

# FUR ANIMAL RESEARCH

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## Introduction: Dr. Hugh Hildebrandt

*Fur Commission USA and Joint Mink Research Committee Adviser*

In this research newsletter some of the abstracts and summaries for you to read do not do the final products the researchers put together justice. The full report submitted by Dr. Beth Mason is actually in a booklet form. It has amazing color photos and diagrams and a wealth of information. The Aleutian disease report by Drs. Marta Canuti, Ann P. Britton, and Andrew S. Lang contains colored charts, diagrams and highlighted information. I urge you to take a look at the complete reports in the online library. Computers, high definition photos and researchers imaginations allow information to take on a whole new form not just black and white.

We have also included some information on fur chewing as a focus topic. This is a mix of information I received in the past from Dr. Oldfield, Dr. Gorham along with some online available information. They cover many ideas and issues with fur chewing like size of food, heritability as seen in other species, and chew enrichments. It will give you possibilities to consider for improving your herd.



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***All studies are available in their entirety at [www.FurResearch.org](http://www.FurResearch.org), a free repository for academic research addressing health, welfare, and disease issues affecting the husbandry of fur bearing animals. Originally launched in 2005 by Fur Commission USA as an archive of the work done by the first generation of leading fur animal scientists in North America, we now include more recent material from sources across the globe, to be used as reference tools for current and future researchers, veterinarians, and fur farmers throughout the world. Fur Commission USA does not receive any compensation for this service.***

## Mink Industry Byproduct Report

Verschuren Centre for Sustainability in Energy and the Environment

Cape Breton University | 2016 - 2018

*Dr. Beth Mason; Project Coordinator*

Over the 2017 and 2018 fiscal periods, the Canadian Mink Breeders Association provided matching funding with ACOA (Atlantic Canada Opportunities agency) for the team at the Verschuren Centre for Sustainability, Cape Breton University, to address issues around waste management. Specifically, the goal was to look for alternative and preferably value creation components within the existing waste streams, that if otherwise re-purposed, would be removed from the mixed source streams going to the existing waste management facilities, thereby enhancing optimization of those processes. The study encompassed a range of opportunities for value markets, available to industry members to recover value while offering improvements in existing composting and anaerobic digestion facilities.

One of the seasonal and somewhat problematic waste streams for processors is mink carcass disposal, as these require considerable time and effort to compost, and yet may have restricted market. Our first study explored fermentative and acid hydrolysis of the carcasses, which produces a liquidized protein product, liberates carcass oil for other uses, and separates out the bone for use in separated meals. Although uptake of mink meals in other feed industries may be challenging, this proved to be a rapid and efficient conversion process, allowing product separation to pursue value markets in plant and pet foods. Oil from this process could be combined with the fat recovered at pelting, which is sold on for purification. This process is generally a harsh chemical, costly conversion, but the market for refined oil is high end cosmetic and leather treatment. Hence an alternative, locally available process that achieved this would bring some of the refined oil benefit back to processors here. Utilizing mink fat provided by a processor, a novel green process was developed that clarified oil to the same desired parameters as required for commercial use. This process requires locally available and affordable materials and would allow direct sale.

For composted mink manure/waste there appeared little data on its value in plant production and so controlled plant growth trials were carried out with the cured compost. Use of compost as a peat replacement in potting mix, showed superior performance over the traditional peat alone or peat/sand mix. Barley seedlings grown on the mink compost (77%MC, pH 5.8, C:N of 10.6:1) showed greater root and shoot development, even though all groups received propagation fertilizer mix. Compost showed good nitrogen to phosphorus ratio (2.5:1.9:0.15, N:P:K). Greenhouse seedling production would therefore be a good market for this product, as seedlings would have a growth phase out of contact with mink compost, minimizing any concern over risk of microbial or pathogen transmission. Alternatively, since a large amount of carbonaceous material is present in the compost, it was decided to test pelletizing the material for biomass fuel use. Varying propor-

tions of compost to dry willow chips (grown locally) were pelletized using a large-scale purpose-built densification unit, and product tested for fuel use. The product enhanced willow pellet quality and up to 50% could be included in the mix. The ideal mix was 25% compost and provided high BTU (7700 BTU/lb, 18,000 KJ/kg) which is only about 6% below commercial pellets, though ash content was considerably higher. An attractive outlet for compost would be in industrial biomass burners or on-site operations, and willow or similar woody biomass crop provides additional benefits to a composting facility through its bio-remediation role as a sink for compost tea nutrients, vs constructed wetlands. An additional value creation from compost – bioconversion to insect meal was tested and although black soldier fly larvae (BSFL) could utilize the compost, growth was reduced relative to other ingredients, impacting on yield of protein meal and larvae oil, likely due to high nitrogen and lignin. Pre-composted or segregated food waste would likely be a better substrate for the BSFL in future trials.

Anaerobic digestion, has been successfully utilized for bio-methane production from livestock liquid manures, yet little data exists for mink manure. The anaerobic digester built for this purpose has encountered problems of high acidity and low bio-gas production. Work with this group included testing of various other materials for co-digestion with mink manure to bring the volatile solids and C:N ratio closer to optimum conditions for the specific microbial groups to function and thereby produce maximum bio-gas. Alternative, locally available ingredients have and continue to be tested through a bench bio-methane tester, and larger vessels to explore the optimum ration to feed the digester, as it is evident that mink manure alone will not provide this even with high alkalinity by-products. Work on co-digestion blends will continue as the system readjusts, bearing in mind locally available and seasonal supplies of ingredients such as vegetable waste and dairy by-products. Extraction of nutrient post digestion is also to be explored once steady state is reached, as this will reduce nutrient loading on surrounding acreage and associated transport cost of the system.

In conclusion, a variety of add-on value opportunities were identified and are available to industry members in a full detailed report. Removal of specific materials from the digestion or composting process serves to enhance the efficiency and success of these processes while adding revenue.

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## **Aleutian mink disease virus and related viruses in British Columbia wildlife**

*Drs. Marta Canuti, Ann P. Britton, and Andrew S. Lang*

Parvoviruses are small, resilient, viruses that can cause severe disease in terrestrial carnivores, including mustelids (e.g., mink, marten, otter, and ermine) and their close relatives. These viruses, among which the most well-known is the Aleutian mink disease virus (AMDV), can represent a serious threat both for wild and farmed mustelids, since

they can cause high mortality, reproduction failure, reduced litter size, abortion and reduced body weight. Thanks to advancements in virus discovery methods, several novel parvoviruses of mustelids have been discovered in recent years, but their clinical relevance remains unknown. Since wildlife is the natural reservoir of these viruses, knowing their host and spatial distribution is crucial to avoid introduction into farms. During this study, we screened wild carnivores of insular British Columbia (BC) for all known mustelid parvoviruses (including eight species of amdoparvoviruses, three species of protoparvoviruses and two species of bocaviruses) and potentially novel viruses.

In total we screened 262 samples and identified three viruses: AMDV, canine parvovirus 2 (CPV-2) and feline panleukopenia virus (FPV). A summary of our surveillance is in the fol-

Parvovirus prevalence in insular BC.

|              | Mink<br>N=77      | Marten<br>N=130 | Otter<br>N=22    | Ermine<br>N=27 | Raccoon<br>N=1 | Wolf<br>N=5 | Total<br>N=262    |
|--------------|-------------------|-----------------|------------------|----------------|----------------|-------------|-------------------|
| AMDV         | 32 (41.6%)        | 4 (3.1%)        | 0                | 0              | 0              | 0           | 36 (13.7%)        |
| CPV-2        | 1 (1.3%)          | 0               | 1 (4.5%)         | 0              | 0              | 0           | 2 (0.8%)          |
| FPV          | 4 (5.2%)          | 2 (1.5%)        | 6 (27.3%)        | 0              | 0              | 0           | 12 (4.6%)         |
| <b>Total</b> | <b>36 (46.7%)</b> | <b>6 (4.6%)</b> | <b>7 (31.8%)</b> | <b>0</b>       | <b>0</b>       | <b>0</b>    | <b>49 (18.7%)</b> |

We sequenced the positive samples and studied the genetic characteristics of the identified viruses. AMDV strains belonged to two different, but closely related, clades and they were very close to viruses identified in mink farms worldwide. They were not related to other amdoparvoviral strains identified in mainland BC in wild skunks and mink. Although there are currently no mink farms on Vancouver Island, there was active mink farming there until 1999, and we believe that the viruses we identified are farm derived strains that successfully managed to spread among wild populations, perpetuating until today. CPV-2 strains were 99.9% identical to each other and were closely related to CPV-2 viruses we previously found in raccoons in mainland BC, suggesting the circulation in BC of only one CPV-2 strain. Although we previously only found FPV in Vancouver Island raccoons, we believe that the two CPV-2 viruses identified in this study originated from raccoons, where CPV-2 prevalence is high. The FPVs were more genetically diverse as they fell into three different clades, indicating the simultaneous circulation of multiple strains. These viruses were sometimes very similar to viruses we previously identified in raccoons in this area. This high diversity could be due to a longer presence of this virus in this region, to multiple different viral introductions, or a combination of both factors.

In conclusion, parvoviruses are not only present in the wildlife of insular BC, but they are also efficiently transmitted and maintained among and within mustelid populations. These viruses had different prevalence among the various hosts, but viruses identified in different hosts were genetically similar, demonstrating active viral exchange between four local animal species. The ecological overlap between the host species explains the frequent viral exchange we observed in the studied populations. However, host susceptibility and viral transmission dynamics may also influence viral spread across different wild

populations. Follow-up studies involving a larger number of samples from mainland BC are crucial to obtain a complete picture of the epidemiology of parvoviruses in BC and to estimate the potential risk for farms derived by the presence of parvoviruses in wildlife.

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## **Aleutian Disease Virus (ADV) Heating Study**

*Madison Sokacz, Dr. Steve Bursian, Tasia Taxis, Jane Link, Dr. John Easley*

Aleutian Disease Virus (ADV) is well known for the economic impacts it has on the world's mink industry. Eradicating ADV from farms remains a constant struggle for ranchers due to the lack of information and understanding of the virus. Michigan State University, in collaboration with Dr. John Easley, conducted a study to investigate the effect of different temperatures on ADV infectivity. The study consisted of four different heat treatment groups of isolated ADV virus. The four treatment groups were: 80 °C for 1 hour, 80 °C for 2 hours, 70 °C for 1 hour, and 70 °C for 2 hours. In addition, there was a positive control group (unheated virus) and a negative control group (no virus). All mink challenged with the 80 °C-treated virus tested negative for ADV via PCR while all animals challenged with the 70 °C-treated virus were infected with ADV at the end of the 28-day trial. Thus, the optimal temperature for the heat treatment of equipment that could be ADV contaminated, such as nest boxes, is 80 °C, for at least one hour.

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## **Development of Genetic Markers for Detection of Aleutian Disease Resistance**

*Cepica A.1, Anistoroaei R.2, Iwamoto T.1, Christensen K.3, Markakis M.4, Dobbin E1.*

It has been accepted that ADV eradication effort on farms, in regions, and indeed in countries is practically impossible, because of the frequent reintroduction from infected animals that remain undetected, often also because infected animals at the time of testing were in very early stages of infection and did not produce antibody yet. Where the ADV eradication was indeed accomplished for a short period of time, the infection was eventually reintroduced in spite of the efforts to keep it out. Thus, even in the cases where there was a de-population by pelting of all of the animals, followed by thorough disinfection, frequent reintroduction have occurred by a) latently infected restocking animals, b) wildlife, c) contaminated vehicles, d) feed, e) as well as contaminated people entering the farms under eradication. For all of these reasons, "eradication" must be historically judged unequivocally as only "illusory". This meant that the farmers were erroneously made to believe that if they followed every detail of the recommended protocols, they could keep the virus and the disease at bay. This strategy seemed logical, recommended, and workable approach to AD elimination from farms after the first report of Cho, H. J., and Greenfield, J., (1978), even though careful reading of the paper reveals AD reappearance during the duration of their study. Therefore, farmers were blamed

erroneously for the eradication failures, because we know now, that in the case of ADV eradication of virus from animal populations is practically impossible. This is unlike the situation with some other viruses, for example herpesvirus infections (pseudorabies of swine, IBR of cattle etc.), where eradication is possible. The reasons for this are beyond the scope of this article, but suffice to say that not all viruses behave the same when it comes to probability of successful eradication. While some viruses are relatively easy to eradicate, e.g. those that induce sterile immunity /no virus present after the immune response is mounted, or if the virus enters long period of latency/herpesviruses/, or where efficacious vaccination is possible.

***In the case of ADV, the following features of the ADV infection minimize the likelihood of success of eradication:***

1. Firstly, *the infected animals shed the virus with unpredictable frequency during the entire period of infection.* In many viral other infections, after the period of disease, the virus is either cleared for life, or it retreats into latency for long period of times, where infectious virus is not shed. In this case, the infected animals can be identified by antibody tests, and removed from the affected farms before the infection can be reactivated, which happens rarely (all herpesviruses). This is the reason why herpesviruses (e.g., pseudorabies) are relatively easily eradicated.
2. *The AD virus is extremely resistant to environmental removal by inactivation/disinfection (heat, UV light, disinfectants).* This is a very uncommon property for a virus, as compared to bacteria most viruses are relatively susceptible to inactivation.
3. **Vaccination is not possible** in principle, as immune response to ADV induced by previous infection with a virus of lower pathogenicity, or a vaccine (whether inactivated or live attenuated /weakened virus/) not only does not prevent infection and disease, but actually potentiates the disease.

**Research Strategy for the solution to the Aleutian disease associated losses world-wide:**

***Even though the virus originally in 1950s, before the disease was described in Aleutian mink strain, was not causing noticeable mortalities among the farmed wild mink, heavy mortalities and reduction of reproduction appeared and spread ubiquitously in all farmed color strains of mink after the mutated Aleutian mink strain was interbred with wild farmed mink to produce new color varieties.***

In order to inherit susceptibility to A. disease, the newly produced color strains of mink, did not need to inherit the full genetic mutation causing the Chediak-Highashi syndrome of the original Aleutian color mutation which was simultaneously responsible for creation of the attractive pelt color and high susceptibility to A. disease. However, the Chediak-Highashi-associated other, until now unknown genes, inherited from the Aleutian mink strain introduced into some animals of the new color strains *loss of the disease resistance* seen in the original wild mink. This occurred in a varied proportion of mink, depending on the mink strain). Even though *all mink of these new color variants, as well as wild mink does get infected and develop antibody as evidence of the infection, only a varied proportion of the animals from among the "new color strains" (again depending on the color strain) remained resistant to the disease.*

*The nature of the gene/s responsible for the disease have been so far unknown, as well as the inheritance pattern, but they decide which infected animal stays healthy for life and which animal gets sick and dies, and which of the females loses reproductive ability.*

It would make sense to only breed animals that have the ability to resist the disease following the infection. In order to do this, a **sensitive** test was necessary that would determine **early** into the infection, which of the infected animals is on the way to a healthy life (disease resistant), and which is on the way to acute or slow dying (disease susceptible). *Such a test can be applied for selection of breeding animals (both females and males), in order to prevent passing of the defective genetics onto the progeny.*

The test fulfilling the criteria has been available following the development (Cepica et al., 2012), in **MALDI-TOF determination of IgG:Albumin**, and it is currently delivered by the Regional Diagnostic Laboratory at the Atlantic Veterinary College, Charlottetown, P.E.I., Canada). However, this selection is **only possible in infected mink**, and no selection for AD disease resistance is possible where eradication is still practiced (e.g., Denmark). Because the trade of the breeding animals between the countries practicing eradication on one side, and practicing selection for resistance on the other, is necessary, research into the DNA markers of the Aleutian disease resistance described here, was necessary.

#### **Simplified methodology:**

- A) The DNA of two cohorts of infected mink were completely sequenced; 1. MALDI-TOF IgG:Albumin <5 (98 disease susceptible animals) and 2. MALDI-TOF IgG:Albumin >8 (98 disease resistant animals)
- B) The sequences were analysed by complex and extensive bioinformatics computer programs to identify the area/s of the genome where these two groups might differ.
- C) *The area of significant differences among the resistant and susceptible animals could be then targeted for development of a DNA based test, in order to identify uninfected animals as either A. disease resistant or A. disease susceptible.*

#### **Results:**

After over 2 years of efforts, we are pleased to report that such area of DNA, responsible for determination of resistance versus susceptibility to A. **disease**, has been identified as the gene coding for "**GATOR complex protein NPRL3 isoform X6**". The function of the gene has been described in other animal species, as capable of dealing with the excess of immunoglobulin created in the course of A. *disease*.

Comparison of the number of homozygotes for the alternative variant of that sequence among the A. *disease* susceptible and *disease* resistant mink, indicates very high statistical significance (confidence) regarding the DNA sequence difference between those animals that are **disease resistant** and **disease susceptible**. Therefore, this gene sequence is definitely a prospective candidate for development of the DNA based test for AD resistance vs. susceptibility among ADV uninfected mink.

## Fur Chewing: Effects on Reproduction

*Gugolek, A., M.O. Lorek and A. Hartman. Studies on the relationship between fur damage in mink, reproduction results and the occurrence of this defect in offspring. SCIENTIFUR 25(4):115-116. 2001*

Causes of fur chewing in mink have been debated and it has not been clear whether this undesirable trait is inherited. Studies in Poland addressed this problem and also investigated the effects of fur chewing on reproduction. Two groups of pastel mink were involved (24 females and 12 males whose fur was damaged on the tail and sides of the body, and 31 females and 15 males whose fur was not damaged) as controls. The animals were bred within these groups (damaged x damaged and control x control). It appeared that fur chewing was an inherited defect. In the fur-damaged group 19% of the kits born chewed their fur. Chewing was observed on the rail and neck. The tail-chewing was thought to be self-inflicted while that on the neck and body was attributed to other mink in the same cage.

As far as reproduction was concerned the worst kit-rearing results were found in the females with fur damage. Males with fur damage appeared fairly normal and exhibited normal sexual activity. Culling of mink showing fur-chewing tendencies is recommended and it was suggested that animals who chewed their own fur also had a tendency to damage the fur of others in the same cage.

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## Additional foraging elements reduce abnormal behaviour – fur-chewing and stereotypic behaviour – in farmed mink (*Neovison vison*)

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*Applied Animal Behaviour Science*

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We investigated whether provision of additional appetitive and consummatory elements of foraging reduces baseline stress and abnormal behaviour – in terms of fur-chewing and stereotypic behaviour – in farmed mink. We studied 200 juveniles ( $n = 100$  females and 100 males) during the 5-month growth period with plenty of feed, and subsequently the females as adults during the 2-month feed restriction period before mating. The mink were distributed in four equally sized groups: (i) FARM, conventional finely ground feed ( $< 8$  mm) without additional foraging elements; (ii) ROPE, access to biting ropes; (iii) CONS, chunky feed (parts up to 42 mm), replacing conventional feed; (iv) BOTH, access to both biting ropes and chunky feed. In growing mink, biting ropes reduced fur-chewing ( $P = 0.044$ ) and chunky feed reduced stereotypic behaviour ( $P = 0.038$ ) and fur-chewing in female mink ( $P = 0.019$ ). During the season of feed restriction, the wear/tear of biting ropes increased. Females on the chunky diet had a higher concentra-

tion of faecal cortisol metabolites ( $P = 0.033$ ), probably due to a more severe slimming resulting in a 6.2% lower body weight ( $P = 0.006$ ) than the mink on the finely ground diet; still the chunky diet reduced time spent in pre-feeding stereotypies ( $P = 0.001$ ). In the restrictively fed females, fur-chewing was reduced both by access to biting ropes ( $P = 0.005$ ) and chunky feed ( $P = 0.007$ ). Consequently, 54% of group FARM mink displayed fur-chewing compared to 21% in group BOTH. In conclusion, stereotypic behaviour was reduced by provision of chunky feed, increasing the consummatory element in daily foraging. Fur-chewing was reduced upon access to either biting ropes or chunky feed in female mink throughout the study. Our findings support frustrated foraging, mainly consummatory, behind abnormal behaviour.

## Determination of the Genetic Component of Fur-Chewing in Chinchillas (*Chinchilla lanigera*) and Its Economic Impact

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Fur-chewing is a common behavioral disorder developed by chinchillas kept in confinement that can indicate a past or present welfare problem. It also has a negative productive impact associated. The aim of this study was to determine the genetic component of fur-chewing, and the effect of this undesired behavior on fur price in a commercial fur-farming system of chinchillas (*Chinchilla lanigera*). The data for the analysis was derived from a commercial population of 10,196 chinchillas, recorded between the years 1990 and 2011. For determining differences in fur price according to presence of fur-chewing behavior, analysis of variance (ANOVA) was used, considering 3007 animals. For estimation of variance components of fur-chewing a sire-dam threshold (probit) mixed model was used, using data of 9,033 individuals, and then heritability on the underlying liability scale was calculated. The analysis revealed a significant negative impact on fur price from fur-chewing chinchillas ( $p$ -value  $< 0.05$ ). In addition, the study showed that fur-chewing presents significant genetic variation, with an estimated heritability of 0.16. The presentation of fur-chewing should be taken into account when selecting broodstock in these systems, in order to reduce the number of affected individuals.

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