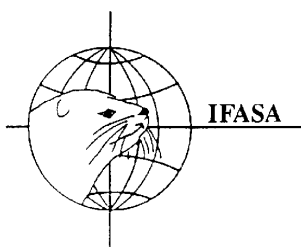
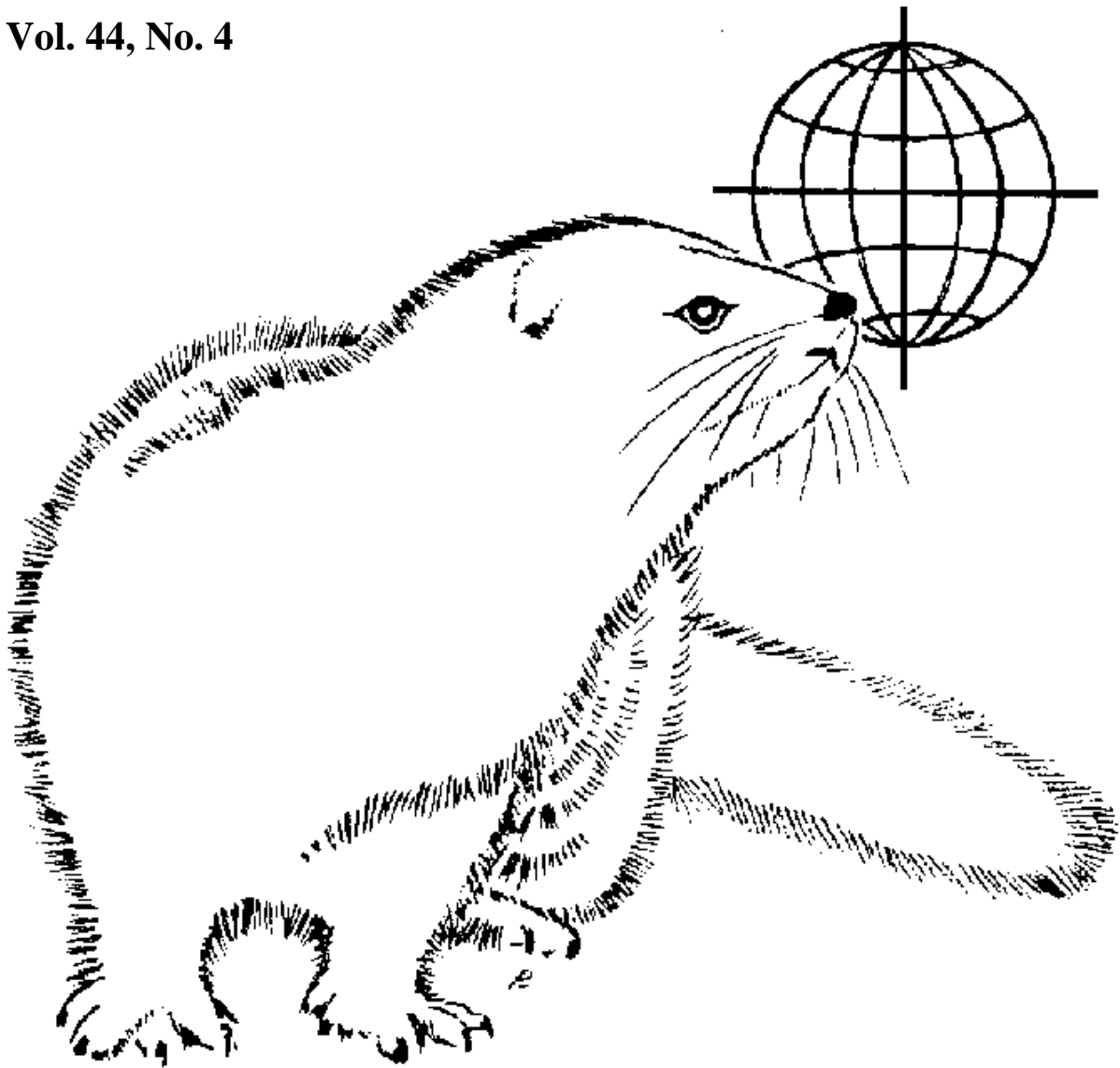


# SCIENTIFUR

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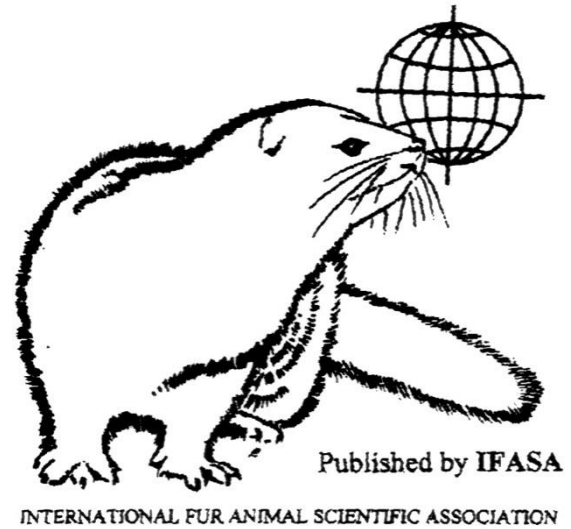
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## Notes from the Editor

So far, COVID-19 cases have been reported in mink on farms in Denmark, the Netherlands and Spain in Europe and in Utah in the USA. In Denmark 41 farms, all located in the same area were affected. In the Netherlands this number is 52. In Spain only one farm was affected. In Utah, mink on two farms were infected.

Various strategies have been applied to cope with Corona virus infections on mink farms. Initially, all mink on infected farms were culled in Denmark, which applied to three farms. Subsequently, severe biosafety restrictions and increased monitoring particularly in exposed areas were imposed on farms by the Danish authorities to avoid culling of mink. With additional new cases, the culling strategy was applied again. In the Netherlands, mink on farms infected with Corona virus were culled and COVID-19 has led to earlier phasing out of Dutch fur farming. The initial plan of a permanent closure in 2024 has been changed to a shutdown in March 2021. In Spain, mink on the infected farm were culled, while an isolation strategy was imposed on the two farms in Utah.

Based on the results of recent Danish and Dutch studies, it was concluded that Corona virus was initially introduced from humans to mink farms but also that transmission of virus from mink to humans is possible. Transmission among farms was also shown and ascribed to human movement between farms, common feed supply or farm cats.

The approach, based on extensive biosafety initiatives on farms and monitoring of farms but no culling allows research that can determine whether a mink population will act as a reservoir for the virus, or whether the mink will gain immunity and the virus die out. Thus, the outcome of this approach could potentially provide important understanding of the nature of COVID-19.

The XII International Scientific Congress in Fur Animal Production (IFASA Congress 2020), to be held in Warsaw, Poland on 24-26 August 2021, replaces the planned 2020 conference that was canceled due to the COVID-19 pandemic. The congress is held in collaboration between the International Fur Animal Scientific Association (IFASA) and the Polish Society of Animal Production (PSAP).

Deadlines for new registrations, change of already submitted abstract and papers or submissions of new abstracts and papers will be announced in October 2020. For further updates and information, please consult: <https://ifasa2020.pl/>. The IFASA Congress is an important forum for researchers in fur animal production to gather to present and discuss recent research and outline research to address future challenges. An interesting and well-attended congress is foreseen in 2021.

Vivi Hunnicke Nielsen

Editor Scientifur



## BREEDING, GENETICS AND REPRODUCTION

### KIT is involved in melanocyte proliferation, apoptosis and melanogenesis in the Rex Rabbit

Shuaishuai Hu<sup>1</sup>, Yang Chen<sup>1,2</sup>, Bohao Zhao<sup>1</sup>, Naisu Yang<sup>1</sup>, Shi Chen<sup>1</sup>, Jinyu Shen<sup>1</sup>, Guolian Bao<sup>3</sup>, Xins-heng Wu<sup>1,2</sup>

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#### Background

Melanocytes play an extremely important role in the process of skin and coat colors in mammals which is regulated by melanin-related genes. Previous studies have demonstrated that KIT is implicated in the process of determining the color of the coat in Rex rabbits. However, the effect of KIT on the proliferation and apoptosis of melanocytes and melanogenesis has not been clarified.

#### Methods

The mRNA and protein expression levels of KIT were quantified in different coat colored rabbits by qRT-PCR and a Wes assay. To identify whether KIT functions by regulating of melanogenesis, KIT over-expression and knockdown was conducted in melanocytes, and KIT mRNA expression and melanin-related genes TYR, MITF, PMEL and DCT were quantified by qRT-PCR. To further confirm whether KIT influences melanogenesis in melanocytes, melanin content was quantified using NaOH lysis after over-expression and knockdown of KIT. Melanocyte proliferation was estimated using a CCK-8 assay at 0, 24, 48 and 72 h after transfection, and the rate of apoptosis of melanocytes was measured by fluorescence-activated cell sorting.

#### Results

KIT mRNA and protein expression levels were significantly different in the skin of Rex rabbits with different color coats ( $P < 0.05$ ), the greatest levels observed in those with black skin. The mRNA expression levels of KIT significantly affected the mRNA expression of the pigmentation-related genes TYR, MITF, PMEL and DCT ( $P < 0.01$ ). Melanin content

was evidently regulated by the change in expression patterns of KIT ( $P < 0.01$ ). In addition, KIT clearly promoted melanocyte proliferation, but inhibited apoptosis.

#### Conclusions

Our results reveal that KIT is a critical gene in the regulation of melanogenesis, controlling proliferation and apoptosis in melanocytes, providing additional evidence for the mechanism of pigmentation of animal fur.

PeerJ. 2020; 8: e9402.

Published online 2020 Jun 18.

Doi: 10.7717/peerj.9402

## NUTRITION, FEEDING AND MANAGEMENT

### Type A Trichothecene Diacetoxyscirpenol-Induced Emesis Corresponds to Secretion of Peptide YY and Serotonin in Mink

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The trichothecene mycotoxins contaminate cereal grains and have been related to alimentary toxicosis resulted in emetic response. This family of mycotoxins comprises type A to D groups of toxic sesquiterpene chemicals. Diacetoxyscirpenol (DAS), one of the most toxic type A trichothecenes, is considered to be a potential risk for human and animal health by the European Food Safety Authority. Other type A trichothecenes, T-2 toxin and HT-2 toxin, as well as type B trichothecene deoxynivalenol (DON), have been previously demonstrated to induce emetic response in the mink, and this response has been associated with the plasma elevation of neurotransmitters peptide YY (PYY) and serotonin (5-hydroxytryptamine, 5-HT). However, it is found that not all the type A and type B trichothecenes have the capacity to induce PYY and 5-HT. It is necessary to identify the

roles of these two emetogenic mediators on DAS-induced emesis. The goal of this study was to determine the emetic effect of DAS and relate this effect to PYY and 5-HT, using a mink bioassay. Briefly, minks were fasted one day before experiment and given DAS by intraperitoneally and orally dosing on the experiment day. Then, emetic episodes were calculated and blood collection was employed for PYY and 5-HT test. DAS elicited robust emetic responses that corresponded to upraised PYY and 5-HT. Blocking the neuropeptide Y2 receptor (NPY2R) diminished emesis induction by PYY and DAS. The serotonin 3 receptor (5-HT3R) inhibitor granisetron totally restrained the induction of emesis by serotonin and DAS. In conclusion, our findings demonstrate that PYY and 5-HT have critical roles in DAS-induced emetic response.

*Toxins (Basel)*. 2020 Jun; 12 (6): 419.  
Published online 2020 Jun 25.  
Doi: 10.3390/toxins12060419

### High Trophic Niche Overlap between a Native and Invasive Mink Does Not Drive Trophic Displacement of the Native Mink during an Invasion Process

Karla García,<sup>1,2</sup> Carola Sanpera<sup>1</sup>, Lluís Jover<sup>1</sup>, Santiago Palazón<sup>1,3</sup>, Joaquim Gosálbez<sup>1</sup>, Konrad Górski<sup>2,4</sup>, Yolanda Melero<sup>5</sup>

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Invasive species are widely recognized to negatively affect native species through both direct and indirect interactions. When diet overlap between the native and invasive species increases, their competitive interaction is expected to increase too. This in turn may lead to displacement of one of the species. However,

the specific mechanisms of the diet displacement are still unclear. In this study, we analysed the diet and diet overlap between the critically endangered European mink and the invasive American mink during the invasion process of the latter species by means of stable isotope analyses. We found a significant diet overlap between the native and invasive mink when they co-occur, an important individual variation of diet, and no significant change of diet of the native species in response to the arrival of the invasive mink. These results suggest significant competitive pressure imposed on the native European mink by the invasive American mink. As such, urgent implementation of control measures of invasive species is needed to ensure the viability and conservation of endangered European mink populations.

*Animals (Basel)*. 2020 Aug; 10 (8): 1387.  
Published online 2020 Aug 10.  
Doi: 10.3390/ani10081387

### Effects of Gut Microbiome and Short-Chain Fatty Acids (SCFAs) on Finishing Weight of Meat Rabbits

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Understanding how the gut microbiome and short-chain fatty acids (SCFAs) affect finishing weight is beneficial to improve meat production in the meat rabbit industry. In this study, we identified 15 OTUs and 23 microbial species associated with finishing weight using 16S rRNA gene and metagenomic sequencing analysis, respectively. Among these, butyrate-producing bacteria of the family Ruminococcaceae were positively associated with finishing weight, whereas the microbial taxa related to intestinal damage and inflammation showed opposite effects. Furthermore, interactions of these microbial taxa were firstly found to be associated with finishing weight. Gut microbial functional capacity analysis revealed that CAZymes, such as galactosidase, xylanase, and glucosidase, could significantly affect finishing weight, given their roles in regulating nutrient digestibility. GOs related to the metabolism of several carbohydrates and amino acids also showed



important effects on finishing weight. Additionally, both KOs and KEGG pathways related to the membrane transportation system and involved in aminoacyl-tRNA biosynthesis and butanoate metabolism could act as key factors in modulating finishing weight. Importantly, gut microbiome explained nearly 11% of the variation in finishing weight, and our findings revealed that a subset of metagenomic species could act as predictors of finishing weight. SCFAs levels, especially butyrate level, had critical impacts on finishing weight, and several finishing weight-associated species were potentially contributed to the shift in butyrate level. Thus, our results should give deep insights into how gut microbiome and SCFAs influence finishing weight of meat rabbits and provide essential knowledge for improving finishing weight by manipulating gut microbiome.

*Front. Microbiol.*, 11 August 2020  
Doi.org/10.3389/fmicb.2020.01835

#### **Autochthonous Strain *Enterococcus faecium* EF2019 (CCM7420), Its Bacteriocin and Their Beneficial Effects in Broiler Rabbits—A Review**

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Weaning is the most important and critical period in rabbits breeding; the cecal digestion is very complex and only small dietary and/or environmental changes can disturb the stable microbial population/fermentation and gut health, leading to digestive dysbiosis and increased morbidity, often with fatal outcome and big economic losses. Control of the microbiota, prevention of digestive disturbances and improving gut health and immunity can be achieved through the natural substances application in rabbit nutrition. While probiotics are frequently used in rabbit farms, the in vivo administration of bacteriocins (antimicrobial substances produced by bacteria, which usually also possess probiotic properties) in these animals is often limited and has become an area of research activity. Moreover, the most of probiotic strains used in rabbits are non-autochthonous (have a different origin

than the rabbits ecosystem). Therefore, our study focused on improving rabbits' health using the autochthonous strain *Enterococcus faecium* EF2019 (CCM7420) and its enterocin (Ent7420) in broiler rabbits. The antibacterial and anticoccidial effect of additives was observed, with good colonization ability of the CCM7420 strain. Both additives showed a tendency to modulate the serum biochemistry parameters and to improve the immunity, jejunal morphology, weight gains, feed conversion ratio and meat quality (physicochemical traits and mineral content).

*Animals (Basel)*. 2020 Jul; 10 (7): 1188.  
Published online 2020 Jul 14.  
Doi: 10.3390/ani10071188

## **BEHAVIOUR AND WELFARE**

### **Barren housing and negative handling decrease the exploratory approach in farmed mink**

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*Applied Animal Behaviour Science*  
Volume 222, January 2020, 104901  
Doi: 10.1016/j.applanim.2019.104901

## **HEALTH AND DISEASE**

### **A Bivalent Human Adenovirus Type 5 Vaccine Expressing the Rabies Virus Glycoprotein and Canine Distemper Virus Hemagglutinin Protein Confers Protective Immunity in Mice and Foxes**

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The development of a safe and efficient multivalent vaccine has great prospects for application. Both rabies virus (RABV) and canine distemper virus (CDV) are highly infectious antigens, causing lethal diseases in domestic dogs and other carnivores worldwide. In this study, a replication-deficient human adenovirus 5 (Ad5)-vectored vaccine, rAd5-G-H, expressing RABV glycoprotein (G) and CDV hemagglutinin (H) protein was constructed. The RABV G and CDV H protein of rAd5-G-H were expressed and confirmed in infected HEK-293 cells by indirect immunofluorescence assay. The rAd5-G-H retained a homogeneous icosahedral morphology similar to rAd5-GFP under an electron microscope. A single dose of 10<sup>8</sup> GFU of rAd5-G-H administered to mice by intramuscular injection elicited rapid and robust neutralizing antibodies against RABV and CDV. Flow cytometry assays indicated that the dendritic cells and B cells in inguinal lymph nodes were significantly recruited in rAd5-G-H-immunized mice in comparison with the mock and rAd5-GFP groups. rAd5-G-H also activated the Th1- and Th2-mediated cell immune responses against RABV and CDV in mice, which contributed to 100% survival of a lethal-dose RABV challenge without any clinical signs. In foxes, a single dose of 10<sup>9</sup> GFU of rAd5-G-H could elicit high levels of neutralizing antibodies against both RABV and CDV in comparison with the mock and rAd5-GFP groups. All foxes in the rAd5-GFP and mock groups died, while the foxes inoculated with rAd5-G-H all survived and showed no clinical signs of disease after being challenged with a lethal wild-type CDV strain. These results suggested that rAd5-G-H has great potential as a bivalent vaccine against rabies and canine distemper in highly susceptible dogs and wildlife animals.

*Front Microbiol.* 2020; 11: 1070.

*Published online 2020 Jun 16.*

*Doi: 10.3389/fmicb.2020.01070*

### **Molecular epidemiology of Aleutian mink disease virus from fecal swab of mink in northeast China**

Mingwei Tong<sup>1,2</sup>, Na Sun<sup>2</sup>, Zhigang Cao<sup>2</sup>, Yuening Cheng<sup>2</sup>, Miao Zhang<sup>2</sup>, Shipeng Cheng<sup>2</sup>, Li Yi<sup>2</sup>

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### **Background**

Aleutian mink disease parvovirus (AMDV) causes Aleutian mink disease (AMD), which is a serious infectious disease of mink. The aim of this study was to get a better understanding of the molecular epidemiology of AMDV in northeast China to control and prevent AMD from further spreading. This study for the first time isolated AMDV from fecal swab samples of mink in China.

### **Results**

A total of 157/291 (54.0%) of the fecal swab samples were positive for AMDV. Of these, 23 AMDV positive samples were randomly selected for sequence alignment and phylogenetic analysis based on the acquired partial fragments of VP2 gene with the hypervariable region. Comparative DNA sequence analysis of 23 AMDV isolates with a reference nonpathogenic (AMDV-G) strain revealed 8.3% difference in partial VP2 nucleotide sequences. Amino acid alignment indicated the presence of several genetic variants, as well as one single amino acid residue deletion. The most concentrated area of variation was located in the hypervariable region of VP2 protein. According to phylogenetic analysis, the Chinese AMDV strains and the other reference AMDV strains from different countries clustered into three groups (clades A, B and C). Most of the newly sequenced strains were found to form a Chinese-specific group, which solely consisted of Chinese AMDV strains.

### **Conclusion**

These findings indicated that a high genetic diversity was found in Chinese AMDV strains and the virus distribution were not dependent on geographical origin. Both local and imported AMDV positive species were prevalent in the Chinese mink farming population. The genetic evidence of AMDV variety and epidemic isolates have importance in mink farming practice.

*BMC Microbiol.* 2020; 20: 234.

*Published online 2020 Aug 1.*

*Doi: 10.1186/s12866-020-01910-8*

## Molecular epidemiology of Aleutian mink disease virus causing outbreaks in mink farms from Southwestern Europe: a retrospective study from 2012 to 2019

Alberto Prieto<sup>1</sup>, Ricardo Fernández-Antonio<sup>1,2</sup>, Gonzalo López-Lorenzo<sup>1</sup>, José Manuel Díaz-Cao<sup>1</sup>, Cynthia López-Novo<sup>1</sup>, Susana Remesar<sup>1</sup>, Rosario Panadero<sup>1</sup>, Pablo Díaz<sup>1</sup>, Patrocinio Morrondo<sup>1</sup>, Pablo Díez-Baños<sup>1</sup>, Gonzalo Fernández<sup>1</sup>

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### Background

Aleutian mink disease virus (AMDV) causes major economic losses in fur-bearing animal production. The control of most AMDV outbreaks is complex due to the difficulties of establishing the source of infection based only on the available on-farm epidemiological data. In this sense, phylogenetic analysis of the strains present in a farm may help elucidate the origin of the infection and improve the control and biosecurity measures.

### Objectives

This study had the following aims: characterize the AMDV strains from most outbreaks produced at Spanish farms between 2012–2019 at the molecular level, and assess the utility of the combined use of molecular and epidemiological data to track the possible routes of infection.

### Methods

Thirty-seven strains from 17 farms were partially sequenced for the NS1 and VP2 genes and analyzed phylogenetically with other strains described worldwide.

### Results

Spanish AMDV strains are clustered in four major clades that generally show a good geographical correlation, confirming that most had been established in Spain a long time ago. The combined study of phylogenetic results and epidemiological information of each farm suggests that most of the AMDV outbreaks since 2012 had been produced by within-farm reservoirs, while a few of them may have been due to the introduction of the virus through international trade.

### Conclusion

The combination of phylogenetic inference, together with epidemiological data, helps assess the possible origin of AMDV infections in mink farms and improving the control and prevention of this disease.

*J Vet Sci.* 2020 Jul; 21(4): e65. English.

Published online Jul 15, 2020.

Doi.org/10.4142/jvs.2020.21.e65

## First expert elicitation of knowledge on drivers of emergence of the COVID-19 in pets

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Infection with the Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) induces the coronavirus infectious disease 19 (COVID-19). Its pandemic form in human population and its probable animal origin, along with recent case reports in pets, make drivers of emergence crucial in domestic carnivore pets, especially cats, dogs and ferrets. Few data are available in these species; we first listed forty-six possible drivers of emergence of COVID-19 in pets, regrouped in eight domains (i.e. pathogen/disease characteristics, spatial-temporal distance of outbreaks, ability to monitor, disease treatment and control, characteristics of pets, changes in climate conditions, wildlife interface, human activity, and economic and trade activities). Secondly, we developed a scoring system per driver, then elicited scientific experts ( $N = 33$ ) to: (a) allocate a score to each driver, (b) weight the drivers scores within each domain and (c) weight the different domains between them. Thirdly, an overall weighted score per driver was calculated; drivers were ranked in decreasing order. Fourthly, a regression tree analysis was used to group drivers with comparable likelihood to play a role in

the emergence of COVID-19 in pets. Finally, the robustness of the expert elicitation was verified. Five drivers were ranked with the highest probability to play a key role in the emergence of COVID-19 in pets: availability and quality of diagnostic tools, human density close to pets, ability of preventive/control measures to avoid the disease introduction or spread in a country (except treatment, vaccination and reservoir(s) control), current species specificity of the disease-causing agent and current knowledge on the pathogen. As scientific knowledge on the topic is scarce and still uncertain, expert elicitation of knowledge, in addition with clustering and sensitivity analyses, is of prime importance to prioritize future studies, starting from the top five drivers. The present methodology is applicable to other emerging pet diseases.

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### **Coronaviruses in cats and other companion animals: Where does SARS-CoV-2/COVID-19 fit?**

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### **Cardiopulmonary nematodes of wild carnivores from Denmark: Do they serve as reservoir hosts for infections in domestic animals?**

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The cardiopulmonary nematodes *Angiostrongylus vasorum*, *Crenosoma vulpis*, *Capillaria aerophila* and *Aelurostrongylus abstrusus*, are a cause of concern in the scientific and veterinary community, potentially causing significant disease in domestic animals. To investigate the potential of wild carnivores as reservoir hosts to these parasites, a total of 1041 animals from seven regions of Denmark were sampled: 476 raccoon dogs (*Nyctereutes procyonoides*), 367 red foxes (*Vulpes vulpes*), 123 American mink (*Neovison vison*), 31 beech martens (*Martes foina*), 30 Eurasian otters (*Lutra lutra*) and 14 polecats (*Mustela putorius*). Hearts and lungs were collected and examined for cardiopulmonary parasites. *Capillaria aerophila* was identified using morphology, whereas *A. vasorum* and *C. vulpis* were identified by a duplex real-time PCR, and *A. abstrusus* by conventional PCR. This is the first Danish report of *A. vasorum* and *C. vulpis* infections in raccoon dogs, mink and polecats, and of *C. aerophila* in raccoon dogs and beech martens. In addition, this is the first time *A. vasorum* and *C. vulpis* have been identified in wild animals from the island of Bornholm, just as it is the first report of *C. vulpis* in American mink, and *C. vulpis* and *A. vasorum* in polecats in Europe. The prevalence of *A. vasorum* appears to have increased in red foxes in Denmark compared to previous studies, while *C. vulpis* and *C. aerophila* prevalences are lower. Our data show that several wild carnivores can serve as reservoir hosts for *A. vasorum*, *C. vulpis* and *C. aerophila* in Denmark, and

that *A. vasorum* appears more abundant than previously reported. It is speculated that the *A. vasorum* increase might relate to increased snail abundance, which may be due to a rise in mean yearly temperatures in Denmark.

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*Crenosoma vulpis* L1

*Angiostrongylus vasorum* L1

*Aelurostrongylus abstrusus* L1

*Capillaria aerophila*  
adult female



## Obituary



### **Gunnar Jørgensen 1933 – 2019**

Recently, some sad news reached to us telling that the founder of Scientifur and IFASA, Gunnar Jørgensen, passed away last year in 2019.

Gunnar Jørgensen was the leading figure in the Danish fur animal research community for decades. He was head of the Department for Research in Fur Animals at the National Institute of Animal Science in Denmark from 1965 to 1993. His main scientific contribution was on feeding and nutrition of fur animals, especially on protein digestibility in mink. With Gunnar Jørgensen as leader, the department staff increased from just two to nine scientists when the department was located in Hillerød north of Copenhagen. After the successful moving of the National Institute of Animal Science to Foulum close to Viborg, in 1989, the number of scientific employees was increased even more. Besides heading the department from 1965 to 1993, Gunnar was also heavily involved in the international collaboration between fur animal scientists. The Nordic Association of Agricultural

Scientists (NJF) had a strong advocate in Gunnar who participated in all NJF seminars for many years.

Gunnar felt strongly for international collaboration between scientists and he initiated and was chair of the Organising Committee of the First International Congress on Fur Animals in 1976 in Helsinki, Finland. Here he presented his idea of a publication Scientifur, which in the form of short abstracts would collect and spread information about research on fur animals all around the world. He was a devoted editor of Scientifur for many years and through this work, many international friendships were initiated. He was the main organizer of the second international congress in 1980 in Vedbæk, Denmark. The third congress was held in 1984 in Versailles, France.

At the fourth international congress in Toronto, Canada in 1988, Gunnar initiated the formation of the International Fur Animal Scientific Association (IFASA) at the gala dinner at the post congress tour in Fox Hills Resort in Wisconsin, USA. Naturally,

Gunnar was elected for the IFASA board from 1988 until 2000.

Since the foundation of IFASA all subsequent congresses: 1988 in Toronto, Canada, 1992 in Oslo, Norway, 1996 in Warsaw, Poland, 2000 in Kastoria, Greece, 2004 in 'S-Hertogenbosch, The Netherlands, 2008 in Halifax, Canada, 2012 in Copenhagen, Denmark and 2016 in Helsinki, Finland has been organised under the auspices of IFASA. The congress proceedings have been published as parts of Scientifur and due to Gunnar, can therefore be found on the IFASA website at [www.ifasanet.org](http://www.ifasanet.org).

Gunnar Jørgensen celebrated his 35<sup>th</sup> anniversary at the National Institute of Animal Science on the 30<sup>th</sup> of April 1993 and retired soon thereafter. As a 'Contribution in Honour of Gunnar Jørgensen' the Report 720 from the National Institute of Animal Science, Denmark, was written and published for the anniversary. The report sums up the professional career of Gunnar as well as the history of Scientifur, IFASA and the scientific status of the institute. In honour of the late Gunnar Jørgensen, [the report](#) can now be found at the IFASA website.

After his retirement, Gunnar and his wife Synnøve moved to Drammen in Norway. I had the pleasure of visiting them some years ago when we collected the Scientifur archive from the Norwegian Fur Breeders Association in Oslo. For many years, Gunnar and Synnøve spent the coldest winter month in Spain.

Synnøve told that Gunnar passed away after having suffered from cancer for some time. He died on July 16<sup>th</sup> 2019 shortly after their 40<sup>th</sup> wedding anniversary. Synnøve still lives in their house in Drammen.

Gunnar will always be remembered as one of the Grand Old Men of Fur Animal Science. Our thoughts and sympathy go to Synnøve.

Steen H. Møller, President of IFASA



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