SCIENTIFUR

SCIENTIFIC INFORMATION IN FUR ANIMAL PRODUCTION

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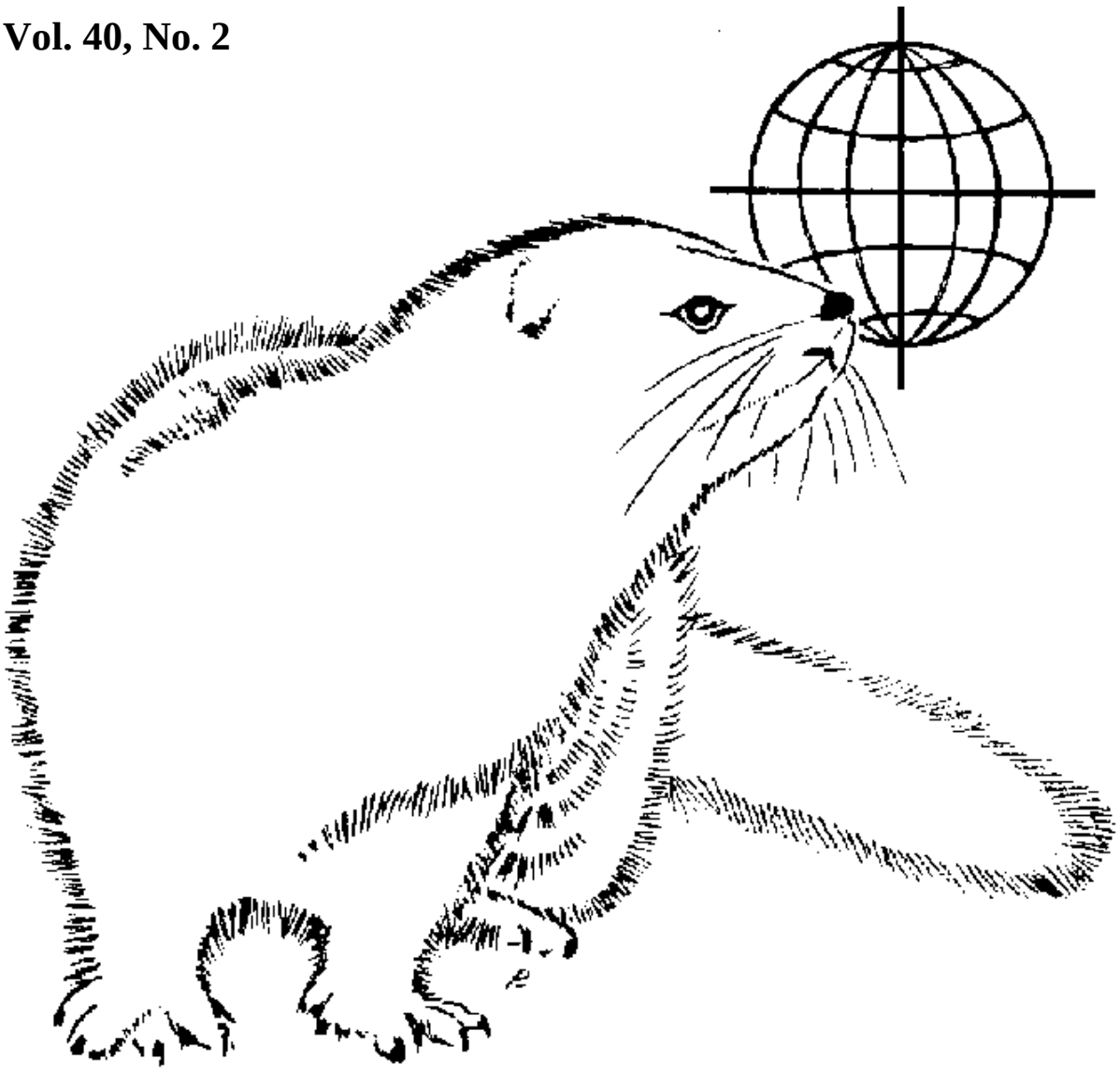

IFASA

INTERNATIONAL FUR ANIMAL SCIENTIFIC ASSOCIATION

SCIENTIFUR scientific information for those involved in fur animal production is published by the International Fur Animal Scientific Association (IFASA).

SCIENTIFUR is the focal point for fur animal researchers all over the world and serves as a platform for scientific and other communication among researchers and others who are interested in the production of fur bearing animals. As such **SCIENTIFUR** contains reports of both basic and applied research as well as abstracts of publications published elsewhere and information regarding congresses, scientific meetings etc.

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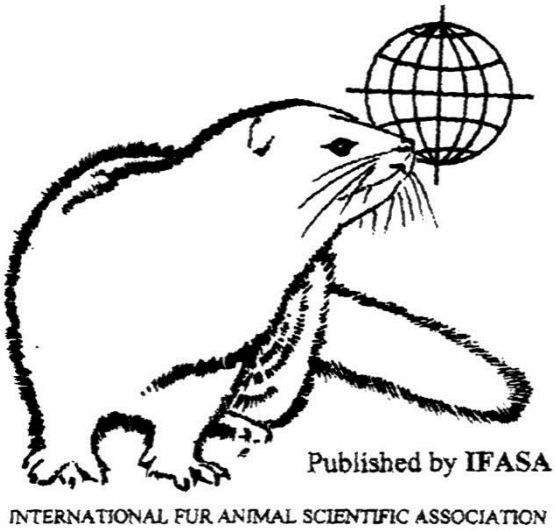

Notes from the Editor

The International Fur Animal Scientific Congress has been held every fourth year since 1976. The first congress was held in Helsinki on the initiative of the Nordic Association of Agricultural Scientists. Since 1992, the international congresses have been arranged under the auspices of IFASA established in 1988. This year - 40 years after the first meeting - the International Fur Animal Scientific Congress will again be held in Helsinki in Finland. The XIth IFASA Congress is organized by ProFur from 23rd to 28th August 2016. An interesting program is set up for the congress. New research is presented within health and diseases including a special focus on *Aleutian* disease. New results of research within breeding, genetics, and reproduction, nutrition, feeding and management and behaviour and welfare are also presented. A preliminary program is available at: http://ifasanet.org/congress/2016/IFASA%20Program_preml_v060616.pdf. Registration can be performed at the IFASA webpage: http://ifasanet.org/. The registration deadline is 25th July 2016.

At the First International Scientific Congress in 1976, the Scandinavian countries, under the auspices of Nordic Association of Agricultural Scientists were urged to establish and send out a newsletter with fur animal production theme. This newsletter should serve to communicate both scientific and other news between researchers in the field all over the world. The board of Nordic Association of Agricultural Scientists, Subsection for Fur Animals realised the decision and a Scientifur Introductory Issue was launched in November 1976. The name, Scientifur, stresses that the principal aim of the newsletter is to communicate at a scientific level concerning problems about fur breeding. Focus was an international newsletter with short articles and abstracts from all over the world. Thus, like the International Fur Animal Scientific Congress Scientifur can celebrate its 40 anniversary in 2016.

It is a special pleasure to announce the publication of a new book "More about Beautiful Fur Animals - genetics of colours, fur, defects and diseases". In 1988, the book "Beautiful Fur Animals – and their colour genetics" was published with information of the inheritance of colour types. However, since 1988 many new mutants have been observed and in 2013 the Committee for Breeding and Genetics, NJF Working Group for Fur Animals decided to gather information about new mutants and combination types to a supplementary publication. It has now resulted in the new book which describes single gene effects of both colour and hair types as well as genetic diseases and abnormalities. "More about Beautiful Fur Animals - genetics of colours, fur, defects and diseases" is primarily directed to fur farmers and advisors but the book will like "Beautiful Fur Animals – and their colour genetics" be valuable for educational purposes and a basis for further research.

The need and interest in research of simply inherited traits in fur animals appears from an abstract in this issue of Scientifur which deals with genomic analysis of a gum disease - a proliferative gingival disease called hereditary hyperplastic gingivitis (HHG) - in foxes.

Research also for the minor fur animal species is in demand. Therefore, I am glad that four abstracts dealing with chinchilla are included in this issue of Scientifur.

Vivi Hunnicke Nielsen

Editor Scientifur

BREEDING, GENETICS AND REPRODUCTION

De novo assembly and mink characterization of farmed blue fox (Alopex lagopus) global transcriptome using Illumina paired-end sequencing

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The blue fox (Alopex lagopus), a coat-color variant of the Arctic fox, is a domesticated fur-bearing mammal. In the present study, transcriptome data generated from a pool of nine different tissues were obtained with Illumina HiSeq2500 paired-end sequencing technology. After filtering from raw reads, 32,358,290 clean reads were assembled into 161,269 transcripts and 97,252 unigenes by the Trinity fragment assembly software. Of the assembled unigenes, 37,967 were annotated in the National Center for Biotechnology Information (NCBI) Non-Redundant (NR) protein database and 26,264 in the Swiss-Prot database. Among the annotated unigenes, 24,839 and 24,267 were assigned using the Gene Ontology (GO) and euKaryotic Orthologous Groups (KOG) databases, respectively. Altogether, 17,057 unigenes were mapped onto 227 pathways using the Kyoto Encyclopedia of Genes and Genomes database. In addition, 6394 simple sequence repeats were identified by examining 12,965 unigenes (>1 kb), which could contribute to the development of molecular markers. This study generated transcriptome data for the blue fox that will promote further progress in expression profiling studies, and provide a good annotation basis for genomic studies.

Genet. Mol. Res. 2016:15(1)
doi: 10.4238/gmr.15017603

Genomic analysis of gum disease and hypertrichosis in foxes

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Since the 1940s, a proliferative gingival disease called hereditary hyperplastic gingivitis (HHG) has been described in the farmed silver fox, Vulpes vulpes (Dyrendahl and Henricson 1960). HHG displays an autosomal recessive transmission and has a pleiotropic relationship with superior fur quality in terms of length and thickness of guard hairs. An analogous human disease, hereditary gingival fibromatosis (HGF), is characterized by a predominantly autosomal dominant transmission and a complex etiology, occurring either as an isolated condition or as a part of a syndrome. Similar to HHG, the symptom most commonly associated with syndromic HGF is hypertrichosis. Here we explore potential mechanisms involved in HHG by comparison to known genetic information about hypertrichosis co-occurring with HGF, using an Affymetrix canine genome microarray platform, quantitative PCR, and candidate gene sequencing. We conclude that the mitogen-activated protein kinase pathway is involved in HHG, however despite involvement of the mitogen-activated protein kinase kinase 6 gene in congenital hypertrichosis with gingival fibromatosis in humans, this gene did not contain any fixed mutations in exons or exon-intron boundaries in HHG-affected foxes, suggesting that it is not causative of HHG in the farmed silver fox population. Differential up-regulation of MAP2K6 gene in HHG-affected foxes does implicate this gene in the HHG phenotype.

Genet Mol Res. 2016:15(2)
doi: 10.4238/gmr.15025363

A fast and robust method for whole genome sequencing of the Aleutian Mink Disease Virus (AMDV) genome

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J Virol Methods. 2016:234:43-51
doi: 10.1016/j.jviromet.2016.03.010

Genetic characterization of the complete genome of an Aleutian mink disease virus isolated in north China

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The genome of a highly pathogenic strain of Aleutian disease mink virus (AMDV-BJ) isolated from a domestic farm in North China has been determined and compared with other strains. Alignment analysis of the major structural protein VP2 revealed that AMDV-BJ is unique among 17 other AMDV strains. Compared with the nonpathogenic strain ADV-G, the 3' end Y-shaped hairpin was highly conserved, while a 4-base deletion in the 5' U-shaped terminal palindrome resulted in a different unpaired "bubble" group near the NS1-binding region of the 5' end hairpin which may affect replication efficiency in vivo. We also performed a protein analysis of the NS1, NS2, and new-confirmed NS3 of AMDV-BJ with some related AMDV DNA sequence published, providing information on evolution of AMDV genes. This study shows a useful method to obtain the full-length genome of AMDV and some other parvoviruses.

Virus Genes. 2016: 52(4):463-73
doi: 10.1007/s11262-016-1320-3

Reduced Genetic Diversity and Increased Structure in American Mink on the Swedish Coast following Invasive Species Control

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Eradication and population reductions are often used to mitigate the negative impacts of non-native invasive species on native biodiversity. However, monitoring the effectiveness of non-native species control programmes is necessary to evaluate the efficacy of these measures. Genetic monitoring could provide valuable insights into temporal changes in demographic, ecological, and evolutionary processes in invasive populations being subject to control programmes. Such programmes should cause a decrease in effective population size and/or in genetic diversity of the targeted non-native species and an increase in population genetic structuring over time. We used microsatellite DNA data from American mink (Neovison vison) to determine whether the removal of this predator on the Koster Islands archipelago and the nearby Swedish mainland affected genetic variation over six consecutive years of mink culling by trappers as part of a population control programme. We found that on Koster Islands allelic richness decreased (from on average 4.53 to 3.55), genetic structuring increased, and effective population size did not change. In contrast, the mink population from the Swedish coast showed no changes in genetic diversity or structure, suggesting the stability of this population over 6 years of culling. Effective population size did not change over time but was higher on the coast than on the islands across all years. Migration rates from the islands to the coast were almost two times higher than from the coast to the islands. Most migrants leaving the coast were localised on the southern edge of the archipelago, as expected from the direction of the sea current between the two sites. Genetic monitoring provided valuable information on temporal changes in the population of American mink suggesting that this approach can be used to evaluate and improve control programmes of invasive vertebrates.

PLoS One. 2016:11(6)
doi: 10.1371/journal.pone.015797

Polyamine-Mediated Effects of Prolactin Dictate Emergence from Mink Obligate Embryonic Diapause

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Biol Reprod. 201:;95(1):6.
doi: 10.1095/biolreprod.116.139204

Estradiol stimulates glycogen synthesis whereas progesterone promotes glycogen catabolism in the uterus of the American mink (Neovison vison)

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Anim Sci J. 2016
doi: 10.1111/asj.12564

Mink aging is associated with a reduction in ovarian hormone release and the response to FSH and ghrelin

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Theriogenology. 2016
doi: 10.1016/j.theriogenology.2016.04.007

The Uterus Duplex Bicollis, Vagina Simplex of Female Chinchillas

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The available literature describing the morphology of the female chinchilla's uterine cervix varies and includes phrases such as 'the cervical canal,' 'a single cervix,' and 'the cervix;' alternatively, some publications describe 2 cervices. In this report, we provide an anatomically correct and definitive description of the uterine cervical morphology of the laboratory chinchilla. We further propose revised, anatomically precise nomenclature to characterize the female chinchilla reproductive tract as a whole.

J Am Assoc Lab Anim Sci. 2016:55(2):155-60
doi: 10.1016/j.theriogenology.2016.04.007

New computerized staging method to analyze mink testicular tissue in environmental research

A. Fakhrzadeh[1], E. Spörndly-Nees[2], E. Ekstedt[2], L. Holm[2], C.L. Hendriks[1]

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Environ Toxicol Chem. 2016
doi: 10.1002/etc.3517

Bioactive Effect of the Preparation Biostyl on the Reproductive Function of Different Genotypes of American Mink

O.V. Trapezov, E.I. Zemljanitskajia, O.V.Rasputina, I.V. Naumkin & L.I. Trapezova.

The different role of coat color mutations in the American mink on the per os effect of the biologically active preparation Biostyl was shown. The number of kits per female was the same in all control genotypes, including Standard (+/+ +/+), sapphire (a/a p/p), and lavender (a/a m/m): 4.4 ± 0.4, 4.4 ± 0.5, and 4.3 ± 0.5, respectively. Experimental groups of these genotypes have shown a great contrast among each other: stimulation of the reproductive function was 5.2 ± 0.3 in Standard minks, while suppression of the reproductive function was 3.8 ± 0.6, and 2.3 ± 0.5 in the double recessive mutants sapphire and lavender, respectively. The differentiation in body mass between experimental and control newborn Standard kits was not revealed. A significant decrease in the body mass of newborn experimental sapphire kits as compared to control group in a sex-specific manner was registered.

Genetika 2016:52(1):126-30.

NUTRITION, FEEDING AND MANAGEMENT

Pseudorabies in farmed foxes fed pig offal in Shandong province, China

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Pseudorabies (PR, Aujeszky's disease) is an acute, highly contagious viral disease resulting in major economic losses to the swine industry. PR is endemic in wild and domestic animals, although its natural host is the pig. Here, we report an outbreak of PR in foxes on a fur-producing farm in Yuncheng county, Shandong, China, that were fed pig offal. The diagnosis of PR was based on nervous signs and standard PCR methods and by isolation of PRV from fox brain tissue in Vero cells. The diagnosis was confirmed by an indirect immunofluorescence assay and electron microscopy. Phylogenetic analysis of a partial (804 nt) viral glycoprotein gC gene sequence indicated that it was likely to be a field strain closely related to a cluster of PRV previously identified in China.

Arch Virol. 2016:161(2):445-8.
doi: 10.1007/s00705-015-2659-9

BEHAVIOUR AND WELFARE

Play in juvenile mink: litter effects, stability over time, and motivational heterogeneit

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HEALTH AND DISEASE

Identification of a novel Aleutian mink disease virus B-cell epitope using a monoclonal antibody against VP2 protein

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Virus Res. 2016
doi: 10.1016/j.virusres.2016.06.014

Accuracy of enzyme-linked immunosorbent assays for quantification of antibodies against Aleutian mink disease virus

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J Virol Methods. 2016: 235:144-151
doi: 10.1016/j.jviromet.2016.06.004

Progression of experimental chronic Aleutian mink disease virus infection

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Background
Aleutian mink disease virus (AMDV) is found world-wide and has a major impact on mink health and welfare by decreasing reproduction and fur quality. In the majority of mink, the infection is subclinical and the diagnosis must be confirmed by serology or polymerase chain reaction (PCR). Increased knowledge based on a systematically description of clinical signs, pathology and histopathology might be a tool to reduce the risk of infection from subclinically infected mink to AMDV free herds. The aim of this study was to give a histopathological description of the progression of a chronic experimental infection with a currently circulating Danish strain of AMDV, Saeby/DEN/799.1/05. These results were compared with the pathogenesis of previously published AMDV stains.

Results
This experimental AMDV infection resulted in only decreased appetite and soft or discolored feces, primarily within the first 8 weeks after AMDV inoculation. Gross pathology revealed few and inconsistent findings mainly associated with the liver, spleen and kidneys. The majority of the AMDV inoculated wild type mink (n = 41) developed various histopathological changes consistent with AMDV infection in one or more organs: infiltrations of mononuclear cells in liver, kidney and brain, reduced density of lymphocytes and increased numbers of plasma cells in lymph nodes and spleen. Natural infection, as occurred in the sentinel sapphire mink (four of six mink), progressed similar to the experimentally inoculated mink.

Conclusions
Experimental AMDV inoculation mainly resulted in subclinical infection with unspecific clinical signs and gross pathology, and more consistent histopathology appearing at any time after AMDV inoculation during the 24 weeks of observation. Thus, the observed histopathology substantiates AMDV infection and no correlation to time of inoculation was found. This confirms that diagnosing AMDV infection requires serology and/or PCR and the Saeby/DEN/799.1/05 AMDV strain results in histopathology consistent with other AMDV strains.

Acta Vet Scand. 2016: 58(1):3.
doi: 10.1186/s13028-016-0214-7

Genetic analysis of porcine circovirus type 2 from dead minks

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Circovirus infection is a growing problem in the field of veterinary and public health. It is associated with enteric diseases in both mammalian and avian hosts. In this study, we detected and isolated porcine circovirus strains in the tissue samples of minks that died from diarrhea in Shandong Province, China. We sequenced the whole genome of two porcine strains of Circovirus, designated as MiSD-1 and MiSD-2, which were 97.34% similarity on nucleotide sequence and closely related to porcine circovirus type 2 (PCV2), but distantly related to mink circoviral species. Phylogenetically MiSD-1 and MiSD-2 are a part of the PCV2b genotype cluster, which is a highly prevalent genotype worldwide. The closer relationship of MiSD-1 and MiSD-2 to PCV2 from pigs than to other mink circoviral species may be evidence of cross-species transmission and considerable zoonotic potential.

Gen Virol. 2016
doi: 10.1099/jgv.0.000529

Naturally occurring recombination in ferret coronaviruses revealed by complete genome Characterization

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Ferret coronaviruses (FRCoVs) exist as an enteric and a systemic pathotype, of which the latter is highly

lethal to ferrets. To our knowledge, this study provides the first full genome sequence of an FRCoV, tentatively called FRCoV-NL-2010, which was detected in 2010 in ferrets in the Netherlands. Phylogenetic analysis showed that FRCoV-NL-2010 is most closely related to mink CoV, forming a separate clade of mustelid alphacoronavirus that split off early from other alphacoronaviruses. Based on sequence homology of the complete genome we propose that these mustelid coronaviruses may be assigned to a new species. Comparison of FRCoV-NL-2010 with the partially sequenced ferret systemic coronavirus MSU-1 and ferret enteric coronavirus MSU-2 revealed that recombination in the spike, 3c and envelope genes occurred between different FRCoVs.

J Gen Virol. 2016
doi: 10.1099/jgv.0.000520

First report of Cryptosporidium canis in foxes (Vulpes vulpes) and raccoon dogs (Nyctereutes procyonoides) and identification of several novel subtype families for Cryptosporidium mink genotype in minks (Mustela vison) in China

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Infect Genet Evol. 2016:41:21-5.
doi: 10.1016/j.meegid.2016.03.016

Roles of three amino acids of capsid proteins in mink enteritis parvovirus replication

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Virus Res. 2016: 222:24-28
doi: 10.1016/j.virusres.2016.05.019

First report of Filaria martis Gmelin, 1790 in the European mink, Mustela lutreola (Linnaeus, 1761)

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The riparian European mink (Mustela lutreola), currently surviving in only three unconnected sites in Europe, is now listed as a critically endangered species according to the IUCN. Habitat loss and degradation, anthropic mortality, interaction with the feral American mink (Neovison vison), and infectious diseases are among the principal causes of its decline. Surveys of helminth parasites of this host that also include focus on subcutaneous potentially pathogenic helminths such as those belonging to the genus Filaria are very scarce. We report here the presence of specimens of Filaria martis in the subcutaneous connective tissues of three M. lutreola individuals from Spain. This is the first finding of a subcutaneous nematode in a representative of the genus Mustela. The report also enlarges the known range of the definitive hosts of this nematode. These worms were mainly located in the dorsal region of mink and more rarely in the knees, elbows, and hips. Skin sloughing

was only observed in one M. lutreola with both septicaemia and an associated high burden of F. martis. Therefore, more attention should be paid to potentially pathogenic helminths when designing conservation programs dedicated to M. lutreola.

Parasitol Res. 2016:115(6):2499-503.
doi: 10.1007/s00436-016-5021-6

Concurrent infection with Mycobacterium avium subsp. hominissuis and Giardia duodenalis in a chinchilla (Chinchilla lanigera f. dom.)

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A 3-year-old, female chinchilla (Chinchilla lanigera f. dom.) suffered from prolonged vaginal discharge. Sonographically, multiple nodules were detected in the uterus, and the lung showed a diffuse radiodensity. Ovario-hysterectomy was performed and histology of the uterus revealed a severe multifocal pyogranulomatous metritis with myriads of acid-fast rod-shaped bacilli. Microbiological culture of formalin-fixed uterine tissue and a native vaginal swab resulted in the growth of mycobacteria that were identified as Mycobacterium (M.) avium subsp. hominissuis. The animal was euthanized and pathomorphological examination revealed severe multifocal granulomatous inflammation of lung, mediastinal and mesenteric lymph nodes, intestine, pancreas and kidneys. In addition, an infection of the small intestine with Giardia duodenalis was confirmed immunohistochemically. This is the first report describing a concurrent infection with M. avium subsp. hominissuis and Giardia duodenalis in a chinchilla. Both pathogens represent a potential health risk especially for young or immunosuppressed persons, in particular if infected animals show unspecific clinical symptoms.

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Therapeutic effect of Pseudomonas aeruginosa phage YH30 on mink hemorrhagic Pneumonia

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Definitive Hosts of Versteria Tapeworms (Cestoda: Taeniidae) Causing Fatal Infection in North America

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We previously reported fatal infection of a captive Bornean orangutan with metacestodes of a novel taeniid tapeworm, Versteria sp. New data implicate mustelids as definitive hosts of these tapeworms in North America. At least 2 parasite genetic lineages circulate in North America, representing separate introductions from Eurasia.

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An invasive species as an additional parasite reservoir: Trichinella in introduced American mink (Neovison vison)

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Seroprevalence and Risk Factors of Toxoplasma gondii Infection in Farmed Minks (Neovison vison) in Northeastern and Eastern China

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Toxoplasma gondii is an important intracellular parasite, which can infect endothermic vertebrate animals, including minks (Neovison vison). However, information on T. gondii infection in minks in China is limited. Therefore, we investigated the seroprevalence and risk factors of T. gondii infection in minks in northeastern and eastern China. A total of 1499 mink blood samples were randomly collected from eight cities between March 2014 and January 2015 in northeastern and eastern China, and antibodies to T. gondii were examined using the modified agglutination test. Overall, the seroprevalence of T. gondii infection was 8.14% in the examined minks. The T. gondii seroprevalence was different among cities (ranging from 1.85% in Changchun to 15.75% in Dalian), genders (4.31% in male and 6.22% in female), seasons (spring: 11.64%; summer: 7.34%; autumn: 7.37%; and winter: 7.32%), and ages (young: 5.79%; subadult: 5.03%; and adult: 11.08%). Region and age were considered as risk factors for T. gondii infection. These results provided baseline data for the prevention and control of T. gondii infection in minks in China.

Vector Borne Zoonotic Dis. 2016:16(7):485-8.
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Urolithiasis in chinchillas: 15 cases (2007 to 2011).

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Urinalysis in chinchillas (Chinchilla lanigera)

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OBJECTIVE To evaluate urine variables in chinchillas (Chinchilla lanigera). DESIGN Evaluation study. SAMPLE Urine samples from 41 chinchillas. PROCEDURES Voided urine samples were collected from clinically normal chinchillas that were exhibited during a breeder exposition. Urinalysis was performed within 1 hour after collection. Urine specific gravity (USG) was measured before and after centrifugation with a handheld veterinary refractometer. Urine dipstick analysis and microscopic sedimentation examination were performed on all samples. Additionally, a urine sulfosalicylic acid (SSA) precipitation test and quantitative protein analysis were performed on samples with sufficient volume. RESULTS 17 of 41 (41%) samples had a USG ≥ 1.050, and USG ranged from 1.014 to > 1.060. The USG before centrifugation did not differ significantly from that after centrifugation. Protein was detected in all urine samples on dipstick analysis. The SSA precipitation test yielded negative results for all samples tested. Results of the quantitative protein analyses were not correlated with the results of the dipstick analyses or SSA tests. The recorded pH for

all samples was 8.5, which was the upper limit of detection for the reagent strip. Glucose and ketones were detected in 5 and 6 samples, respectively. Crystals were observed in 28 of 41 (68%) samples; 27 of those samples contained amorphous crystals. CONCLUSIONS AND CLINICAL RELEVANCE Urinalysis results for clinically normal chinchillas were provided. For chinchilla urine samples, measurement of USG by refractometry prior to centrifugation is acceptable and protein concentration should be determined by quantitative protein analysis rather than dipstick analysis or the SSA test.

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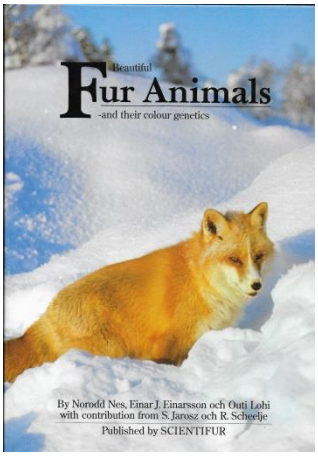

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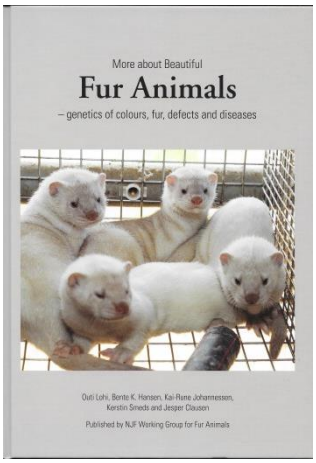

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