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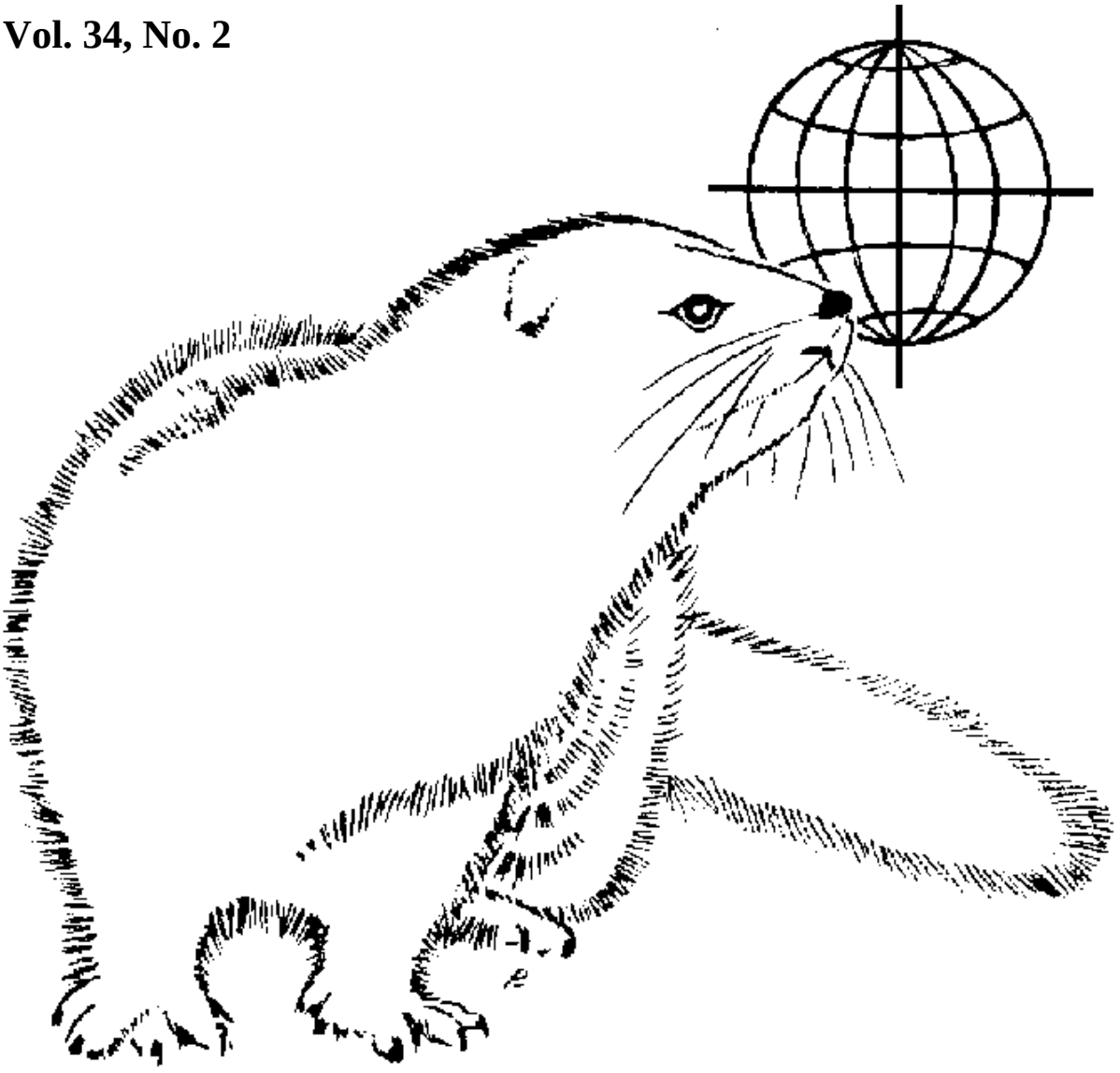

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Notes from the Editor

This issue of Scientifur 34, 2 contains a reviewed publication presenting a study of the effect of dietary ascorbic acid supplementation on tissue vitamin A and vitamin E levels and antioxidant enzyme activity in both standard and sapphire mink.

This issue presents also abstracts dealing with molecular genetic studies in fox and mink. Compared to other animal husbandry species, molecular genetic studies in fur animals are still in the making. A meiotic linkage map of the silver fox is aligned and compared to the dog genome.

Abstracts presenting linkage maps and molecular characterization of color variants in mink are presented as well. Other abstracts inform about studies e.g. dealing with Aleutian mink disease virus infection and behaviour.

Submission to Scientifur of results from all scientific investigations regarding fur animal production is encouraged. It is the aim that all scientific work related to fur animal production should be reported in Scientifur.

Vivi Hunnicke Nielsen
Editor Scientifur

Effect of dietary ascorbic acid supplementation on tissue vitamin A and vitamin E levels and antioxidant enzyme activity in standard and sapphire mink (*Neovison vison*)

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Abstract

The effect of high content of dietary ascorbic acid (vitamin C) on vitamin A and the antioxidant system, vitamin E, the level of glutathione (GSH) and enzymes, superoxide dismutase (SOD) and catalase (CAT) in mink tissues has been studied. There were two experimental groups of mink, sapphire and standard brown, and 100 mg of vitamin C per mink were supplemented to their diet for 20 days. The study has shown that the vitamin A concentration in the tissues of the experimental mink decreased compared with the controls. The vitamin E content in serum and many tissues of both experimental groups of mink was higher than in the control groups. The concentration of vitamin E in the kidney of the experimental sapphire mink (10.66±1.6 μg/g) was significantly lower in comparison with the control group (36.87±14.16) and the experimental brown mink (20.97±6.12). SOD and CAT activities and level of GSH changed slightly. The results show that in sapphire mink the vitamins A and E level changed more intensively than in standard mink with the ascorbic acid high dose.

Keywords: antioxidant system, ascorbic acid, catalase, glutathione, mink, superoxide dismutase, vitamin A, vitamin E.

Introduction

The ascorbic acid possesses a wide spectrum of antioxidant properties and it is found practically in all tissues of mammals. In the organism vitamin C functions as part of the complex system of biological antioxidants consisting of enzymatic and nonenzymatic parts (Menyschikova *et al*., 2006). The key enzymes of the antioxidant system are SOD and CAT, and low-molecular antioxidants include vitamins A, E, C and glutathione.

Fur animals as the majority of mammals are capable of synthesizing ascorbic acid in the organism. Ascorbic acid added to the diet of mink increased the hemoglobin level and erythrocytes number, improved milk production in females and newborn viability. Fur animals assimilated vitamin A better in the diet with vitamin C, and as an antioxidant the ascorbic acid can replace a larger part of tocopherol required by the animal. The increased vitamin C content in the diet raised the tocopherol level in blood plasma and tissues, and also partially removed clinical signs of avitaminosis E. It is known that in the sapphire mink the congenital lysosomes defect similar to Chediak-Higashi syndrome in humans and some animals is observed (Uzenbaeva *et al*., 2007). When treated with large doses of ascorbic acid, this shows positive effects on leukocytes function (Carr & Frei, 1999). Despite considerable positive effects there exist data on negative influence of large quantities of dietary ascorbic acid on mink

(Helgebostad, 1984). Mink of different genotypes possess a number of physiological and morpho-biochemical peculiarities. The mink genotype also influences the antioxidant system and its activity under the influence of various environmental factors (Ilyina *et al.*, 2007). The purpose of this study was to make comparative research of the influence of high levels of ascorbic acid on the antioxidant system in tissues of sapphire and standard dark brown mink.

Materials and Methods

Animals, diet and treatment groups

Two colour types of mink (*Neovison vison*), standard and sapphire, were used. All the animals were healthy. Five-month-old mink (females and males) of each colour were divided into control and experimental groups. Initial body weight of dark brown males was ~ 2.0 kg, sapphire males ~ 1.57 kg; dark brown females ~ 1.28 kg and sapphire females ~ 1.10 kg. The standard (n=8) and sapphire (n=5) control animals were fed with a standard farm diet. The metabolizable energy (ME) is calculated on the basis of table values for feed ingredients. Diet composition (g/418 kJ of ME) was: meat soft by-products (5-10), meat-bone by-products (6-10), fish meal (15-20), minced fish (3-5), cooked grain (14.5-15.5), vegetables (8-10), dried yeast (2), tallow (1-2). The content of vitamin A in the diet was 500 IU; vitamin E – 15 mg per mink. In three weeks before the slaughter period the animals received no extra vitamin A. Two experimental groups of mink (standard, n=7; sapphire, n=4) were fed with the same basal diet supplemented with 100 mg of vitamin C of mink daily for 20 days. All the animals had water *ad libitum*.

Sampling and assay methods

Samples of tissues were collected during the slaughter period in November. On day 20, the control and experimental mink were sampled for blood serum, liver, kidney, heart, lungs, spleen and skeletal muscle. All samples were stored at – 25°C. The concentration of retinol and α-tocopherol in the blood serum and tissues was determined by high performance liquid chromatography method as previously described (Skurihin & Dvinskaya, 1989). Proteins in the samples were precipitated by ethanol. Retinol and α-tocopherol were extracted by n-hexane. Chromatographic separation was carried out by a microcolumn chromatograph with ultraviolet detector. The sample volume introduced into the column was 10 µl.

The total SOD activity was determined by the adrenochromic method based on the spontaneous autooxidation of epinephrine with the formation of end products with have an absorbance peak at 480 nm (Misra & Fridovich, 1972). This reaction depends on the presence of superoxide anions and is specifically inhibited by SOD. The amount of enzyme that caused 50% inhibition of epinephrine autooxidation is defined as 1 unit (U). Catalase activity was evaluated by measuring the decrease in H_2O_2 concentration at 240 nm (Bears & Sizes, 1952).The GSH was determined by the method of Ellman in the presence of 5,5'-dithiobis-(2-nitrobenzoic acid) (Sedlak & Lindsay, 1968). The results were expressed in mmol GSH per 100 g of raw tissue. The data were expressed as mean ± SD. The Mann-Whitney's *U* test was used for comparison between the mink groups.

Results and discussion

The results have shown that the diet with added ascorbic acid decreased the vitamin A concentration practically in all investigated tissues in the experimental mink of both colors (Fig.1, A). The most significant changes of the retinol content were observed in kidneys, while in the sapphire mink similar decrease in the vitamin A content occurred not only in this tissue ($p \leq 0.05$) but also in blood serum ($p \leq 0.05$). Vitamin A was not detectable in all other tissues.

The concentration of vitamin A in kidneys of the mink investigated was much higher than that found in the liver. This contradicts with earlier findings, which showed that the kidney of mink contain lower concentrations of vitamin A compared to the liver. The metabolism of vitamin A is tightly regulated. As in blood, the vitamin A concentration in tissues is dependent on the amount of vitamin A supplied with the diet. One explanation of the observed variation in vitamin A concentration in the kidney of mink may be that differences in the dietary vitamin A intake might exist due to the influence of vitamin A level in the kidney (Raila et al., 2001). On the whole, these results may suggest a significant contribution of the kidney in the vitamin A metabolism in mink.

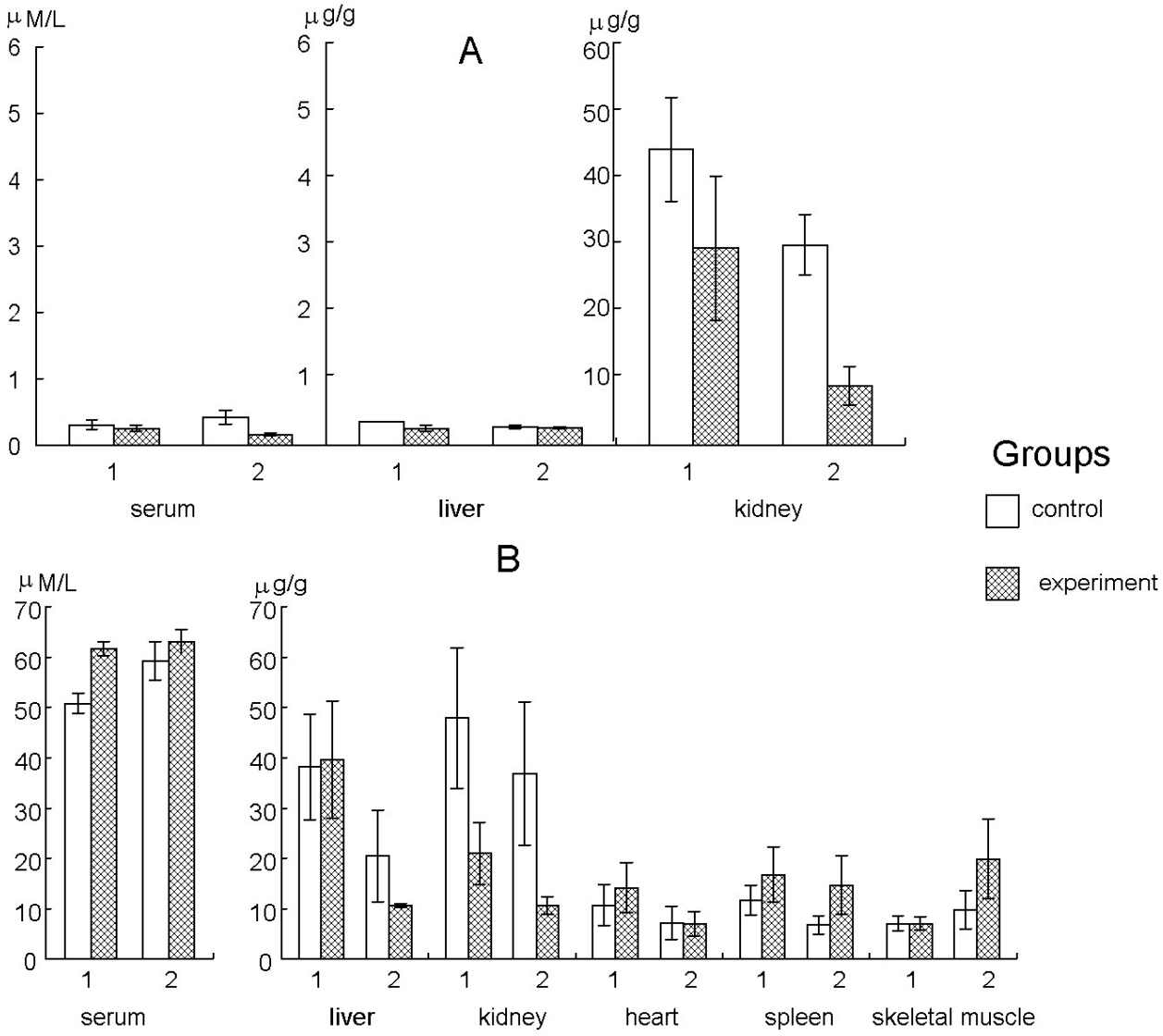

Fig. 1. Effects of ascorbic acid on tissue concentration of vitamins A (A) and E (B) in standard (1) and sapphire (2) mink (Mean ± SD).

The increase of the vitamin C content in the diet increased the vitamin E level in blood plasma and tissues. In our experiment tocopherol concentration also increased in the majority of tissues in the experimental groups (Fig.1, B) while tocopherol concentration in the kidney decreased. The reduction of tocopherol content in the kidney of experimental mink shows the increasing loading on this organ connected with its excretory function leading to the organism detoxication. As a result of long application of high dose of vitamin C in the diet a significant amount of oxalic acid is synthesized which causes adverse effect on kidneys (Menyschikova *et al.*, 2006). In our experiment, the vitamin E concentration decreased in the mink kidney in both experimental groups, but is more significant in the sapphire mink - more than three times in comparison with the control group and more than twice in comparison with the brown mink. The tocopherol concentration in the sapphire mink also decreased in the liver. However, there were no significant differences between groups of mink. Probably, that subtle effect of ascorbic acid on antioxidant vitamins can still be observed with longer time experiment and a higher number of animals per group than those used in our study.

Table 1. Effect of ascorbic acid on antioxidant enzymes activities and level of GSH in tissues of standard and sapphire mink.

Tissues	Colour type	SOD activity, U/g tissue		CAT activity, μmol H_2O_2/min·g tissue		GSH, mmol/100 g tissue	
		control group	experimental group	control group	experimental group	control group	experimental group
Liver	brown	416.92±30.80	556.57±43.24*	552.68±32.36	704.89±29.69*	0.16±0.01	0.20±0.01
	sapphire	487.92±44.27	540.49±12.93	579.84±38.92	484.26±57.97	0.24±0.01	0.24±0.01
Kidney	brown	108.60±16.50	103.28±12.40	81.20±4.03	83.30±6.39	0.43±0.03	0.34±0.01*
	sapphire	122.36±25.88	107.67±9.54	69.14±8.64	67.93±4.15	0.39±0.02	0.40±0.02
Heart	brown	69.33±5.18	73.66±6.55	15.08±1.35	18.25±2.49	0.35±0.01	0.36±0.03
	sapphire	46.33±4.83	33.38±9.81	16.26±2.14	16.11±3.51	0.27±0.04	0.27±0.01
Lungs	brown	45.02±7.53	41.85±7.55	30.92±3.51	25.52±2.69	0.23±0.01	0.24±0.01
	sapphire	16.95±6.72	52.81±17.19	29.08±2.35	27.87±2.84	0.23±0.02	0.18±0.01*
Spleen	brown	121.43±6.00	121.40±10.67	15.38±1.55	14.90±2.47	0.23±0.03	0.23±0.03
	sapphire	120.22±11.62	128.90±12.38	17.41±4.20	15.05±0.96	0.18±0.03	0.19±0.05
Skeletal muscle	brown	66.08±8.63	96.60±10.98*	19.74±3.60	30.65±6.57	0.16±0.01	0.19±0.02*
	sapphire	102.89±10.78	98.16±9.78	24.98±7.73	24.93±4.36	0.12±0.01	0.13±0.02

* – significantly different from control group.

The unequal degree of metabolism intensity in mink of different genotypes influences their ability to reserve vitamins in tissues, and antioxidant enzymes activities. In the liver of standard mink, activation of both SOD and CAT is noted (Table 1). The decrease of antioxidant enzymes activity in the sapphire mink heart is noted while changes in the standard mink not were found. The greatest difference in SOD activity in the sapphire and standard mink is found in the lung – in the sapphire mink it increased more than three times and in the standard mink it remained unchanged.

The influence of ascorbic acid on the level of GSH in mink was expressed by the way of the decreased content in lung of sapphire mink. It is known that an important function of GSH is reduction of dehydroascorbic acid, the oxidized form of vitamin C. The lung which is directly exposed to oxygen is particularly sensitive to the effects of GSH deficiency. Decreased level of GSH in kidney of the experimental brown mink was also registered (Table 1). Simultaneously, no significant influence of ascorbic acid on the level of GSH in other mink tissues was observed.

The results of the experiment indicate that the antioxidant system reaction on high amounts of dietary ascorbic acid in the standard and sapphire mink were different. The ascorbic acid caused more changes in the sapphire mink vitamins A and E concentrations as compared with those in the brown mink. In the kidney, both vitamins content decreased, and changes were more significant in sapphire mink. Obviously, the kidney was the basic target of vitamin C as their excretory function was amplified. The intensification of nonenzymatic antioxidants, vitamins A and E resulted in minor changes of SOD and CAT activities and the GSH level. In conclusion, even considerable content of the ascorbic acid in the diet had no significant influence on the antioxidant system in mink.

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Uzenbaeva L.B., Golubeva A.G., Ilukha V.A., Tutyunnik N.N. 2007. The specific of blood leukocyte structure in the mink (*Mustela vison* Schreber, 1777) with various genotypes. Vestnik VOGiS, 11 (1), 155 – 161. (in Russian).

A meiotic linkage map of the silver fox, aligned and compared to the canine genome

A.V. Kukekova, L.N. Trut, I.N. Oskina, J.L. Johnson, S.V. Temnykh, A.V. Kharlamova, D.V. Shepeleva, R.G. Gulievich, S.G. Shikhevich, A.S. Graphodatsky, G.D. Aguirre, G.M. Acland

A meiotic linkage map is essential for mapping traits of interest and is often the first step toward understanding a cryptic genome. Specific strains of silver fox (a variant of the red fox, *Vulpes vulpes*), which segregate behavioral and morphological phenotypes, create a need for such a map. One such strain, selected for docility, exhibits friendly dog-like responses to humans, in contrast to another strain selected for aggression. Development of a fox map is facilitated by the known cytogenetic homologies between the dog and fox, and by the availability of high resolution canine genome maps and sequence data. Furthermore, the high genomic sequence identity between dog and fox allows adaptation of canine microsatellites for genotyping and meiotic mapping in foxes. Using 320 such markers, we have constructed the first meiotic linkage map of the fox genome. The resulting sex-averaged map covers 16 fox autosomes and the X chromosome with an average inter-marker distance of 7.5 cM. The total map length corresponds to 1480.2 cM. From comparison of sex-averaged meiotic linkage maps of the fox and dog genomes, suppression of recombination in pericentromeric regions of the metacentric fox chromosomes was apparent, relative to the corresponding segments of acrocentric dog chromosomes. Alignment of the fox meiotic map against the 7.6x canine genome sequence revealed high conservation of marker order between homologous regions of the two species. The fox meiotic map provides a critical tool for genetic studies in foxes and identification of genetic loci and genes implicated in fox domestication.

Genome Research, 2007: 17, 387-399

The first linkage map of the American mink (*Mustela vison*)

R. Anistoroaei, A. Menzorov, O. Serov, A. Farid, K. Christensen

Described herein, the first microsatellite linkage map for the American mink consists of 85 microsatellite markers resolved into 17 linkage groups. The map was constructed using 92 F(1) progeny from five sire families created by crossing mink with different colour types. The linkage groups ranged from 0 to 137 cM. These linkage groups were assigned to 12 of the 14 mink autosomes using a somatic cell hybrid panel. The total map covered 690 sex-averaged Kosambi units with an average marker spacing of 8 cM. This map will facilitate further genetic mapping of monogenic characters and QTL.

Animal Genetics, 2007: 38, 384-388

An extended anchored linkage map and virtual mapping for the American mink genome based on homology to human and dog

R. Anistoroaei, S. Ansari, A. Farid., B. Benkel, P. Karlskov-Mortensen, K. Christensen

In this report we present an extended linkage map of the American mink (Neovison vison) consisting of 157 microsatellite markers and comprising at least one linkage group for each of the autosomes. Each linkage group has been assigned to a chromosome and oriented by fluorescence in situ hybridization (FISH) and/or by means of human/dog/mink comparative homology. The average interval between markers is 8.5 cM and the linkage groups collectively span 1340 cM. In addition, 217 and 275 mink microsatellites have been placed on human and dog genomes, respectively. In conjunction with the existing comparative human/dog/mink data, these assignments represent useful virtual maps for the American mink genome. Comparison of the current human/dog assembled sequential map with the existing Zoo-FISH-based human/dog/mink maps helped to refine the human/dog/mink comparative map. Furthermore, comparison of the human and dog genome assemblies revealed a number of large synteny blocks, some of which are corroborated by data from the mink linkage map.

Genomics 2009: 94, 204-210

Immunocytological analysis of meiotic recombination in the American mink (*Mustela vison)*

P.M. Borodin., E.A. Basheva., A.L. Zhelezova

Using immunolocalization of MLH1, a mismatch repair protein that marks crossover sites along synaptonemal complexes, we estimated the total length of the genetic map, the recombination rate and crossover distribution in the American mink (Mustela vison). We prepared spreads from 130 spermatocytes of five male minks and mapped 3320 MLH1 foci along 1820 bivalents. The total recombination length of the male mink genome, based on the mean number of MLH1 foci for all chromosomes, was 1327 cM. The overall recombination rate was estimated to be 0.48 cM/Mb. In all bivalents, we observed prominent peaks of MLH1 foci near the distal ends and a paucity of them near the centromeres. This indicates that genes located at proximal regions of the chromosomes should display much tighter genetic linkage than physically equidistant markers located near the telomeres.

Animal Genetics, 2009: 40, 235-238

Albinism in the American mink (*Neovison vison*) is associated with a *tyrosinase* nonsense mutation

R. Anistoroaei, M. Fredholm, K. Christensen, T. Leeb

Albino phenotypes are documented in various species including the American mink. In other species the albino phenotypes are associated with *tyrosinase* (*TYR*) gene mutations; therefore *TYR* was considered the candidate gene for albinism in mink. Four microsatellite markers were chosen in the predicted region of the *TYR* gene. Genotypes at the markers *Mvi6025* and *Mvi6034* were found to be associated with the *albino* phenotype within an extended half-sib family. A BAC clone containing *Mvi6034* was mapped to chromosome 7q1.1-q1.3 by fluorescent *in situ* hybridization. Subsequent analysis of genomic *TYR* sequences from wild-type and albino mink samples identified a nonsense mutation in exon 1, which converts a TGT codon encoding cysteine to a TGA stop codon (c.138T>A, p.C46X; EU627590). The mutation truncates more than 90% of the normal gene product including the putative catalytic domains. The results indicate that the nonsense mutation is responsible for the *albino* phenotype in the American mink.

Animal Genetics, 2008: 39, 645–648

Molecular characterization of the Himalayan mink

B.F. Benkel, K. Rouvinen-Watt, H. Farid, R. Anistoroaei

A rare color variant of the American mink (*Neovison vison*), discovered on a ranch in Nova Scotia and referred to as the "*marbled*" variety, carries a distinctive pigment distribution pattern resembling that found in some other species, e.g., the Siamese cat and the Himalayan mouse. We tested the hypothesis that the color pattern in question light-colored body with dark-colored points (ears, face, tail, and feet) is due to a mutation in the melanin-producing enzyme tyrosinase (TYR) that results in temperature-sensitive pigment production. Our study shows that marbled mink carry a mutation in exon 4 of the *TYR* gene (c.1835C > G) which results in an amino acid substitution (p.H420Q). The location of this substitution corresponds to the amino acid position that is also mutated in the TYR protein of the Himalayan mouse. Thus, the marbled variant is more aptly referred to as the Himalayan mink.

Mammalian Genome, 2009: 20, 256–259

Chromosomal Mapping of Canine-Derived BAC Clones to the Red Fox and American Mink Genomes

A.V. Kukekova, N.V. Vorobieva, V.R. Beklemisheva, J.L. Johnson, S.V. Temnykh, D.V. Yudkin, L.N. Trut, C. Andre, F. Galibert, G.D. Aguirre, G.M. Acland, A.S. Graphodatsky

High-quality sequencing of the dog (*Canis lupus familiaris*) genome has enabled enormous progress in genetic mapping of canine phenotypic variation. The red fox (*Vulpes vulpes*), another canid species, also exhibits a wide range of variation in coat color, morphology, and behavior. Although the fox genome has not yet been sequenced, canine genomic resources have been used to construct a meiotic

linkage map of the red fox genome and begin genetic mapping in foxes. However, a more detailed gene-specific comparative map between the dog and fox genomes is required to establish gene order within homologous regions of dog and fox chromosomes and to refine breakpoints between homologous chromosomes of the 2 species. In the current study, we tested whether canine-derived gene–containing bacterial artificial chromosome (BAC) clones can be routinely used to build a gene-specific map of the red fox genome. Forty canine BAC clones were mapped to the red fox genome by fluorescence in situ hybridization (FISH). Each clone was uniquely assigned to a single fox chromosome, and the locations of 38 clones agreed with cytogenetic predictions. These results clearly demonstrate the utility of FISH mapping for construction of a whole-genome gene-specific map of the red fox. The further possibility of using canine BAC clones to map genes in the American mink (*Mustela vison*) genome was also explored. Much lower success was obtained for this more distantly related farm-bred species, although a few BAC clones were mapped to the predicted chromosomal locations.

Journal of Heredity 2009: 100 (Supplement 1), S42-S53

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.

Canadian Veterinary Journal 2010: 51 (1): 75-77

Rapid development of fasting-induced hepatic lipidosis in the American mink (*Neovison 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 (*Neovison 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 phosphate-idylcholine 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

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 (17.93.6 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-P_2ase), phosphoenol-pyruvate carboxykinase (PEPCK), and pyruvate kinase (PKM_2) 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, F_1-generation kits exposed to protein restriction during foetal life (FLP1; 10.3 g) had a lower birth weight (p=0.004) than did F_1-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-P_2ase mRNA (p=0.007) and of PKM_2 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.

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Evaluation of methane-utilising bacteria products as feed ingredients for monogastric animals

M. Overland, A.H. Tauson, K. Shearer, A. Skrede

Bacterial proteins represent a potential future nutrient source for monogastric animal production because they can be grown rapidly on substrates with minimum dependence on soil, water, and climate conditions. This review summarises the current knowledge on methane-utilising bacteria as feed ingredients for animals. We present results from earlier work and recent findings concerning bacterial protein, including the production process, chemical composition, effects on nutrient digestibility, metabolism, and growth performance in several monogastric species, including pigs, broiler chickens, mink (*Mustela vison*), fox (*Alopex lagopus*), Atlantic salmon (*Salmo salar*), rainbow trout (*Oncorhynchus mykiss*), and Atlantic halibut (*Hippoglossus hippoglossus*). It is concluded that bacterial meal (BM) derived from natural gas fermentation, utilising a bacteria culture containing mainly the methanotroph *Methylococcus capsulatus* (Bath), is a promising source of protein based on criteria such as amino acid composition, digestibility, and animal performance and health. Future research challenges include modified downstream processing to produce value-added products, and improved understanding of factors contributing to nutrient availability and animal performance.

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Stereotypic behaviour in farm mink (*Neovison vison*) 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 ~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.

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