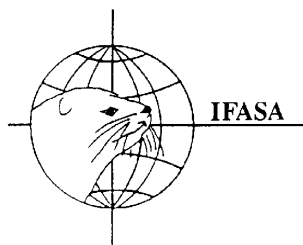
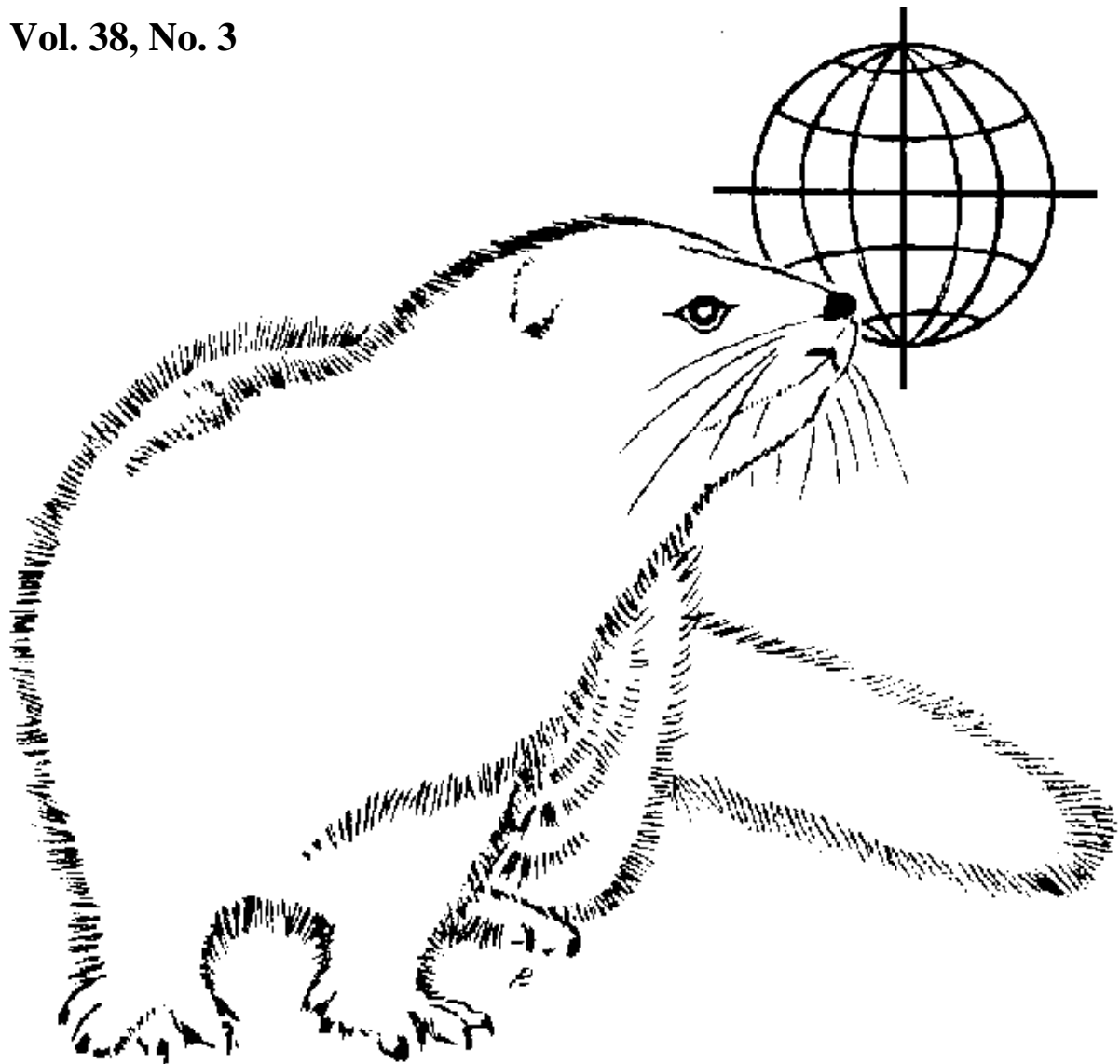


SCIENTIFUR

SCIENTIFIC INFORMATION IN FUR ANIMAL PRODUCTION

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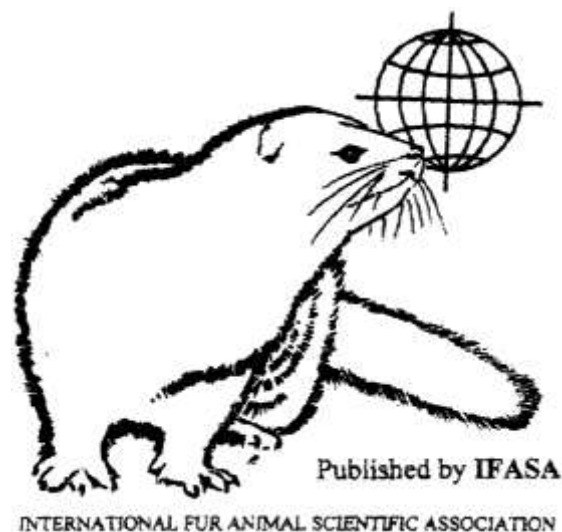
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Notes from the Editor

Group housing has increased in Europe since it was adopted in 1999. It may be advantageous for the production but can lead to unwanted aggressions between animals. Research results presented in this volume of *Scientifur* show that genetic selection which includes both direct and indirect genetic effects for aggression-related traits can reduce the frequency of bite marks and thus probably increase welfare in group-housed mink.

Aleutian mink disease or plasmacytosis is a serious disease causing considerable economic losses for the mink industry. Control of the disease demands actions in several areas. This includes methods to identify the virus (AMVD) in the mink but also in the surrounding environment on the farms, methods to eliminate the virus on farms and also an understanding of the spread of the virus in the population. Studies are referred to where AMDV is characterized, where new methods are presented to detect the virus both in mink and in the environment,

where solutions are sought to inactivate the virus in the environment e.g. in manure and where the molecular epidemiology is studied.

The 65th Annual Meeting of the European Association of Animal Production (EAAP), Copenhagen was held in Denmark 25-29 August 2014: <http://www.eaap2014.org>
Efforts were made to include fur animal research among the presentations. Ten oral presentations were given within mink research with topics within genetics, reproduction, nutrition, management, behaviour and welfare.

Attention should be given to the following upcoming meeting:

The Abildgaard Seminar: "Mink Health and Welfare", Copenhagen, Denmark 6-7 November 2014.

Further information can be obtained: (hammer@sund.ku.dk).

Vivi Hunnicke Nielsen
Editor *Scientifur*

BREEDING, GENETICS AND REPRODUCTION**Association of MITF gene with hearing and pigmentation phenotype in Hedlund white American mink (*Neovison vison*)**

M.N. Markakis, V.E. Soedring, V. Dantzer, K. Christensen, R. Anistoroaei

J. Gen. 2014: 93(2): 477-481

<http://www.ias.ac.in/jgenet/Vol93No2/temp/jgen-13-505.pdf>

Indirect genetic effects contribute substantially to heritable variation in aggression-related traits in group-housed mink (*Neovison vison*)

S.W. Alemu, P. Bijma, S.H. Møller, L. Janss, P. Berg

Since the recommendations on group housing of mink (*Neovison vison*) were adopted by the Council of Europe in 1999, it has become common in mink production in Europe. Group housing is advantageous from a production perspective, but can lead to aggression between animals and thus raises a welfare issue. Bite marks on the animals are an indicator of this aggressive behaviour and thus selection against frequency of bite marks should reduce aggression and improve animal welfare. Bite marks on one individual reflect the aggression of its group members, which means that the number of bite marks carried by one individual depends on the behaviour of other individuals and that it may have a genetic basis. Thus, for a successful breeding strategy it could be crucial to consider both direct (DGE) and indirect (IGE) genetic effects on this trait. However, to date no study has investigated the genetic basis of bite marks in mink.

A model that included DGE and IGE fitted the data significantly better than a model with DGE only, and IGE contributed a substantial proportion of the heritable variation available for response to selection. In the model with IGE, the total heritable variation expressed as the proportion of phenotypic variance (T_2) was six times greater than classical heritability (h^2). For instance, for total bite marks, T_2 was equal to 0.61, while h^2 was equal to 0.10. The genetic correlation between direct and indirect effects ranged from 0.55 for neck bite marks to 0.99 for tail bite marks. This positive correlation suggests

that mink have a tendency to fight in a reciprocal way (giving and receiving bites) and thus, a genotype that confers a tendency to bite other individuals can also cause its bearer to receive more bites.

Both direct and indirect genetic effects contribute to variation in number of bite marks in group-housed mink. Thus, a genetic selection design that includes both direct genetic and indirect genetic effects could reduce the frequency of bite marks and probably aggression behaviour in group-housed mink.

Genet. Sel. Evol. 2014: 46(1): 30

doi: 10.1186/1297-9686-46-30

<http://www.ncbi.nlm.nih.gov/pubmed/24884874>

Microsatellite polymorphism and its association with body weight and selected morphometrics of farm red fox (*Vulpes vulpes* L.)

M. Zatoń-Dobrowolska, A. Mucha, H. Wierzbicki, D. Morrice, M. Moska, M. Dobrowolski, P. Przysiecki

Polymorphism of 30 canine-derived microsatellites was studied in a group of 200 red foxes kept on 2 Polish farms. 22 out of 30 microsatellites were selected to study association between marker genotypes and body weight (BW), body length (BL), body circumference (BC), tail length (TL), ear height (EH), length of the right front limb (FRLL), length of the right rear limb (RRLL), length of the right front foot (FRFL) and length of the right rear foot (RRFL). A total of 112 alleles and 243 genotypes were found at 22 autosomal microsatellite loci. Three monomorphic loci deemed as uninformative were excluded from the study. The association between marker genotypes and the studied traits was analysed using general linear model (GLM) procedure and least squares means (LSM). Linkage disequilibrium (LD) was estimated to assess non-random association between microsatellite loci. Out of 19 microsatellites studied four markers showed no association with the studied traits, three markers had a significant effect on one trait, and another three markers had significant effect on two traits. Among ten microsatellites with significant effect on four economically important traits (BW, BL, BC, TL) four were associated with two characters: marker FH2613 with BW and BC, marker FH2097 with BL and BC, marker ZUBECA6

with BW and BC, whereas marker REN75M10 was associated with BL and TL. The strongest LD (r^2 ranged from 0.15 to 0.33) was estimated between nine loci with significant effect on economically important traits (BW, BL, BC, TL).

J. Appl. Genet. 2014: [Epub ahead of print]

<http://www.ncbi.nlm.nih.gov/pubmed/24819338>

Effect of age and breeding season on sperm acrosin activity in the arctic fox (*Alopex lagopus* L.)

K. Stasiak, B. Janicki

The objective of this study was to determine the effect of age and reproductive season on selected properties of semen from the arctic fox, *Alopex lagopus* L. The experiment used 40 ejaculates collected manually from 6 animals (3 foxes aged one year and 3 foxes older than three years). Statistically less semen (0.39 cm³) was collected from the young compared to the older animals, and the ejaculates obtained were characterized by higher concentration of spermatozoa (195.04 x 10⁶/cm³). In turn, sperm acrosomal extracts from the older animals contained statistically more acrosin (6,4 mU/10⁶ spermatozoa). In the sperm acrosomal extracts prepared during the first semen sampling, the mean acrosin activity did not exceed 2.3 mU/million spermatozoa. At subsequent semen sampling dates, the activity of the analysed enzyme increased to reach 7.72 mU/million spermatozoa. In the extracts obtained from the semen collected at the end of the breeding season of arctic foxes, the acrosin activity again reached a value obtained at the beginning of the season.

Pol. J. Vet. Sci. 2014: 17(1):177-179

Environmental pollutants and alterations in the reproductive system in wild male mink (*Neovison vison*) from Sweden

S. Persson, U. Magnusson

Chemosphere 2014: 4(120C): 237-245 doi: 10.1016/j.chemosphere.2014.07.009

<http://www.ncbi.nlm.nih.gov/pubmed/25103085>

Gene mapping as a method for verifying sequence localization based on interspecific chromosome painting (ZOO-FISH)

M. Bugno-Poniewierska, B. Słota, K. Pawlina, L. Potocki, A. Gurgul, E. Słota, J. Klukowska-Rötzler

The results obtained in the present study made it possible to place selected markers on the physical map of the arctic fox genome. With the use of fluorescence in situ hybridization (FISH) the GHR (3q24) and 1110 (1q21.1-21.2) genes and the FH2537 (5q11.3) microsatellite were localized on arctic fox chromosomes. The results confirmed previously proposed homologies using the ZOO-FISH technique, except for the 1110 gene. This suggests that the gene underwent a rearrangement (an inversion) that changed its localization compared to the dog.

Folia. Biol. 2014: 62(1): 17-21

<http://www.ncbi.nlm.nih.gov/pubmed/24745145>

Uterine Glycogen Metabolism in Mink during Estrus, Embryonic Diapause and Pregnancy

M. Dean, J. Hunt, L. McDougall, J. Rose

We have determined uterine glycogen content, metabolizing enzyme expression and activity in the mink, a species that exhibits obligatory embryonic diapause, resulting in delayed implantation. Gross uterine glycogen concentrations were highest in estrus, decreased 50% by diapause and 90% in pregnancy ($P \leq 0.05$). Endometrial glycogen deposits, which localized primarily to glandular and luminal epithelia, decreased 99% between estrus and diapause ($P \leq 0.05$) and were nearly undetectable in pregnancy. Glycogen synthase and phosphorylase proteins were most abundant in the glandular epithelia. Glycogen phosphorylase activity (total) in uterine homogenates was higher during estrus and diapause, than pregnancy. While glycogen phosphorylase protein was detected during estrus and diapause, glycogen synthase was almost undetectable after estrus, which probably contributed to a higher glycogenolysis/glycogenesis ratio during diapause. Uterine glucose-6-phosphatase 3 gene expression was greater during diapause, when compared to estrus ($P \leq 0.05$) and supports the hypothesis that glucose-6-phosphate

resulting from phosphorylase activity was dephosphorylated in preparation for export into the uterine lumen. The relatively high amount of hexokinase-1 protein detected in the luminal epithelia during estrus and diapause may have contributed to glucose trapping after endometrial glycogen reserves were depleted. Collectively, our findings suggest to us that endometrial glycogen reserves may be an important source of energy, supporting uterine and conceptus metabolism up to the diapausing blastocyst stage. As a result, the size of uterine glycogen reserves accumulated prior to mating may in part, determine the number of embryos that survive to the blastocyst stage, and ultimately litter size.

J. Reprod. Dev. 2014: [Epub ahead of print]

<http://www.ncbi.nlm.nih.gov/pubmed/25225159>

NUTRITION, FEEDING AND MANAGEMENT

Nutrient-specific compensatory feeding in a mammalian carnivore, the mink, *Neovison vison*

K. Jensen, S.J. Simpson, V.H. Nielsen, J. Hunt, D. Raubenheimer, D. Mayntz

Balancing of macronutrient intake has only recently been demonstrated in predators. In particular, the ability to regulate carbohydrate intake is little studied in obligate carnivores, as carbohydrate is present at very low concentrations in prey animal tissue. In the present study, we determined whether American mink (*Neovison vison*) would compensate for dietary nutritional imbalances by foraging for complementary macronutrients (protein, lipid and carbohydrate) when subsequently given a dietary choice. We used three food pairings, within which two macronutrients differed relative to each other (high v. low concentration), while the third was kept at a constant level. The mink were first restricted to a single nutritionally imbalanced food for 7 d and then given a free choice to feed from the same food or a nutritionally complementary food for three consecutive days. When restricted to nutritionally imbalanced foods, the mink were willing to overingest protein only to a certain level ('ceiling'). When subsequently given a choice, the mink compensated for the period of nutritional imbalance by selecting the nutritionally complementary food in the food choice pairing. Notably, this rebalancing

occurred for all the three macronutrients, including carbohydrate, which is particularly interesting as carbohydrate is not a major macronutrient for obligate carnivores in nature. However, there was also a ceiling to carbohydrate intake, as has been demonstrated previously in domestic cats. The results of the present study show that mink regulate their intake of all the three macronutrients within limits imposed by ceilings on protein and carbohydrate intake and that they will compensate for a period of nutritional imbalance by subsequently selecting nutritionally complementary foods.

Br. J. Nutr. 2014: 20: 1-8.

<http://www.ncbi.nlm.nih.gov/pubmed/25141190>

Ileal, colonic and total tract nutrient digestibility in dogs (*Canis familiaris*) compared with total tract digestibility in mink (*Neovison vison*)

M.T. Tjernsbekk, A.H. Tauson, O. Ahlstrøm

Mink (*Neovison vison*) was studied as a model for the determination of ileal crude protein (CP) and amino acid (AA) digestibility in dogs (*Canis familiaris*). Apparent ileal digestibility (AID) and apparent colonic digestibility (ACD) in dogs and apparent total tract digestibility (ATTD) in dogs and mink were measured for dry matter (DM), main nutrients and AA. Standardised ileal digestibility (SID) of CP and AA in dogs was calculated. Twelve dogs and 12 mink divided into three groups were fed one out of three diets differing in CP digestibility. In dogs, AID of CP was lower (74.4%) than ATTD (83.5%) ($p < 0.001$). The ATTD of CP in mink (77.8%) did not differ from AID, ACD (78.5%) and SID (79.6%) in dogs. Digestibility of AA followed the same pattern, and, except for Thr and Ser, ATTD in mink was very close to SID in dogs. Also, AID was close to ATTD in mink for several AA. High correlations were found between methods for digestibility of CP and most AA ($p < 0.01$) and for AA ranking with respect to digestibility level ($p < 0.001$). In dogs, ether extract digestibility was approximately 96% at all sites, while DM, starch and total carbohydrate digestibility increased from ileal to faecal level ($p < 0.01$). Mink ATTD of DM and main nutrients was closest to ACD in dogs. It was concluded that mink

is a suitable model for the determination of AID and SID of CP and AA in dogs.

Arch. Anim. Nutr. 2014; 68(3): 245-261. doi: 10.1080/1745039X.2014.915137

<http://www.ncbi.nlm.nih.gov/pubmed/24870271>

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 foetuses 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 foetuses. 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 foetuses 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>

Effects of different sources and levels of copper on growth performance, nutrient digestibility, and elemental balance in young female mink (*Mustela vison*)

X. Wu, T. Zhang, Z. Liu, J. Zheng, J. Guo, F. Yang, X. Gao

An experiment was conducted in a 3 × 3 + 1 factorial experiment based on a completely randomized design to evaluate the effects of different sources of copper on growth performance, nutrient digestibility and elemental balance in young female mink on a corn-fishmeal-based diet. Animals in the control group were fed a basal diet (containing 8.05 mg Cu/kg DM; control), which mainly consisted of corn, fish meal, meat bone meal, and soybean oil, with no copper supplementation. Minks in other nine treatments were fed basal diets supplemented with Cu from reagent-grade copper sulfate, tribasic copper chloride (TBCC) and copper methionate. Cu concentrations of experiment diets were 10, 25, and 40 mg/kg copper. A metabolism trial of 4 days was conducted during the last week of experimental feeding. Final body weight and average daily gain increased (linear and quadratic, P<0.05) as Cu increased in the diet; maximal growth was seen in the Cu25 group. Cu supplementation slightly improved the feed conversion rate (P=0.095). Apparent fat digestibility was increased by copper level (P=0.020). Retention nitrogen was increased by copper level (linear, P=0.003). Copper source had a significant effect on copper retention with Cu-Met and copper sulfate treatments retention more than TBCC treatments (P<0.05). Our results indicate that mink can efficiently utilize added dietary fat and that Cu plays an important role in the digestion of dietary fat in mink, and mink can efficiently utilize Cu-Met and CuSO₄.

Biol. Trace Elem. Res. 2014; 160(2): 212-221
doi: 10.1007/s12011-014-0054-0.

<http://www.ncbi.nlm.nih.gov/pubmed/24962642>

Effects of different dietary manganese levels on growth performance and N balance of growing mink (*Neovison vison*)

H.H. Zhang, N. Zhou, T.T. Zhang, K. Bao, C. Xu, X.C. Song, G.Y. Li

Two experiments were conducted to study the effects of dietary manganese levels on growth performance, nutrients digestibility, and N balance of minks during growing period. In experiment 1, 75 healthy male minks (60 days old) were selected and randomly divided into five groups with different types of diet. The diet was supplemented with 0 (control), 50, 100, 300, and 600 ppm of manganese as MnSO₄ of dry matter (DM) in basic diet, respectively. From early July to middle September, the results showed that the final body weights of minks were significantly affected by diets ($P < 0.05$). Average daily gains (ADG) were significantly higher in the 300-ppm manganese group than those in other groups. The ratio of feed to body weight gain (F/G) was significantly affected by manganese level ($P < 0.05$). In experiment 2, 45 male minks (75 days old) with the same body weight were selected from each group of experiment 1 to carry out the nutrient digestion and N-balance tests which lasted for 4 days for the collection of the feces and urine, and the diets and treatment codes were same as in experiment 1. The results showed that no significant differences were found in DM, crude protein (CP), and crude carbohydrate (CC) digestibility among all groups ($P > 0.05$), but ether extract (EE) and gross energy (GE) digestibility were all the highest in the 300-ppm group. N intake and fecal N were similar among all groups ($P > 0.05$). Urinary N was lower in the 300-ppm group; in contrast, N retention was higher in this group ($P < 0.05$). In conclusion of experiment 1 and experiment 2, the diet supplemented with 300 ppm of manganese (as manganese sulfate) could improve the growth performance and increase the EE and GE digestibility of mink during the growing period and moreover reduce the nitrogen emissions to the environment, and the optimal total manganese level in mink's diet was 409.16 in DM during the growing period.

Biol. Trace Elem. Res. 2014: 160(2): 206-211
doi: 10.1007/s12011-014-0008-6

<http://www.ncbi.nlm.nih.gov/pubmed/24958021>

Effects of dietary copper on nutrient digestibility, tissular copper deposition and fur quality of growing-furring mink (*Mustela vison*)

X. Wu, Z. Liu, T. Zhang, Y. Yang, F. Yang, X. Gao

The present study investigated the effects of dietary copper (Cu) on growth performance and fur quality in growing-furring minks. One hundred and five standard dark female minks were randomly assigned to seven groups with the following dietary treatments: basal diet with no supplemental Cu (control) and basal diet supplemented with either 6, 12, 24, 48, 96 or 192 mg/kg Cu from copper sulphate, respectively. Our data showed that final body weight ($P = 0.033$), daily gain ($P = 0.029$) and fat digestibility ($P = 0.0006$) responded to increasing levels of Cu. The activity of glutamic-oxalacetic transaminase (GOT) and glutamic-pyruvic transaminase (GPT) in serum increased (linear and quadratic, $P < 0.05$) as Cu increased in the diet. Increasing Cu improved total protein (TP) and albumin (ALB) (quadratic, $P < 0.05$). The level of ceruloplasmin (CER) responded in a linear ($P < 0.0001$) and quadratic ($P < 0.0001$) form with increasing level of Cu. Colour intensity of those minks pelted suggested that relatively high levels of supplemental Cu have a beneficial effect on intensifying hair colour of dark mink but did not affect leather thickness. Liver Cu and plasma Cu concentrations of the mink linearly ($P < 0.0001$) responded to increasing levels of Cu. Our results indicate that growing-furring mink can efficiently utilize added dietary fat and that Cu plays an important role in the digestion of dietary fat in growing-furring mink, and supplemental dietary Cu in growing-furring mink promotes fat digestion and improve hair colour.

Biol. Trace Elem. Res. 2014: 158(2): 166-175. doi: 10.1007/s12011-014-9933-7. [Epub 2014 Mar 26]

<http://www.ncbi.nlm.nih.gov/pubmed/24668161>

Dietary copper supplementation improves pelt characteristics of female silver fox (*Vulpes fulva*) during the winter fur-growing season

W. Zhong, H. Liu, G. Luo, Z. Chang, F. Liu, J. Zhao, D. Li, Z. Yue, H. Zhang, G. Li

Copper has an essential role in normal fur pigmentation and fur quality. This study evaluated the effects of cupric citrate (CuCit) supplementation on growth, nutrients metabolism and pelt characteristics of the female silver fox (*Vulpes fulva*). Fifty age-matched female silver foxes with similar body weights were randomly divided into five dietary groups for 58 days during the winter fur-growing season. The basal diet contained 4.92 mg/kg copper. Groups I-V were supplemented with 6, 30, 60, 90 or 150 mg Cu from CuCit per 1 kg dry matter basal diet. Serum alkaline phosphatase activity was significantly higher ($P < 0.05$) in those fed 90 mg/kg Cu than those fed 150 mg/kg Cu. Pelt total thickness was significantly higher ($P < 0.05$) in those fed 30 mg/kg Cu than foxes fed 6 mg/kg Cu supplemented diet, but were similar to the other groups. Length of guard hair was significantly lower ($P < 0.05$) in those fed 90 mg/kg Cu than fed 6 mg/kg Cu and 30 mg/kg Cu, but were similar to the other groups. Length of underhair was significantly higher ($P < 0.05$) in those fed 6 mg/kg Cu than those fed 90 mg/kg Cu, but was similar to the other groups. Considering decreasing environmental contamination and improving pelt performance, supplementing 30 mg/kg Cu from CuCit (actual copper 35 mg/kg dry matter) is appropriate for female silver fox.

Anim. Sci. J. 2014: 85(7): 757-762. doi: 10.1111/asj.12208

<http://www.ncbi.nlm.nih.gov/pubmed/24798300>

Methylmercury accumulation and elimination in mink (*Neovison vison*) hair and blood: Results of a controlled feeding experiment using stable isotope tracers

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Concentrations of metals in hair are used often to develop pharmacokinetic models for both animals and humans. While data on uptake are available, elimination kinetics are less well understood; stable isotope tracers provide an excellent tool for measuring uptake and elimination kinetics. In the present study, methylmercury (MeHg) concentrations through time were measured in the hair and blood of mink (*Neovison vison*) during a controlled 60-day feeding experiment. Thirty-four mink were

fed a standard fish-based diet for 14 days at the end of which (day 0), 4 mink were sacrificed to determine baseline MeHg concentrations. From day 0 to day 10, the remaining mink were fed Diet #1 consisting of the base diet supplemented with $0.513 \pm 0.013 \mu\text{g Me}^{199}\text{Hg/g}$ and $0.163 \pm 0.003 \mu\text{g Me}^{201}\text{Hg/g}$. From day 10 to day 60, mink were fed Diet #2, i.e., the base diet supplemented with $0.175 \pm 0.024 \mu\text{g Me}^{201}\text{Hg/g}$. Animals were sacrificed periodically to determine accumulation of Me^{201}Hg in blood and hair over the entire 60 day period and the elimination of Me^{199}Hg over the last 50 days. Hair samples collected from each mink and cut into 2.0-mm lengths, indicate that both isotopes of MeHg first appeared in the hair closest to the skin at approximately day 10 with concentrations in the hair reaching steady state from day 39 onwards. The elimination rate of Me^{199}Hg from the blood was 0.05/day and the ratio of MeHg in the hair: blood was 119. A large fraction of MeHg (22% to > 100%) was stored in the hair suggesting that in fur-bearing mammals, hair is a major route of elimination of MeHg from the body

Environ. Toxicol. Chem. 2014. doi: 10.1002/etc.2762 [Epub ahead of print]

<http://www.ncbi.nlm.nih.gov/pubmed/25258205>

The effect of different fat sources in the diet on the composition of adipose tissue in arctic foxes (*Alopex lagopus* L.)

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The study investigated the effect of vegetable and animal fat in the feed ration on the fatty acid profile of reserve fat in the arctic fox. Varying proportions of saturated and unsaturated fats in the feed ration comprised the experimental factor. In order to differentiate contents of saturated and unsaturated fatty acids in the experimental feed rations, various percentages of rapeseed oil and turkey fat were applied. The subcutaneous and circum-organal fat in this study differed considerably in terms of contents of individual fatty acids and between individual groups of acids. The circum-organal fat contained much higher amounts of unsaturated acids, but at the same time it was characterized by a lower amount of monounsaturated acids. Significant differences were also found in the contents of as

many as 11 fatty acids. Recorded results indicate a potential modification of reserve fat in the arctic fox, a model representative of carnivorous animals (Carnivora). The possibility of the partial substitution of animal fat with vegetable oil (rape oil) in the nutritive diet of arctic foxes was confirmed.

Folia. Biol. 2014: 62(2): 127-133

[http://www.ncbi.nlm.nih.gov/pubmed/?term=The+effect+of+different+fat+sources+in+the+diet+on+the+composition+of+adipose+tissue+in+arctic+foxes+\(Alopex+lagopus+L.\)](http://www.ncbi.nlm.nih.gov/pubmed/?term=The+effect+of+different+fat+sources+in+the+diet+on+the+composition+of+adipose+tissue+in+arctic+foxes+(Alopex+lagopus+L.))

Ferret Nutrition

C.A. Johnson-Delaney

Vet. Clin. North Am. Exot. Anim. Pract. 2014: 17(3): 449-470. doi: 10.1016/j.cvex.2014.05.008

<http://www.ncbi.nlm.nih.gov/pubmed/25155665>

Comparative morphology of the lingual papillae and their connective tissue cores in the tongue of the American mink, (*Neovison vison*)

K. Yoshimura, Y. Fukue, R. Kishimoto, J. Shindo, I. Kageyama

We observed the morphology of the lingual papillae (filiform, conical, fungiform, and vallate papillae, and lateral organ) and their connective tissue cores (CTCs) in the American mink (*Neovison vison*) using light and scanning electron microscopy. Filiform papillae were distributed on the apex linguae and rostral regions of the corpus linguae. Conical papillae were distributed over the caudal region and absent in the radix linguae. Numerous ridges were present in the radix linguae. Four to six vallate papillae were situated at the border between the corpus and radix linguae. Instead of foliate papillae, a pair of lateral organs was situated on the caudal edge of the corpus. The epithelial surface of each filiform papilla consisted of a single main process and 10-12 accessory processes. Notably, filiform papillae in the apex linguae exhibited morphological variation, and some were dome-like and lacked processes. In contrast, filiform papillae on the rostral part were not variable, were extended

to a sharp tip, were associated with an eosinophilic stratum corneum, and lacked nuclei. The CTCs of the filiform papillae consisted of a main core and slender accessory cores surrounding a concavity. Those in the apex linguae were similar in appearance and consisted of main and adjacent accessory cores. The fungiform papillae had a dome-like epithelial surface and their CTCs were columnar, with upper concavities and flanges. The simplified lingual morphology of the American mink, particularly in the filiform papillae in the apex linguae, may be influenced by its diet and semiaquatic lifestyle.

Zoolog. Sci. 2014: 31(5): 292-299. doi: 10.2108/zs130214

<http://www.ncbi.nlm.nih.gov/pubmed/24832902>

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

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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 µg/g in kidney (68 %) and from 1 to 5 µg/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 µg/g and 82 % of liver samples had concentrations below 1 µg/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: 23(5): 767-778. doi: 10.1007/s10646-014-1213-y
<http://www.ncbi.nlm.nih.gov/pubmed/24573774>

HEALTH AND DISEASE

Evidence of endoplasmic reticulum stress and liver inflammation in the American mink *Neovison vison* with benign hepatic steatosis

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We investigated the presence of inflammatory signs in the progression of fatty liver disease induced by fasting. Sixty standard black American mink (*Neovison vison*) were fasted for 0, 1, 3, 5, or 7 days and one group for 7 days followed by re-feeding for 28 days. Liver sections were evaluated histologically and liver mRNA levels indicating endoplasmic reticulum (ER) stress, adipogenic transformation, and inflammation were assessed by quantitative real-time PCR. After 3 days of fasting, the mink had developed moderate liver steatosis. Increased hyaluronan reactivity in lymphocytic foci but no Mallory-Denk bodies were seen in livers of the mink fasted for 5-7 days. Up-regulation of glucose-regulated protein, 78 kDa was observed on day 7 indicating ER stress, especially in the females. Liver lipoprotein lipase and monocyte chemoattractant protein 1 mRNA levels increased in response to 5-7 days of food deprivation, while tumor necrosis factor α (TNF- α) was the highest in the mink fasted for 5 days. The expression of the genes of interest, except for TNF- α , correlated with each other and with the liver fat content. The mRNA levels were found to change more rapidly below n-3/n-6 polyunsaturated fatty acid ratio threshold of 0.15. Following re-feeding, hepatocyte morphology and mRNA abundance returned to pre-fasting levels. Within the studied timeframe, evidence for ER stress, adipogenic transformation, and liver inflammation suggested incipient transition from steatosis to steatohepatitis with potential for development of more severe liver disease. This may

present a possibility to influence disease progression before histologically observable steatohepatitis.

J. Comp. Physiol. B. 2014: [Epub ahead of print]

<http://www.ncbi.nlm.nih.gov/pubmed/25079677>

Inactivation of Aleutian mink disease virus through high temperature exposure in vitro and under field-based composting conditions

I. Hussain, G.W. Price, A.H. Farid

Vet. Microbiol. 2014: 173(1-2): 50-58. doi: 10.1016/j.vetmic.2014.07.014. [Epub 2014 Jul 25]

<http://www.ncbi.nlm.nih.gov/pubmed/25139658>

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: 184: 14-19. doi: 10.1016/j.virusres.2014.02.007

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

Application of real-time PCR to detect Aleutian Mink Disease Virus on environmental farm sources

A. Prieto, J.M. Díaz-Cao, R. Fernández-Antonio, R. Panadero, P. Díaz, C. López, P. Morrondo, P. Díez-Baños, G. Fernández

Vet. Microbiol. 2014: pii: S0378-1135(14)00364-2. doi: 10.1016/j.vetmic.2014.07.024. [Epub ahead of print]

<http://www.ncbi.nlm.nih.gov/pubmed/25183237>

Validation of an automated ELISA system for detection of antibodies to Aleutian mink disease virus using blood samples collected in filter paper strips

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Aleutian mink disease virus (AMDV) is the cause of a chronic immune complex disease, Aleutian disease (AD), which is common in mink-producing countries. In 2005, implementation of an AMDV eradication programme in Finland created a need for an automated high-throughput assay. The aim of this study was to validate an AMDV-VP2 -recombinant antigen ELISA, which we developed earlier, in an automated assay format for the detection of anti-AMDV antibodies in mink blood and to determine the accuracy of this test compared with the reference standard (counter-current immunoelectrophoresis, CIEP).

A blood sampling method based on filter paper 12-strips (blood combs) and a device to introduce these strips to an ELISA plate for elution of the samples was developed. Blood and serum samples were collected from 761 mink from two farms with low (2%) and high (81%) seroprevalences of AMDV infection in 2008. ELISA sensitivity and specificity were estimated with a Bayesian 2-test 2-population model that allowed for conditional dependence between CIEP and ELISA. Agreement between the two tests was assessed with kappa statistic and proportion agreement.

The sensitivity and specificity of the automated ELISA system were estimated to be 96.2% and 98.4%, respectively. Agreement between CIEP and ELISA was high, with a kappa value of 0.976 and overall proportion agreement of 98.8%.

The automated ELISA system combined with blood comb sampling is an accurate test format for the detection of anti-AMDV antibodies in mink blood and offers several advantages, including improved blood sampling and data handling, fast sample throughput time, and reductions in costs

Virol. J. 2014: 11:141. doi: 10.1186/1743-422X-11-141

Testing for aleutian mink disease virus in the river otter (*Lontra canadensis*) in sympatry with infected American mink (*Neovison vison*)

J. Bowman, A.G. Kidd, L.A. Nituch, C. Sadowski, A. L. Schulte-Hostedde

Aleutian mink disease virus (AMDV) occurs in the American mink (*Neovison vison*) in wild populations and on mink farms and can cause illness

and death. The North American river otter (*Lontra canadensis*) may be exposed to AMDV because of shared space and habitat with mink. Using serology and real-time PCR, we tested river otters across Ontario for AMDV infection. We found no evidence of infection in otters, a surprising finding given the sympatric distribution, niche overlap, and close phylogenetic relationship of the river otter and the American mink. Our results are consistent with the hypothesis that the major point of spillover of AMDV between mink farms and wildlife is manure and composting carcasses on mink farms. Mink farms in Ontario are generally in agricultural landscapes; it is unlikely that river otter use these habitats and thus are likely not exposed to AMDV. We found no evidence that AMD is an important disease for the river otters in Ontario.

J. Wildl. Dis. 2014: 50(3): 689-693. doi: 10.7589/2013-10-286

<http://www.ncbi.nlm.nih.gov/pubmed/24807350>

Molecular characterization of the small nonstructural 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.

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

Development of a PCR-RFLP assay for the detection and differentiation of canine parvovirus and mink enteritis virus

C. Zhang, Y. Yu, H. Yang, G. Li, Z. Yu, H. Zhang, H. Shan

J. Virol. Methods. 2014: pii: S0166-0934(14)00368-1. doi: 10.1016/j.jviromet.2014.09.014 [Epub ahead of print]

<http://www.ncbi.nlm.nih.gov/pubmed/25256910>

Novel circovirus from mink, China

H. Lian, Y. Liu, N. Li, Y. Wang, S. Zhang, R. Hu

A long-established epidemic of enteritis, caused by an unidentified pathogen distinct from parvovirus, has now been recognized in mink. In 2013, we identified a novel circovirus by degenerate PCR and fully sequenced its genome. This virus differs substantially from currently known members of the genus Circovirus and represents a new species.

Emerg. Infect. Dis. 2014; 20(9): 1547-1549. doi: 10.3201/eid2009.140015

Hepeviridae: An expanding family of vertebrate viruses

R. Johne, P. Dremsek, J. Reetz, G. Heckel, M. Hess, R.G. Ulrich

Infect. Genet. Evol. 2014; 27C: 212-229. doi: 10.1016/j.meegid.2014.06.024

<http://www.ncbi.nlm.nih.gov/pubmed/25050488>

Necrotizing and eosinophilic masticatory myositis in farmed mink: a preliminary description

D.B. Needle, C. Hollinger, G.D. Shelton, S.D. Fitzgerald

J. Comp. Pathol. 2014; 151(2-3): 217-227. doi: 10.1016/j.jcpa.2014.04.017

<http://www.ncbi.nlm.nih.gov/pubmed/25016423>

Detection and Characterization of Avastrovirus Associated with Diarrhea Isolated from Minks in China

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Astroviruses are becoming a growing concern in veterinary and public health. Many astrovirus species are associated with enteric diseases have been described in both mammalian and avian hosts. In the present study, 23 fecal samples from diarrheic

minks were collected in Liaoning and Shandong Province, and an investigation of astrovirus was performed using biochemical methods and RT-PCR assay with specific primers. A total of four mink astroviral isolates were detected from sick minks with diarrhea problems. Further sequencing and characterization of the partial ORF1b gene and ORF2 gene segments revealed low sequence identities (20.0-85.3 and 31.8-87.2 %) with known astroviral strains, indicating the emergence of a novel clade of astroviruses. Some new features of the astroviral genome have also been discovered. The phylogenetic tree revealed that all samples were distantly related to mink astrovirus and were closely related to chicken astroviruses and turkey astroviruses. MK/DL-1, MK/DL-2, MK/SD-1, and MK/SD-2 formed a new clade and were found to be more closely related to astroviruses from birds than to other mink strains, indicating past cross-species transmission and considerable zoonotic potential.

Food. Environ. Virol. 2014: [Epub ahead of print]

<http://www.ncbi.nlm.nih.gov/pubmed/24915926>

Viral metagenomic analysis of feces of wild small carnivores

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Recent studies have clearly demonstrated the enormous virus diversity that exists among wild animals. This exemplifies the required expansion of our knowledge of the virus diversity present in wildlife, as well as the potential transmission of these viruses to domestic animals or humans.

In the present study we evaluated the viral diversity of fecal samples (n=42) collected from 10 different species of wild small carnivores inhabiting the northern part of Spain using random PCR in combination with next-generation sequencing. Samples were collected from American mink (*Neovison vison*), European mink (*Mustela lutreola*), European polecat (*Mustela putorius*), European pine marten (*Martes martes*), stone marten (*Martes foina*), Eurasian otter (*Lutra lutra*) and Eurasian badger (*Meles meles*) of the family of Mustelidae; common genet (*Genetta genetta*) of the family of Viverridae; red fox (*Vulpes vulpes*) of the family of Canidae and European wild cat (*Felis silvestris*) of the family of Felidae.

A number of sequences of possible novel viruses or virus variants were detected, including a theilovirus, phleboviruses, an amdovirus, a kobuvirus and picobirnaviruses.

Using random PCR in combination with next generation sequencing, sequences of various novel viruses or virus variants were detected in fecal samples collected from Spanish carnivores. Detected novel viruses highlight the viral diversity that is present in fecal material of wild carnivores.

Virol. J. 2014: 11: 89. doi: 10.1186/1743-422X-11-89

<http://www.ncbi.nlm.nih.gov/pubmed/24886057>

Mink S38G gene polymorphism and atrial fibrillation in the Chinese population: a meta-analysis of 1871 participants

Y.Y. Li, L.S. Wang, X.Z. Lu

Mink gene S38G polymorphism in the β -subunit of slow activating component of the delayed rectifier potassium channel current potassium channel has been associated with increased atrial fibrillation (AF) risk. However, the individual studies results were still controversial. To investigate the association of Mink S38G gene polymorphisms with AF, a meta-analysis including 1871 subjects from six individual studies was conducted. Mink S38G gene polymorphism was significantly related to AF under allelic (OR:1.380, 95% CI:1.200-1.600, $P < 0.00001$), recessive (OR:1.193, 95% CI:1.033-1.377, $P = 0.017$), dominant (OR:1.057, 95% CI:1.025-1.089, $P < 0.00001$), additive (OR:1.105, 95% CI:1.036-1.178, $P = 0.002$), homozygous (OR:1.128, 95% CI:1.068-1.191, $P < 0.00001$), and heterozygous genetic models (OR:1.078, 95% CI:1.014-1.146, $P = 0.016$). A significant association between Mink S38G gene polymorphism and AF risk was found. G allele carriers may predispose to AF.

ScientificWorldJournal 2014: 768681. doi: 10.1155/2014/768681. [Epub 2014]

<http://www.ncbi.nlm.nih.gov/pubmed/24696659>

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, L. Lu, H. Liu, G. Hu, J. Li, Y. Gong, G. Wang, M. Hu, Shiganyan, Y. Liu

Vet. Microbiol. 2014: 170(3-4): 456-461. doi: 10.1016/j.vetmic.2014.02.025. [Epub 2014 Feb 25]

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

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: 11(3): 409-419. doi: 10.1007/s10393-014-0917-z. [Epub 2014 Mar 7]

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

Effect of body condition on tissue distribution of perfluoroalkyl substances (PFASs) in Arctic fox (*Vulpes lagopus*)

C.B. Aas, E. Fuglei, D. Herzke, N.G. Yoccoz, H. Routti

Arctic animals undergo large seasonal fluctuations in body weight. The effect of body condition on the distribution and composition of 16 perfluoroalkyl substances (PFASs) was investigated in liver, blood, kidney, adipose tissue and muscle of Arctic foxes (*Vulpes lagopus*) from Svalbard (n=18, age 1-3 years). PFAS concentrations were generally highest in liver, followed by blood and kidney, while lowest concentrations were found in adipose tissue and muscle. Concentrations of summed perfluorocarboxylic acids and perfluoroalkyl sulfonates were five and seven times higher, respectively, in adipose tissue of lean compared to fat foxes. In addition, perfluorodecanoate (PFDA) and perfluorohexane sulfonate (PFHpS) concentrations in liver, kidney and blood, and, perfluorononanoate (PFNA) in liver and blood, were twice as high in the lean compared to the fat foxes. The ratio between perfluorooctane sulfonamide (FOSA) and its metabolite perfluorooctane sulfonate (PFOS) was lowest in liver, muscle and kidney while significantly higher proportions of FOSA were found in adipose tissue and blood. The results of the present study suggest that toxic potential of exposure to PFAS among other pollutants in Arctic mammals may increase during seasonal emaciation. The results also suggest that body condition should be taken into account when temporal trends of PFASs.

Environ. Sci. Technol. 2014: [Epub ahead of print]

Genetic epidemiology and pathology of raccoon-derived *Sarcoptes* mites from urban areas of Germany

Z. Rentería-Solís, A.M. Min, S. Alasaad, K. Müller, F.U. Michler, R. Schmäsche, U. Wittstatt, L. Rossi, G. Wibbelt

The raccoon, *Procyon lotor* (*Carnivora: Procyonidae*), is an invasive species that is spreading throughout Europe, in which Germany represents its core area. Here, raccoons mostly live in rural regions, but some urban populations are

already established, such as in the city of Kassel, or are starting to build up, such as in Berlin. The objective of this study was to investigate *Sarcoptes* (*Sarcoptiformes: Sarcoptidae*) infections in raccoons in these two urban areas and to identify the putative origin of the parasite. Parasite morphology, and gross and histopathological examinations of diseased skin tissue were consistent with *Sarcoptes scabiei* infection. Using nine microsatellite markers, we genotyped individual mites from five raccoons and compared them with *Sarcoptes* mites derived from fox, wild boar and Northern chamois, originating from Italy and Switzerland. The raccoon-derived mites clustered together with the fox samples and were clearly differentiated from those of the wild boar and chamois samples, which suggest a fox origin for the raccoon mange infection. These results are evidence of the cross-transmission of *S. scabiei* among wild carnivores. Although our results cannot elucidate whether raccoons became infected by frequent interaction with endemically or epidemically infected foxes or whether these cases resulted from occasional contacts among these animal species, they do nevertheless show that pathogens can be shared among urban populations of native and invasive carnivores.

Med. Vet. Entomol. 2014: Suppl 1: 98-103. doi: 10.1111/mve.12079

Unexpected diversity of the cestode *Echinococcus multilocularis* in wildlife in Canada

K.M. Gesy, J.M. Schurer, A. Massolo, S. Liccioli, B.T. Elkin, R. Alisauskas, E.J. Jenkins

Echinococcus multilocularis is a zoonotic cestode with a distribution encompassing the northern hemisphere that causes alveolar hydatid disease in people and other aberrant hosts. *E. multilocularis* is not genetically uniform across its distribution, which may have implications for zoonotic transmission and pathogenicity. Recent findings of a European-type haplotype of *E. multilocularis* in wildlife in one location in western Canada motivated a broader survey of the diversity of this parasite in wildlife from northern and western Canada. We obtained intact adult cestodes of *E. multilocularis* from the intestines of 41 wild canids (wolf - *Canis lupus*, coyote - *Canis latrans*, and red fox - *Vulpes vulpes*), taeniid eggs from 28 fecal

samples from Arctic fox (*Vulpes lagopus*), and alveolar hydatid cysts from 39 potential rodent intermediate hosts. Upon sequencing a 370-nucleotide region of the NADH dehydrogenase subunit 1 (*nad1*) mitochondrial locus, 17 new haplotypes were identified. This constitutes a much higher diversity than expected, as only two genotypes (European and an Asian/North American) had previously been identified using this locus. The European-type strain, recently introduced, may be widespread in wildlife within western Canada, possibly related to the large home ranges and wide dispersal range of wild canids. This study increased understanding of the biogeographic distribution, prevalence and genetic differences of a globally important pathogenic cestode in northern and western Canada.

Int. J. Parasitol. Parasites. Wildl. 2014; 3(2): 81-87
doi: 10.1016/j.ijppaw.2014.03.002

Genetically distinct isolates of *Spirocerca* sp. from a naturally infected red fox (*Vulpes vulpes*) from Denmark

M.N. Al-Sabi, M.S. Hansen, M. Chriél, E. Holm, G. Larsen, H.L. Enemark

Vet. Parasitol. 2014; 205(1-2): 389-396. doi: 10.1016/j.vetpar.2014.07.002

<http://www.ncbi.nlm.nih.gov/pubmed/25060226>

Enteric Colonization by *Staphylococcus delphini* in Four Ferret Kits with Diarrhoea

J.M. Gary, I.M. Langohr, A. Lim, S. Bolin, C. Bolin, I. Moore, M. Kiupel

J. Comp. Pathol. 2014; pii: S0021-9975(14)00136-4
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<http://www.ncbi.nlm.nih.gov/pubmed/25246181>

The first report of *Angiostrongylus vasorum* (Nematoda; Metastrongyloidea) in Poland, in red foxes (*Vulpes vulpes*)

A.W. Demiaszkiewicz, A.M. Pyziel, I. Kuligowska, J. Lachowicz

Angiostrongylus vasorum belongs to the superfamily of Metastrongyloidea. This nematode occurs in foxes, dogs and other predators. The Nematode *A. vasorum* place themselves in the pulmonary artery and its branches, and in the right ventricle and atrium of the heart. Numerous species of land snails are the intermediate hosts of the parasite. In 2013, lungs and hearts of 76 foxes shot in the Forest District Głęboki Bród in Augustowska Primeval Forest were parasitologically necropsied. Four of the examined foxes were infected with the nematode *A. vasorum*, a prevalence of 5.2%. In one fox pericardium there were 6 male and 6 female nematodes. In the remaining three foxes nematodes were localized in the pulmonary artery. In two foxes 2 specimens of nematodes were detected (male and female, and two females) while 1 female was detected in the other fox. This is the first report of the presence of the nematode *A. vasorum* in fox in Poland.

Acta. Parasitol. 2014; 59(4): 758-762.
doi: 10.2478/s11686-014-0290-7

<http://www.ncbi.nlm.nih.gov/pubmed/25236289>

First Characterization in China of *Encephalitozoon cuniculi* in the Blue Fox (*Alopex lagopus*)

X.I. Meng, J. Zheng, X. He, H. Jia, Y. Zhang

Encephalitozoon cuniculi is a microsporidian parasite that infects a wide range of vertebrates, including primates. It has recently emerged as an opportunistic parasite of patients infected with the human immunodeficiency virus. The blue fox (*Alopex lagopus*; also known as the arctic fox) is one of the most susceptible species for

encephalitozoonosis. Here, we report an outbreak of encephalitozoonosis at a fox farm in China. The isolated parasites displayed the typical morphology of *E. cuniculi* as assessed by Masson's trichrome staining. Analysis of the internal transcribed spacer sequence indicated that the isolated parasite is a genotype III strain of *E. cuniculi*. Furthermore, phylogenetic analysis of the PTP1 gene verifies classification of this new strain (termed LN-1) with other genotype III *E. cuniculi* strains, though the PTP3 and SWP1 sequences diverge from the reference strain. This is the first report of encephalitozoonosis in farmed blue foxes in China.

J. Eukaryot. Microbiol. 2014.

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<http://www.ncbi.nlm.nih.gov/pubmed/24995428>

Mapping of polar fox renal cortex proteins using two-dimensional gel electrophoresis and mass spectrometry--a preliminary study

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The aim of the present study was to establish protein map of polar fox (*Alopex lagopus*) renal cortex. Kidney cortex proteins of isoelectric point ranging from 3 to 10 were analysed using two-dimensional

electrophoresis and MALDI-TOF mass spectrometry. Sixteen protein spots corresponding to thirteen different gene products were identified. These proteins were divided into following groups: lipid and fatty acid metabolism, amino acid metabolism, energetic pathways, regulatory proteins, transport proteins and structural proteins. This is the first attempt to create reproducible 2-D map, of renal cortex proteins characteristic for polar foxes, used as animal model for carnivores. It is worth emphasizing that the results of this study may broaden currently available protein databases.

Pol. J. Vet. Sci. 2014: 17(2): 231-237

<http://www.ncbi.nlm.nih.gov/pubmed/24988848>

Evaluation of spore wall protein 1 as an alternative antigen for the diagnosis of Encephalitozoon cuniculi infection of farmed foxes using an enzyme-linked immunosorbent assay

X.I. Meng, J. Zheng, Y. Gao, Y. Zhang, H. Jia

Vet. Parasitol. 2014: 203(3-4): 331-334. doi: 10.1016/j.vetpar.2014.03.011

<http://www.ncbi.nlm.nih.gov/pubmed/24830821>

Actual Mink Research 2014
Meeting at Research Centre Foulum
Faculty of Science and Technology
Aarhus University, Denmark

Can we get more mink kits to survive?

J. Malmkvist

The early kit survival day 0-3 after delivery is one of the critical points, determining the potential of increasing the number of kits produced per delivering female in mink production. Previous studies have documented that birth problems (influenced by e.g. female body condition and nest building materials) increase the risk of early kit mortality, reduced maternal care and kit vitality. The mated females are motivated to build a nest, and present data indicate that the onset of dam nest building can take place as early as 3-4 weeks prior to delivery. Nesting materials of an insufficient nature (e.g. wood shavings only) increase the stress hormone concentration in the dams and reduce kit survival. In contrast, several other types of nesting materials, given in the pre-delivery period, reduce dam stress and improve both in-nest temperatures and kit survival. In a new study, we compare six different combinations of nesting material to mated yearlings, either as simultaneous Free Choice (FC) or as a prepared Mixture (M): 1: FC of straw, wood wool and rabbit wool (N=60), 2: FC of straw, wood wool and lamb's wool (N=60), 3: FC of straw, lamb's wool (N=60), 4: M, straw with 2.5 % lamb's wool (N=60), 5: M, straw with 10 % lamb's wool (N=60), and 6: straw (N=60), all groups with *ad libitum* access in the cage from the time of transfer of the dam to the maternity (after mating March 25) until 7 days after delivery. The hypothesis tested is that high cohesion and increase thermoregulatory capacity of the nest building material is beneficial. The data collection is on-going and include nest building (scored weekly), in-nest climate (temperature and humidity every 15 min. by loggers), kit survival and growth (day 1-7) and dam stress hormone concentration measured non-invasively (faeces cortisol metabolites before and after delivery). Preliminary results are discussed in order to get input to next years' trials on how we

can get more mink kits to survive during the early postnatal period.

Meeting at Research Centre Foulum, Faculty of Science and Technology Aarhus University, Denmark. DCA Report no. 45, September 2014 (in Danish) p. 6-12. Authors' abstract.

Partner preference in captive mink - Paternity correlates with female mink interest in male urine and faeces, not with number of matings or visits of these

C. L. Noera, M. Stelvig, T. Dabelsteen

Chemical communication plays an important role for solitary carnivore species especially during the breeding season. Male and female mink mark their home ranges with urine and faeces and use their sense of smell to find and assess each other during the breeding season. This behaviour and the underlying sensory capacity is likely to be present also in captive mink since mink have been bred in captivity for relatively short time evolutionary speaking.

This study tested females of the American wild type mink in the breeding season using free choice experiments with two males. The results show a correlation between female mink interest in male urine and faeces and the same male minks' chance of paternity. 17 out of 20 females showed a preference for the same male mink over a four days stimulus preference trial (presenting male urine and faeces). 19 females were subjected to a successive partner preference test. All but one female mated with both males on two or more days. However, 12 of the females had offspring, which could be assigned to only one male by DNA paternity tests, and 10 of these females' choice of partner during the stimulus preference test (urine and faeces) correlated with the actual partner of their offspring. Contrary to this there were no correlations between

paternity and partner preference (free choice of two male mink).

The results suggest that we may use urine and faeces samples from possible mates to test, which mate a female will prefer to farther its offspring. This may reduce the need for matings with more males as well as aggression between the two sexes.

Meeting at Research Centre Foulum, Faculty of Science and Technology Aarhus University, Denmark. DCA Report no. 45, September 2014 (in Danish) p. 13-21. Authors' abstract.

High milk production if mink dams are fed ad libitum from parturition

M.N. Pinkalski, S.H. Møller

Abstract

According to Danish legislation it is not allowed to wean mink kits before they are 8 weeks old. But the welfare of the mother and the kits are often suffering as she has no or very little milk left at eight weeks, and no chance of escaping the kits. We wanted to investigate if changing the feeding strategy in the beginning of the lactation period could prolong the period and thereby improve the welfare of mother and kits. 50 female mink were fed ad libitum and 50 female mink were fed restrictively in the first four weeks of the lactation period. 5 females were then killed from each treatment in each of the following weeks after birth; 4, 6, 7 and 8, to be able to measure and weigh the mammary gland tissue. The result showed that six weeks after birth the female fed ad libitum had significantly more mammary gland tissue than females fed restrictively. By 7 weeks there was no difference in the amount of tissue. We also investigated the effect of litter size on the amount of mammary tissue, but this did not seem to have an effect. Though the milk production did not last longer when the females were fed ad libitum, we showed that the females had more milk available in the period from 4-7 weeks after birth.

Meeting at Research Centre Foulum, Faculty of Science and Technology Aarhus University, Denmark. DCA Report no. 45, September 2014 (in Danish) p. 22-27. Authors' abstract.

ERFA-groups can work effectively with animal welfare with methods from stable schools

B.I.F. Henriksen

The aim of the study was to evaluate if stable schools can be a useful tool for farmers to improve management for the benefit of mink welfare. Stable schools are knowledge exchange between farmers that are working towards a common goal, being able to give good and practical advice to each other. The concept is based on Farmer field schools, developed and used in developing countries, were the common learning process and equality among participants of a group are characteristic. Several Danish mink farmers are familiar with ERFA-groups which also are farmers meeting together. These groups do often invite an advisor, and focus on general issues instead of farm specific problems. The intensive and more binding stable schools with only farmers and a facilitator has not been tested on mink farms.

We therefore established two stable schools with farmers from five mink farms in 2013. The meetings were on the respective farms, and every farm was visited once within a year. The host-farmer presented two challenges he/she wanted to work with and get inputs to from the group, and one success story. Qualitative interviews were conducted with the farmers to evaluate their perception of stable schools.

The first results from the study show that the farmers were generally very positive to the structural way of working. They especially emphasized the importance of a person leading and facilitating the process. It came up that some of the farmers would try to implement methods from stable schools into their ERFA-group, like facilitation or letting the host-farmer chose what to discuss at the meeting. It did not seem to be any problems in discussing challenges relevant for other periods than the actual day of the farm-visit. One problem might be that some challenges were common on several farms, and had already been discussed several times when the last host-farmer should choose what to work with. Some of the participants in the stable school had done several changes in their management as a result of the discussions in the group. Others had not made any changes, but joined the group mainly to share their experiences with the others in the group.

Based on the preliminary results from the study, and results from other studies of stable schools we can conclude that farmers are generally very positive to the systematically way of working in the groups, and do see animal welfare as an important issue to work with.

Meeting at Research Centre Foulum, Faculty of Science and Technology Aarhus University, Denmark. DCA Report no. 45, September 2014 (in Danish) p. 28-33. Authors' abstract.

Investigation of Anhedonia in farm mink

T. Schou, C. Pertoldi, J. Malmkvist

The housing conditions on mink farms and the minks' reaction to the environment indicate that some farmed mink may experience stress of an intermittent type for longer periods. However there is a lack of indicators of intermediate chronic stress in farm mink. Psychological and physical chronic stress has shown to increase the risk of developing depression and disease for both humans and animals. Because of the similarity of depression symptoms between animals and humans, an animal model of depression has been developed for rodents. With the use of a chronic unpredictable mild stress paradigm (CMS) depression can be elicited in rodents. Anhedonia (defined as: a decreased capacity to experience pleasure of normal rewarding stimuli) is one of three core symptoms of major depression and is used as an indicator of elicited depression in rodents. Anhedonic rodents have a reduced rewarding sensitivity when examining normally rewarding stimuli such as sweet solutions. The reduced rewarding sensitivity cause reduced rewarding value of the substances, which is measured by reduced preference or consumption rate. Further, several studies have examined side effects of anhedonia e.g. reduced exploration, reduced aggression, reduced sexual activity, reduced weight, increased conflict behaviour and increased craving-like behaviour. The aim of this study was to develop a similar method of measuring anhedonia in farm mink. Thus this thesis is divided into two sections: 1) investigating substances that mink find rewarding for use in an anhedonia test; 2) Investigating anhedonia in farm mink.

1) The rewarding value of manipulated farm feed (MFF) and wet cat feed (WCF) were tested to identify a rewarding substance. The rewarding value

was measured as consumption rate. The mink females found WCF 26.8% more rewarding compared to the MFF. The rewarding values were found useable for an anhedonia test.

2) With the use of several well-known welfare assessment procedures (Faecal Cortisol metabolites, Stick test, Novel Object test, Stereotypy observation, Fur chewing evaluation and weight) and the rewarding value of WCF and MFF a test for the occurrence of anhedonia in farm mink was developed and carried out. The test did not find that dams with high kit loss (used as a measure of pre-pregnancy and prenatal stress) were in greater risk of having anhedonia in comparison with dams with a total kit survival. In addition a correlation test was performed. Mink females with low body weight were found to show signs of anhedonia with positive correlations for the following four measures: 1) decreased consumption rate; 2) decreased exploration; 3) decreased aggression; 4) increased conflict behaviour (in the Stick test). Thus, these variables were – as expected - correlated for anhedonic mink females as found in rodents. However some conflicting correlations were also found as consumption rate was positively correlated with craving-like behaviour and conflict behaviour in the Novel Object test. These results indicate that there is a potential and a need for further investigation and development of an anhedonia test for farm mink. The need of an anhedonia test has been emphasized in the WelFur protocol for farm mink as a positive emotional state is one of 12 welfare assessment criteria (Mononen *et al.* 2012), which is affected by an animal's depressive state.

Meeting at Research Centre Foulum, Faculty of Science and Technology Aarhus University, Denmark. DCA Report no. 45, September 2014 (in Danish) p. 34-39. Authors' abstract.

Early weaning and separation to group housing may reduce the number of bite-marks in the leather side of mink pelts

S. H. Møller, S.W. Hansen

A selection experiment has shown that bite-marks in mink can be efficiently reduced when the indirect genetic effects of social interaction between the mink in a cage is included in group selection. Environmental factors, however, also has significant effect on the number of bite-marks, and the total

number of bite-marks was first reduced after four years of selection. We therefore tested the hypothesis that early weaning and separation to group housing would reduce the number of bite-marks in the leather side of the pelts. Weaning and separation at seven weeks was tested against weaning at eight weeks and separation at eleven weeks on the research farm at Aarhus University and at a private farm. Early weaning and separation to group housing reduced the number of bite-marks significantly at the private farm but not at the research farm. It was concluded that the age at weaning and separation is not a key factor in relation to bite-marks in mink. The search for environmental or management factors affecting the number of bite-marks in mink therefore continues.

Meeting at Research Centre Foulum, Faculty of Science and Technology Aarhus University, Denmark. DCA Report no. 45, September 2014 (in Danish) p. 40-43. Authors' abstract.

Production and welfare consequences by keeping female mink in groups, in standard cage vs. climbing cage and having access to tubes with large and small diameter

S.W. Hansen

The aims of this experiment were three fold; 1) to elucidate the production and welfare consequences of keeping 2, 3 or 4 females together in climbing cages throughout the growing season (July to November), 2) to document the production and welfare consequences of keeping pairs of mink (male-female) in climbing cages instead of in standard cages and 3) to investigate whether a large (12 cm) or small (4 cm) diameter of the tubes used as enrichment affects the occurrence of fur chewing in mink differently.

The experiment included 312 mink distributed on five groups kept in standard cages or climbing cages. Half of the mink in each group had access to a large tube and the other half access to a small tube (Table 1). All mink had access to one shelf, nest box and water and were fed ones a day. In the climbing cages was the shelf placed in the top cage.

Table 1. Experimental design

Group	Cages (N)	Mink (N)	Tubes	Cage type
MFC: 1 female + 1 male	24	48	Large/ small	Climbing
MFS: 1 female + 1 male	24	48	Large/ small	Standard
F2: 2 females	24	48	Large/ small	Standard
F3: 3 females	24	72	Large/ small	Climbing
F4: 4 females	24	96	Large/ small	Climbing
Total	120	312		

The mink were weighed 3 times and the feed allowance registered daily automatically. The behaviour and location of the mink were observed by scan sampling 8 times with 1 hour interval in 8 days (8h-16h) distributed throughout the experimental period. In November, all the mink were killed individually by Co2 and labeled with an ID number in the nose. The bodies were examined for injuries, wounds, swellings of especially the skin of the tip of the tail and fur chewing. In connection with the pelting process, the bright leather side of the matured pelt was examined for bite marks.

The main consequences of housing more than two females in the same cage were an increase in the number of bite marks and an increased risk of injuries. The number of females in the cage reduces the use of the shelf and if the females were more than two, they were resting more together than if they were kept in pairs. The number of females did not affect the use of nest box or activity. Two and three females together had the best growth and the highest incidence of fur chewing than four females or male-female pairs.

The two types of cages did not affect the females' use of the cage differently. Females with access to first floor in the climbing cage reduced their stay in bottom cage accordingly. Cage type had no effect on the females' use of the nest box. After the autumnal equinox, the use of the shelf was not different in the standard cage or climbing cage. The location of the females alone or together with the male was independent of cage type. There was no indication that females kept in pairs with a male were resting more alone in climbing cages than in standard cages. The activity was highest in females in standard cage. Cage type had no effect on the incidence of fur chewing, bite marks or wounds and

did not affect growth or feed allocation (ad libitum feeding). The temperament of the females was independent of the cage type. It can thus be concluded that housing female mink with a male in a climbing cage does not reduce the welfare, but it was hard to document welfare improvement compared to housing in standard cages. The diameter of the tubes did not affect the occurrence of fur chewing.

Meeting at Research Centre Foulum, Faculty of Science and Technology Aarhus University, Denmark. DCA Report no. 45, September 2014 (in Danish) p. 44-54. Authors' abstract.

Simulations give the most effective breeding plans

K. Meier, A.C. Sørensen, J.P. Thirstrup, M.S. Lund

Today, the use of breeding schemes with breeding value estimation is possible for the individual Mink farmer. However, the traits of interest differ in complexity and thus breeding progress differs for the individual traits. One way to optimize breeding for complex traits is by using genomic selection. We used stochastic simulations to evaluate genomic selection in Mink breeding. By comparing the current breeding scheme with different scenarios of genomic selection, we assessed the genetic gain and total economic gain for the traits analysed.

Our results show that total economic gain is higher using genomic selection compared to traditional breeding. The gain varies dependent on the accuracy and genotyping strategy. Even though only 10% of the males are genotyped and the accuracy is low, total economic gain is higher compared to traditional breeding. Our results also show that it is possible to increase genetic gain for litter size, pregnancy rate and skin quality, complex traits that have been difficult to improve with traditional breeding.

Meeting at Research Centre Foulum, Faculty of Science and Technology Aarhus University, Denmark. DCA Report no. 45, September 2014 (in Danish) p. 55-59. Authors' abstract.

Low correlation between fur quality traits evaluated on live animals and on skin after pelting suggests evaluations performed on live animals as a less effective selection method

J. Thirstrup, J. Jensen, K. Meier, A.C. Sørensen, M.S. Lund

The quality and size of the skin is important for the price of the mink. Therefore, there has been genetic selection for large skin of high quality. Animals are selected for either breeding or culling in November before pelting, but the prices are determined based on skin evaluations after pelting. Selection for high skin quality and large skin size is therefore performed on live animals and is an indirect measure of skin quality.

The aim of the analysis was to estimate genetic variance and co-variance of fur quality traits, weight, and skin size evaluated on live animals in November and on skin after pelting. The analysis was performed in order to evaluate if selection on live animals is effective as indication for skin evaluations. Heritabilities were calculated from the estimated variance components.

Four thousand four hundred and eighty mink born and raised at Aarhus University research farm in Foulum in 2013 were evaluated for general quality, wool density, silkiness and weights in November before pelting. Three thousand five hundred and eighty-eight of those mink were evaluated for the same three fur quality traits as well as skin size after pelting. Variance and co-variance were estimated using Average Information Restricted Maximum Likelihood (AI-REML) algorithms implemented in the DMU package for analyzing multivariate mixed models.

Heritabilities were in the range 0.11 – 0.57 for traits evaluated on live animals and were in the range 0.29 – 0.63 for traits evaluated on skin. Correlations between single traits evaluated on live animals and skin, respectively, were in the range 0.32 – 0.81. Furthermore, we found negative correlations between weight of live animals and fur quality traits evaluated on skin in the range of -0.36 – -0.41.

Correlations below 1 for single traits indicate that selection potential is not fully explored. Furthermore, negative correlations between weights of live animals and fur quality traits evaluated on skin potentially can result in deterioration of quality,

if selection primarily is aimed at increased skin size and hence mink with high weight are selected. We therefore recommend either index selection on multiple traits simultaneously, selection based on skin and pedigree information and/or genomic selection as more effective breeding plans. Especially genomic selection would be effective in utilizing quality traits measured after pelting.

Meeting at Research Centre Foulum, Faculty of Science and Technology Aarhus University, Denmark. DCA Report no. 45, September 2014 (in Danish) p. 60-64. Authors' abstract.

Experimental wounds in mink – a tool to investigate wound healing, assessment and management

A. Jespersen, A.S. Hammer, H.E. Jensen

Wounds are a significant contributor to mink mortality during growth season and can be used as an indicator for reduced welfare in mink production. Loss of mink due to wounds and injuries on pelts equals lost profit. To minimize these issues it is both important that we know how to treat wounds effectively and when it is no longer acceptable from a welfare perspective to keep a wounded mink alive. This choice should be made through wound assessment based on objective criteria established through solid investigations of wound healing processes. For the purpose of characterizing the wound healing processes in mink, we have developed a wound model that can be used to answer a variety of questions related to how we should handle wound problems in a clinical setting. The model is preferred over spontaneously occurring wounds because it gives the opportunity to standardize animal material and study conditions to increase statistical significance. The experiments are carried out in healthy mink under general anesthesia. After clipping and aseptic preparation of the wound site, a square, 2x2 cm full thickness piece of skin is removed from the back midline and/or the side of the neck with scalpels and scissors. The anesthesia is reversed and the mink are returned to their cages with regular observation and pain medication on the first day after surgery. The wound conditions thus are comparable to those of spontaneously occurring wounds. After a predetermined time period defined by the specific purpose of the study, the mink are euthanized and

subjected to full necropsy and sampling of tissue for histopathological investigation. The wound model is currently being used to study individual differences and time perspectives in wound healing, the relationship between wound related pain, stress and behavior, topical wound treatment, wound infections and the effect of feed protein content on wound healing.

Meeting at Research Centre Foulum, Faculty of Science and Technology Aarhus University, Denmark. DCA Report no. 45, September 2014 (in Danish) p. 65-70. Authors' abstract.

Dietary supplements to a low protein diet may affect the incidence of hepatic lipidosis in mink

C.F. Matthiesen, A-H. Tauson

Hepatic lipidosis, i.e. hepatic lipid infiltration, is multifactorial and may be caused by a number of factors such as low protein provision, feed deprivation, rapid accretion or mobilisation of body fat, all resulting in metabolic and nutritional imbalances. Our objectives were to investigate if supplementation of a low protein diet with nutrients acting as methyl donors, antioxidants or having insulinogenic properties could lower the incidence of hepatic lipidosis in growing mink from August to November when mortality, caused by hepatic lipid infiltration, often is high.

Seventy-two young mink, 36 females and 36 males, were used in the study. The animals were allocated to six treatment groups each consisting of 6 males and 6 females. The control group was fed a conventional farm feed (29.6:54.2:16.2% of metabolisable energy (ME) from protein: fat: carbohydrate) whereas the 5 experimental groups were fed a low protein diet (20% of ME from protein, prepared by adding 5.5% corn starch, 3.5 corn oil, 6% potato mash powder, 1% sugar beet pulp and 8% water to the control diet) and supplemented with the crystalline amino acids alanine (0.8% - negative control - group 1), taurine (0.5% - group 2), arginine (0.5% - group 3), and methionine (0.5% - group 4) or the carbohydrate dextrose (2.5% of the corn starch was replaced with dextrose - group 5). Feed intake was recorded as an average per group per day. The animals were weighed and blood sampled once every third week. The liver was removed and the liver and body weights were recorded of all animals that died during the

experiment. All remaining animals were euthanized at the end of the experiment when liver, kidney and body weights were recorded. All livers were frozen for later analysis. Liver weight was significantly affected ($P < 0.001$) by dietary treatment, status (dead or alive) ($P < 0.001$) and interactions between dietary treatment and status ($P < 0.001$). This resulted in significantly heavier livers among animals diagnosed with hepatic lipidosis compared to livers from euthanized animals without hepatic lipidosis.

A low protein diet (20% of ME from protein) with lower content of all amino acids compared to a traditional farm feed, increased the incidence of fatty livers. If the methionine content of the low protein diet was just above the methionine content of the farm feed there was no evidence of fatty livers. These results were confirmed by the chemical composition of the liver where there was no difference in fat content in the livers of the mink fed a low protein with a methionine level just above the methionine of the control group fed with traditional farm feed.

Meeting at Research Centre Foulum, Faculty of Science and Technology Aarhus University, Denmark. DCA Report no. 45, September 2014 (in Danish) p. 71-77. Authors' abstract.

How can we get more water for mink kits in late lactation

T.N. Clausen, P.F. Larsen

Water supply is very important for welfare and growth of mink in late lactation. Lactating females' milk production is up to 200 ml per day around day 28 and therefore she has a high need of good quality water. The drinking water system is very important for the kits, drip water system or rabbit water bowls in late lactation have been shown to be of benefit. In this study we focused on adding fibers or Feed binders to increase the water content in the feed and make it easier for the kits to fulfill their need of water. Results show that the choice of fiber is important for improving the water balance for the mink kits and so far the perfect fiber has not been found.

Meeting at Research Centre Foulum, Faculty of Science and Technology Aarhus University, Denmark. DCA Report no. 45, September 2014 (in Danish) p. 78-82. Authors' abstract.

**6th International Conference on the Assessment of Animal Welfare
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Assessment score of mink in the nursing period decreases with date of assessment

B.I.F. Henriksen, S.H. Moller

Abstract no. 19 in Proceeding at 6th International Conference on the Assessment of Animal Welfare at Farm and Group Level, pp 98

DOI: 10.3921/978-90-8686-798-1

Development of the WelFur on-farm welfare assessment protocol for the Finn raccoon

Koistinen, H. Huuki, J. Mononen, L. Ahola

Abstract no. 58 in Proceeding at 6th International Conference on the Assessment of Animal Welfare at Farm and Group Level, pp 137

DOI: 10.3921/978-90-8686-798-1

Test of procedures for observation of stereotypy in mink during winter

S.H. Moller, S.W. Hansen, B.I.F. Henriksen

Abstract no. 24 in Proceeding at 6th International Conference on the Assessment of Animal Welfare at Farm and Group Level, pp 98

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WelFur mobile, a mobile application for measurements in farms

M. Reichstadt, R. Botreau and Y. Gaudron

Abstract no. 68 in Proceeding at 6th International Conference on the Assessment of Animal Welfare at Farm and Group Level, pp 147

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The development of the fox protocol: the second refinement phase

J. Mononen, T. Koistinen, H. Huuki, L. Ahola

Abstract no. 57 in Proceeding at 6th International Conference on the Assessment of Animal Welfare at Farm and Group Level, pp 136

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Implementation of the WelFur protocols for farmed fur animals

L. Ahola, H. Huuki, J. Mononen, T. Koistinen

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