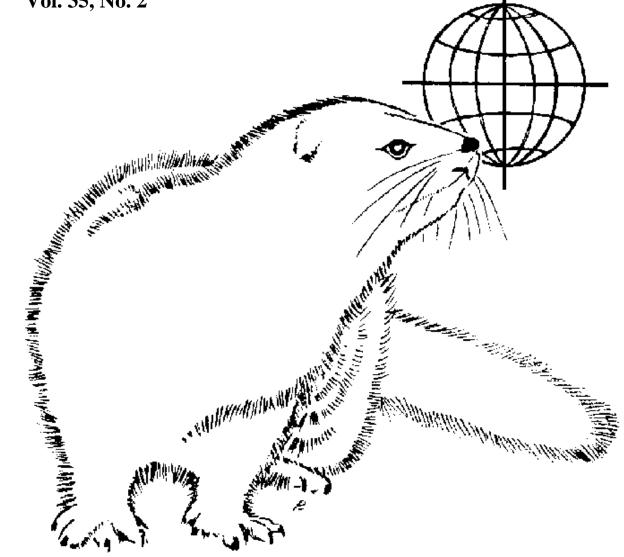
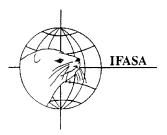
SCIENTIFUR

SCIENTIFIC INFORMATION IN FUR ANIMAL PRODUCTION

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INTERNATIONAL FUR ANIMAL SCIENTIFIC ASSOCIATION

SCIENTIFUR - scientific information in Fur Animal Production.

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Notes from the Editor

This volume of Scientifur presents the preliminary program for the Xth International Scientific Congress in Fur animal Production. The IFASA Congress will be held in Copenhagen in Denmark, August 21-24,2012.

Efficient use of feed is important in fur animal production. Feed expenses make up a considerable part of production costs and inefficient use of feedstuff causes undesirable discharge of nutrients to the environment. Abstracts are presented with suggestion of dietary protein content and selection conditions, respectively which improve feed utilization. Welfare is constantly in focus. The relationship between stress and stereotypic behaviour is reported in another abstract. An abstract demonstrates that mink homozygous for the Aleutian allele show the characteristic formation of abnormally large granules in leukocytes. Furthermore, a new differential diagnostic test is presented that identify the vaccine and fields strains of Canine distemper virus. Another study shows that mink coronavirus possess high genomic variability.

Vivi Hunnicke Nielsen Editor Scientifur



CONGRESS

PRELIMINARY PROGRAM

COPENHAGEN

DENMARK

21.8 — 24.8 2012



PRELIMINARY PROGRAM

TUESDAY AUGUST 21

09.00 - 13.30	Arrival, registration at Copenhagen Scandic
13.30 - 22.00	Pre-congress event at Kopenhagen Fur

WEDNESDAY AUGUST 22

Morning	Opening Ceremony
0	Welcome by Chairman of the Danish Fur Breeders Association / CEO
	Speech by the Danish Agricultural Minister
	Speech by the president of IFASA
	Guest speaker
	Plenary/parallel: Health & Disease
	Moderator: Tove Clausen & Anne Sofie Hammer
12.30 - 13.30	Lunch
Afternoon	Excursion to Kronborg/Frederiksborg/Amalienborg Castle
	Membership meeting and election

THURSDAY AUGUST 23

Morning	Plenary/parallel: Nutrition, Feeding, & Management
	Moderator: Jan Elnif & Tor Michael Lassen
12.00 - 13.00	Lunch
Afternoon	Plenary/parallel: Breeding, Genetics, & Reproduction
	Moderator: Vivi Hunniche Nielsen & Anne-Helene Tauson
	Coffee break
	Plenary/parallel: Theme on "WelFur for mink and foxes"
	Moderator: Steen H. Møller & Jakko Mononen
	Poster session
19.00	Gala Dinner

FRIDAY AUGUST 24

Morning	Plenary/parallel: Behaviour & Welfare
	Moderator: Leif Lau Jeppesen & Steffen W. Hansen
	Closing Ceremony
	best oral presentation and best poster
12.30 - 13.30	Lunch

Plenaries and sessions will be oral presentations.

Special focus themes:

Within the program, we aim to dedicate two to three sessions to pre-defined focus themes, such as: Aleutian disease, N-reduction or Limits to body size and condition. Different aspects of these themes will be approached through presentations from different disciplines such as health, disease, nutrition, feeding, breeding, genetics, behavior, welfare, management & ethics.

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Effects of diets with different protein and dlmethionine levels on the growth performance and N-balance of growing minks

H. Zhang, G.Y. Li, E.J. Ren, X.M Xing, Q Wu, F.H. Yang

This study was performed to evaluate the effects of diets with different protein and dl-methionine (Met) levels on nitrogen (N) retention, nutrient digestibility, growth performance, and some blood parameters in growing minks. Eighty healthy male minks were selected and randomly divided into five groups with different types of diet. The dietary protein levels, expressed as percentage of dry matter (DM), were 36% (HP) and 28% (LP), corresponding to average 363g and 295g protein/kg DM, respectively. LP was supplemented with Met (0.3%), 0.6% and 0.9% DM); the codes were LP+M1, LP+M2 and LP+M3, respectively. From July to middle of September, the average daily gain and feed: gain ratio (F/G) of the minks that received the diet with 0.6% Met added to the low protein diet was better than feeding HP and other groups. Fecal N and Urinary N of group LP+M2 were the lowest one, in contrast, the daily retention of N was the highest one. Digestibility of DM and CP were not affected by different diets, but digestibility of fat declined with dietary protein level decreasing. Serum urea nitrogen (SUN) was affected by different protein and Met levels. Considering all factors the best performance could be observed offering LP+M2, the prime level of Met was 13.87 g/kg DM in dietary, and 258.5 g digestible protein kg(-1) DM was enough for mink in growing period. Furthermore, addition of Met in low protein diets for minks would be beneficial in terms of reduced feed expenses and lower nitrogen emissions to the environment.

J Anim Physiol Anim Nutr (Berl), 2011: Jun 3. doi: 10.1111/j.1439-0396.2011.01160.x. [Epub ahead of print]

Response to selection and genotype-environment interaction in mink (*Neovison vison*) selected on ad libitum and restricted feeding

V.H. Nielsen, S.H. Møller, B.K. Hansen, P. Berg

Mink were selected for high November weight (AL line) and low feed conversion ratio (FC line) on ad

libitum feeding and for high November weight on restricted feeding (RF line). After three generations of selection, the average estimated breeding value for November weight was 533, 326, and 150 g in males and 168, 82, and -85 g in females in the AL, RF, and FC lines. The breeding value for feed conversion ratio was -1.39, -0.84 and -0.68 kg feed kg⁻¹ gain in males and -0.39, -0.31 and -0.23kg feed kg⁻¹ gain in females in the selection lines. In generation 4, the AL, RF and FC lines were tested on both ad libitum and restricted feeding. The estimated breeding value for November weight in males in the AL line (533 g) was significantly greater than that in the RF line (384 g) on ad libitum feeding. The corresponding values on restricted feeding were 297 and 326 g, respectively, which were not significantly different. This indicates genotype×environment interaction. In the AL line, selection improved feed conversion ratio by increased appetite. In the RF line, it was improved by increased feed utilization. Environmental sensitivity in males, estimated from breeding values for November weight was 236 g in the AL line and 58 g in the RF line suggesting that the RF line was more robust to changes in feeding conditions. A smaller litter size in the AL line (4.1) than in the RF line (5.6) indicates that selection for large weight affects reproduction.

Can J Anim Sci, 2011: 91(2), 231-237

On the origin of a domesticated species: Identifying the parent population of Russian silver foxes (*Vulpes vulpes*)

M.J. Statham, L.N. Trut, B.N. Sacks, A.V. Kharlamova, I.N. Oskina, R.G. Gulevich, J.L. Johnson, S.V. Temnykh, G.M. Acland, A.V. Kukekova

The foxes at Novosibirsk, Russia, are the only population of domesticated foxes in the world. These domesticated foxes originated from farm-bred silver foxes (Vulpes vulpes), whose genetic source is unknown. In this study we examined the origin of the domesticated strain of foxes and two other farmbred fox populations (aggressive and unselected) maintained in Novosibirsk. To identify the phylogenetic origin of these populations we sequenced two regions of mtDNA, cytochrome b and D-loop, from 24 Novosibirsk foxes (8 foxes

from each population) and compared them with corresponding sequences of native red foxes from Europe, Asia, Alaska and Western Canada, Eastern Canada, and the Western Mountains of the USA. We identified seven cytochrome b - D-loop haplotypes in Novosibirsk populations, four of which were previously observed in Eastern North America. The three remaining haplotypes differed by one or two base change from the most common haplotype in Eastern Canada. $\Phi(ST)$ analysis showed significant differentiation between Novosibirsk populations and red fox populations from all geographic regions except Eastern Canada. No haplotypes of Eurasian origin were identified in the Novosibirsk populations. These results are consistent with historical records indicating that the original breeding stock of farm-bred foxes originated from Prince Edward Island, Canada. Mitochondrial DNA data together with historical records indicate two stages in the selection of domesticated foxes: the first includes captive breeding for ~50 years with unconscious selection for behaviour; the second corresponds to over 50 further years of intensive selection for tame behaviour.

Biol J Linn Soc Lond, 2011: 103(1), 168-175

Stress and stereotypic behaviour in mink (*Mustela vison*): A focus on adrenocortical activity

J. Malmkvist, L.L. Jeppesen, R. Palme

We examined whether female mink with low (LS) and high (HS) occurrence of stereotypic behaviour differ in their adrenocortical activity in baseline conditions or in response to immobilisation (Experiment 1), handling, adrenocorticotropic hormone (ACTH) challenge (Experiment 2) and excretion of circulating cortisol (Experiment 3). Faeces are the predominating excretory route of cortisol (83%), with peak concentrations after 4.2 h (urine: 3.4 h). Faecal cortisol metabolites (FCMs) reflected changes in relation to handling/ACTH challenge. In Experiment 1 (n = 162), HS mink had approximately 54% higher baseline level of FCM than LS mink (P < 0.001), with markedly elevated FCM on the days after an immobilisation stressor. In Experiment 2 (n = 48), LS and HS mink did not differ in adrenocortical activity after an ACTH challenge. However, HS mink reacted more in response to handling, evident in the FCM level 4-20 h after the handling (P = 0.001). In Experiment 3 (n = 16), the excretion of infused (3)H-cortisol did not differ between LS and HS mink. Stereotypic behaviour is concurrent with higher baseline concentrations of FCM, which cannot be explained by a greater adrenocortical reactivity or a different excretion of the circulating cortisol. Instead, we conclude that mink with a high level of stereotypic behaviour have a greater perception of stress, or increased sensitivity to stressors at the pituitary level.

Stress, 2011: Mar 27. [Epub ahead of print]

Pregnancy Detection in Putatively Unmated Mink (*Mustela vison*) by Serum Progesteron Level

L. Felska-Blaszczyk, B. Lasota, M. Sulik, A. Maslowska, M. Dziadosz, B. Blaszczyk, P. Blaszczyk

The aim of this study was to determine whether blood plasma progesterone is a reliable indicator of pregnancy in mink at an early stage of gestation. We also attempted to establish the threshold value of progesterone as a pregnancy indicator. The analysis was carried out at a production farm on 42 standard female mink aged 1 year, which were grouped both according to the observed success of mating ("mated" and "unmated") and the level of blood progesterone measured afterwards serum ("pregnant" and "nonpregnant"). It was next verified whether a particular female had been assigned to the proper group in the first place. An analysis of accuracy of mating success assessment within the group of unmated females revealed that more than one-third of decisions were wrong, since some females that had been considered unmated ultimately whelped. This suggests that mating supervision by farm workers lacks reliability. A progesterone test for verification of such management decisions should limit the risk of error. We suggest that progesterone tests could be carried out using the threshold values 1.9 ng/ml and 20 ng/ml in blood sampled on 25 March and 8 April, respectively, although some level of uncertainty should be taken into account.

J Reprod Dev, 2011: Mar 8. [Epub ahead of print]

Effect of mutations affecting coat color on the blood lymphocyte structure in the American mink (*Mustela vison* Schreber, 1777)

L.B. Uzenbaeva, O.V. Trapezov, A.G. Kizhina, V.A. Iliukha, L.I. Trapezova, N.N. Tiutiunnik

American minks with different genotypes containing the Aleutian coat color allele in the homozygous state, including the single recessive Aleutian (a/a); double recessive sapphire (a/a p/p)and lavender (m/m a/a); triple recessive violet (m/m a/a p/p); and dominant-recessive cross sapphire (S/+ a/a p/p), sapphire leopard (S(K)/+ a/a p/p), and shadow sapphire (S(H)/+ a/a p/p) minks, as well as American minks without the Aleutian allele, including the standard (+/+); single recessive silverblue (p/p) and hedlund-white (h/h); double recessive pearl (k/k p/p), Finnish topaz (t(S)/t(S) b/b); incompletely dominant royal silver (S(R)/+), standard leopard (S(K)/+), and black crystal (C(R)/+); and dominant-recessive snowy topaz (C(R)/+ t(S)/t(S) b/b) and Kujtezhy-spotted (S(K)/+b/b) minks have been studied. Homozygosity for the a allele has been found to disturb the subcellular structure of leukocyte, namely the formation of abnormally large granules.

Genetika, 2011: 47(1), 87-94

Differentiation of canine distemper virus isolates in fur animals from various vaccine strains by reverse transcription-polymerase chain reactionrestriction fragment length polymorphism according to phylogenetic relations in china

F. Wang, X. Yan, X. Chai, H. Zhang, J. Zhao, Y. Wen, W. Wu

In order to effectively identify the vaccine and field strains of Canine distemper virus (CDV), a new differential diagnostic test has been developed based on reverse transcription-polymerase chain reaction (RT-PCR) and restriction fragment length polymorphism (RFLP). We selected an 829 bp fragment of the nucleoprotein (N) gene of CDV. By RFLP analysis using BamHI, field isolates were distinguishable from the vaccine strains. Two fragments were obtained from the vaccine strains by RT-PCR-RFLP analysis while three were observed in the field strains. An 829 nucleotide region of the CDV N gene was analyzed in 19 CDV field strains

isolated from minks, raccoon dogs and foxes in China between 2005 and 2007. The results suggest this method is precise, accurate and efficient. It was also determined that three different genotypes exist in CDV field strains in fur animal herds of the north of China, most of which belong to Asian type. Mutated field strains, JSY06-R1, JSY06-R2 and JDH07-F1 also exist in Northern China, but are most closely related to the standard virulent strain A75/17, designated in Arctic and America-2 genetype in the present study, respectively.

Virol J, 2011: 8, 85

Histopathologic and immunohistochemical lesions in liver of mink infected with Aleutian disease virus

A. Valdovska, M. Pilmane

Parvovirus of Aleutian disease causes mainly damage to kidneys, but immune complexes deposition and damage may occur also in other organs. In mink farms of Latvia the liver dystrophy or hepatic lipidosis of mink is widely distributed. The goal of this study was to examine probability of liver damage and regeneration of mink infected with Aleutian disease virus. Liver injury was assessed histologically. The mink liver demonstrated inflammation of liver parenchyma and foci of fatty liver. In immunohistochemistry, during liver regeneration the matrix metalloproteinases MMP-9, vascular endothelial growth factor and beta-defensin 2 expressions were lower, but MMP-2 and nerve growth factor receptor p75 expression was increased.

Pol J Vet Sci, 2011:14(1), 69-76

Molecular characterization of a new species in the genus Alphacoronavirus associated with mink epizootic catarrhal gastroenteritis

A.N. Vlasova, R. Halpin, S. Wang, E. Ghedin, D.J. Spiro, L.J. Saif

A coronavirus (CoV) previously shown to be associated with catarrhal gastroenteritis in mink (Mustela vison) was identified by electron microscopy in mink faeces from two fur farms in

Wisconsin and Minnesota in 1998. A pancoronavirus and a genus-specific RT-PCR assay were used initially to demonstrate that the newly discovered mink CoVs (MCoVs) were members of the genus Alphacoronavirus. Subsequently, using a random RT-PCR approach, full-genomic sequences were generated that further confirmed that, phylogenetically, the MCoVs belonged to the genus Alphacoronavirus, with closest relatedness to the recently identified but only partially sequenced (fragments of the polymerase, and full-length spike, 3c, envelope, nucleoprotein, membrane, 3x and 7b genes) ferret enteric coronavirus (FRECV) and coronavirus (FRSCV). ferret systemic The molecular data presented in this study provide the first genetic evidence for a new coronavirus associated with epizootic catarrhal gastroenteritis outbreaks in mink and demonstrate that MCoVs possess high genomic variability and relatively low overall nucleotide sequence identities (91.7%) between contemporary strains. Additionally, the new MCoVs appeared to be phylogenetically distant from human (229E and NL63) and other alphacoronaviruses and did not belong to the species Alphacoronavirus 1. It is proposed that, together with the partially sequenced FRECV and FRSCV, they comprise a new species within the genus Alphacoronavirus.

J Gen Virol, 2011: 92, 1369-79

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Keywords in alphabetic order if not included in the title.

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