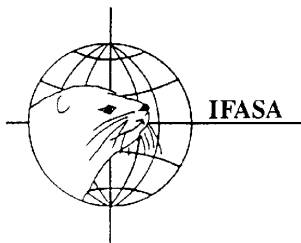
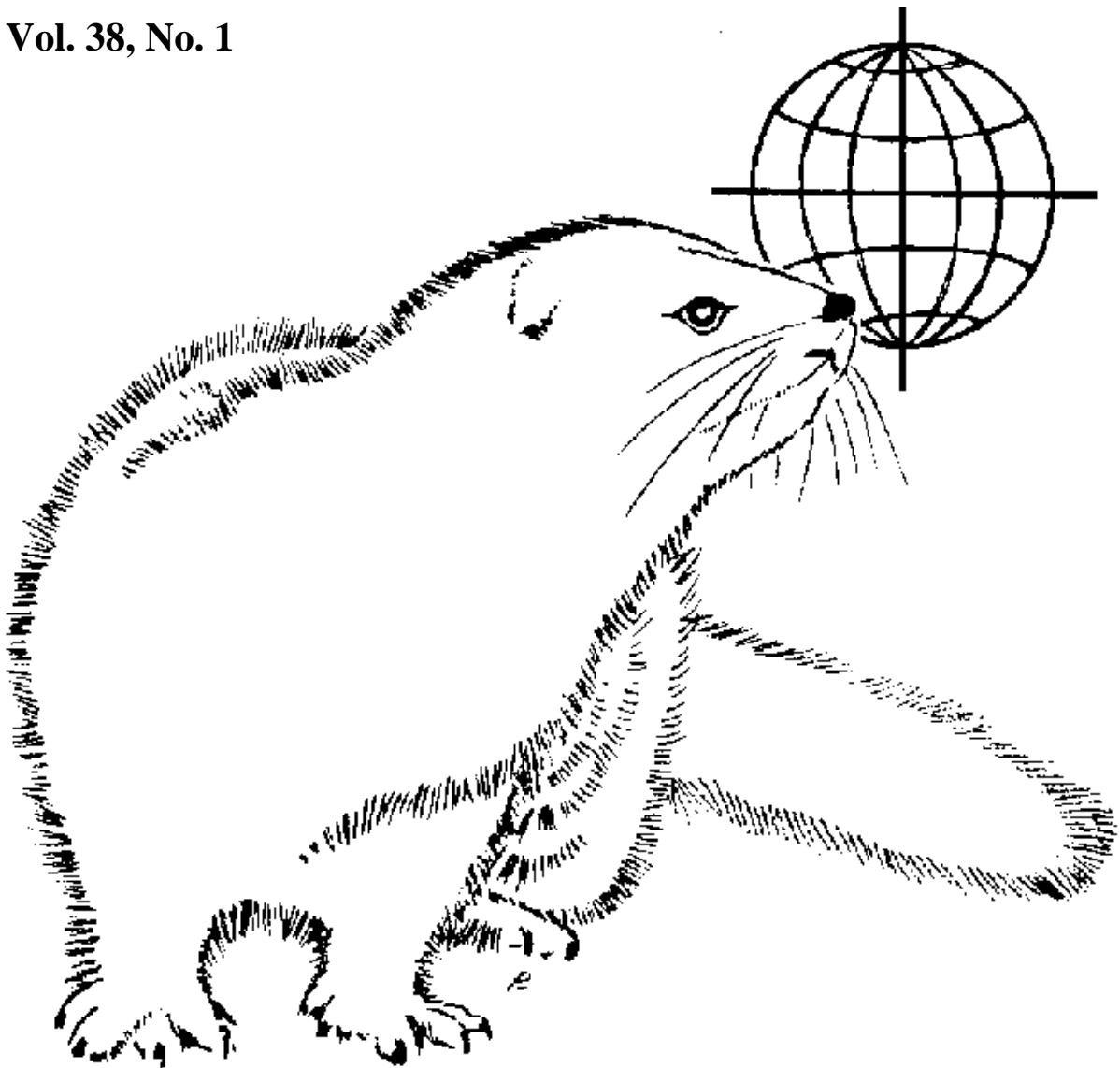


SCIENTIFUR

SCIENTIFIC INFORMATION IN FUR ANIMAL PRODUCTION

Vol. 38, No. 1



INTERNATIONAL FUR ANIMAL SCIENTIFIC ASSOCIATION

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SCIENTIFUR is the contact link between fur animal researchers all over the world and serves as an outlet for scientific and other communication between researchers and others who are interested in the production of fur bearing animals. As such **SCIENTIFUR** contains reports of scientific and applied nature as well as abstracts of information published elsewhere and information regarding congresses, scientific meetings etc.

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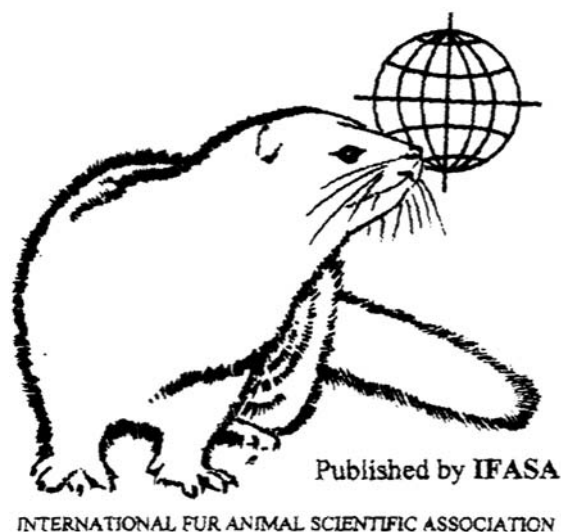
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Notes from the Editor

The 65th Annual Meeting of the European Association of Animal Production (EAAP) will be held in Copenhagen 25-29 August 2014. In this year's congress, there will be several theatre and poster presentations focusing on fur animal research. Furthermore, one of the four technical tours will include a visit to the mink research farm at Copenhagen University and to the Danish fur auction house Kopenhagen Fur, where there e.g. will be presentation of fur grading. Kopenhagen Fur will also man a stand in the hall during the congress. Further information about the congress can be obtained at: <http://www.eaap2014.org/>

The Nordic NJF meeting dealing with all aspects of fur animal research will this year be held in Denmark from 30th September to 3rd October.

Attention should also be given to the Abildgaard Seminar "Mink Health and Welfare", which will take place at Copenhagen University in Denmark 6th to 7th November 2014. The main topics will be fatty liver disease and skin lesions and healing. The subjects will be addressed in oral presentations, posters and workshops. For more information: (hammer@sund.ku.dk).

Many abstracts in this volume of Scientifur deal with diseases. This includes a study of the effect of the feeding intensity on the severity of fatty liver in mink.

Vivi Hunnicke Nielsen
Editor Scientifur

BREEDING, GENETICS AND REPRODUCTION**An American mink (*Neovison vison*) transcriptome**

K. Christensen, R. Anistoroaei

HiSeq2000 Illumina pair-end sequenced transcript data originating from a pool of four different tissues of a wild-type American mink yielded approximately 90 Gb of raw data. Subsequently, unique contigs were assembled by a combined approach using velvet and phrap. Of these assembled contigs, about 136 000 match the dog genome and nearly 30 000 contigs match the human transcriptome at more than 17 000 unique gene locations. Gene annotation for these contigs was performed employing custom-made scripts run in combination with comparative sequence similarity search and alignment in the dog and human genome using blast algorithms. Transcripts representing five genes known to be associated with pigmentation were reliably aligned against large mink genomic contigs derived from BAC clones. Sequence comparison between transcript and genomic data revealed seven SNPs. In this study, we generated and annotated mink transcript sequences representing more than 16 000 known genes. This is the first comprehensive transcriptome for the American mink genome, which will facilitate further development in mink expression profiling studies and provide a good annotation basis in the perspectives of a whole genome sequencing project. The project was deposited at EMBL database with the accession number PRJEB1260.

Anim. Genet. 2014; 45(2): 301-303
doi: 10.1111/age.12113 [Epub 2014: Jan 21.]

<http://www.ncbi.nlm.nih.gov/pubmed/24444022>

Development and characterization of polymorphic microsatellite markers for Chinese raccoon dog (*Nyctereutes procyonoides procyonoides*)

S.Q. Yan, Y.M. Li, C.Y. Bai, X.M. Ding, W.J. Li, J.N. Hou, Z.H. Zhao, J.H. Sun

Chinese raccoon dog (*Nyctereutes procyonoides procyonoides*) is one of the most important fur-bearing animal species. Information about the

genetic background of farmed Chinese raccoon dogs is limited. In this study, 17 polymorphic microsatellite markers were isolated and identified from an (AC)_n-microsatellite-enriched library of Chinese raccoon dogs. The number of alleles per locus ranged from 2 to 8 based on 48 individuals tested. The expected and observed heterozygosity and polymorphism information content per locus ranged from 0.383 to 0.8378, 0.3200 to 0.8696, and 0.3047 to 0.7947, respectively. Cross-species amplification of these loci in 2 other Canidae species indicated that 9 and 11 of these loci could also be amplified successfully in the arctic and silver fox, respectively. These microsatellite loci developed in the present report will provide useful tools for population genetic studies, individual identification, and phylogenetic analysis in the Chinese raccoon dog and other Canidae species.

Genet. Mol. Res. 2013; 12(4): 6351-6355
doi: 10.4238/2013.December.6.2

<http://www.ncbi.nlm.nih.gov/pubmed/24390984>

Foetal life protein provision of mink (*Neovison vison*) changes the relative mRNA abundance of some hepatic enzymes regulating fat metabolism

C.F. Matthiesen, M.A. Casañas, A.H. Tauson

The nutrient provision to pregnant females has high impact on the growth and metabolism of their offspring. The objective was to investigate if the expression of hepatic enzymes regulating the fat metabolism was affected in fetuses and adult female mink born by dams fed either a low or an adequate level of protein during late gestation. The relative abundances of acetyl coenzyme A carboxylase (ACC), fatty acid synthase (FAS) and carnitine palmitoyl transferase 1 (CPT1) mRNA were determined by qualitative polymerase chain reaction in the livers of F0- and F1-generation dams and in F1-generation fetuses. Low protein provision during foetal life resulted in a lower expression of FAS in foetal liver but a tendency towards increased expression in the liver of adult dams. There was a tendency towards an effect of life stage of the animal on the expression of ACC resulting in a higher expression among F1 fetuses exposed to low protein during foetal life than F0 dams fed a low protein diet during late gestation. The expression of CPT1 was significantly lower

among dams exposed to low protein provision during foetal life than controls, possibly indicating a lower rate of mitochondrial β -oxidation. Further investigations are needed to clarify the consequences of these changes for the fat metabolism.

Arch Anim. Nutr. 2014; 68(2): 159-169
doi: 10.1080/1745039X.2014.889506

<http://www.ncbi.nlm.nih.gov/pubmed/24646153>

Ideal body condition improves reproductive performance and influences genetic health in female mink

L. Boudreau, B. Benkel, T. Astatkie, K. Rouvinen-Watt

Anim. Reprod. Sci. 2014; 145(1-2): 86-98
doi: 10.1016/j.anireprosci.2014.01.004
[Epub 2014: Jan 1.]

<http://www.ncbi.nlm.nih.gov/pubmed/24486009>

NUTRITION, FEEDING AND MANAGEMENT

The use of chemical markers for the identification of farm escapees in feral mink populations

M. Brzeziński, A. Zalewski, A. Niemczynowicz, I. Jarzyna, M. Suska-Malawska

Variations in the contaminant burden in feral and ranch mink, resulting from differences in their diet, may permit the identification of farm escapees. However, this is only possible in the case of contaminants that accumulate to significantly different levels in the two groups of animals. The main objective of this study was to identify chemical markers whose concentrations differ between feral and ranch mink, by analyzing the accumulation of 13 chemical elements in liver and kidney samples. Total mercury levels were up to 15-fold higher in kidney, and up to 7-fold higher in liver of feral mink compared with ranch mink. The majority of feral mink samples analyzed for mercury, contained concentrations that ranged from 1 to 5 $\mu\text{g/g}$ in kidney (68 %) and from 1 to 5 $\mu\text{g/g}$ in

liver (70 %). In comparison, the organs of ranch mink had significantly lower levels of mercury: 95 % of kidney samples had concentrations below 1 $\mu\text{g/g}$ and 82 % of liver samples had concentrations below 1 $\mu\text{g/g}$. Small geographical variations in Hg levels were observed in mink from the four studied feral populations. Significant differences in Cu concentrations between ranch and feral mink were also detected, with low variation within the two groups. Less pronounced differences were recorded for other chemical elements. These data suggest that Hg and Cu may be used as chemical markers for the identification of first generation mink farm escapees.

Ecotoxicology. 2014: Feb 27. [Epub ahead of print]

<http://www.ncbi.nlm.nih.gov/pubmed/24573774>

HEALTH AND DISEASE

Diagnosing Aleutian mink disease infection by a new fully automated ELISA or by counter current immunoelectrophoresis: A comparison of sensitivity and specificity

R. Dam-Tuxen, J. Dahl, T.H. Jensen, T. Dam-Tuxen, T. Struve, L. Bruun

J. Virol. Methods. 2014: 199: 53-60
doi: 10.1016/j.jviromet.2014.01.011
[Epub 2014: Jan 23.]

<http://www.ncbi.nlm.nih.gov/pubmed/24462658>

Molecular epidemiology of Aleutian mink disease virus in China

Z. Wang, W. Wu, B. Hu, H. Zhang, X. Bai, J. Zhao, L. Zhang, X. Yan

Virus Res. 2014: 20:184C: 14-19
doi: 10.1016/j.virusres.2014.02.007
[Epub ahead of print]

<http://www.ncbi.nlm.nih.gov/pubmed/24561116>

Monitoring chronic infection with a field strain of Aleutian mink disease virus

T.H. Jensen, A.S. Hammer, M. Chriél

Vet. Microbiol. 2014: 31:168(2-4): 420-427
 doi: 10.1016/j.vetmic.2013.11.041
 [Epub 2013 Dec 16.]

<http://www.ncbi.nlm.nih.gov/pubmed/24389253>

Establishment of stably transfected cells constitutively expressing the full-length and truncated antigenic proteins of two genetically distinct mink astroviruses

M.R. Bidokhti, K. Ullman, T.H. Jensen, M. Chriél, A. Mottahedin, M. Munir, A.M. Andersson, O. Detournay, A.S. Hammer, C. Baule

Astroviruses are becoming a growing concern in veterinary and public health. To date there are no registered vaccines against astrovirus-induced disease, mostly due to the difficulty to cultivate astroviruses to high titer for vaccine development using conventional techniques. As means to circumvent this drawback, we have developed stably transfected mink fetal cells and BHK21 cells constitutively expressing the full-length and truncated capsid proteins of two distinct genotypes of mink astrovirus. Protein expression in these stably transfected cells were demonstrated by strong signals as evaluated by in-situ PLA and IFA, and confirmed by Western blotting. The recombinant full-length and truncated proteins induced a high level of antibodies in mink, evaluated by ELISA, demonstrating their immunogenicity. In a challenge experiment in mink, a reduction in presentation clinical signs and virus shedding was observed in mink kits born from immunized females. The gene integration and protein expression were sustained through cell passage, showing that the used approach is robust and reliable for expression of functional capsid proteins for vaccine and diagnostic applications.

PLoS One. 2013: 23:8(12): e82978, 13 pp.
 doi:10.1371/journal.pone.0082978.eCollection
 2013

<http://www.ncbi.nlm.nih.gov/pubmed/24376619>

Wildlife reservoirs of canine distemper virus resulted in a major outbreak in Danish farmed mink (*Neovison vison*)

R. Trebbien, M. Chriél, T. Struve, C.K. Hjulsager, G. Larsen, L.E. Larsen

A major outbreak of canine distemper virus (CDV) in Danish farmed mink (*Neovison vison*) started in the late summer period of 2012. At the same time, a high number of diseased and dead wildlife species such as foxes, raccoon dogs, and ferrets were observed. To track the origin of the outbreak virus full-length sequencing of the receptor binding surface protein hemagglutinin (H) was performed on 26 CDV's collected from mink and 10 CDV's collected from wildlife species. Subsequent phylogenetic analyses showed that the virus circulating in the mink farms and wildlife were highly identical with an identity at the nucleotide level of 99.45% to 100%. The sequences could be grouped by single nucleotide polymorphisms according to geographical distribution of mink farms and wildlife. The signaling lymphocytic activation molecule (SLAM) receptor binding region in most viruses from both mink and wildlife contained G at position 530 and Y at position 549; however, three mink viruses had an Y549H substitution. The outbreak viruses clustered phylogenetically in the European lineage and were highly identical to wildlife viruses from Germany and Hungary (99.29% - 99.62%). The study furthermore revealed that fleas (*Ceratophyllus sciurorum*) contained CDV and that vertical transmission of CDV occurred in a wild ferret. The study provides evidence that wildlife species, such as foxes, play an important role in the transmission of CDV to farmed mink and that the virus may be maintained in the wild animal reservoir between outbreaks.

PLoS One. 2014: 13:9(1): e85598, 11 pp.
 doi: 10.1371/journal.pone.0085598 eCollection
 2014

<http://www.ncbi.nlm.nih.gov/pubmed/24454897>

Molecular characterization of the small non-structural proteins of parvovirus Aleutian mink disease virus (AMDV) during infection

Q. Huang, Y. Luo, F. Cheng, S.M., Best, M.E. Bloom, J. Qiu

Virology. 2014: 452-453: 23-31
doi: 10.1016/j.virol.2014.01.005
[Epub 2014: Jan 28.]

<http://www.ncbi.nlm.nih.gov/pubmed/24606679>

Establishment of a rescue system for an autonomous Parvovirus mink enteritis virus

D. Yuan, J. Wang, Z. Li, Y. Mao, J.Z. Sun, J. Xi, S. Wang, Q. Hou, B. Yi, W. Liu

Virus Res. 2014: 22:183C: 1-5
doi: 10.1016/j.virusres.2014.01.012
[Epub ahead of print]

<http://www.ncbi.nlm.nih.gov/pubmed/24463297>

The identification, typing, and antimicrobial susceptibility of *Pseudomonas aeruginosa* isolated from mink with hemorrhagic pneumonia

J. Qi, L. Li, Y. Du, S. Wang, J. Wang, Y. Luo, J. Che, J. Lu, H. Liu, G. Hu, J. Li, Y. Gong, G. Wang, M. Hu, Shiganyan, Y. Liu

Vet. Microbiol. 2014: pii: S0378-1135(14)00115-1
doi:10.1016/j.vetmic.2014.02.025
[Epub ahead of print]

<http://www.ncbi.nlm.nih.gov/pubmed/?term=24629901>

High feeding intensity increases the severity of fatty liver in the American mink (*Neovison vison*) with potential ameliorating role for long-chain n-3 polyunsaturated fatty acids

M.F. Dick, J. Hurford, S. Lei, A.M. Mustonen, P. Nieminen, K. Rouvinen-Watt K.

Rapid body fat mobilization, obesity, and an inadequate supply of n-3 polyunsaturated fatty acids

(PUFA) have been suggested to play roles in the etiology of fatty liver in the American mink (*Neovison vison*). This study examined the effects of feeding intensity and dietary fat source on fatty liver induced by fasting. In a multi-factorial design, 3 different fat sources (herring oil, rich in n-3 PUFA, soya oil, rich in n-6 PUFA, and canola oil, rich in n-9 monounsaturated fatty acids) were fed to mink at a low and high feeding intensity for 10 weeks, followed by an overnight or a 5-day fasting treatment to induce fatty liver.

Fasting led to the development of fatty liver with increased severity in the mink fed at the high feeding intensity. The herring oil diet, high in long-chain n-3 PUFA, was found to decrease the severity of fatty liver in the mink at the high feeding intensity.

Preventing excessive weight gain and increasing dietary intake of n-3 long-chain PUFA may help prevent excessive lipid accumulation during prolonged periods of fasting or inappetence by promoting hepatic fatty acid oxidation.

Acta. Vet. Scand. 2014: 56:5: 1-9

doi: 10.1186/1751-0147-56-5

<http://www.ncbi.nlm.nih.gov/pubmed/24438337>

Invasive American Mink: Linking Pathogen Risk Between Domestic and Endangered Carnivores

M.A. Sepúlveda, R.S. Singer, E.A. Silva-Rodríguez, A. Eguren, P. Stowhas, K. Pelican

Infectious diseases, in particular canine distemper virus (CDV), are an important threat to the viability of wild carnivore populations. CDV is thought to be transmitted by direct contact between individuals; therefore, the study of species interactions plays a pivotal role in understanding CDV transmission dynamics. However, CDV often appears to move between populations that are ecologically isolated, possibly through bridge hosts that interact with both species. This study investigated how an introduced species could alter multihost interactions and act as a bridge host in a novel carnivore assemblage of domestic dogs (*Canis familiaris*), invasive American mink (*Neovison vison*), and threatened river otters (*Lontra provocax*) in southern Chile. We found that rural dogs interact with mink near farms whereas in riparian habitats, minks and river otters shared the same latrines with both species visiting

sites frequently within time intervals well within CDV environmental persistence. No interactions were observed between dogs and otters at either location. Both dog and mink populations were serologically positive for CDV, making the pathogen transfer risk to otters a conservation concern. Altogether, introduced mink in this

ecosystem have the potential to act as bridge hosts between domestic dogs and endangered carnivores.

Ecohealth. 2014: Mar 7. [Epub ahead of print]

<http://www.ncbi.nlm.nih.gov/pubmed/24604545>

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SCIENTIFUR/Faculty of Agricultural Sciences, Aarhus University, P.O. Box 14, DK-8830 Tjele, Denmark or

E-mail: Scientifur@agrsci.dk

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Summary/Abstract, which should not exceed 150 words.

Keywords in alphabetic order if not included in the title.

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