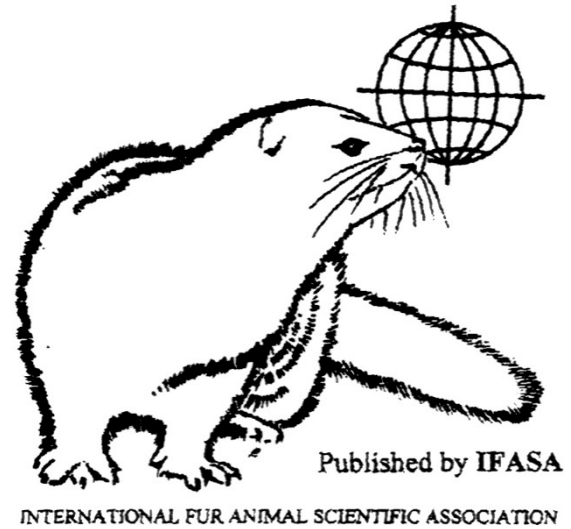
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Notes from the Editor

Eradication of Aleutian Disease (AD) has not been successful. This calls for actions to limit the influence that the disease has on the production. New results from a study of the association of reproductive performance of female mink and the individual AD status suggest that selection for females with low AD values will improve the reproduction performance and thus that a farm disease control program in combination with selection are valuable tools in the control of the effect of Aleutian Mink Disease. Furthermore, mapping of transmission of Aleutian Mink Disease Virus (AMDV) forms the basis for understanding the spread of the virus among farms. Results in an abstract published here suggest that phylogenetic analyses based on whole-genome sequencing is the tool to use in such a mapping. On infected farms, it is shown that there is a high environmental contamination, which needs to be considered in developing disinfection procedures.

Control of the embryonic diapause requires regulation at molecular level. New promising candidates for the molecular control of embryonic diapause in mammals have been detected in a recent study, which is reported in this issue of *Scientifur*. A study of European polecat suggests that the function of a protein inhibitor dominating the protein profile at embryo implantation is to protect against damage caused by proteinases released simultaneously.

The all-embracing goal of fur animal production is the production of high quality fur. However, fur animals like other farm animals also have the potential of being used as a model in human research. Abstracts in this issue suggest that mink can be used in the study of *Pseudomonas aeruginosa* mediated rhinosinusitis and that chinchilla can be used as a novel animal model of human pregnancy.

Vivi Hunnicke Nielsen

Editor *Scientifur*

BREEDING, GENETICS AND REPRODUCTION**The effect of color type on early wound healing in farmed mink (*Neovison vison*)**

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Background:

Individual differences of mink, including color type, are speculated to affect the course of wound healing, thereby impacting wound assessment and management on the farms, as well as the assessment of wounds in forensic cases. In this study, we examined the effect of color type on early wound healing in farmed mink. Full thickness excisional wounds (2 × 2 cm) were made on the back in 18 mink of the color types Brown, Silverblue and Blue Iris. Gross and microscopic pathology of the wounds was evaluated 2 days post-wounding together with degree of wound size reduction, presence of bacteria and blood analyses.

Results:

Pathological examination on day 2 showed the greatest mean wound size reduction in Brown mink (11.0 %) followed by Blue Iris (7.9 %) and Silverblue (1.6 %). Bacteria were cultured from all wounds, and predominantly *Staphylococcus* species were recovered in mixed or pure culture. Histopathology from day 2 wounds showed a scab overlying necrotic wound edges, which were separated from underlying vital tissue by a demarcation zone rich in

polymorphonuclear leukocytes. Fibroblasts and plump endothelial cells were more numerous in the deeper tissues. Complete blood count parameters were within normal ranges in most cases, however, the mink showed mildly to markedly decreased hematocrit and six mink of the color types Silverblue and Blue Iris showed moderately elevated numbers of circulating segmented neutrophils on day 2. There was a marked increase in concentration of serum amyloid A from day 0 to day 2 in all color types.

Conclusions:

We have described differences in early wound healing between mink of the color types Brown, Silverblue and Blue Iris by use of an experimental wound model in farmed mink. The most pronounced difference pertained to the degree of wound size reduction which was greatest in Brown mink, followed by Blue Iris and Silverblue, respectively.

BMC Vet Res. 2017 May 22; 13(1):135.

Doi: 10.1186/s12917-017-1052-1.

Embryo arrest and reactivation: potential candidates controlling embryonic diapause in the tamar wallaby and mink

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Biol Reprod. 2017 April 1; 96(4): 77-894.

Doi: 10.1093/biolre/iox019.

A retrospective cohort study estimating the individual Aleutian disease progress in female mink using a VP2 ELISA and its association to reproductive performance

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Prev Vet Med. 2017 May 1; 140:60-66.

Doi: 10.1016/j.prevetmed.2017.02.010.

Epub 2017 Feb 24.

Reproductive parameters of critically endangered European mink (*Mustela lutreola*) in captivity

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Anim Reprod Sci. 2017 Jun; 181:86-92.

Doi: 10.1016/j.anireprosci.2017.03.019.

Epub 2017 Mar 31.

Pulse of inflammatory proteins in the pregnant uterus of European polecats (*Mustela putorius*) leading to the time of implantation

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Uterine secretory proteins protect the uterus and conceptuses against infection, facilitate implantation, control cellular damage resulting from implantation, and supply pre-implantation embryos with nutrients. Unlike in humans, the early conceptus of the European polecat (*Mustela putorius*; ferret) grows and develops free in the uterus until implanting at about 12 days after mating. We found that the proteins appearing in polecat uteri changed dramatically with time leading to implantation. Several of these proteins have also been found in pregnant uteri of other eutherian mammals. However, we found a combination of two increasingly abundant proteins that have not been recorded before in pre-placentation uteri. First, the broad-spectrum proteinase inhibitor α_2 -macroglobulin rose to dominate the protein profile by the time of implantation. Its functions may be to limit damage caused by the release of proteinases during implantation or infection, and to control other processes around sites of implantation. Second, lipocalin-1 (also known as tear lipocalin) also increased substantially in concentration. This protein has not previously been recorded as a uterine secretion in pregnancy in any species. If polecat lipocalin-1 has similar biological properties to that of humans, then it may have a combined function in antimicrobial protection and transporting or scavenging lipids. The changes in the uterine secretory protein repertoire of European polecats is therefore unusual, and may be representative of pre-placentation supportive uterine secretions in mustelids (otters, weasels, badgers, mink, wolverines) in general.

Doi: 10.1098/rsos.161085

NUTRITION, FEEDING AND MANAGEMENT**Effects of maternal treatment with β -hydroxy- β -methylbutyrate and 2-oxoglutaric acid on femur development in offspring of minks of the standard dark brown type**

Tomaszewska E.¹, Dobrowolski P.², Świetlicka I.³, Muszyński S.³, Kostro K.⁴, Jakubczak A.⁵, Taszkun I.⁶, Żmuda A.⁴, Rycerz K.⁷, Blicharski T.⁸, Jaworska-Adamu J.⁷

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J Anim Physiol Anim Nutr (Berl). 2017 May 15. Doi: 10.1111/jpn.12742. [Epub ahead of print]

Using energy budgets to combine ecology and toxicology in a mammalian sentinel species

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Process-driven modelling approaches can resolve many of the shortcomings of traditional descriptive and non-mechanistic toxicology. We developed a

simple dynamic energy budget (DEB) model for the mink (*Mustela vison*), a sentinel species in mammalian toxicology, which coupled animal physiology, ecology and toxicology, in order to mechanistically investigate the accumulation and adverse effects of lifelong dietary exposure to persistent environmental toxicants, most notably polychlorinated biphenyls (PCBs). Our novel mammalian DEB model accurately predicted, based on energy allocations to the interconnected metabolic processes of growth, development, maintenance and reproduction, lifelong patterns in mink growth, reproductive performance and dietary accumulation of PCBs as reported in the literature. Our model results were consistent with empirical data from captive and free-ranging studies in mink and other wildlife and suggest that PCB exposure can have significant population-level impacts resulting from targeted effects on fetal toxicity, kit mortality and growth and development. Our approach provides a simple and cross-species framework to explore the mechanistic interactions of physiological processes and ecotoxicology, thus allowing for a deeper understanding and interpretation of stressor-induced adverse effects at all levels of biological organization.

Sci Rep. 2017 Apr 7; 7:46267.

Doi: 10.1038/srep46267.

Estimating population density and connectivity of American mink using spatial capture-recapture

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Ecol Appl. 2016 Jun;26(4): 1125-1135.

Doi: 10.1890/15-0315.

Relationship type affects the reliability of dispersal distance estimated using pedigree inferences in partially sampled populations: A case study involving invasive American mink in Scotland

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HEALTH AND DISEASE

Evolutionary analysis of whole-genome sequences confirms inter-farm transmission of Aleutian mink disease virus

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Aleutian mink disease virus (AMDV) is a frequently encountered pathogen associated with mink farming. Previous phylogenetic analyses of AMDV have been based on shorter and more conserved parts of the genome, e.g. the partial NS1 gene. Such fragments are suitable for detection but are less useful for elucidating transmission pathways while sequencing entire viral genomes provides additional informative sites and often results in better-resolved phylogenies. We explore how whole-genome sequencing can benefit investigations of AMDV transmission by reconstructing the relationships between AMDV field samples from a Danish outbreak. We show that whole-genome phylogenies are much better resolved than those based on the partial NS1 gene sequences extracted from the same alignment. Well-resolved

phylogenies contain more information about the underlying transmission trees and are useful for understanding the spread of a pathogen. In the main case investigated here, the transmission path suggested by the tree structure was supported by epidemiological data. The use of molecular clock models further improved tree resolution and provided time estimates for the viral ancestors consistent with the proposed direction of spread. It was however impossible to infer transmission pathways from the partial NS1 gene tree, since all samples from the case farms branched out from a single internal node. A sliding window analysis showed that there were no shorter genomic regions providing the same phylogenetic resolution as the entire genome. Altogether, these results suggest that phylogenetic analyses based on whole-genome sequencing taking into account sampling dates and epidemiological data is a promising set of tools for clarifying AMDV transmission.

J Gen Virol. 2017 Jun 13.

Doi: 10.1099/jgv.0.000777. [Epub ahead of print]

Distribution of Aleutian mink disease virus contamination in the environment of infected mink farms

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Vet Microbiol. 2017 May; 204:59-63.

Doi: 10.1016/j.vetmic.2017.04.013.
Epub 2017 Apr 14.

Experimental *Pseudomonas aeruginosa* mediated rhino sinusitis in mink

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Int J Pediatr Otorhinolaryngol. 2017 May; 96: 156-163.

Doi: 10.1016/j.ijporl.2016.12.037.
Epub 2016 Dec 27.

Detection of viromes of RNA viruses using the next generation sequencing libraries prepared by three methods

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Virus Res. 2017 Jun 2; 237: 22-26.

Doi: 10.1016/j.virusres.2017.05.003.
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First description of *Cryptosporidium ubiquitum* XIIa subtype family in farmed fur animals

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Epub 2017 Apr 19.

Fatal *Acinetobacter Baumannii* Infection in the critically endangered European mink (*Mustela lutreola*)

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The present study reports the first case of fatal *Acinetobacter baumannii* infection in the critically endangered European mink (*Mustela lutreola*). Gross examination revealed a severe, diffuse hemorrhagic pneumonia and generalized congestion as main features. Microscopically, the main lesions were an acute, severe fibrinous-hemorrhagic pneumonia associated with proliferation of coccobacilli and generalized acute-subacute congestion. Cultures yielded *A. baumannii*; the species was confirmed by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry and the strain presented a multidrug-resistant pattern. The results are not only of conservation concern but also of public health concern given *A. baumannii* is one of the most important pathogens implicated in nosocomial infections in humans.

J Zoo Wildl Med. 2017 Mar; 48(1): 220-223.
Doi: 10.1638/2016-0082.1.

Full genetic characterization and epidemiology of a novel amdoparvovirus in striped skunk (*Mephitis mephitis*)

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Amdoparvovirus is a newly defined parvoviral genus that contains four species (Carnivore amdoparvovirus 1-4), including the well-known Aleutian mink disease virus (AMDV). Amdoparvoviruses cause an immune-associated and often lethal wasting syndrome in Mustelidae and Caninae hosts. In this study, we molecularly investigated amdoparvoviruses detected in 44 striped skunks (*Mephitis mephitis*) found dead in and around Vancouver, British Columbia, Canada. Some of the animals exhibited pathological changes compatible with amdoparvovirus-associated disease. The nearly complete genomic sequence was obtained for seven different strains and our analyses show how this virus, which we named skunk amdoparvovirus (SKAV), should be classified as a separate species within the genus (proposed Carnivore amdoparvovirus 5). We detected co-infections, recombinant genomes, at least three separate viral lineages, and preliminary evidence for geographic

segregation of lineages. Furthermore, we proved that similar viruses, only partially characterized in previous studies and labeled as AMDV, circulate in skunks from other distant areas of North America (Ontario and California) and found evidence for spillover events in mink (*Neovison vison*). Although SKAVs are capable of causing disease in infected animals, a high proportion of sub-clinical infections has been observed, suggesting these animals might act as asymptomatic carriers and pose a threat to wild and captive carnivores. Finally, we highlight the need for more specific diagnostic tests and further molecular investigations to clarify the epidemiology and host- and geographical distributions of amdoparvoviruses in terrestrial carnivores, especially because the whole spectrum of viral diversity in this group is likely still unknown.

Emerg Microbes Infect. 2017 May 10; 6(5): e30.
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The chinchilla as a novel animal model of pregnancy

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Several parameters are important when choosing the most appropriate animal to model human obstetrics, including gestation period, number of fetuses per gestation and placental structure. The domesticated long-tailed chinchilla (*Chinchilla lanigera*) is a well-suited and appropriate animal model of pregnancy that often will carry only one offspring and has a long gestation period of 105-115 days. Furthermore, the chinchilla placenta is of the haemomonochorial labyrinthine type and is therefore comparable to the human villous haemomonochorial placenta. This proof-of-concept study demonstrated the feasibility in laboratory settings, and demonstrated the potential

of the pregnant chinchilla as an animal model for obstetric research and its potential usefulness for non-invasive measurements in the placenta. We demonstrate measurements of the placental and fetal metabolism (demonstrated *in vivo* by hyperpolarized MRI and *in vitro* by qPCR analyses), placental vessels (demonstrated *ex vivo* by contrast-enhanced

CT angiography) and overall anatomy (demonstrated *in vivo* by whole-body CT).

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