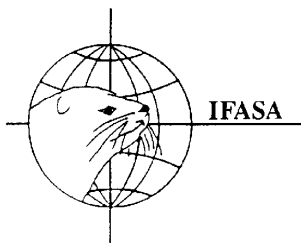
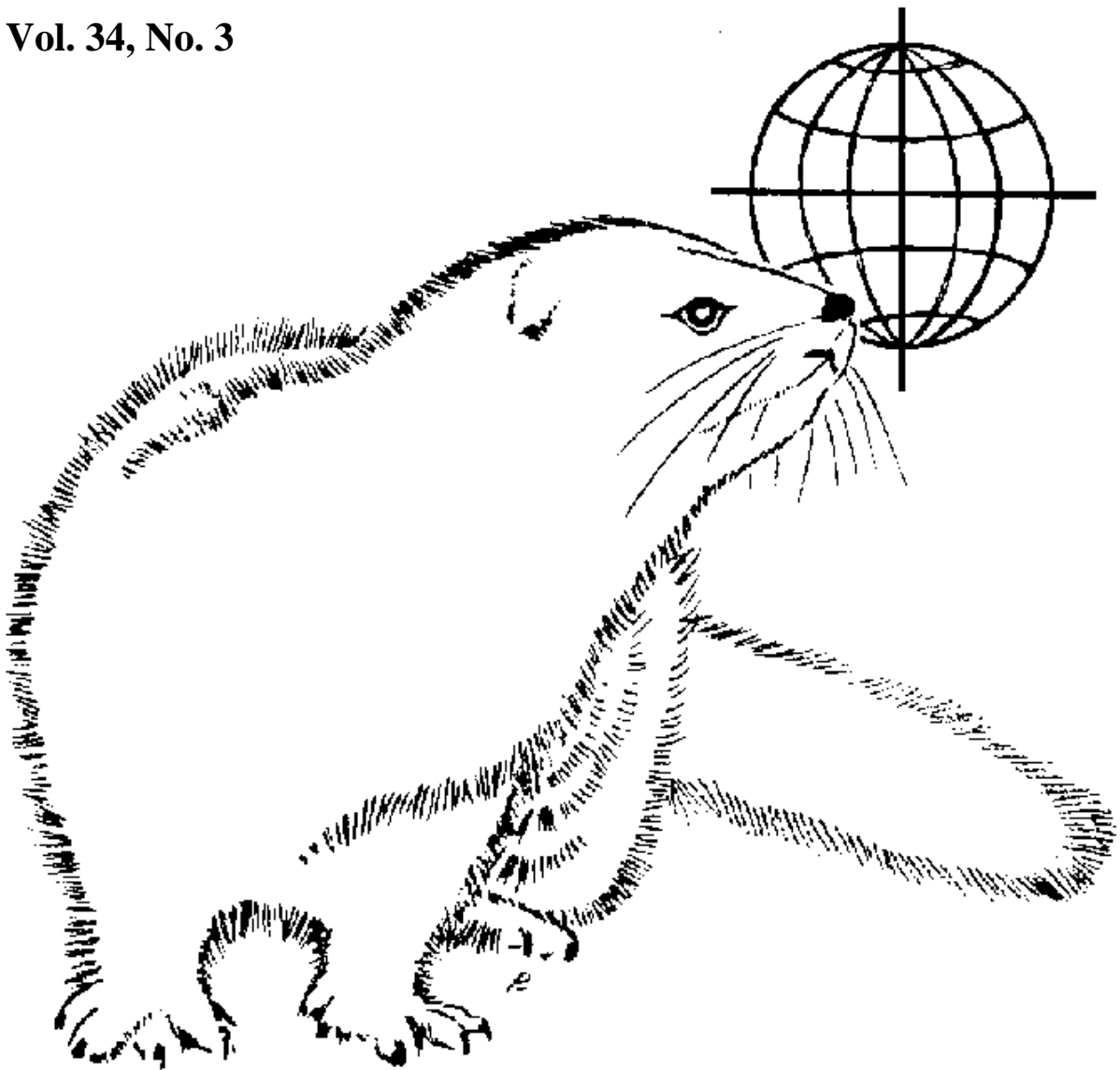


SCIENTIFUR

SCIENTIFIC INFORMATION IN FUR ANIMAL PRODUCTION

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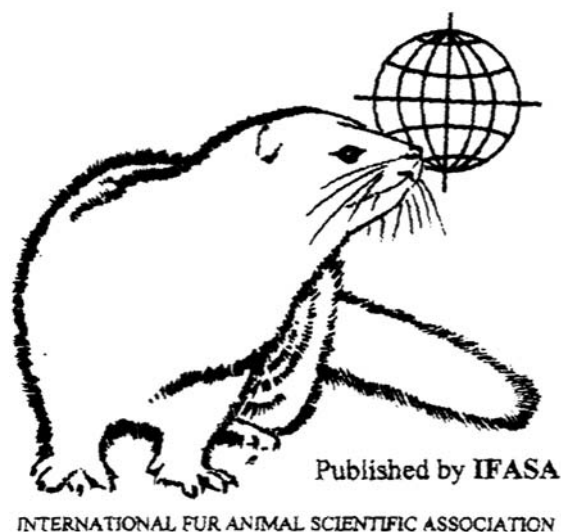
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1.	Contents	31
2.	Notes	33
3.	Abstracts	35
	Animal evolution during domestication: the domesticated fox as a model	35
	<i>L. Trut, I. Oskina, A. Kharlamova</i>	
	Stereotypic behaviour in farm mink (<i>Neovision vison</i>) can be reduced by selection	35
	<i>B.K. Hansen, L.L. Jeppesen, P. Berg</i>	
	Effect of late gestation low protein supply to mink (<i>Mustela vison</i>) dams on reproductive performance and metabolism of dam and offspring	35
	<i>C.F. Matthiesen, D. Blache, P.D. Thomsen, N.E. Hansen, A.H. Tauson</i>	
	Feeding mink (<i>Neovision vison</i>) a protein-restricted diet during pregnancy induces higher birth weight and altered hepatic gene expression in the F(2) offspring	36
	<i>C.F. Matthiesen, D. Blache, P.D. Thomsen, A.H. Tauson</i>	
	Rapid development of fasting-induced hepatic lipidosis in the American mink (<i>Neovision vison</i>): effects of food deprivation and re-alimentation on body fat depots, tissue fatty acid profiles, hematology and endocrinology	36
	<i>K. Rouvinen-Watt, A.M. Mustonen, R. Conway, C. Pal, L. Harris, S. Saarela, U. Strandberg, P. Nieminen</i>	
	Effects of monorecessive and double recessive mutations affecting coat color on the monoamine content of the brain of the American mink (<i>Mustela vison</i> Schreber, 1777)	37
	<i>O.V. Trapezov, L.I. Trapezova, T.A. Alekhina, D.V. Klochkow, Iu.N. Ivanov</i>	
	Association analysis between SNPs of the growth hormone receptor gene and growth traits in arctic fox	37
	<i>Z.H. Du, Z.Y. Liu, X.J. Bai</i>	
	Association of MC3R gene polymorphisms with body weight in the red fox and comparative gene organization in four canids	37
	<i>A. Skorczyk, K. Flisikowski, M. Szydlowski, J. Cieslak, R. Fries, M. Switonski</i>	

A survey of Aleutian mink disease virus infection of feral American mink in Nova Scotia	38
<i>A.H. Farid, P. Rupasinghe, J.L. Mitchell, K. Rouvinen-Watt</i>	
The capsid proteins of Aleutian mink disease virus activate caspases and are specifically cleaved during infection	38
<i>F. Cheng, A.Y. Chen, S.M. Best, M.E. Bloom, D. Pintel, J. Qiu</i>	
Molecular analysis of the nucleoprotein gene of canine distemper virus isolated from clinical cases of the disease in foxes, minks and dogs	38
<i>L. Adaszek, S. Winiareczyk, J. Maj, L. Jankowski, A. Zietek-Barszcz, M. Skrzypczak</i>	
Analysis of the vp2 gene sequence of a new mutated mink enteritis parvovirus strain in PR China	39
<i>J. Zuo, J. Rao, H. Xu, L. Ma, B. Li, Y. Wang, X. Cai, W. Han, L. Lei, B. Liu</i>	
Detection of a novel astrovirus in brain tissue of mink suffering from shaking mink syndrome using viral metagenomics	39
<i>A.L. Blomström, F. Widén, A.S. Hammer, S. Belák, M. Berg</i>	
Outbreak of neonatal diarrhea in farmed mink kits (<i>Mustella vison</i>) associated with enterotoxigenic <i>Staphylococcus delphini</i>	40
<i>D.G. Sledge, P.K. Danieu, C.A. Bolin, S.R. Bolin, A. Lim, B.C. Anderson, M. Kiupel</i>	
Detection of <i>Neospora caninum</i> from farm-bred young blue foxes (<i>Alopex lagopus</i>) in China	40
<i>X. Yu, N. Chen, D. Hu, W. Zhang, X. Li, B. Wang, L. Kang, X. Li, Q. Liu, K. Tian</i>	
4. Symposiums, congresses etc.	41
Actual Fur Research 2010	
Meeting at the Faculty of Agricultural Sciences, Aarhus University, Denmark	
Hunting fur trait genes	41
<i>V.H. Nielsen, R.M. Anistoroaei, B. Guldbrantsen, K. Christensen, M. Fredholm</i>	
Correlations between feed efficiency, activity and health	41
<i>B.M. Damgaard, S.W. Hansen</i>	
A metabolomic approach to describe the metabolism in mink	41
<i>M.S. Hedemann</i>	
Measurement of stress in Mink	42
<i>J. Malmkvist</i>	
Influence of fibre in diet on mating behaviour and reproduction success	42
<i>A. Spangberg, J. Malmkvist</i>	
Health and welfare in mink – New Danish rules and initiatives	42
<i>S.H. Møller</i>	
Why environmental enrichment and does it improve the welfare of the mink?	43
<i>S.W. Hansen</i>	
Is selection for reduced aggression in group housing possible?	43
<i>P. Berg, S.H. Møller</i>	

Notes from the Editor

Studies in fur animals cover many research areas. It appears from the abstracts published in this issue of *Scientifur*. A study is performed to study domestication using the domesticated fox as a model. In another study, it is shown that behaviour may be changes by selection. It is also shown that a sub-optimal diet during pregnancy may influence birth weight in the following generations in mink. The effect of food deprivation and re-alimentation is reported in another abstract. Furthermore, associations between gene polymorphisms and growth traits are shown. Knowledge of pathogens and control of diseases is essential.

Abstracts are given describing studies of Aleutian mink disease virus, canine distemper virus, mink enteritis parvovirus, a new astrovirus, *Staphylococcus delphini* and *Neospora caninum*.

At the yearly meeting at the Faculty of Agricultural Sciences, Aarhus University, Denmark held 21th September results of the most recent Danish fur animal research are presented for the fur animal industry and fur animal production advisors. This issue of *Scientifur* brings abstracts from this meeting.

Vivi Hunnicke Nielsen
Editor *Scientifur*

Animal evolution during domestication: the domesticated fox as a model

L. Trut, I. Oskina, A. Kharlamova

We review the evolution of domestic animals, emphasizing the effect of the earliest steps of domestication on its course. Using the first domesticated species, the dog (*Canis familiaris*), for illustration, we describe the evolutionary peculiarities during the historical domestication, such as the high level and wide range of diversity. We suggest that the process of earliest domestication via unconscious and later conscious selection of human-defined behavioral traits may accelerate phenotypic variations. The review is based on the results of a long-term experiment designed to reproduce early mammalian domestication in the silver fox (*Vulpes vulpes*) selected for tameability or amenability to domestication. We describe changes in behavior, morphology and physiology that appeared in the fox during its selection for tameability, which were similar to those observed in the domestic dog. Based on the data of the fox experiment and survey of relevant data, we discuss the developmental, genetic and possible molecular genetic mechanisms underlying these changes. We ascribe the causative role in evolutionary transformation of domestic animals to the selection for behavior and to the neurospecific regulatory genes it affects.

Bioessays 2009, 31(3), 349-360

Stereotypic behaviour in farm mink (*Neovision vision*) can be reduced by selection

B.K. Hansen, L.L. Jeppesen, P. Berg

In this article we present the first estimation of genetic variation of stereotypic behaviour (SB). Stereotypic behaviour is defined as an unvarying behaviour without any specific goal or function repeated at least five times. All types of SB were included in the analyses. Altogether 1484 adult mink females of the brown colour type were assessed for behaviour traits: SB, active or inactive behaviour, staying in nest box. Genetic correlations were based on estimates of additive genetic (co)variances obtained from a trivariate linear animal model fitted to behaviour traits, body weight

and litter size. The SB has an intermediate genetic variation (h^2 approximately 0.3) and divergent selection for SB confirmed that the frequency of SB can be altered by selection. The results confirmed the hypotheses of negative genetic correlation between SB and body weight and negative genetic correlation between body weight and litter size. The hypotheses of positive correlation between SB and active behaviour and SB and litter size were not confirmed. Consequences of selection for reduced SB can be changes in other behaviour traits, body weight and litter size, depending on the genetic correlation between the traits.

J Anim Breed Genet, 2010: 127(1), 64-73

Effect of late gestation low protein supply to mink (*Mustela vison*) dams on reproductive performance and metabolism of dam and offspring

C.F. Matthiesen, D. Blache, P.D. Thomsen, N.E. Hansen, A.H. Tauson

Protein malnutrition in utero that induces permanent changes in metabolism has been investigated intensively in various animals in recent years, but to the best of our knowledge, not yet in the mink, a strict carnivore. In the present study, minks were fed either a low-protein (LP) diet, i.e., with a protein:fat:carbohydrate ratio of 14:51:35% of metabolisable energy (ME), or an adequate-protein diet (AP), i.e. 29:56:15% of ME, from when implantation was completed until parturition (17.9 +/- 3.6 days). Respiration and balance experiments were performed during both gestation and lactation. Plasma concentrations of leptin, IGF-1, and insulin were determined by radioimmunoassay; the relative abundances of glucose-6-phosphatase (G-6-Pase), fructose-1,6-bisphosphatase (Fru-1,6-P2ase), phosphoenol-pyruvate carboxykinase (PEPCK), and pyruvate kinase (PKM2) were determined in liver, and abundances of adiponectin and leptin in adipose tissue were determined by real-time quantitative PCR (q PCR). The protein supply only affected quantitative metabolism traits during the period of differentiated feeding. The dietary composition was reflected in the nitrogen metabolism and substrate oxidation, but no effects remained during lactation. The LP dams tended to have a smaller liver mass in relation to body weight than did AP dams (2.5% vs.

2.9%; $p = 0.09$), significantly less leptin mRNA ($p < 0.05$), and 30.6% fewer kits per mated female ($p = 0.03$). Furthermore, F1-generation kits exposed to protein restriction during foetal life (FLP1; 10.3 g) had a lower birth weight ($p = 0.004$) than did F1-generation kits exposed to adequate protein (FAP1; 11.3 g). Differences remained significant until 21 days of age (120.4 g vs. 127.6 g; $p = 0.005$). The FLP1 foetuses displayed a lower abundance of Fru-1,6-P2ase mRNA ($p = 0.007$) and of PKM2 mRNA ($p = 0.002$) than did FAP1 foetuses. Whether these changes during foetal life cause permanent changes in the glucose homeostasis of the offspring and result in the transmission of epigenetic phenotypic changes, as seen in the rat, needs further investigation.

Arch Anim Nutr, 2010: 64(1), 56-76

Feeding mink (*Neovision vison*) a protein-restricted diet during pregnancy induces higher birth weight and altered hepatic gene expression in the F(2) offspring

C.F. Matthiesen, D. Blache, P.D. Thomsen, A.H. Tauson

Malnutrition during foetal life can induce modifications in the phenotype of an individual. The present study aimed to observe effects of low foetal life protein provision on modifications of the phenotype and changes in the progeny of 1-year-old female mink (F(1) generation) offspring of mothers fed a low-protein diet. Traits studied included reproductive performance, energy and protein metabolism, and key hepatic enzymes associated with glucose homeostasis and metabolic hormones. The F(0) generation offspring were fed either a low-protein (14 % of metabolisable energy (ME) from protein - FLP1) or an adequate-protein (29 % of ME from protein - FAP1) diet for the last 17.9 (sd 3.6) d of gestation. The F(1) dams were studied at birth and at 1 year of age, during their first reproductive cycle, after maintenance on an adequate diet from birth and thereafter. Metabolic traits during gestation and lactation were largely unaffected by foetal life protein provision, but birth weight in the F(2) generation was higher ($P = 0.003$) among FLP2 kits than among FAP2 kits. Furthermore, the relative abundance of pyruvate kinase mRNA was significantly ($P=0.007$) lower, and fructose-1,6-

bisphosphatase mRNA tended ($P=0.08$) to be lower in FLP2 foetuses than in FAP2 foetuses, showing some similar difference in the F(2) generation and F(1) generation foetuses, suggesting an effect on some hepatic enzymes affecting glucose homeostasis being transmitted from the F(1) to the F(2) generation. These findings indicate that even though energy and nitrogen metabolism displayed no effect of protein provision during early life, programming effects still appeared at the molecular level in the following generation.

Br J Nutr, 2010: 104(4), 544-553

Rapid development of fasting-induced hepatic lipidosis in the American mink (*Neovision vison*): effects of food deprivation and re-alimentation on body fat depots, tissue fatty acid profiles hematology and endocrinology

K. Rouvinen-Watt, A.M. Mustonen, R. Conway, C. Pal, L. Harris, S. Saarela, U. Strandberg, P. Nieminen

Hepatic lipidosis is a common pathological finding in the American mink (*Neovision vison*) and can be caused by nutritional imbalance due to obesity or rapid body weight loss. The objectives of the present study were to investigate the timeline and characterize the development of hepatic lipidosis in mink in response to 0-7 days of food deprivation and liver recovery after 28 days of re-feeding. We report here the effects on hematological and endocrine variables, body fat mobilization, the development of hepatic lipidosis and the alterations in the liver lipid classes and tissue fatty acid (FA) sums. Food deprivation resulted in the rapid mobilization of body fat, most notably visceral, causing elevated hepatosomatic index and increased liver triacylglycerol content. The increased absolute amounts of liver total phospholipids and phosphatidylcholine suggested endoplasmic reticulum stress. The hepatic lipid infiltration and the altered liver lipid profiles were associated with a significantly reduced proportion of n-3 polyunsaturated FA (PUFA) in the livers and the decrease was more evident in the females. Likewise, re-feeding of the female mink resulted in a more pronounced recovery of the liver n-3 PUFA. The rapid decrease in the n-3/n-6 PUFA ratio in response to food deprivation could trigger an inflammatory

response in the liver. This could be a key contributor to the pathophysiology of fatty liver disease in mink influencing disease progression.

Lipids, 2010: 45(2), 111-128

Effects of monorecessive and double recessive mutations affecting coat color on the monoamine content of the brain of the American mink (*Mustela vison Schreber, 1777*)

O.V. Trapezov, L.I. Trapezova, T.A. Alekhina, D.V. Klochkow, Iu.N. Ivanov

The effects of mutations affecting the coat color on the dopamine, noradrenaline, and serotonin contents of the hypothalamus and brainstem of the American mink have been studied. The sample comprised standard (+/+) and mutant minks, including the monorecessive pastel (b/b), silver-blue (p/p), and white hedlund (h/h) and the combination double recessive sapphire (a/a p/p) and pearl (k/k p/p) ones. The dopamine content of the brainstem of the monorecessive pastel (b/b) and silver-blue (p/p) minks has been found to be higher than in standard (+/+) minks. Conversely, the homozygosity for two coat color loci in double recessive pearl minks (k/k p/p) significantly decreases the noradrenaline and serotonin contents of the hypothalamus. In addition, monorecessive and double recessive minks differ from each other in the serotonin contents of the midbrain and medulla.

Genetika 2009: 45(12), 1641-1645

Association analysis between SNPs of the growth hormone receptor gene and growth traits in arctic fox

Z.H. Du, Z.Y. Liu, X.J. Bai

Using single-strand conformation polymorphism (PCR-SSCP) and DNA sequencing, single nucleotide polymorphisms (SNPs) of growth hormone receptor (GHR) gene were detected in an arctic fox population. Correlation analysis between GHR polymorphisms and growth traits were carried out using the appropriate model. Four SNPs, G3A in the 5'UTR, C99T in the first exon, T59C and G65A

in the fifth exon were identified on the arctic fox GHR gene. The G3A and C99T polymorphisms of GHR were associated with female fox body weight (P<0.05) and the T59C and G65A polymorphisms of GHR were associated with male fox body weight (P<0.05) and the skin length of the female fox (P<0.01). Therefore, marker assisted selection on body weight and skin length of arctic foxes using these SNPs can be applied to get big and high quality arctic foxes.

Yi Chuan, 2010: 32(6), 599-605

Association of MC3R gene polymorphisms with body weight in the red fox and comparative gene organization in four canids

A. Skorzcyk, K. Flisikowski, M. Szydlowski, J. Cieslak, R. Fries, M. Switonski

There are five genes encoding melanocortin receptors. Among canids, the genes have mainly been studied in the dog (MC1R, MC2R and MC4R). The MC4R gene has also been analysed in the red fox. In this report, we present a study of chromosome localization, comparative sequence analysis and polymorphism of the MC3R gene in the dog, red fox, arctic fox and Chinese raccoon dog. The gene was localized by FISH to the following chromosome: 24q24-25 in the dog, 14p16 in the red fox, 18q13 in the arctic fox and NPP4p15 in the Chinese raccoon dog. A high identity level of the MC3R gene sequences was observed among the species, ranging from 96.0% (red fox - Chinese raccoon dog) to 99.5% (red fox - arctic fox). Altogether, eight polymorphic sites were found in the red fox, six in the Chinese raccoon dog and two in the dog, while the arctic fox appeared to be monomorphic. In addition, association of several polymorphisms with body weight was analysed in red foxes (the number of genotyped animals ranged from 319 to 379). Two polymorphisms in the red fox, i.e. a silent substitution c.957A>C and c.*185C>T in the 3'-flanking sequence, showed a significant association (P < 0.01) with body weight.

010 May 12 [Epub ahead of print]

A survey of Aleutian mink disease virus infection of feral American mink in Nova Scotia

A.H. Farid, P. Rupasinghe, J.L. Mitchell, K. Rouvinen-Watt

Spleen samples from 14 mink that were trapped in 4 counties of Nova Scotia were tested for the presence of the Aleutian mink disease virus (AMDV) by polymerase chain reaction. Viral DNA was not detected in samples from Kings County (n = 2), but was detected in all the mink sampled from Colchester (n = 2) and Halifax (n = 6) counties, and 3 of 4 mink from Yarmouth County. The high level of AMDV-infected mink in Colchester and Halifax counties may pose a serious threat to the captive mink and wild animal populations. Because treatment of infected free-ranging mink is not an option, AMDV control strategies for the captive mink should be primarily focused on bio-security to protect clean ranches.

Can Vet J, 2010: 51(1), 75-77

The capsid proteins of Aleutian mink disease virus activate caspases and are specifically cleaved during infection

F. Cheng, A.Y. Chen, S.M. Best, M.E. Bloom, D. Pintel, J. Qiu

Aleutian mink disease virus (AMDV) is currently the only known member of the genus Amdovirus in the family Parvoviridae. It is the etiological agent of Aleutian disease of mink. We have previously shown that a small protein with a molecular mass of approximately 26 kDa was present during AMDV infection and following transfection of capsid expression constructs (J. Qiu, F. Cheng, L. R. Burger, and D. Pintel, *J. Virol.* 80:654-662, 2006). In this study, we report that the capsid proteins were specifically cleaved at aspartic acid residue 420 (D420) during virus infection, resulting in the previously observed cleavage product. Mutation of a single amino acid residue at D420 abolished the specific cleavage. Expression of the capsid proteins alone in Crandell feline kidney (CrFK) cells reproduced the cleavage of the capsid proteins in virus infection. More importantly, capsid protein

expression alone induced active caspases, of which caspase-10 was the most active. Active caspases, in turn, cleaved capsid proteins *in vivo*. Our results also showed that active caspase-7 specifically cleaved capsid proteins at D420 *in vitro*. These results suggest that viral capsid proteins alone induce caspase activation, resulting in cleavage of capsid proteins. We also provide evidence that AMDV mutants resistant to caspase-mediated capsid cleavage increased virus production approximately 3- to 5-fold in CrFK cells compared to that produced from the parent virus AMDV-G at 37 degrees C but not at 31.8 degrees C. Collectively, our results indicate that caspase activity plays multiple roles in AMDV infection and that cleavage of the capsid proteins might have a role in regulating persistent infection of AMDV.

J Virol, 2010: 84(6), 2687-2696

Molecular analysis of the nucleoprotein gene of canine distemper virus isolated from clinical cases of the disease in foxes, minks and dogs

L. Adaszek, S. Winiarczyk, J. Maj, L. Jankowski, A. Zietek-Barszcz, M. Skrzypczak

In this study, we used RT-PCR to detect and characterize canine distemper virus isolated from 9 naturally infected foxes, 3 minks and 3 dogs in Poland by amplifying and sequencing a portion of the NP gene. A 293-bp fragment of the CDV NP gene was amplified by RT-PCR. Sequencing of the PCR products from the isolates led to the identification of 3 sequence variants. The mostly representative polymorphic variant No. 1 showed high homology with Chinese isolate of CDV with a accession number EF 375619. The sequences of all isolates from this polymorphic variants compared with the sequences of other polymorphic variants obtained in the study and with European and American isolates sequences from GenBank showed the conservative nucleotides changes in positions 57, 132, 143, 159 and 237. These mutations can indicate that in this part of Europe there are new variants of CDV.

Pol J Vet Sci, 2009: 12(4) 433-437

Analysis of the vp2 gene sequence of a new mutated mink enteritis parvovirus strain in PR China

J. Zuo, J. Rao, H. Xu, L. Ma, B. Li, Y. Wang, X. Cai, W. Han, L. Lei, B. Liu

Mink enteritis virus (MEV) causes a highly contagious viral disease of mink with a worldwide distribution. MEV has a linear, single-stranded, negative-sense DNA with a genome length of approximately 5,000 bp. The VP2 protein is the major structural protein of the parvovirus encoded by the vp2 gene. VP2 is highly antigenic and plays important roles in determining viral host ranges and tissue tropisms. This study describes the bionomics and vp2 gene analysis of a mutated strain, MEV-DL, which was isolated recently in China and outlines its homologous relationships with other selected strains registered in Genbank.

The MEV-DL strain can infect F81 cells with cytopathic effects. Pig erythrocytes were agglutinated by the MEV-DL strain. The generation of MEV-DL in F81 cells could infect mink within three months and cause a disease that was similar to that caused by wild-type MEV. A comparative analysis of the vp2 gene nucleotide (nt) sequence of MEV-DL showed that this was more than 99% homologous with other mink enteritis parvoviruses in Genbank. However, the nucleotide residues at positions 1,065 and 1,238 in the MEV-DL strain of the vp2 gene differed from those of all the other MEV strains described previously. It is noteworthy that the mutation at the nucleotide residues position 1,238 led to Asp/Gly replacement. This may lead to structural changes. A phylogenetic tree and sequence distance table were obtained, which showed that the MEV-DL and ZYL-1 strains had the closest inheritance distance.

A new variation of the vp2 gene exists in the MEV-DL strain, which may lead to structural changes of the VP2 protein. Phylogenetic analysis showed that MEV-DL may originate from the ZYL-1 strain in DaLian.

Viol J, 2010: 7, 124

Detection of a novel astrovirus in brain tissue of mink suffering from shaking mink syndrome using viral metagenomics

A.L. Blomström, F. Widén, A.S. Hammer, S. Belák, M. Berg

In 2000, farmed mink kits in Denmark were affected by a neurological disorder. The characteristic clinical signs included shaking, staggering gait, and ataxia. The disease, given the name "shaking mink syndrome", was reproduced by inoculation of brain homogenate from affected mink kits to healthy ones. However, the etiology remained unknown despite of intensive efforts. In this study random amplification and large-scale sequencing were used and an astrovirus was detected in the brain tissue of three experimentally infected mink kits. This virus was also found in the brain of three mink kits naturally displaying the disease, but not in the six healthy animals investigated. The complete coding region of the detected astrovirus was sequenced and compared to both a mink astrovirus associated with pre-weaning diarrhea and to a recently discovered human astrovirus associated to a case of encephalitis in a boy with x-linked agammaglobulinemia. The identities were 80.4% and 52.3%, respectively, showing that the virus described in this study were more similar to the pre-weaning diarrhea mink astrovirus. For the non-structural coding regions the sequence identity was around 90% when compared to the astrovirus, which is associated with pre-weaning diarrhea in mink. The region coding for the structural protein was more diverse, only showing a 67% sequence identity. This finding is of interest not only because the detected virus may be the etiological agent of the shaking mink syndrome but also as this is one of the first descriptions of an astrovirus found in the central nervous system of animals.

J Clin Microbiol, 2010 [Epub ahead of print]

Outbreak of neonatal diarrhea in farmed mink kits (*Mustella vison*) associated with enterotoxigenic *Staphylococcus delphini*

D.G. Sledge, P.K. Danieau, C.A. Bolin, S.R. Bolin, A. Lim, B.C. Anderson, M. Kiupel

An outbreak of diarrhea on a large commercial mink farm affected 5,000 of 36,000 neonatal mink kits, with 2,000 dying within a 2-week period. Affected kits were severely dehydrated, and their furcoats and paws were covered with yellow- to green-tinged mucoid feces. On necropsy, the small intestines of examined animals were markedly distended by serous to mucoid fluid. Microscopically, there was prominent colonization of the intestinal villar epithelium by gram-positive bacterial cocci in the absence of inflammation and morphologic changes in villous enterocytes. The colonizing bacteria were phenotypically identified as belonging to the *Staphylococcus intermedius* group of bacteria. This was confirmed by nucleic acid sequence analysis of the 16S ribosomal RNA gene. Further nucleic acid sequencing of polymerase chain reaction (PCR) amplicons from the superoxide dismutase gene and the heat shock protein 60 gene differentiated the isolate as *Staphylococcus delphini*. Production of staphylococcal enterotoxins A and E was demonstrated with a commercial ELISA-based immunoassay. Sequencing of PCR amplicons confirmed the presence of the enterotoxin E gene, but PCR amplification of the enterotoxin A, B, C, or D genes was not successful. Although direct causation was not confirmed in this study, the authors postulate that the observed hypersecretory diarrhea in these

mink kits was the result of colonization of the small intestine by *S delphini* and subsequent production of enterotoxin.

Vet Pathol, 2010: 47(4), 751-757

Detection of *Neospora caninum* from farm-bred young blue foxes (*Alopex lagopus*) in China

X. Yu, N. Chen, D. Hu, W. Zhang, X. Li, B. Wang, L. Kang, X. Li, Q. Liu, K. Tian

Neospora caninum has been detected in several wild mammalian species, i.e., deer, coyotes, dingoes, and foxes. Farm-bred foxes were rarely reported to be affected by the parasite. In this study, we detected for the first time the infection of *N.caninum* in farm-bred young blue foxes (*Alopex lagopus*) in China. *Neospora*-like tissue cysts were observed in brains and kidneys of the foxes by histopathological and immunohistochemical examinations. One hundred and three sera from the clinically normal vixens were tested for the presence of *N.caninum* and *Toxoplasma gondii* antibodies by two commercial ELISA test kits. Twenty-eight of 103 (27.2%) sera were positive for *N. caninum* and 1 serum (0.97%) was positive for *T. gondii*. A portion of the *Nc5* gene of *N. caninum* was amplified from the DNA extracted from the fox brains by semi-nested PCR, further confirmed the existence of *N. caninum* among the farm-bred fox herd in China.

J Vet Med Sci, 2009: 71(1), 113-115

Actual Fur Research 2010
Meeting at the Faculty of Agricultural Sciences
Aarhus University, Denmark
28 September 2010

Hunting fur trait genes

V.H. Nielsen, R.M. Anistoroaei, B. Guldbrantsen, K. Christensen, M. Fredholm

A 3-generations population (F₂-design) was established to map QTL (genes) for fur quality traits in mink. In the parental generation (generation 1), American short nap mink were crossed with Nordic wildmink. Recordings of fur quality traits were made at Kopenhagen Fur. At this point, chromosomes 2 and 6 have been genotyped for 10 and 8 markers, respectively. The results of the analyses revealed QTL for guard hair, hair length, pelt quality and size of the pelt on chromosome 2. On chromosome 6, QTL were detected for type, guard hair and fur quality. Identification of genes for fur quality traits allows DNA-based selection to be used to improve fur quality quickly and efficiently.

Meeting at the Faculty of Agricultural Sciences, University of Aarhus, Denmark. Internal Report Husbandry no. 28, September 2010 (in Danish) p. 4. Authors' abstract.

Correlations between feed efficiency, activity and health

B. M. Damgaard, S.W. Hansen

The body weight of the mink has been increasing during the last years and investigations have documented the possibility of increasing the feed efficiency by selection programs. The aim of the present study was to investigate activity, body weight and immune status in mink with high and low residual feed intake (RFI) during restrictive and

ad libitum feeding. The study included 30 mink, where half of the mink had high RFI and the other half had low RFI. The results showed that the difference in RFI between the two groups can not unequivocally be attributed to differences in mean activity between the two groups, but there was a tendency (P=0.092) to a higher activity for group RFI-High than for group RFI-Low. Furthermore, restrictive feeding of mink with high RFI resulted in immune suppression and mink that concentrated its activity to the period up to feeding at the expense of activity at different times of day.

Meeting at the Faculty of Agricultural Sciences, University of Aarhus, Denmark. Internal Report Husbandry no. 28, September 2010 (in Danish) p. 9. Authors' abstract.

A metabolomic approach to describe the metabolism in mink

M.S. Hedemann

Blood samples were collected from mink with high and low residual feed intake. One blood sample was taken during a period where the mink were fed restrictively and two samples were taken during a period where the mink were fed ad libitum. The blood samples were analyzed using a metabolomic approach. Using this method, the complete set of small-molecule metabolites present in a sample is analyzed. One of the advantages of this method is that it is explorative. There was no clear difference between mink with low and high residual feed intake but the data will be subjected to further analysis. There were marked differences in the plasma from mink fed restrictively and mink fed ad

libitum. Two metabolites, present in higher concentration in mink fed restrictively than in mink fed ad libitum, have been identified so far. These metabolites are betaine and carnitine. Further metabolites await identification.

Meeting at the Faculty of Agricultural Sciences, University of Aarhus, Denmark. Internal Report Husbandry no. 28, September 2010 (in Danish) p. 16. Authors' abstract.

Measurement of stress in Mink

J. Malmkvist

Stress is as an element in the evaluation of animal welfare. Additionally, the measurement of stress can be applied when effects of different aspects of breeding, cage environment and management of mink are compared. But what is stress and how can it be measured? Is abnormal behaviour linked to stress in mink? At the meeting new results and methods for estimating stress in mink are presented. One method is based upon measuring the concentration of cortisol metabolites in faeces from mink. This non-invasive method is in many aspects beneficial, in comparison to blood sampling procedures. In experiments with radio-labelled cortisol injection, the main part of cortisol is in mink excreted via faeces (83 %), rather than via the urine (17 %). The metabolism of cortisol is not different between mink with low or high occurrence of stereotypic behaviour. This knowledge can be used to better understand the link between e.g. abnormal behaviour and stress in farmed mink.

Meeting at the Faculty of Agricultural Sciences, University of Aarhus, Denmark. Internal Report Husbandry no. 28, September 2010 (in Danish) p. 21. Authors' abstract.

Influence of fibre in diet on mating behaviour and reproduction success

A. Spangberg, J. Malmkvist

A fibrous diet has been suggested used to increase the mink's satiety during the feed restricted winter

period. This study aims to describe possible consequences of a fibrous diet on mating/reproductive success in female farmed mink. The present study also aims at describing the female mink's mating behaviour, as only few details about the mating behaviour in captivity are known. In addition, a better understanding of the mating behaviour may help to identify when a mating trial is problematic and thus should be ended. We found no significant effects on mating behaviour and reproductive success after using the fibrous diet. Furthermore, we found that several aspects of the mating behaviour often depend on the female's previous mating success during the mating season and on the success of a mating trial.

Meeting at the Faculty of Agricultural Sciences, University of Aarhus, Denmark. Internal Report Husbandry no. 28, September 2010 (in Danish) p. 29. Authors' abstract.

Health and welfare in mink – New Danish rules and initiatives

S.H. Møller

Almost everybody related to the Danish mink production have been affected since a very critical television programme produced by an animal activist group was broadcasted on a public service network on October 27. 2009. Many farmers have had an extraordinary control visit by the authorities in the autumn of 2009, and in 2010 all Danish farmers will be inspected. The Danish Fur Breeders Association have made an effort to inform all farmers about the current regulations, their interpretation and in assisting the farmers to comply to all rules and regulations on housing, management and documentation. Much have been achieved, but regarding cage enrichments and written documentation, many farmers are not there yet.

The fur animal science was not affected directly, apart from providing documented figures on the issues raised on TV: Morbidity, mortality and the incidences of wounds and bites, as well as the general health and welfare of farm mink in Denmark. A press release leads to a few opportunities to present this knowledge on TV and

Radio. Our major involvement have been as advisors for the authorities in the Ministry of Agriculture and the Ministry of Justice, as the faculty of Agricultural Sciences in Foulum has an obligation to gather the scientific knowledge and make this knowledge available to the authorities, at their request.

The Minister of Agriculture formed a working group in order to develop suggestions for the content and practical implementation of new rules and regulations on:

1. Mandatory education of all new mink farmers and educational updates for all farmers every 3 years
2. Mandatory health advisory agreements between mink farmers and veterinary practitioners including 4 to 6 annual advisory visits to all Danish mink farms
3. A branch codex on how to comply with all current rules and regulations relating to health and welfare. To be developed by the Danish Fur Breeders Association and approved by the authorities.

The paper describes the results reached by the working group, the political and scientific rationale behind each part, and a personal comment on how the farmers and their mink will be affected and can make the best of the new rules and regulations.

Meeting at the Faculty of Agricultural Sciences, University of Aarhus, Denmark. Internal Report Husbandry no. 28, September 2010 (in Danish) p. 38. Authors' abstract.

Why environmental enrichment and does it improve the welfare of the mink?

S.W. Hansen

The desire to improve the animals' welfare has caused an increasing interest for environmental enrichment in the western part of the world. At the same time it is the intention that environmental enrichments must be based on research results documenting that the enrichments improve the animals' welfare. The purpose of this presentation is, based on published research results, to give a status on the kinds of enrichments examined, which

effect they have had on the mink and whether it has been documented that they improve the mink's welfare. In the Danish Act of Law on fur animals it is requested that mink have access to straw and a shelf or a tube. Straw is used for insulation in the nest and as a cover on top of the nest and thus it has mainly been examined as a part of the nest environment. Furthermore, straw may have an effect as chewing object, however, this function has only been examined to a limited extent. The welfare effect of loose tubes in the cage has been examined in combination with several other enrichment objects but the examination of mink's welfare when only being allocated loose tubes is limited. It is possible that the material, form and size of the tubes may influence how the tubes affect the mink's welfare. Shelves seem to function as observation post for mink. Access to shelves decreases the activity and the occurrence of stereotypi, which is estimated to be positive for the mink's welfare. In order to be able to take constructively part in the discussion and legislation on environmental enrichments on Danish farms it is important to have documented knowledge about what is working, how does it work, why does it work, and which alternatives will improve the mink's welfare in the best and cheapest way. If this knowledge is non-existing it can be difficult to ensure that the future enrichment actually does benefit the mink's welfare.

Meeting at the Faculty of Agricultural Sciences, University of Aarhus, Denmark. Internal Report Husbandry no. 28, September 2010 (in Danish) p. 50. Authors' abstract.

Is selection for reduced aggression in group housing possible?

P. Berg, S.H. Møller

There is evidence from several species (e.g. poultry) that selection can contribute to reducing aggression in groups, and selection thus could be one way of reducing aggression in groups of mink in group housing. On this background, a selection experiment was started, aiming at reducing the number of bite marks on the skin side. This study describes variation in bite marks in the first generation. The study includes evaluation of bite marks on a total of 640 mink in group housing and 289 of their full sibs

in standard cages (two animals). In group housing significantly more bite marks are observed than on the corresponding full sibs in standard cages. In addition, there seems to be a weak relationship between number of bite marks in group housing and standard cages. In group housing the females are generally more bitten than males, though the most bitten male has on average more bite marks than the least bitten female. A higher correlation between number of bite marks are observed between animals of the same sex (the two males and the two females) than between sexes in group housing. This indicates that bite marks to a large extent is due to fights within sexes.

A large variation between full sibs/cages was found in the number of bite marks. Heritability was estimated to be 0,17, but this is not expected to reveal all genetic variability. This supports that genetic differences are an important factor contributing to the number of bite marks. Selection for reduced number of bite marks continues in the years to come.

Meeting at the Faculty of Agricultural Sciences, University of Aarhus, Denmark. Internal Report Husbandry no. 28, September 2010 (in Danish) p. 61. Authors' abstract.

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