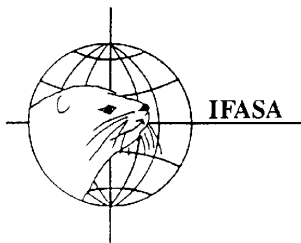
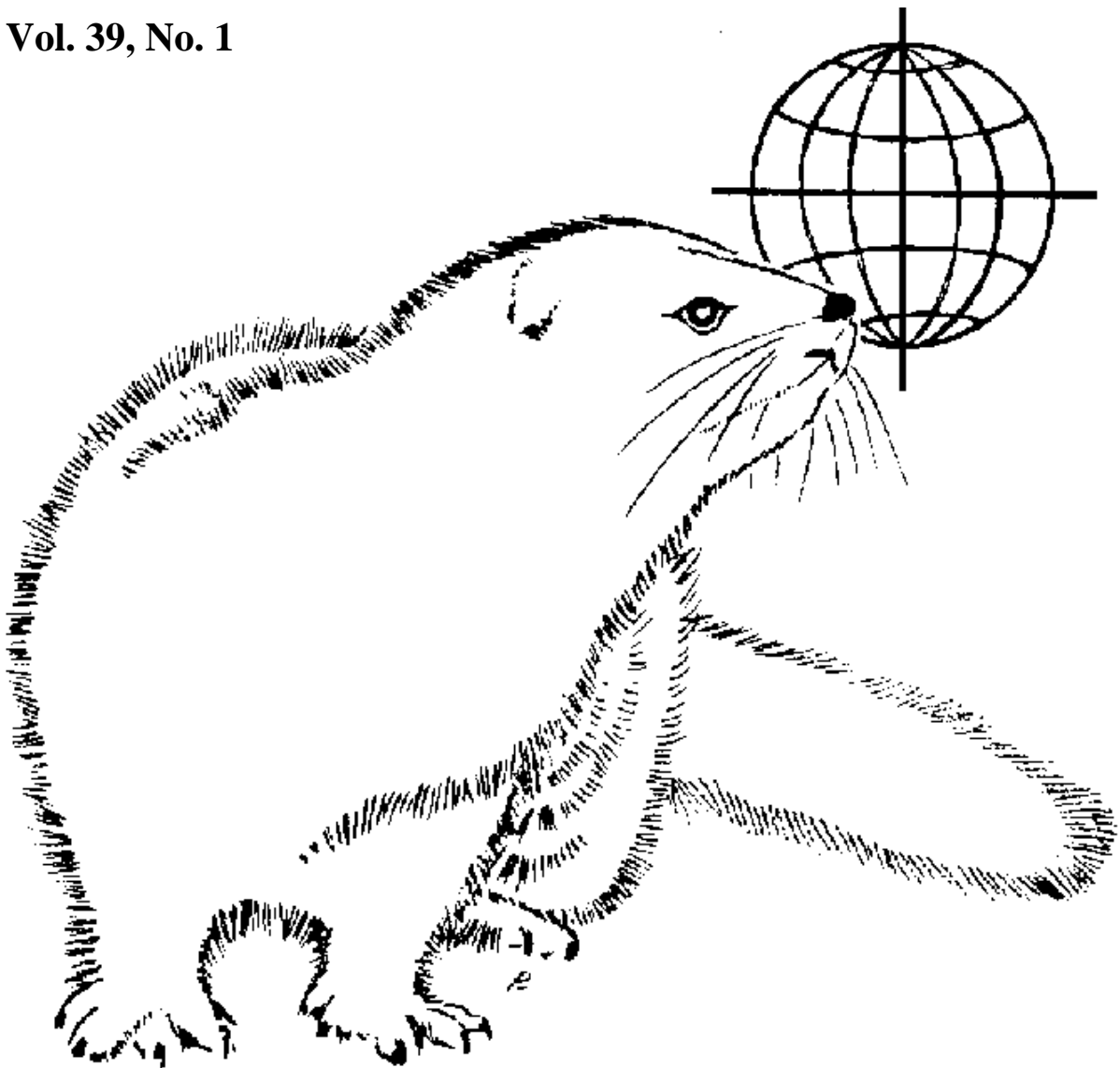


# SCIENTIFUR

SCIENTIFIC INFORMATION IN FUR ANIMAL PRODUCTION

Vol. 39, No. 1



INTERNATIONAL FUR ANIMAL SCIENTIFIC ASSOCIATION

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**Vivi Hunnicke Nielsen**  
**SCIENTIFUR**  
**P.O. Box 14**  
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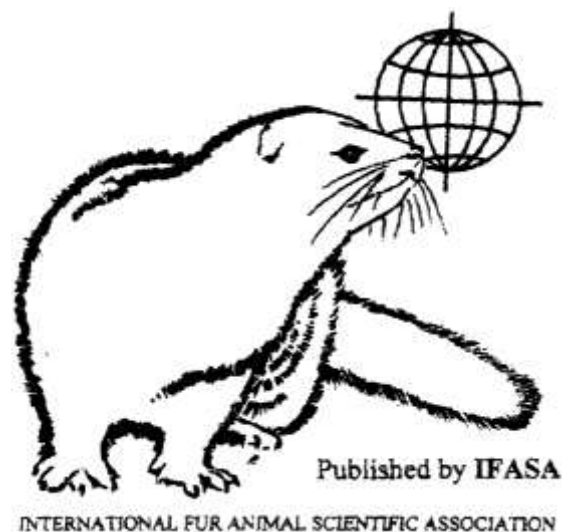
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## Notes from the Editor

It has previously been shown that mink raised on a farm at 42 degree N latitude under natural light conditions adapted when moved to an artificial light regimen corresponding to 45 degrees S latitude. Thus, their furring and reproductive cycles became in phase with the altered light regimen. A paper dealing with the effect of latitude on the antioxidant status in racoon dogs is published in this volume of *Scientifur*. The study which was conducted with the aim of comparing the antioxidant status in racoon dogs farmed in Poland at 50°5'N and in

Russia at 57°5'N. The results may similarly suggest an effect of latitude. Thus, it was observed that racoon dogs from higher latitudes possess a larger antioxidant capacity than animals from lower latitudes.

This year, the Nordic NJF meeting will be held in Åbo in Finland from 29 September to 1 October 2015. Further information can be obtained at: [tml@kopenhagenfur.com](mailto:tml@kopenhagenfur.com)

Vivi Hunnicke Nielsen  
Editor *Scientifur*



## ***Investigation of antioxidant system in raccoon dogs from different geographical zones in the autumn period***

*T.N Ilyina, V.A. Ilyukha, I.V. Baishnikova, S.N. Sergina, \*S. Łapinski  
Institute of Biology, Karelian Research Centre, Russian Academy of Sciences,  
Petrozavodsk, Russia*

*\*Agricultural University of Krakow, Krakow, Poland*

*E-mail: [ilyina@bio.krc.karelia.ru](mailto:ilyina@bio.krc.karelia.ru)*

*Keywords: antioxidant system, catalase, glutathione, raccoon dog, superoxide dismutase, vitamins A and E*

### **Abstract**

The aim of the study was to compare the antioxidant status in farmed raccoon dogs (*Nyctereutes procyonoides* Gray) in Poland and Russia. Tissue samples (liver, kidney, heart, lung, spleen, skeletal muscle) were collected in the late autumn when animals show willingness to winter conditions and examined for indicators of the antioxidant system – vitamin A and E content, reduced glutathione (GSH) level and activities of superoxide dismutase (SOD) and catalase. The largest difference between raccoon dogs farmed in Poland and Russia for indicators of the antioxidant system was found in the liver. Our results might suggest that raccoon dogs from higher latitudes possess stronger antioxidant capacity than animals from lower latitudes but confounding of latitude with nutrient intake as well as farm environment cannot be excluded.

### **Introduction**

Several mammalian species occur in habitats where seasonal changes of environmental parameters are predictable throughout the year. Changes in the natural photoperiod (day length) trigger modifications in many physiological, morphological, and behavioral processes that are believed to promote survival in seasonally breeding animals (Goldman, 2001). Photoperiodic changes are mostly pronounced at higher latitudes and it has been proposed that this proximate factor is primarily used by species occurring at latitudes above 30° where the photoperiodic signal is strongest (Bradshaw & Holzapfel, 2007). Seasonality results in metabolic adjustments that include changes in the antioxidant defense system that protects organisms

against the excess of reactive oxygen species (ROS) and this plays an important role in adaptation to environmental factors. The antioxidant system includes enzymes such as superoxide dismutase (SOD) and catalase, and low-molecular antioxidants such as glutathione (GSH) and vitamin E and A.

The farmed raccoon dog (*Nyctereutes procyonoides* Gray) is a suitable model for studying of seasonal changes in metabolism. The raccoon dog is the only *Canidae* which spends several winter months in a burrow in hibernation (winter dormancy). Therefore, its autumnal fattening and natural weight loss in winter and spring are greater than in other *Canidae*: in farm animals it changes from about 12 to 7 kg (Mustonen et al., 2007). However, farmed raccoon dogs from Poland and North-West of Russia do not hibernate. The animals only reduce the locomotor activity and consume less feed. It seems that the fattening accompanied by insulin resistance can evoke increased ROS generation, which stimulates the activity of the antioxidant system in this species (Mustonen et al., 2007; Sergina et al., 2013). However, it remains unclear whether geographical differences influence antioxidant capacity in such seasonal mammal as raccoon dogs. The aim of this investigation was to conduct a comparative study of various indicators of the antioxidant system activity in raccoon dogs from different geographical localities.

### **Materials and Methods**

Raccoon dog males and females from two localities - Poland, Krakow region (50°5'N) and Russia, Pskov region (57°5'N) - were used. Both groups of animals (n=5, 2 males and 3 females in each group)

were kept in standard farming conditions as recommended for the species. The raccoon dogs in Poland were fed a diet consisting of chicken products, meat and bone mass (77%), extruded wheat (12%), wheat bran (1%), dried beet pulp (2%), vegetable oil (1%), and water (7%). The content of vitamin A in the diet was 1000 IU, vitamin E – 17 mg, selenium – 0.02 mg, selenium chelate – 0.0003 mg per animal per day.

The raccoon dogs in Russia were given feed consisting of meat and fish products (67.1%), cooked grain (20.52%), vegetable (0.24%), fat (7.59%), milk products (0.24%), dried yeast (4.31%). The content of vitamin A in the diet was 1000 IU; vitamin E – 15 mg per animal per day without selenium addition.

Samples of tissues (liver, kidney, spleen, lung, heart and skeletal muscles) were collected during the slaughter season in November and examined for indicators of antioxidant system. The total SOD activity was determined by the adrenochromic method based on the spontaneous autooxidation of epinephrine with the formation of end products which have an absorbance peak at 480 nm (Misra & Fridovich, 1972). Catalase activity was evaluated by measuring the decrease in H<sub>2</sub>O<sub>2</sub> concentration at 240 nm (Bears & Sizes, 1952). The GSH level was determined by the method of Ellman as previously described (Sedlak & Lindsay, 1968). The tissue concentrations of vitamins A (retinol) and E ( $\alpha$ -tocopherol) were determined by high performance liquid chromatography method (Skurihin & Dvinskaya, 1989). Data are presented as mean  $\pm$  standard error of mean (SEM). Statistical analysis was performed with Mann-Whitney's U-test. The research was carried out using the facilities of the Equipment Sharing Centre of the Institute of Biology, Karelian Research Centre of Russian Academy of Sciences.

## Results and discussion

Latitude is important in determining seasonal regulation due to photoperiod in raccoon dogs of the temperate zone. In this study the levels of GSH, retinol and  $\alpha$ -tocopherol as well as antioxidant enzymes' activities were measured in tissues of raccoon dogs from colder (Russia) and warmer (Poland) localities. The results of our investigation are summarized in Fig. 1, 2. The data indicate

similarity in tissue antioxidant enzyme activities in raccoon dog and other mammals: liver has the highest SOD and catalase activities among the tissues investigated. The data suggest differences in some indicators between animals from the two regions. The largest differences between values were observed in liver and skeletal muscles. Liver SOD activity, GSH content and vitamin levels were significantly higher in animals from the colder region than in raccoon dogs from the warmer region. Also skeletal muscle of raccoon dog from the colder region had greater enzymes' activities but lower  $\alpha$ -tocopherol level than animals from the warmer region.

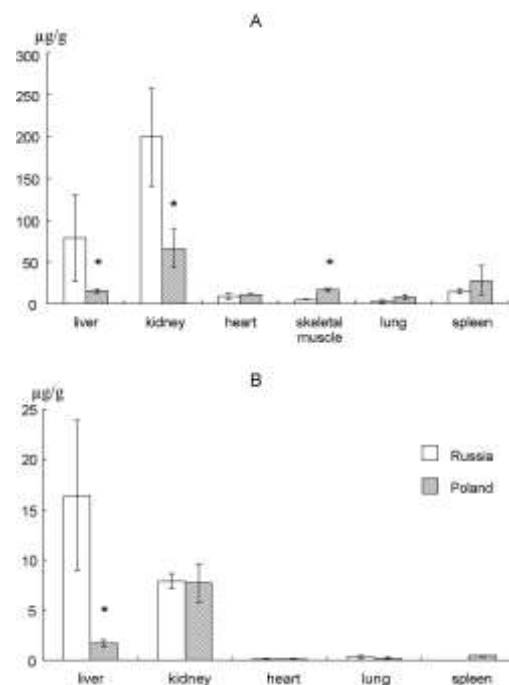


Fig. 1. Vitamins E (A) and A (B) content in tissues of raccoon dogs from different regions.

These tissues are involved in glucose metabolism that increases in the autumnal process of energy storage (as lipids and glycogen) that subsequently will be transformed into wintertime energy expenditure (Mustonen et al., 2007). Regulation of the suprachiasmatic clock is now considered to imply the synchronization of circadian oscillators contained in most peripheral organs like liver, heart, or white adipose tissue. These peripheral organs are thought to play a critical role in tissue-specific physiology (Mendoza et al., 2008). Changes in the antioxidant enzymes' activities allow an understanding of the modifications of biochemical



pathways, as the SOD synthesis is known to be regulated by oxygen level (Misra & Fridovich, 1972) and the catalase synthesis is activated by  $H_2O_2$  (Aebi & Wyss, 1978) formed in both reaction of superoxide dismutation and oxidase reactions.

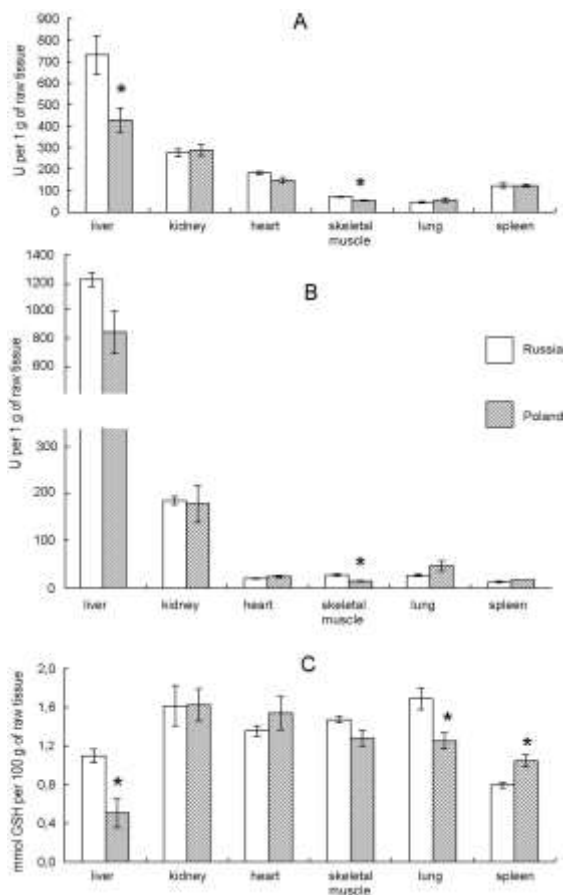


Fig. 2. Activity of SOD (A), catalase (B) and glutathione level (C) in tissues of raccoon dogs from different regions.

The Russian raccoon dogs had a significantly higher content of  $\alpha$ -tocopherol in the kidney than the Polish animals. The accumulation, transport and tissue delivery of  $\alpha$ -tocopherol, a key vitamin E form, involve molecular, biochemical, and cellular processes closely related to overall lipid and lipoprotein homeostasis (Rigotti, 2007). It has been reported that the vitamin E accumulation in animal tissues in autumn may induce hibernation (Kalabuhov, 1985). Vitamin E is the most important natural antioxidant and sufficient intake is important especially in the northern regions before the winter period connected with significant metabolic changes.

The retinol content in the raccoon dog kidney was relatively similar in both groups and the other tissues contain low vitamin A level or the retinol concentration was not detected. Previous research has shown that Canids tissues are low carotenoids accumulators despite consuming diets that contained low to moderate levels of carotenoids (Slifka et al., 1999).

Additionally, Russian raccoon dogs had higher GSH content in lung and lower value in spleen than Polish animals. These differences might be associated with more severe climatic conditions in the colder than in the warmer region. However no differences in the values between animals from different localities were detected in heart that demonstrated high stability of antioxidant defense in this tissue. Perhaps, the difference in GSH levels is associated with the degree of inclusion in oxidation reactions.

Changes in photoperiod are believed to promote survival in seasonally breeding animals and trigger modifications in many physiological processes (Goldman, 2001). In conclusion, raccoon dogs from the colder locality with a shorter photoperiod had in general higher values of antioxidants than animals from the warmer locality with a longer photoperiod. In accordance with previous investigations of photoperiod effects in various geographical localities in other species (Dark et al., 1983), the results of our study show higher antioxidant capacity of raccoon dog from the northerly locality than of those from the southerly region. These results may indicate that the raccoon dog displays considerable geographical variation in energy requirements and use of the photoperiod as an anticipatory cue for predicting the onset of winter. Such differences could be related to the availability of energy and the relative severity of climatic conditions in Russian locality. However, further studies including detailed information of nutrient content and feed intake and standardized farming conditions at different latitudes are needed to substantiate the conclusions.

### Acknowledgments

This study was supported by the President of the Russian Federation grant for Leading Scientific School # 1410.2014.4 and the grant for Russian–Polish Interacademic Cooperation. We extend

special thanks to Dr Hieronim Zurek from the “Władkowice” fur farm (Poland) for providing animals.

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## BREEDING, GENETICS AND REPRODUCTION

### The complete mitochondrial genome of silver fox (*Caniformia: Canidae*)

W.L. Sun, W. Zhong, K. Bao, L.H. Liu, Y. Ya-Han, Z. Wang, G.Y. Li

**Abstract** Silver fox is color variant of *Vulpes vulpes*. At present, there are few studies on phylogeny of *Canidae* and *Caniformia*. In this article, we determined and described the complete mitogenome of silver fox for the first time, which is 16,723 bp in length, containing 13 protein-coding genes, 2 rRNA genes, 22 tRNA genes, one origin of replication on the light-strand ( $O_L$ ) and a putative control region (CR). The overall base composition is 31.4% A, 27.9% T, 26.0% C, 14.7% G, respectively, with a AT bias (59.3%). Ten protein-coding genes use the initiation codon ATG while ND2, ND3 and ND5 use ATA. Most of them have TAA as the stop codon, except ND2 uses TAG, Cytb uses AGA, and COX3, ND3, ND4 use an incomplete stop codon TA. The information is expected to provide useful molecular data for further taxonomic and phylogenetic studies of *Canidae* and *Caniformia*.

*Mitochondrial DNA. 2015: 25:1-3. [Epub ahead of print]*

### Genomic resources notes

*Genomic Resources Development Consortium*  
M. Baratti, F. Cattonaro, T. Di Lorenzo, D.M. Galassi, V. Iannilli, A. Iannucci, J. Jensen, P.F. Larsen, R.O. Nielsen, C. Pertoldi, D. Postolache, J.M. Pujolar, E. Randi, A. Ruiz-Gonzalez, J.P. Thirstrup, G.G. Vendramin, A. Zalewski

This article documents the public availability of (i) RAD sequencing data and validated SNPs for the American mink *Neovison vison* and (ii) Transcriptome resources for two nonmodel freshwater crustacean species, the copepod *Eucyclops serrulatus* and the amphipod *Echinogammarus veneris*.

*Mol. Ecol. Resour. 2015: 15(2): 458-459*  
*doi: 10.1111/1755-0998.12368*

### The complete sequence of the mitochondrial genome of Arctic fox (*Alopex lagopus*)

S.Q. Yan, P.C. Guo, Y. Yue, W.H. Li, C.Y. Bai, Y.M. Li, J.H. Sun, Z.H. Zhao

**Abstract** In the present study, the complete mitochondrial genome sequence of Arctic fox (*Alopex lagopus*) was determined for the first time. It has a total length of 16,656 bp, and contains 13 protein-coding genes, 22 tRNA genes, 2 ribosome RNA genes and 1 control region. The nucleotide composition is 31.3% for A, 26.2% for C, 14.8% for G and 27.7% for T, respectively. The D-loop region located between tRNA<sup>Pro</sup> and tRNA<sup>Phe</sup> contains a (ACACGTACACGCAT)<sub>18</sub> tandem repeat array. The data will be useful for the investigation of the genetic structure and diversity in the natural and farmed population of Arctic foxes.

*Mitochondrial DNA. 2015: 28:1-2. [Epub ahead of print]*

### Platinum coat color in red fox (*Vulpes vulpes*) is caused by a mutation in an autosomal copy of KIT

J.L. Johnson, A. Kozysa, A.V. Kharlamova, R.G. Gulevich, P.L. Perelman, H.W. Fong, A.V. Vladimirova, I.N. Oskina, L.N. Trut, A.V. Kukekova

The red fox (*Vulpes vulpes*) demonstrates a variety of coat colors including platinum, a common phenotype maintained in farm-bred fox populations. Foxes heterozygous for the platinum allele have a light silver coat and extensive white spotting, whereas homozygosity is embryonic lethal. Two KIT transcripts were identified in skin cDNA from platinum foxes. The long transcript was identical to the KIT transcript of silver foxes, whereas the short transcript, which lacks exon 17, was specific to platinum. The KIT gene has several copies in the fox genome: an autosomal copy on chromosome 2 and additional copies on the B chromosomes. To identify the platinum-specific KIT sequence, the genomes of one platinum and one silver fox were sequenced. A single nucleotide polymorphism (SNP) was identified at the first nucleotide of KIT intron 17 in the platinum fox. In platinum foxes, the A allele of the SNP disrupts the donor splice site and causes exon 17, which is part of a segment that encodes a conserved tyrosine kinase domain, to be

skipped. Complete cosegregation of the A allele with the platinum phenotype was confirmed by linkage mapping (LOD 25.59). All genotyped farm-bred platinum foxes from Russia and the US were heterozygous for the SNP (A/G), whereas foxes with different coat colors were homozygous for the G allele. Identification of the platinum mutation suggests that other fox white-spotting phenotypes, which are allelic to platinum, would also be caused by mutations in the KIT gene.

*Anim. Genet.* 2015: doi: 10.1111/age.12270 [Epub ahead of print Feb. 6]

## NUTRITION, FEEDING AND MANAGEMENT

### **Influence of Dietary Zinc and Copper on Apparent Mineral Retention and Serum Biochemical Indicators in Young Male Mink (*Mustela vison*)**

X. Wu, Z. Liu, J. Guo, C. Wan, T. Zhang, H. Cui, F. Yang, X. Gao

An experiment was conducted in a  $3 \times 3$  (Cu  $\times$  Zn) factorial experiment based on a completely randomized design to evaluate the effects of dietary copper and zinc on apparent mineral retention and serum biochemical indicators in young male mink on a corn-fish meal based diet. Animals were fed basal diets supplemented with Cu from copper sulfate (CuSO<sub>4</sub>) and Zn from zinc sulfate (ZnSO<sub>4</sub>). Supplemental Cu levels were 0, 15, and 30 mg/kg copper, respectively, while supplemental Zn levels were 0, 150, and 300 mg/kg, respectively. A metabolism trial of 4 days was conducted during the last week of experimental feeding. Blood samples were collected via the toe clip to determine blood hematology and blood metabolites. Copper excretion, retention, and digestibility were influenced by dietary copper ( $P < 0.05$ ), however, there was also a zinc-copper interaction. Copper digestibility and retention were substantially reduced when zinc was added to the low copper diet but showed little change with zinc supplementation of the high copper diet. Both plasma Cu and plasma Zn were influenced by dietary level of the respective mineral ( $P < 0.05$ ). There was no influence of dietary copper on plasma zinc; however, high Zn in the diet reduced plasma Cu concentrations. There was a zinc-copper interaction for plasma Cu ( $P = 0.053$ ). Cu-Zn superoxide dismutase (Cu-Zn

SOD) activity tended to be influenced by dietary zinc ( $P = 0.065$ ) and dietary copper ( $P = 0.035$ ). Dietary copper had a significant effect on ceruloplasmin (CER) and triglyceride (TG) concentrations ( $P < 0.05$ ). Our results show that moderately high Zn in the diet (Zn:Cu ratio of 40:1) significantly reduce the apparent Cu digestibility. Our results also show that moderately high Cu in the diet increases Cu retention, but not reduces Zn absorption, and moderately high Zn in the diet reduced plasma Cu concentrations and CER activity.

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### **Copper bioavailability, blood parameters, and nutrient balance in mink**

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

A  $3 \times 3 + 1$  factorial experiment was conducted based on a completely randomized design to evaluate the effects of different sources of copper on plasma metabolites, nutrient digestibility, relative copper bioavailability, and retention of some minerals in male mink. Animals in the control group were fed a basal diet, which mainly consisted of corn, fish meal, meat and bone meal, and soybean oil, with no copper supplementation. Mink in the other 9 treatments were fed the basal diet supplemented with Cu from reagent-grade copper sulfate (CuSO<sub>4</sub>), tribasic copper chloride (TBCC), or copper methionine (CuMet). Copper concentrations of the experimental diets were 50, 100, and 150 mg Cu/kg DM. Blood samples were collected via the toe clip at the end of study (d 42) to determine blood hematology and blood metabolites. A metabolism trial of 4 d was conducted during the last week of experimental feeding. There was a linear ( $P < 0.01$ ) effect of dose of Cu on plasma Cu concentrations, ceruloplasmin concentration, and Cu-Zn superoxide dismutase activity. A linear response to Cu dose was noted for fat ( $P < 0.05$ ) digestibility. Supplemental dose of Cu linearly increased ( $P < 0.05$ ) liver Cu and decreased ( $P < 0.05$ ) liver Zn level but did not alter liver Fe. The concentration of liver Cu of the mink fed with TBCC and CuMet diets was greater ( $P < 0.05$ ) than that fed CuSO<sub>4</sub>. Compared with CuSO<sub>4</sub> (100%), relative bioavailability values of TBCC were 104 and 104%, based on serum

ceruloplasmin and liver copper, respectively, and relative bioavailability values of CuMet were 130 and 111%. CuMet and TBCC are more bioavailable than CuSO<sub>4</sub>. In conclusion, the relative bioavailability of CuMet obtained in this study was greater than that of CuSO<sub>4</sub> and TBCC. Dose of Cu had an important effect on the regulating ceruloplasmin concentration, Cu-Zn superoxide dismutase activity, and the digestion of dietary fat in mink.

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## BEHAVUOUR AND WELFARE

### **Does the selection of fox for tame and aggressive behavior changes their ability to focus attention, and training the motor skills?**

[No authors listed]

Foxes long time selected for tame and aggressive behavior were compared on ability to focus attention on the object of food reinforcement. Attenuation of this behavior and rate of training for motor skills also has been examined. Maximal duration of eye focusing was significantly higher in aggressive foxes, in comparison with tame ones. Our experiments allowed divide the group of tame foxes into two subgroups "calm" and "emotional", on the base of emotionality and motor activity during tests. Features of behavior of these two subgroups steadily differed in all tests. "Calm" tame foxes at the extinction test continued the trained skill longer than "emotional" and aggressive ones. Tame foxes were more successful than aggressive in the training for motor skills. The possible reasons of the data obtained are discussed.

*Zh. Vyssh. Nerv. Deiat. Im. I P Pavlova.* 2014: 64(5): 521-530

## HEALTH AND DISEASE

### **Aleutian mink disease virus in free-ranging mustelids in Finland - a cross-sectional epidemiologic and phylogenetic study**

A. Knuuttila, K. Aaltonen, A.M. Virtala, H. Henttonen, M. Isomursu, A. Leimann, T. Maran, U. Saarma, P. Timonen, O. Vapalahti, T. Sironen

Aleutian mink disease virus (AMDV) can cause severe immune complex-mediated disease in American mink. AMDV has also been detected in several other mustelid species with potential negative impact on their health and population. A molecular and cross-sectional epidemiologic study was conducted to gain data on the prevalence, distribution, transmission, and diversity of AMDV strains in Finnish free-ranging mustelids and risk factors associated with infection. The presence of anti-AMDV antibodies and/or AMDV DNA was tested from 308 samples representing eight mustelid species and 17 administrative regions. Positive samples were detected across the country and in 54% (31/57) of feral American mink, 27% (7/26) of European badgers, and 7% (1/14) of European polecats. Samples from Eurasian otters, European pine martens, least weasels, stoat, and wolverine were negative. Major risk factors for infection were the species American mink with 335 and badger with 74 times higher odds than other species and the years 2006-2009 with 5 times higher odds than years 2010-2014. No clustering according to species, geographical origin, or year was evident in phylogeny, except for four divergent sequences from Estonian badgers that formed a separate phylogroup distinct from other AMDV strains. This study showed that AMDV is prevalent in certain species of Finnish free-ranging mustelids and widely distributed across the country. Furthermore, the free-ranging mustelids carry both strains similar to those found in farmed mink, but also distinct strains that may represent novel amdoparvoviruses.

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### **Aleutian mink disease virus in striped skunks (*Mephitis Mephitis*): Evidence for cross-species spillover**

L.A. Nituch, J. Bowman, P.J. Wilson, A.I. Schulte-Hostedde

Aleutian mink disease virus (AMDV) causes a parvovirus infection, initially characterized in American mink (*Neovison vison*), that may have harmful effects on wild populations of susceptible animals. In North America, where American mink are native, the origin, host range, and prevalence of AMDV in wild species is not clear. We studied

striped skunks (*Mephitis mephitis*) and raccoons (*Procyon lotor*) to determine whether species sympatric with mink are potential reservoirs in the transmission of AMDV to wild mink and mink farms. Antibodies to AMDV were detected in 41% of skunk serum samples (143/347) and AMDV nucleic acids were detected in 32% (14/40) of skunk spleen samples by PCR, indicating that AMDV exposure and infection were frequent in skunks. We detected no AMDV antibodies in 144 raccoon blood samples. Phylogenetic analysis revealed a newly identified AMDV haplogroup consisting of isolates from Ontario skunks and a free-ranging domestic mink from Ontario. Our findings of frequent AMDV infection in skunks, close genetic similarity between skunk and mink AMDV isolates, and evidence of AMDV transmission from skunks to mink support the hypothesis that skunks may be acting as alternative hosts and reservoirs of AMDV to wild mink through cross-species virus spillover

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**Development of a nanoparticle-assisted PCR (nanoPCR) assay for detection of mink enteritis virus (MEV) and genetic characterization of the NS1 gene in four Chinese MEV strains**

*J. Wang, Y. Cheng, M. Zhang, H. Zhao, P. Lin, L. Yi, M. Tong, S. Cheng*

**Background:** Mink enteritis virus (MEV) causes mink viral enteritis, an acute and highly contagious disease whose symptoms include violent diarrhea, and which is characterized by high morbidity and mortality. Nanoparticle-assisted polymerase chain reaction (nanoPCR) is a recently developed technique for the rapid detection of bacterial and viral DNA. Here we describe a novel nanoPCR assay for the clinical detection and epidemiological characterization of MEV.

**Results:** This assay is based upon primers specific for the conserved region of the MEV NS1 gene, which encodes nonstructural protein 1. Under optimized conditions, the MEV nanoPCR assay had a detection limit of  $8.75 \times 10^1$  copies recombinant plasmids per reaction, compared with  $8.75 \times 10^3$  copies for conventional PCR analysis. Moreover, of 246 clinical mink samples collected from five provinces in North-Eastern China, 50.8% were scored MEV positive by our nanoPCR assay,

compared with 32.5% for conventional PCR. Furthermore no cross reactivity was observed for the nanoPCR assay with respect to related viruses, including canine distemper virus (CDV) and Aleutian mink disease parvovirus (AMDV). Phylogenetic analysis of four Chinese wild type MEV isolates using the nanoPCR assay indicated that they belonged to a small MEV clade, named the China type, in the MEV/FPLV cluster, and were closely clustered in the same location.

**Conclusions:** Our results indicate that the MEV China type clade is currently circulating in domestic minks in China. We anticipate that the nanoPCR assay we have described here will be useful for the detection and epidemiological and pathological characterization of MEV.

*BMC Vet. Res.* 2015: 13:11(1): 1. [Epub ahead of print]

**Isolation and Characterization of a "phiKMV-Like" Bacteriophage and Its Therapeutic Effect on Mink Hemorrhagic Pneumonia**

*Z. Cao, J. Zhang, Y.D. Niu, N. Cui, Y.Ma, F. Cao, L. Jin, Z. Li, Y. Xu*

The objective of this study was to investigate the potential of using phages as a therapy against hemorrhagic pneumonia in mink both in vitro and in vivo. Five *Pseudomonas aeruginosa* (*P. aeruginosa*) strains were isolated from lungs of mink with suspected hemorrhagic pneumonia and their identity was confirmed by morphological observation and 16S rDNA sequence analysis. Compared to *P. aeruginosa* strains isolated from mink with hemorrhagic pneumonia in 2002, these isolates were more resistant to antibiotics selected. A lytic phage vB\_PaeP\_PPA-ABTNL (PPA-ABTNL) of the Podoviridae family was isolated from hospital sewage using a *P. aeruginosa* isolate as host, showing broad host range against *P. aeruginosa*. A one-step growth curve analysis of PPA-ABTNL revealed eclipse and latent periods of 20 and 35 min, respectively, with a burst size of about 110 PFU per infected cell. Phage PPA-ABTNL significantly reduced the growth of *P. aeruginosa* isolates in vitro. The genome of PPA-ABTNL was 43,227 bp (62.4% G+C) containing 54 open reading frames and lacked regions encoding known virulence factors, integration-related proteins and antibiotic resistance

determinants. Genome architecture analysis showed that PPA-ABTNL belonged to the "phiKMV-like Viruses" group. A repeated dose inhalational toxicity study using PPA-ABTNL crude preparation was conducted in mice and no significantly abnormal histological changes, morbidity or mortality were observed. There was no indication of any potential risk associated with using PPA-ABTNL as a therapeutic agent. The results of a curative treatment experiment demonstrated that atomization by ultrasonic treatment could efficiently deliver phage to the lungs of mink and a dose of 10 multiplicity of infection was optimal for treating mink hemorrhagic pneumonia. Our work demonstrated the potential for phage to fight *P. aeruginosa* involved in mink lung infections when administered by means of ultrasonic nebulization.

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eCollection 2015

**Molecular epidemiology of Aleutian mink disease virus (AMDV) in Estonia, and a global phylogeny of AMDV**

A. Leimann, A. Knuuttila, T. Maran, O. Vapalahti, U. Saarma

*Virus Res*. 2015; 2: 199C: 56-61  
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**Canine distemper virus DNA vaccination of mink can overcome interference by maternal antibodies**

T.H. Jensen, L. Nielsen, B. Aasted, C. Pertoldi, M. Blixenkronne-Møller

*Vaccine*. 2015; 10;33(11):1375-81  
doi: 10.1016/j.vaccine.2015.01.029. [Epub ahead of print Jan 28]

**Molecular characterization of H9N2 influenza virus isolated from mink and its pathogenesis in mink**

L. Peng, C. Chen, H. Kai-Yi, Z. Feng-Xia, Z. Yan-Li, L. Zong-Shuai, Z. Xing-Xiao, J. Shi-Jin, X. Zhi-Jing

*Vet. Microbiol*. 2015; 23: 176(1-2): 88-96  
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