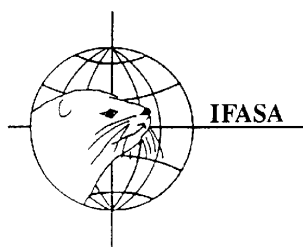
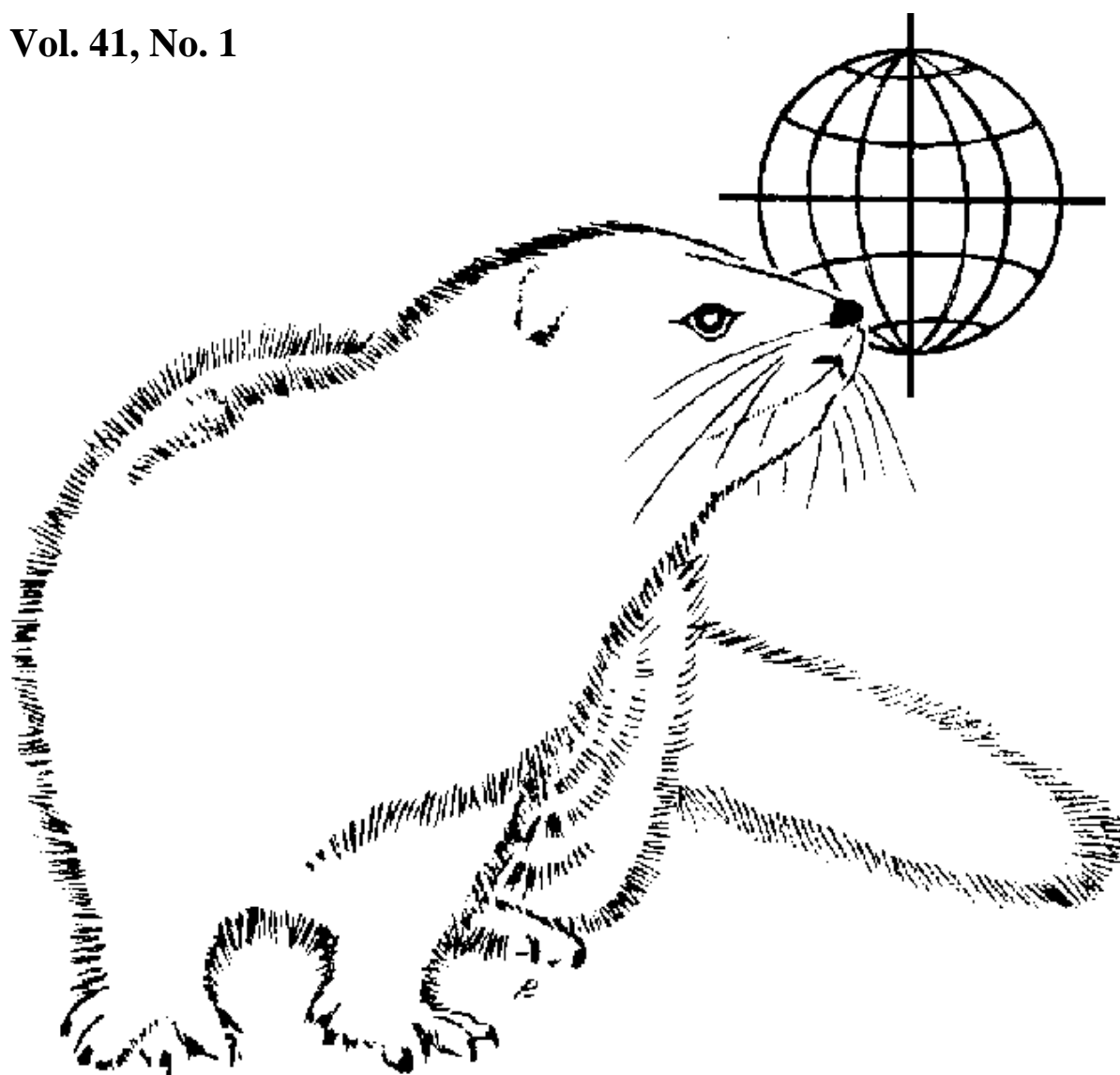


# SCIENTIFUR

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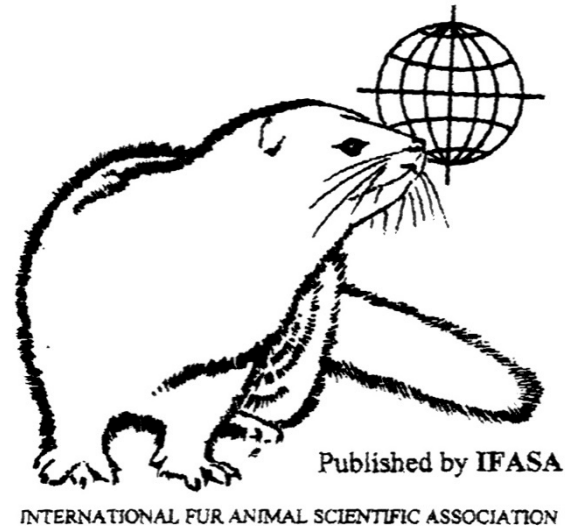
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## Notes from the Editor

In the beginning of 2017, Welfur, a European welfare assessment programme, was launched for certification at 4000 fur animal farms in Europe. The welfare indicators applied are developed for farmed mink and foxes in the Welfur project initiated voluntarily in 2009 by the European fur sector. The Welfur assessment protocol is based on four welfare principles: “Good feeding”, “Good housing”, “Good health” and “Appropriate behaviour” as in the European Welfare Quality® project that focused on cattle, pigs and poultry and was completed in 2009. Welfur is a tool for improved management and documentation of good welfare at the farm and also for traceability purposes.

The Welfur certification is research-based and independent and benefits from former sustained and extensive research in fur animals as well as research initiated to support the programme. It is the ambition that only certified skins will be sold in the major European auction houses from 2020. This

issue of Scientifur brings a report of the status and perspectives of Welfur for mink.

Obligate embryonic diapause is observed during gestation in mink like in other species of carnivores. New research results provide an understanding of the regulation of this diapause. The findings suggest that polyamines, synthesized under the control of pituitary prolactin, are the uterine factor the absence of which is responsible for embryonic diapause in mustelid carnivores. An abstract describing the results are given in Scientifur 41.1.

Since the turn of year 2017, Birthe Ømark Jensen has taken up the position as secretary of Scientifur. Birthe is an experienced bilingual secretary. A warm welcome to Birthe.

Vivi Hunnicke Nielsen

Editor Scientifur





**BREEDING, GENETICS AND REPRODUCTION****Heterozygosity for Mutations Affecting Coat Pigmentation in the American Mink (*Neovison vison*) Enhances Structural Stability of Adrenal Cortex under Stress Conditions**

Trapezo O.V.<sup>1</sup>, Luzenko N.D.<sup>1</sup> & Trapezova L.I.<sup>1</sup>

<sup>1</sup>*Institute of Cytology and Genetics, Siberian Branch, Russian Academy of Sciences, Novosibirsk, Russia.*

The results of the study of the effects of heterozygosity for mutations affecting coat pigmentation on the response to the environmental stress caused by extreme feeding conditions are provided. The animals with the following genotypes were taken into the study: homozygotes standard (+/+), hedlund white (h/h), and aleutian (a/a) and heterozygotes hedlund white (h/+) and aleutian (a/+). The animals homozygous for the aleutian mutation (a/a) showed a statistically lower growth rate than the animals of other genotypes both in the control and in the experiment ( $p < 0.05$ ). Under the control conditions, the animals homozygous for both the wild type standard allele (+/+) and the mutant hedlund white (h/h) and aleutian (a/a) alleles showed the evident tendency for the zona fasciculata and zona reticularis of the adrenal cortex broadening compared to the experimental conditions. At the same time, in the animals heterozygous for the hedlund white (h/+) and the aleutian (a/+) mutations, a clear tendency for increasing size of the zona fasciculata and zona reticularis under the experimental conditions was observed. In the heterozygous animals, although we observed single destructive changes in the adrenal cortex under stress conditions, they were much less profound than in the homozygous ones. This may be related to the broader range of morphological adaptation in the heterozygotes, which gives them the possibility of more significant enlargement of the secreting zone to provide for its adequate functioning.

*Genetika*, 2016: 52(4):488-92.

Doi: 10.1134/S1022795416030169

**Interplay between aggression, brain monoamines and fur color mutation in the American mink**

Kulikov A.V.<sup>1</sup>, Bazhenova E.Y.<sup>1</sup>, Kulikova E.A.<sup>2</sup>, Fursenko D.V.<sup>1</sup>, Trapezova L.I.<sup>3</sup>, Terenina E.E.<sup>4</sup>, Mormede P.<sup>4</sup>, Popova N.K.<sup>2</sup> & Trapezov O.V.<sup>3</sup>.

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*Genes Brain Behav.* 2016: 15(8): 733-740.

Doi: 10.1111/gbb.12313. Epub 2016

**From single nucleotide substitutions up to chromosomal deletions: genetic pause of leucism-associated disorders in animals**

Fleck K., Erhardt G. & Lühken G.

Leucism is characterized by a complete or partial white skin and hair in combination with pigmented irides, which can be vivid blue or heterochromatic. This is due to a complete or partial lack of melanocytes. The underlying pathogenesis is a disturbed emigration or differentiation of neural crest-derived cells. Therefore, leucistic phenotypes can be associated with defects, which mainly impair sensory organs and nerves. In humans, a well-known example is the Waardenburg syndrome. Leucism-associated disorders were also described in mouse, rat, hamster, rabbit, mink, cat, dog, pig, sheep, llama, alpaca, cattle and horse. In some of these species already identified causal mutations affect the genes EDN3, EDNRB, KIT, MITF, PAX3, SILV and SOX10. Defect alleles represent different types of genetic variation, ranging from single nucleotide substitutions up to larger chromosomal deletions. Some of the defect alleles produce desired coat color patterns. In some but not all cases, available genetic tests enable breeders to avoid production of animals affected by a leucism-associated disorder.

*Berl. Munch Tierarztl. Wochenschr. 2016: 129 (7-8): 269-81.*

### **Mitochondrial DNA haplotypes are associated with performance traits in Raccoon dogs\***

Ślaska B.<sup>1\*\*</sup>, Zięba G.<sup>1</sup>, Rozempolska-Rucińska I.<sup>1</sup>, Jeżewska-Witkowska G.<sup>1</sup>, Nisztuk S.<sup>1</sup>, Horecka B.<sup>1</sup> & Zoń A.<sup>2</sup>

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<sup>2</sup>*Experimental Station of the National Research Institute of Animal Production, Chorzełów, Poland.*

Given the important function fulfilled by mitochondria in cells, the relationship between mitochondrial DNA polymorphism and economically important traits has been investigated for many farm animal species. However, no such information is available for farm fur-bearing animals. Therefore, we have evaluated three fragments of mitochondrial genes: *MT-COI* (cytochrome c oxidase subunit I), *MT-COII* (cytochrome c oxidase subunit II), and *MT-CYTB* (cytochrome b) for their association with performance traits in raccoon dogs. The results obtained in this study indicate that the candidate gene *MT-COII* can be involved in the development of hair coat. Hair coat quality was significantly associated with the m.A7446 polymorphism. Raccoon dogs of genotype m.G7446 had significantly better hair coat quality in comparison with animals of genotype m.A7446. In the case of the other eight polymorphisms identified, no significant differences were found in the values of the six assessed traits (body weight, body size and conformation, colour type, hair coat purity, hair coat quality, total score of conformation traits) between the alternative genotypes. Six polymorphisms were found in the *MT-COII* gene sequence and, accordingly, three haplotypes: A (AAGAAA - respectively in positions 7125, 7194, 7221, 7287, 7446, 7578), B (AAGAGA), and C (GCAGGG) were distinguished. Animals with haplotype B and C were characterised by a significantly better hair coat quality in comparison.

Given the important function fulfilled by mitochondria in cells, the relationship between

mitochondrial DNA polymorphism and economically important traits has been investigated for many farm animal species. However, no such information is available for farm fur-bearing animals. Therefore, we have evaluated three fragments of mitochondrial genes: *MT-COI* (cytochrome c oxidase subunit I), *MT-COII* (cytochrome c oxidase subunit II), and *MT-CYTB* (cytochrome b) for their association with performance traits in raccoon dogs. The results obtained in this study indicate that the candidate gene *MT-COII* can be involved in the development of hair coat. Hair coat quality was significantly associated with the m.A7446 polymorphism. Raccoon dogs of genotype m.G7446 had significantly better hair coat quality in comparison with animals of genotype m.A7446. In the case of the other eight polymorphisms identified, no significant differences were found in the values of the six assessed traits (body weight, body size and conformation, colour type, hair coat purity, hair coat quality, total score of conformation traits) between the alternative genotypes. Six polymorphisms were found in the *MT-COII* gene sequence and, accordingly, three haplotypes: A (AAGAAA - respectively in positions 7125, 7194, 7221, 7287, 7446, 7578), B (AAGAGA), and C (GCAGGG) were distinguished. Animals with haplotype B and C were characterised by a significantly better hair coat quality in comparison with raccoon dogs of haplotype A. Given the important function of mitochondria in biochemical processes related to economically important traits and animal healthiness, the investigations should be continued and extended on other functional and health traits.

*Animal Science Papers and Reports vol. 34 (2016) no. 3, 293-302.*

### **Regulation of diapause in carnivores**

Fenelon J.C.<sup>1</sup>, Lefèvre P.L.<sup>1</sup>, Banerjee A.<sup>1</sup>, & Murphy B.D.<sup>1</sup>.

<sup>1</sup>*Centre de recherche en reproduction animale, Faculté de médecine vétérinaire, Université de Montréal, St-Hyacinthe, QC, Canada.*

*Reprod. Domest Anim. 2016.*

*Doi: 10.1111/rda.12835. [Epub ahead of print]*

**Hormonal stimulation of American mink (*Neovison vison*) females during mating improves reproduction parameters**

Seremak B.<sup>1</sup>, Dziadosz-Stys M.<sup>1</sup>, Felska-Blaszczyk L.<sup>2</sup> & Lasota B.<sup>1</sup>

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The aim of the study was to determine the effect of hormonal stimulation during the mating season on reproduction performance in American mink females and a selection of both the hormonal formulation and its dosage. The study involved one-year-old females of American mink (*Neovison vison*) of the pearl color morph. The females received one of two hormonal formulations, F1 or F2, with a single injection administered 24 h before planned mating. The formulations contained: (F1) a pituitary gonadotropin releasing hormone analogue, and (F2) freeze-dried, crystalline serum gonadotropin (PMSG) of a strong FSH- and LH-like effect. Each formulation was administered in three dosage levels. The hormonal stimulation applied 24 h before the planned mating significantly reduced the number of sterile females, also brought a significant increase in the average litter size, from 1.05 to 1.35 kits, and in the average number of live births, from 1.03 to 1.98. Of the two formulations tested, the analogue of pituitary gonadotropin releasing hormone (F1) at a dose of 36 IU proved to be the most effective; its application allowed attaining the highest reproductive parameters. Using hormonal stimulation of the female mink during the mating can be effectively put into practice on the farm and may in consequence improve the profitability of the production cycle.

*Annals of Warsaw University of Life Sciences – SGGW*

*Animal Science, No 55 (1), 2016: 119–126*

*(Ann. Warsaw Univ. Life Sci. – SGGW, Anim. Sci. 55 (1), 2016)*

**The Transcriptomic Evolution of Mammalian Pregnancy: Gene Expression Innovations in Endometrial Stromal Fibroblasts.**

Kin K.<sup>1</sup>, Maziarz J.<sup>2</sup>, Chavan A.R.<sup>1</sup>, Kamat M.<sup>3</sup>, Vasudevan S.<sup>3</sup>, Birt A.<sup>3</sup>, Emera D.<sup>4</sup>, Lynch V.J.<sup>5</sup>, Ott T.L.<sup>3</sup>, Pavlicev M.<sup>6</sup> & Wagner G.P.<sup>7</sup>.

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*Genome Biol. Evol.*, 2016: 8(8): 2459-73.

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**Epidermal Growth Factor Promotes Proliferation and Migration of Follicular Outer Root Sheath Cells via Wnt/ $\beta$ -Catenin Signaling**

Zhang H.<sup>1</sup>, Nan W., Wang S, Zhang T., Si H., Yang F. & Li G.

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*Cell Physiol. Biochem.* 2016: 39(1): 360-70.

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### **Sperm kinematic, head morphometric and kinetic-morphometric subpopulations in the blue fox (*Alopex lagopus*)**

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This work provides information on the blue fox ejaculated sperm quality needed for seminal dose calculations. Twenty semen samples, obtained by masturbation, were analyzed for kinematic and morphometric parameters by using CASA-Mot and CASA-Morph system and principal component (PC) analysis. For motility, eight kinematic parameters were evaluated, which were reduced to PC1, related to linear variables, and PC2, related to oscillatory movement. The whole population was divided into three independent subpopulations: SP1, fast cells with linear movement; SP2, slow cells and nonoscillatory motility; and SP3, medium speed cells and oscillatory movement. In almost all cases, the subpopulation distribution by animal was significantly different. Head morphology analysis generated four size and four shape parameters, which were reduced to PC1, related to size, and PC2, related to shape of the cells. Three morphometric subpopulations existed: SP1: large oval cells; SP2: medium size elongated cells; and SP3: small and short cells. The subpopulation distribution differed between animals. Combining the kinematic and morphometric datasets produced PC1, related to morphometric parameters, and PC2, related to kinematics, which generated four sperm subpopulations - SP1: high oscillatory motility, large and short heads; SP2: medium velocity with small and short heads; SP3: slow motion small and

elongated cells; and SP4: high linear speed and large elongated cells. Subpopulation distribution was different in all animals. The establishment of sperm subpopulations from kinematic, morphometric, and combined variables not only improves the well-defined fox semen characteristics and offers a good conceptual basis for fertility and sperm preservation techniques in this species, but also opens the door to use this approach in other species, included humans.

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### **NUTRITION, FEEDING AND MANAGEMENT**

#### **Protein and amino acid bioavailability of extruded dog food with protein meals of different quality using growing mink () as a model**

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The present study evaluated growing mink () as a model for dietary protein quality assessment of protein meals used in extruded dog foods. Three foods with similar CP content but of different protein quality were produced using different protein meals. The protein meals varied with respect to CP digestibility and AA composition and included lamb meal (LBM), poultry meal (PM), and fish meal (FM) with low, intermediate, and high protein quality, respectively. Nitrogen balance, BW gain, protein efficiency ratio (PER), and apparent total tract digestibility (ATTD) were used as measures of protein and AA bioavailability in growing mink. Standardized ileal digestibility (SID) was used to measure protein and AA bioavailability in adult dogs (). The mink study (3 × 3 Latin square design) included 12 kits aged 8 to 11 wk. The dog study included 12 dogs divided in 3 groups allocated to 1 of the experimental diets. The growing mink responded in accordance with the different AA

supply between diets, as determined by the first limiting AA. The LBM diet deviated from the other diets with lower ( $< 0.001$ ) values for N retention, BW gain, and PER, and the diets differed ( $< 0.001$ ) in ATTD of CP and all AA, except for hydroxyproline. Retention of N was 0.66, 1.04, and 1.18 g·kg<sup>-1</sup>·d; BW gain was 8.2, 26.8, and 35.3 g/d; PER was 0.38, 1.39, and 1.71; and ATTD of CP was 66.8, 73.8, and 82.1% for the LBM, PM, and FM diets, respectively. In dogs, SID of CP and AA differed ( $\leq 0.017$ ) between diets and was generally lowest for the LBM diet, intermediate for the PM diet, and greatest for the FM diet. For CP, SID was 71.5, 80.2, and 87.0% for the LBM, PM, and FM diets, respectively. The contents of digestible CP and AA (based on SID) covered the minimal requirement for adult dogs set by the NRC for all diets, except for the content of digestible Met + Cys in the LBM diet. Despite this, dietary content of Met + Cys in the LBM diet agreed with the recommended level set by the NRC and the Association of American Feed Control Officials for adult dogs but was below the level recommended by the European Pet Food Industry Federation. It was concluded that growth studies with mink kits can provide valuable information in protein quality assessment of extruded dog foods. Furthermore, the study showed that to ensure nutritional adequacy of dog food and to be able to compare protein quality of dog foods, information on AA composition and digestibility is crucial.

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**Fetal life malnutrition was not reflected in the relative abundances of adiponectin and leptin mRNAs in adipose tissue in male mink kits at 9.5 weeks of age**

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Malnutrition in fetal life and during suckling have in some animal studies resulted in adaptive changes related to the fat and glucose metabolism, which in the long term might predispose the offspring for metabolic disorders such as obesity later in life. The objective was to study the effect of fetal life malnutrition in male mink on the gene expression of leptin and adiponectin in different adipose tissue sites.

Thirty-two male mink, strict carnivore species, exposed to low (FL) or adequate (FA) protein provision the last  $16.3 \pm 1.8$  days of fetal life and randomly assigned to a low (LP) or adequate (AP) protein diet from 7 to 9.5 weeks of age were used. Adipose tissues (subcutaneous, perirenal and mesenteric) were analyzed using qPCR. Fetal life or post-weaning protein provision did not affect the relative abundances of leptin and adiponectin mRNAs in adipose tissue at 9.5 weeks of age. Relative abundances of leptin and adiponectin mRNAs were different between adipose tissue sites and were significantly higher in subcutaneous than in perirenal and mesenteric tissues.

Fetal life protein malnutrition in male mink, did not result in adaptive changes in the gene expression of leptin and adiponectin mRNAs in adipose tissue at 9.5 weeks of age as found in rodents. However, both leptin and adiponectin mRNAs were significantly differently expressed between tissue sites.

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**Estimating population density and connectivity of American mink using spatial capture-recapture**

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Estimating the abundance or density of populations is fundamental to the conservation and management of species, and as landscapes become more fragmented, maintaining landscape connectivity has become one of the most important challenges for biodiversity conservation. Yet these two issues have never been formally integrated together in a model that simultaneously models abundance while accounting for connectivity of a landscape. We demonstrate an application of using capture-recapture to develop a model of animal density using a least-cost path model for individual encounter probability that accounts for non-Euclidean connectivity in a highly structured network. We utilized scat detection dogs (*Canis lupus familiaris*) as a means of collecting non-invasive genetic samples of American mink (*Neovison vison*) individuals and used spatial capture-recapture models (SCR) to gain inferences about mink population density and connectivity. Density of mink was not constant across the landscape, but rather increased with increasing distance from city, town, or village centers, and mink activity was associated with water. The SCR model allowed us to estimate the density and spatial distribution of individuals across a 388 km<sup>2</sup> area. The model was used to investigate patterns of space usage and to evaluate covariate effects on encounter probabilities, including differences between sexes. This study provides an application of capture-recapture models based on ecological distance, allowing us to directly estimate landscape connectivity. This approach should be widely applicable to provide simultaneous direct estimates of density, space usage, and landscape connectivity for many species.

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### **Outbreak of severe pseudorabies virus infection in pig-offal-fed farmed mink in Liaoning Province, China**

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An outbreak of severe pseudorabies virus (PRV) infection in farmed mink occurred in northern China in late 2014, causing significant economic losses in the local fur industry. Here, we report the first case of a PRV outbreak in mink in northeastern China, caused by feeding farmed mink with raw pork or organs contaminated by PRV. Mink infected with virulent PRV exhibited diarrhea, neurologic signs, and higher mortality, which can be misdiagnosed as highly pathogenic mink enteritis virus (MEV), canine distemper virus (CDV), and food poisoning. However, these were excluded as causative agents by PCR or bacteria isolation. The duration of disease was 3-7 days, and the mortality rate was 80-90%. PRV was characterized using indirect immunofluorescence assays (IFA) and electron microscopy (EM). Phylogenetic analysis based on full-length genome sequences and those of individual genes of this novel virus strain showed that it clustered in an independent branch with several other PRV isolates from China.

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**Rate of exposure of a sentinel species, invasive American mink (*Neovison vison*) in Scotland, to anticoagulant rodenticides**

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**Mean body weight gains in standard mink depending on the number of kits in a litter**

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Mean body weight gains in standard mink depending on the number of kits in a litter. The objective of the study is to determine the effect of litter size from which animals came on their weight at weaning and pre-slaughter, and as a consequence also on their mean daily gains. The study was conducted on a population of 330 minks, divided into groups depending on the size of litter from which they came: I (2–4 kits) – 74 animals (44 ♂, 30 ♀), II (5–7 kits) – 170 animals (92 ♂, 78 ♀), III (8–10 kits) – 86 animals (44 ♂, 42 ♀). We established a significant effect of litter size on body weight at weaning and mean daily gains. Animals from smaller litters were found to have a higher body weight at weaning; whereas higher gains were observed in animals

coming from bigger litters. Pre-slaughter body weight was similar in all assessed groups.

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(*Ann. Warsaw Univ. Life Sci. – SGGW, Anim. Sci.* 55 (2), 2016)

**HEALTH AND DISEASE**

**Transcript Profiling of Toll-Like Receptor mRNAs in Selected Tissues of Mink (*Neovison vison*)**

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Toll-like receptors (TLRs) can recognize conserved molecular patterns and initiate a wide range of innate and adaptive immune responses against invading infectious agents. The aim of this study was to assess the transcript profile of mink TLRs (mTLRs) in mink peripheral blood mononuclear cells (PBMCs) and a range of tissues, and to explore the potential role of mTLRs in the antiviral immune response process. The results indicated that the mTLR partial nucleotide sequences had a high degree of nucleotide identity with ferret sequences (95–98%). Phylogenetic analysis showed that mammalian TLRs grouped into five TLR families, with a closer relationship of the mTLRs with those of ferret than the other mammalian sequences. Moreover, all the mTLRs were ubiquitously expressed in lymphoid organs (spleen and lymph nodes) and PBMCs. Interestingly, the mTLR expression patterns in lung, uterus, and heart showed quite a lot of similarity. Another remarkable observation was the wide expression of mTLR1–3 mRNAs in all tissues. Among the analyzed tissues, skeletal muscle was revealed to being the lowest repertoire of mTLR expression. Additionally, mink PBMCs exposed to the canine distemper virus revealed significant upregulation of mTLR2, mTLR4, mTLR7, and mTLR8 mRNAs, indicating

that mTLRs have a role in innate immunity in the mink. Collectively, our results are the first to establish the basic expression patterns of mTLRs and the relationship between mTLRs and a virus, which will contribute to better understanding of the evolution and the functions of mTLRs in the innate immune system in minks.

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### **High molecular polymorphism of the hypervariable region in the VP2 gene of Aleutian mink disease virus**

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Parvoviruses exhibit extreme genetic plasticity. The VP2 protein, containing a hypervariable region, is of particular importance. A single nucleotide change in this part of the genome and its effect on the amino acid sequence may significantly affect the range of infected hosts, tropism for specific tissues, or virulence. The high polymorphism in the hypervariable region can be exploited for phylogenetic analysis. The aim of this study was to analyze the polymorphism of the VP2 hypervariable region in isolates of the Aleutian mink disease virus (AMDV) infecting Polish mink farms and to determine the phylogenetic relationships between the Polish isolates and genetic variants of the pathogen occurring in other countries. The study compares farms from two regions of Poland. The isolates contained five changes in the amino acid sequence, which had not previously been recorded in the NCBI database. There were 21 changes noted between the genotypes obtained and the sequence of the reference strain [GenBank NC\_001662.1], of which 8 were in the hypervariable region. The isolates identified in our study exhibit a high degree of similarity within the farms, but between farms there is considerable variation in the amino acid sequence of the VP2 protein fragment. Because variants characteristic for farms were obtained, it

will be possible to trace the movement of the virus between farms, and in the longer term to use the characteristic sequences as a marker of the origin of infected animals.

*Acta Virol.*, 2016; 60(4):354-360.  
Doi: 10.4149/av\_2016\_04\_354

### **Driving forces behind the evolution of the Aleutian mink disease parvovirus in the context of intensive farming**

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Aleutian mink disease virus (AMDV) causes plasmacytosis, an immune complex-associated syndrome that affects wild and farmed mink. The virus can also infect other small mammals (e.g., ferrets, skunks, ermines, and raccoons), but the disease in these hosts has been studied less. In 2007, a mink plasmacytosis outbreak began on the Island of Newfoundland, and the virus has been endemic in farms since then. In this study, we evaluated the molecular epidemiology of AMDV in farmed and wild animals of Newfoundland since before the beginning of the outbreak and investigated the epidemic in a global context by studying AMDV worldwide, thereby examining its diffusion and phylogeography. Furthermore, AMDV evolution was examined in the context of intensive farming, where host population dynamics strongly influence viral evolution. Partial NS1 sequences and several complete genomes were obtained from Newfoundland viruses and analyzed along with numerous sequences from other locations worldwide that were either obtained as part of this study or from public databases. We observed very



high viral diversity within Newfoundland and within single farms, where high rates of co-infection, recombinant viruses and polymorphisms were observed within single infected individuals. Worldwide, we documented a partial geographic distribution of strains, where viruses from different countries co-exist within clades but form country-specific subclades. Finally, we observed the occurrence of recombination and the predominance of negative selection pressure on AMDV proteins. A surprisingly low number of immunoeptopic sites were under diversifying pressure, possibly because AMDV gains no benefit by escaping the immune response as viral entry into target cells is mediated through interactions with antibodies, which therefore contribute to cell infection. In conclusion, the high prevalence of AMDV in farms facilitates the establishment of co-infections that can favor the occurrence of recombination and enhance viral diversity. Viruses are then exchanged between different farms and countries and can be introduced into the wild, with the rapidly evolving viruses producing many parallel lineages.

*Virus Evol.*, 2016: 2(1):vew004. *eCollection 2016*  
Doi: 10.1093/ve/vew004

#### **Development of a Peptide ELISA for the diagnosis of Aleutian Mink Disease**

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Aleutian disease (AD) is a common immunosuppressive disease in mink farms worldwide. Since the 1980s, counterimmunoelectrophoresis (CIEP) has been the main detection method for infection with the Aleutian Mink Disease Virus (AMDV). In this study, six peptides derived from the AMDV structural protein VP2 were designed, synthesized, and used as ELISA antigens to detect anti-AMDV antibodies in the sera of infected minks. Serum samples were collected from 764 minks in farms from five different provinces, and analyzed by both CIEP (a gold standard) and peptide ELISA. A peptide designated

P1 (415 aa-433 aa) exhibited good antigenicity. A novel ELISA was developed using ovalbumin-linked peptide P1 to detect anti-AMDV antibodies in mink sera. The sensitivity and specificity of the peptide ELISA was 98.0% and 97.5%, respectively. Moreover, the ELISA also detected 342 early-stage infected samples (negative by CIEP and positive by PCR), of which 43.6% (149/342) were true positives. These results showed that the peptide ELISA had better sensitivity compared with CIEP, and therefore could be preferable over CIEP for detecting anti-AMDV antibodies in serological screening.

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*PLoS One.* 2016: 11(11): e0165793. Doi: 10.1371/journal.pone.0165793. *eCollection 2016.*

#### **Postvaccination wounds associated predominantly with *Arcanobacterium phocae* in minks (*Neovison vison*) at three mink farms**

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Doi: 10.1016/j.virusres.2016. [Epub ahead of print]

#### **Experimental Infection of Mink Enforces the Role of *Arcanobacterium phocae* as Causative Agent of Fur Animal Epidemic Necrotic Pyoderma (FENP)**

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Fur Animal Epidemic Necrotic Pyoderma (FENP) is a severe, often lethal infectious disease affecting all three fur animal species: mink (*Neovision vision*), foxes (*Vulpes lagopus*) and finnraccoons (*Nyctereutes procyonoides*). Previous studies showed an association between *Arcanobacterium phocae* and FENP. An experimental infection was conducted to confirm the ability of *A. phocae* to infect mink either alone or concurrently with a novel *Streptococcus* sp. found together with *A. phocae* in many cases of FENP. Different inoculation methods were tested to study possible routes of transmission. Typical signs, and gross- and histopathological findings for FENP were detected when naïve mink were infected with the tissue extract of mink with FENP, using a subcutaneous/ intradermal infection route. Edema, hemorrhage, necrosis and pus formation were detected in the infection site. A pure culture preparation of *A. phocae* alone or concurrently with the novel *Streptococcus* sp. caused severe acute signs of lethargy, apathy and anorexia and even mortality. The histopathological findings were similar to those found in naturally occurring cases of FENP. In contrast, the perorally infected mink presented no clinical signs nor any gross- or histopathological lesions. This study showed that *A. phocae* is able to cause FENP. The study also indicated that predisposing factors such as the environment, the general condition of the animals, temperature and skin trauma contribute to the development of the disease.

*PLoS One. 2016; 11(12): e0168129. Doi: 10.1371/journal.pone.0168129. eCollection 2016.*

### **Genome analysis of canine astroviruses reveals genetic heterogeneity and suggests possible inter-species transmission**

*Mihalov-Kovács E.<sup>1</sup>, Martella V.<sup>2</sup>, Lanave G.<sup>2</sup>, Bodnar L.<sup>2</sup>, Fehér E.<sup>1</sup>, Marton S.<sup>1</sup>, Kemenesi G.<sup>3</sup>, Jakab F.<sup>3</sup> & Bányai K.<sup>4</sup>*

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### **A novel bocavirus from domestic mink, China**

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Bocaviruses have been found in the feces of humans and a variety of animals, including pigs, cattle, dogs, gorillas, cats, and sea lions. Here, we have characterized the almost complete genome (5224 nt) of a novel bocavirus from feces of domestic minks, which has been provisionally named mink bocavirus. The NS1 protein of mink bocavirus shared 36.9-52 % amino acid sequence identities with those of other known bocaviruses and phylogenetically clustered with bocaviruses from other carnivores. According to the genetic distance-based criteria, mink bocavirus qualifies as a novel species of bocavirus. PCR of feces from a group of domestic minks, which included both healthy animals and animals suffering from diarrhea, revealed that 30 % (9/30) shed virus. However, no association between viral shedding and the presence of diarrhea could be determined.

*Virus Genes., 2016: 52(6): 887-890. Epub 2016.*

*Doi: 10.1007/s11262-016-1380-4*

**Isolation of *Clostridium limosum* from an outbreak of metritis in farmed mink**

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An outbreak of sudden death of pregnant farmed mink in Finland occurred during the busiest whelping period in the spring of 2013. The affected farms were all located in western Finland in a rather narrow geographic area, Ostrobothnia. Dead mink from 22 farms were submitted for laboratory diagnostics to the Finnish Food Safety Authority (Evira). The carcasses were necropsied and tissue specimens were prepared for histology. Samples of internal organs and peritoneal fluid were cultured bacteriologically.

Major pathological findings included hemorrhagic vaginal discharge, severely inflamed uteri with luminal hemorrhagic exudate and dead fetuses. Dead fetuses were present in the peritoneal cavity and associated severe peritonitis occurring as sequela of uterine rupture were found in most minks. Histological findings included hemorrhages, neutrophil infiltrations, degenerative inflammatory cells, edema, fibrin and rod-shaped bacteria on all layers of the uterine wall. In most samples abundant and pure anaerobic bacterial growth of *Clostridium limosum* was found.

This is the first report of *C. limosum* associated metritis in farmed mink. Disease was only observed in pregnant females and the uterus was the primary site of infection. The source of infection and the route of transmission remained unclear, but feed borne transmission was suspected.

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**Permissive XPR1 gammaretrovirus receptors in four mammalian species are functionally distinct in interference tests**

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**Influenza A Virus Surveillance in the Invasive American Mink (*Neovison vison*) from Freshwater Ecosystems, Northern Spain**

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**First international collaborative study to evaluate rabies antibody detection method for use in monitoring the effectiveness of oral vaccination programmes in fox and raccoon dog in Europe**

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*J Virol Methods. 2016: 238:77-85.*

*Doi: 10.1016/j.jviromet.2016.10.006. Epub 2016 .*

**The usefulness of direct agglutination test, enzyme-linked immunosorbent assay and polymerase chain reaction for the detection of *Toxoplasma gondii* in wild animals**

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**Muscle mercury and selenium in fishes and semiaquatic mammals from a selenium-deficient area**

Kalisinska E.<sup>1</sup>, Lanocha-Arendarczyk N.<sup>1</sup>, Kosik-Bogacka D.<sup>2</sup>, Budis H.<sup>3</sup>, Pilarczyk B.<sup>4</sup>, Tomza-Marciniak A.<sup>4</sup>, Podlasinska J.<sup>5</sup>, Cieslik L.<sup>6</sup>, Popiolek M.<sup>7</sup>, Pirog A.<sup>8</sup> & Jedrzejewska E.<sup>9</sup>.

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*Ecotoxicol Environ Saf.*, 2017: 136:24-30.

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**Heavy metal concentrations in female wild mink (*Neovison vison*) in Sweden - Sources of variation and associations with internal organ weights**

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*Biomed Environ Sci.*, 2016: 29(7): 521-3.

Doi: 10.3967/bes2016.068.

**Detection of Multi-drug Resistant *Acinetobacter Lwoffii* Isolated from Soil of Mink Farm**

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*Biomed Environ Sci.* 2016; 29(7): 521-3.

Doi: 10.3967/bes2016.068.

**Calcium-Sensing Receptor and Transient Receptor Ankyrin-1 Mediate Emesis Induction by Deoxynivalenol (Vomitoxin)**

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### **Brains of Native and Alien Mesocarnivores in Biomonitoring of Toxic Metals in Europe**

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Mercury (Hg), lead (Pb) and cadmium (Cd) are involved in mammalian brain damage. However, little is known about Pb and Cd brain levels in

wildlife that reflect the geochemical background. The aims of the study include the estimation of Hg, Pb and Cd concentrations, and the determination of relationships between these elements in the brains of 94 mesocarnivores. Road-killed or hunted animals were obtained from north-western Poland near the Polish-German border. The investigation covered the native Eurasian otter *Lutra lutra*, badger *Meles meles*, pine marten *Martes martes*, beech marten *M. foina*, European polecat *Mustela putorius*, red fox *Vulpes vulpes*, and alien species: feral and ranch American mink *Neovison vison*, raccoon *Procyon lotor* and raccoon dog *Nyctereutes procyonoides*. Depending on the diet and environmental pollution, the carnivore brains accumulated toxic metals in varying amounts. The highest median Hg levels (in mg/kg dry weight, dw) were found in the piscivorous Eurasian otter and feral mink (2.44 and 3.96), Pb in the omnivorous raccoon (0.47), while Cd in minks (~0.06). We indicated that Pb-based ammunition is a significant source of the element in scavengers from hunting area, and we also found a significant correlation between Pb and Cd levels in the fox brain. Finally, this study is the first to suggest background levels for brain Pb and Cd in mesocarnivores (<0.50 and <0.04 mg/kg dw, respectively).

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**Actual Mink Research 20 September 2016**

**Meeting at Research Centre Foulum**

**Faculty of Science and Technology**

**Aarhus University, Denmark**

**The  $\alpha$ -tocopherol supplementation for mink can be reduced**

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The  $\alpha$ -tocopherol (vitamin E) requirement of mink has traditionally been considered very high in comparison to other species (). This was due to the very high content of fats and oils and generally easily perishable ingredients in feed mixtures for mink. Fats and oils are easily oxidised (rancified) if not kept under optimal conditions with respect to temperature and oxidative stability ().  $\alpha$ -Tocopherol acts as an anti-oxidant (prevents oxidation/rancidity) both in the feed and in the body of the mink after ingesting the feed, hence protects the animals against negative physiological effects of rancid fats and oils (). Lately, in Denmark, there has been a change in which ingredients are available for mink feed production towards less fish based offal together with a rapid development in storage and transport conditions of both raw ingredients and ready mixed mink feed in both the mink feed industry and on mink farms. Therefore it seems reasonable to reevaluate existing recommendations for  $\alpha$ -tocopherol supplementation in mink to assess the need for  $\alpha$ -tocopherol under modern production conditions and avoid over-supplementation with  $\alpha$ -tocopherol, which is both physiologically and financially unsound. Studies in mink during growth and pelting seasons 2014 and 2015 with varying  $\alpha$ -tocopherol supplementation have shown that the current  $\alpha$ -tocopherol recommendations for mink feed of 60 to 80 mg/kg feed can be reduced to approximately 40 mg/kg feed when synthetic  $\alpha$ -tocopherol is used. If the natural RRR- $\alpha$ -tocopherol stereoisomer is used the supplied amount of  $\alpha$ -tocopherol can be further reduced to approximately 20 mg/kg feed. However, individual animal, feed,

and farm related conditions should be taken into consideration.

*Meeting at Research Centre Foulum, Faculty of Science and Technology, Aarhus University, Denmark. DCA Report no. 083, September 2016 (in Danish) p. 12-18. Author's abstract.*

**Vitamin B – if added in excess to the feed for mink it will be lost in the urine**

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The present investigation showed that when feeding mink a feed composed of high quality ingredients it is possible to leave out B-vitamins and cholin without inducing deficiencies in the mink. In an experiment, mink were fed four different diets: 1) a diet without addition of B-vitamins and cholin, 2) a diet where 50% of the recommended B-vitamin was added, 3) a control diet with recommended addition of B-vitamin and 4) a diet where liquid vitamin B was added to the control diet. There was no difference in growth and fur quality between the experimental groups. Blood and urine samples from 10 mink in each group were analyzed. In urine, it was possible to detect both intact B-vitamins (vitamin B2, B5, B6, and B9) and metabolites of vitamin B3 and B6. The level of vitamin B9 was very low in mink fed the diet without vitamin B supplementation, and further studies are required to establish the need for vitamin B9. For vitamin B2, B3, B5, and B6 the study showed that the amount of these vitamins was adequate in the feed even without supplementation.

*Meeting at Research Centre Foulum, Faculty of Science and Technology, Aarhus University, Denmark. DCA Report no. 083, September 2016 (in Danish) p. 19-27. Author's abstract.*

### **Protein requirements for gestation and retention in fetal tissue in mink (*Neovison vison*)**

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The knowledge regarding nutrient requirements of pregnant female mink is fairly limited but the importance of gestational nutrition, especially protein provision, has, however, long been recognized. Furthermore, it is well known that mink kits are born altricial, and that their body energy reserves are very limited at birth, but still very little is known about the pattern of fetal growth and the quantitative accretion of nutrients and energy in the body. Because of the delayed implantation, stage in gestation can usually not be determined exactly and this hampers the possibilities to get accurate results. The objectives were to determine the protein requirement during gestation in mink before (BEF, 66 dams) and after (AFT, 40 dams) implantation and to monitor and measure protein and energy retained in fetal tissue during fetal development in pregnant mink dams at different time points after mating (FET). Protein provision made up 10, 15, 20, 25, 30, 35, 40 and 45% of ME (BEF) whereas the two lowest levels were excluded in AFT. Implantation sites, number and survivability of fetuses were determined. Fetal nutrient and energy retention at different time points after mating was investigated with 116 dams (FET). Implantation occurred at a normal rate even at the lowest protein provision, but embryo survival tended to be compromised when protein provided  $\leq 20\%$  of metabolizable energy (ME) in the BEF study. All levels of protein provision AFT supported a similar rate of implantation, number and survival of fetuses. However 20% of ME from protein was numerically lower than 25%-45% of ME in the AFT study. Late fetal growth is exponential, but only 0.6 g protein was retained in individual fetuses 50 days after mating (FET) confirming the low protein requirement for gestation.

Meeting at Research Centre Foulum, Faculty of Science and Technology, Aarhus University, Denmark. DCA Report no. 083, September 2016 (in Danish) p. 28-34. Author's abstract.

### **Probiotics effect on the intestinal flora in mink kits**

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Diarrhea is a frequent cause for disease and mortality in mink kits during their growth period, and one of the main reasons for antibiotic use in mink production. In other production animals and humans probiotics are assumed to have a positive effect on gut health and may have a protective effect in relation to some types of diarrhea. The aim of the study was to investigate the potential effect of probiotic supplied to mink kits in the period before weaning.

To investigate the effect of certain types of probiotics in mink kits, we studied the growth of 73 mink kits of the age 35 to 56 days kept in so-called "kindergardens". The kits were divided into three test groups and once a day the mink kits were treated with one of two probiotics, "*Lactobacillus reuteri*" and "*Actobacillus plantarum* and *Pediococcus acidilactici*". Mink kits in the control group received a placebo treatment without probiotics. The results did not show an effect of either of the two probiotics on growth performance or survival.

Meeting at Research Centre Foulum, Faculty of Science and Technology, Aarhus University, Denmark. DCA Report no. 083, September 2016 (in Danish) p. 35-41. Author's abstract.

### **Several functions of straw to mink**

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According to current Danish legislation, farm mink must have permanent access to straw during housing. However, the best provision method (on top of nest box lid vs. inside the cage) and the mink's use of straw during the entire yearly production cycle are not really known. Therefore,



we investigated several functions of straw for one year. The study focused on whether (i) mink eat straw, in particular during restricted feeding periods before mating, (ii) straw functions as enrichment reducing abnormal behaviour, (iii) mink use straw for nest building outside the reproductive period, (iv) straw is used in maternal nest building, improving litter survival and (v) straw coverage of the nest boxes influences mink behaviour. We used 320 cages of brown mink at the AU-Foulum research farm from January to pelting in November and followed dams and their offspring in 2016. The cages were distributed to four groups (each of 80 cages) according to straw provision (in cage/on top of nest box lid) and type of nest box cover (none, wooden plate or straw). The groups were: S (straw given in the cage, no nest box cover), SC (straw given in the cage, wood plate cover nest box), NB (straw given on top of nest box, straw cover nest box) and SNB (straw in the cage and on top of nest box, straw cover on nest box). Preliminary results suggest that mink used barley straw for several purposes, including eating (in particular during periods of restricted feeding), and nest building (both during the winter period and as part of the maternal behaviour). Mink can pull straw down from the nest box lid for eating; however, they nest build less in case straw only is provided here. Around deliveries the combination of straw in the cage and nest box coverage reduced the number of stillborn kits. We cannot exclude that a covered nest box can be advantageous for first-year dams, whereas no effect was evident in experienced, second-year dams. The experiment continues for the rest of 2016 thus further results will be presented.

*Meeting at Research Centre Foulum, Faculty of Science and Technology, Aarhus University, Denmark. DCA Report no. 083, September 2016 (in Danish) p. 42-47. Author's abstract.*

### **Feeding strategy in the late gestation and the nest box environment's influence on the farmed mink females ability to perform early maternal care**

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In the production of farmed mink, the litter sizes and kit mortality are relatively high, and a majority of the kits that die do so within the first seven days alive. Mink kits are born vulnerable, which makes them dependent on both the female's ability to perform early maternal care and the nest environment. The aim of this master project was to investigate how both feeding strategy in the late gestation and the nest box environment could contribute to improving the female mink's ability to perform early maternal care under different Danish management strategies and thereby increase kit survival and welfare seven days postpartum.

This farm experiment included 3,351 gestated female mink distributed on four farms. The females had the age of one to four years, and seven color types were represented. The litter was counted one and seven days postpartum, and evaluations of the nests were carried out before parturition and postpartum. Moreover, the females' body conditions were assessed before parturition. Data were collected from April 18 or 21 (depending on farm) and ended when the litter had the age of seven days. The results across farms showed no differences in kit survival one or seven days postpartum or in kit mortality between the groups fed 50% restrictedly and the groups fed non-restrictedly in the late gestation. However, on farm level, one of the farms had had more kits in the groups fed non-restrictedly. The results from the tested nest box environment products, easy-brick and easy-strø++, did not indicate a contribution to the improvement of the female mink's ability to perform early maternal care. easy-strø++ reduced the female mink's possibilities to build a nest with top and walls (category score >3). These open nests compared to the closed nests, scored before parturition and postpartum, did not differ in the number of kits alive one or seven days postpartum when straw was used in the top of the nest box.

*Meeting at Research Centre Foulum, Faculty of Science and Technology, Aarhus University, Denmark. DCA Report no. 083, September 2016 (in Danish) p. 48-57. Author's abstract.*

**No effect of human activity or where the access hole is placed between the upper and lower part of cages on the number of bite marks in juvenile group housed mink**

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A 5 generations selection experiment has shown that bite-marks on the leather side of mink pelts can be changed significantly, if the social interactions between the mink in a cage is included in 'group-selection'. In addition to high heritability, profound environmental factors was found to affect the number of bite-marks in both a selection and control line. The total number of bite-marks, therefore, was only reduced after selection in four generations. As early weaning and separation was found not to be

the profound environmental factor, two other candidates for such an environmental factor in group-housing was tested: 1. The level of human activity around the mink. 2. Placing the access hole between the lower and the upper part in the back of the cage. Based on the bite-mark score from the leather side of the skins at pelting, the two environmental factors tested had little and insignificant effect. Thus, the decisive management- or environmental factors affecting the group-selection experiment are still not known.

*Meeting at Research Centre Foulum, Faculty of Science and Technology, Aarhus University, Denmark. DCA Report no. 083, September 2016 (in Danish) p. 58-61. Author's abstract.*

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# WELFUR-MINK

## - STATUS AND PERSPECTIVES

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### WelFur-Mink

In 2009 the European Fur Breeders' Association initiated the "WelFur" project with the purpose of developing a welfare assessment protocol for mink and fox farms, following the standards developed within the framework of the EU Welfare Quality® project. The assessment is based on four welfare principles: "Good feeding", "Good housing", "Good health" and "Appropriate behaviour" including 12 underlying criteria and 22 welfare measurements -to be measured on-farm in three different seasons. WelFur mink has been tested in 12 countries and based on this the protocol is adjusted and optimized. Research efforts focus on the optimization of WelFur without reducing the quality. Electronic data collection gathering ensures that breeders are informed of the results immediately following the assessment. Like other production data these results may be used for production planning purposes in consultation with advisors and veterinarians.

### Background

During the last decades research efforts have focused on how to accurately measure production animal welfare; partly in order to quantify the debate on animal welfare, and partly to assess how different management routines and production systems affect animal welfare. Research results are increasingly used in relation to legislation and authority control of animal welfare as well as ensuring that farmers respect rules and regulations. Further, research results are used in the development of systems for animal welfare assessment.

A welfare assessment describes the welfare at farm-level by means of a series of measurements; i.e. factors that may be measured or assessed and reflect animal welfare. Just like legislation at the time, the first welfare assessments were based on housing system design in order to avoid harmful conditions. Today, welfare assessments include resources provided in the form of housing systems and management routines as well as the ways in which the animals react in the form of health and behaviour (Figure 1). At the same time the assessment includes the animals' positive emotions/experiences instead of simply measuring negative responses. Several research institutions have developed various protocols to assess welfare, however with different purposes. The European Welfare Quality® project ended in 2009. Based on a common foundation the project developed protocols for welfare assessments within various parts of cattle, pig and poultry production. The Welfare Quality® project was

financed via the EU 6th Framework Programme "Food Quality and Food Safety", and, therefore, fur animals were not included.

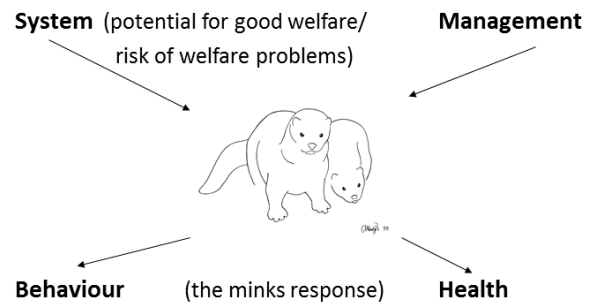


Figure 1 – two types of – and four sources of – information when assessing welfare in mink

Welfare Quality® has set the standard for assessing animal welfare at farm-level in Europe. Assessments are based on one-day observations at the farm to illustrate the four superior welfare principles "Good feeding", "Good housing", "Good health" and "Appropriate behaviour". Within these principles 12 specific animal welfare criteria have been defined; each including a number of registrations of animals, farm management or production systems.

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### Development of WelFur protocol for mink

The WelFur protocols for welfare assessment in mink and fox farms were developed by scientists from six countries in the period from 2009 to 2014, and are based on the Welfare Quality® concept (Møller et al., 2015). The entire process was supervised by a group of highly recognized scientists, including the Welfare Quality® project manager, in order to ensure that fur animal welfare was assessed according to the same principles and standards as applied for other production animals.

Welfare assessments include registrations from three different seasons in a production year – (season 1: Adult breeders during the winter period 2: Adults and kits in the reproduction period 3: Adults and juveniles in the growth period) – to cover the entire

life cycle of mink and to achieve a comprehensive assessment of the welfare within the production system (Figure 2). During each season the animals are exposed to major changes, and health challenges vary within the seasons. In order to reduce this variation the three WelFur observation periods are limited to last from 6 to 8 weeks. The observation periods are as follows: 1. Breeding animals in January-February; 2. Suckling period in May-June, and 3: Growth period from late September and until pelting (Figure 2).

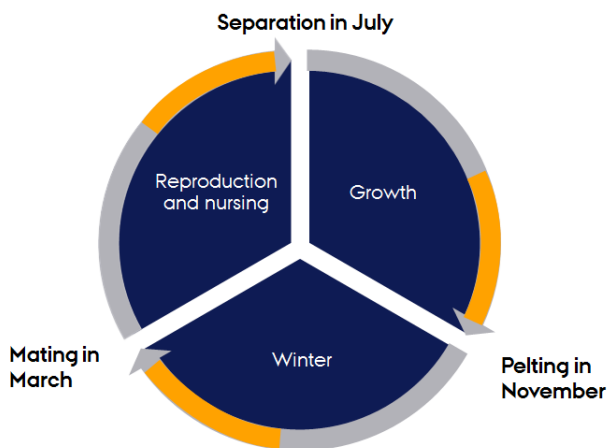


Figure 2 – the three observation periods in WelFur-Mink are marked with orange within the three production seasons “Winter”, “Reproduction and nursing” and “Growth”.

Individual mink farm welfare is assessed according to 22 welfare parameters, covering the 12 welfare criteria that constitute the four welfare principles of Welfare Quality® (Table 1). Measurements are animal-based as far as possible; i.e. they are used to measure animal behaviour or health. If this it is not possible, resource-based measurements are applied instead; i.e. registration of housing systems or management routines.

The measurements have been selected based on an examination of previous research and from thorough discussions between scientists within the area. All measurements have been assessed in relation to validity (do the measurements reflect mink welfare), reliability (are measurements replicable – within and between observers) and feasibility (can they be applied in practice and at reasonable costs).

Assessment of animal-based and resource-based measurements is based on a random sample of animals on the farm, and the welfare of the sample

animals is considered as an estimate for the entire farm. A representative sample consists of 120 cages (20 sections of 6 cages each) during the winter and suckling periods; and 90 cages (15 sections of 6 cages each) during the growth period.

### Going from measurements to a complete assessment

The final welfare assessment at farm-level is based on the calculation of several welfare scores from the on-farm registrations. The assessment is a stepwise weighted sum of scores between the levels; i.e. from 22 measurements to 12 criteria to 4 principles and to 1 overall assessment. This weighted sum is based on an expert panel assessment of the welfare measurements and their importance to animal welfare during various periods as well as the Welfare Quality® guidelines regarding the extent to which good welfare in one area may compensate for poor welfare in another area.

In practice, the weighted sum is achieved by calculating a score between 0 and 100 (100 being the best achievable and 50 a neutral value indicating welfare that is neither good nor poor) for each of the 12 criteria based on on-farm registrations. Next, these 12 scores are combined to produce a value between 0 and 100 for each of the 4 principles and this will eventually result in a classification within one of the four welfare categories. The categories and threshold values have been defined as follows: Best current practice (animal welfare score at highest level with values ranging from 80-100), Good current practice (animal welfare scores ranging from 55-80), Acceptable current practice (animal welfare score is above or equal to minimum requirements ranging from 20-55) and Unacceptable current practice (animal welfare score is low and considered unacceptable).

The categories are not based on average scores for each principle. Thus, a high score in relation to one principle will only to a lesser extent compensate for a very low score in relation to other principles. A farm is classified in the category “Best current practice” if it scores more than 55 on all principles and more than 80 on two of them. Likewise, a farm is considered to correspond to “Good current practice” if it scores more than 20 on all principles and more than 55 on two of them. A farm in the category “Acceptable current practice” scores more than 10 on all principles and more than 20 on three principles. Farms that do not achieve these scores

are considered to correspond to “Unacceptable current practice”.

### Research and testing

The WelFur assessment protocol has been tested in recent years to ensure that the assessment procedure is feasible and practical as well as robust and reliable in relation to various farm conditions and different countries. While developing the protocol it was simultaneously tested in 9 Danish farms in 2011. The WelFur protocol was subsequently tested in 14 Danish farms in 2012-13, in 39 Finnish farms in 2012-14, and in 18 Danish farms in 2014-15. Testing resulted in e.g. an adjustment of individual measurement assessments. The results from the present testing have also been used in studies investigating the importance of the actual observation date to the overall assessment; thus taking this into account if necessary. Finally, in 2015-16 the WelFur protocol was tested in 27 mink farms in 10 European countries in order to test the assessment under different climatic conditions and at farms in countries with different mink production traditions.

Among other results, these tests demonstrated certain challenges in relation to achieving the necessary information from the breeders, e.g. in relation to representative samples. Therefore, a new method has been developed, allowing samples to be taken without previous information. The WelFur assessments were feasible in all countries; however, in relation to some test procedures certain challenges existed, e.g. cage design. Based on experiences from various tests the WelFur assessment protocol is being optimized.

Currently, more projects are carried out at Aarhus University with the purpose of achieving the knowledge necessary to make these optimizations. The examinations e.g. include assessments of animal temperament, when animals are housed in groups, the impact of the observer’s posture as well as various conditions in relation to cage design and arrangement. Research is also carried out with a view to optimizing the protocol and the testing procedures in order to make welfare assessments on individual farms less time-consuming without reducing assessment validity. Finally, additional research efforts focus on examining whether some of the more time-consuming measurements may, in time, be replaced by new and less time-consuming measurements.

### Perspectives

The major part of the tested farms was placed in the category “Good current practice”, some in the “Best current practice” category and a few in “Acceptable current practice” category. Thus, WelFur is able to distinguish between animal welfare levels in different farms. However, there may be significant variation in the scores – in relation to the 4 principles, 12 criteria and 22 measurements – between farms allocated to the same category. This means that there is a huge difference between the areas that the individual farms should work with in order to achieve a higher score or be allocated to a better category at the next assessment. It is, therefore, very important for the farmers to know if they should increase focus on e.g. mortality rates or animal temperament.

In order for the individual farmer to know why his farm was allocated to a certain assessment category, he should be given access to the details of the welfare assessment after the visit. A tablet solution for on-farm recording of WelFur registrations has been developed and allows the farmer to receive a copy of the results immediately after the assessment. The sections observed as part of the WelFur assessment are marked with yellow plastic cards allowing the farmer to see for himself whether the cages observed gave rise to comments. This ensures complete transparency as to the basis of the assessment. Once the final results for the farm in question are available, the individual farmer can consider which production areas should be in focus and also – in cooperation with his advisor – establish goals and plan efforts in order to achieve the goals. Thus, the WelFur assessment results will become part of the farm management together with – and interacting with – all other types of information used by fur breeders to take care of their animals in the best possible way.

In relation to WelFur, Danish fur breeders are well equipped; partly, because they have a long tradition for production management based on actual knowledge of the farm and the animals; and partly because they have well established extension service in the form of advisors and veterinarians who know the farm. In countries without such traditions, national advisors will be educated to assist the farmers with interpretation of results and how to improve when needed.

Table 1. Welfare principles, criteria and measurements used in WelFur Mink

<b>Principle</b>	<b>Criteria</b>	<b>Measurements</b>
1 Good feeding	1 Absence of prolonged hunger	Are mink too thin?
	2 Absence of prolonged thirst	Do all mink have access to drinking water? Do drinking nipples work and are they clean?
2 Good housing	3 Comfort around nesting	Do all mink have access to a nest box? Are nest boxes dry, clean, no sharp edges and no fleas?
	4 Thermal comfort	Are nest boxes protected from wind, direct sun and heat? Are nest boxes isolated, exposed to draught and is bedding material available?
	5 Ease of movement	Sufficient available space for movement?
3 Good health	6 Absence of injuries	Do mink have skin lesions or injuries to the body?
	7 Absence of disease	How many mink died in the period? Are there any sick mink? Mink with diarrhea or impaired movement?
	8 Absence of pain induced by management procedures	Efficient methods of killing mink at pelting or in case of disease or injury?
4 Appropriate behavior	9 Expression of social behaviours	Are mink housed individually, in pairs or groups in the growth season? Weaning procedures?
	10 Expression of other behaviours	Do mink display stereotypic behavior? Are mink given cage enrichment? Do they display fur chewing?
	11 Good human-animal relationship	Are the mink fearful or curious? Frequency and duration of handling?
	12 Positive emotional state	

### **Epilogue**

From January 2017, fur animal welfare assessment according to the WelFur protocol will be available for all European fur breeders. In this connection further information on WelFur is needed. At the annual thematic meeting on current mink research at Aarhus University, held at research center Foulum on 20 September 2016, a presentation on the research status was given. We have made a reprint of the material from the thematic meeting in order to make this information available to all interested parties.

### **Contact**

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Further information in the implementation of WelFur is found at Fur Europe – <http://www.fureurope.eu/fur-policies/welfur/> – as well as national fur breeder organizations.

### **References**

Møller S.H, Hansen S.W, Malmkvist J, Vinke C.M, Lidfors L, Gaborit M, Botreau R. 2015. Welfare assessment protocol for mink. Fur Europe. 182 s.

*Meeting at Research Centre Foulum, Faculty of Science and Technology, Aarhus University, Denmark. DCA Report no. 083, September 2016 (in Danish) p. 62-67. Author's abstract*



## Obituary



### **Secretary Karin Smedegaard 1948-2016**

Secretary Karin Smedegaard passed away 14<sup>th</sup> August 2016. Karin was secretary for Scientifur from 2009 to 2016. She worked with Scientifur concurrently with her position as secretary at Department of Molecular Biology and Genetics at Aarhus University. She was secretary at the Department from 1997 until she retired at the end of 2015.

Karin had a diverse background with regard to both education and employments. She was only 14 years old when she started as a trainee in a hardware store. After finishing this education, she worked in different hardware stores, at an optician, and in insurance and real estate. She became interested in secretarial work and in 1988 she finished an education as bilingual secretary. She started her carrier as a secretary in the Danish Federation of Small and Medium-Sized Enterprises. Then she worked in an engineering company and finally at Aarhus University.

Karin was a very competent secretary who worked with great engagement. At the Department of Molecular Biology and Genetics she had many diverse tasks also far beyond standard secretarial work. She was very supportive for the permanent staff, as well as for PhD students and Postdocs e.g. in relation to travel arrangements. She was attentive and helpful to the many young foreign PhD students and Postdocs, taking care of practical matters for them such as accommodation and contact with public authorities and focused strongly on their well-being.

She was very well liked and respected and she was considered as the Department's grandma.

Karin had great interest in international and social affairs. This engagement was of great advantage both for her work at Department of Molecular Biology and Genetics and for her work with Scientifur. She was very committed to her work seeking at all time to improve present or introduce new procedures. In her work with Scientifur, she participated in the discussion of development and improvement of the journal.

After careful considerations, Karin decided to retire from her work at Department of Molecular Biology and Genetics in late 2015. Fortunately, she decided to continue the work with Scientifur but sadly volume 40.1 was her last task with Scientifur.

The plans after her retirement included travels and visits to friends, nationally and internationally. It is sad, that illness caught up with her so shortly after her retirement. She still had so much to experience and so much to contribute.

Family, friends and many colleagues paid Karin their final respect at the memorial. Karin leaves behind her husband, two children and three grandchildren who lost Karin much too early.

Vivi Hunnicke Nielsen



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**References.** References in the text should be made according to the following examples:

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Nielsen, V.H., Møller, S.H., Hansen, B.K. & Berg, P. (2007). Genotype - environment interaction in mink. *Scientifur*, 31 (3), 89.

Shirali, M., Nielsen, V.H., Møller S.H. & Jensen, J. (2015). Longitudinal analysis of residual feed intake and BW in mink using random regression with heterogeneous residual variance. *Animal*, 8 (10), 1597-1604.

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