

# **Whole genome sequencing of Aleutian disease virus from skunks, raccoons and mink in British Columbia**

**Final report; January 2017**

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## **1. Skunks**

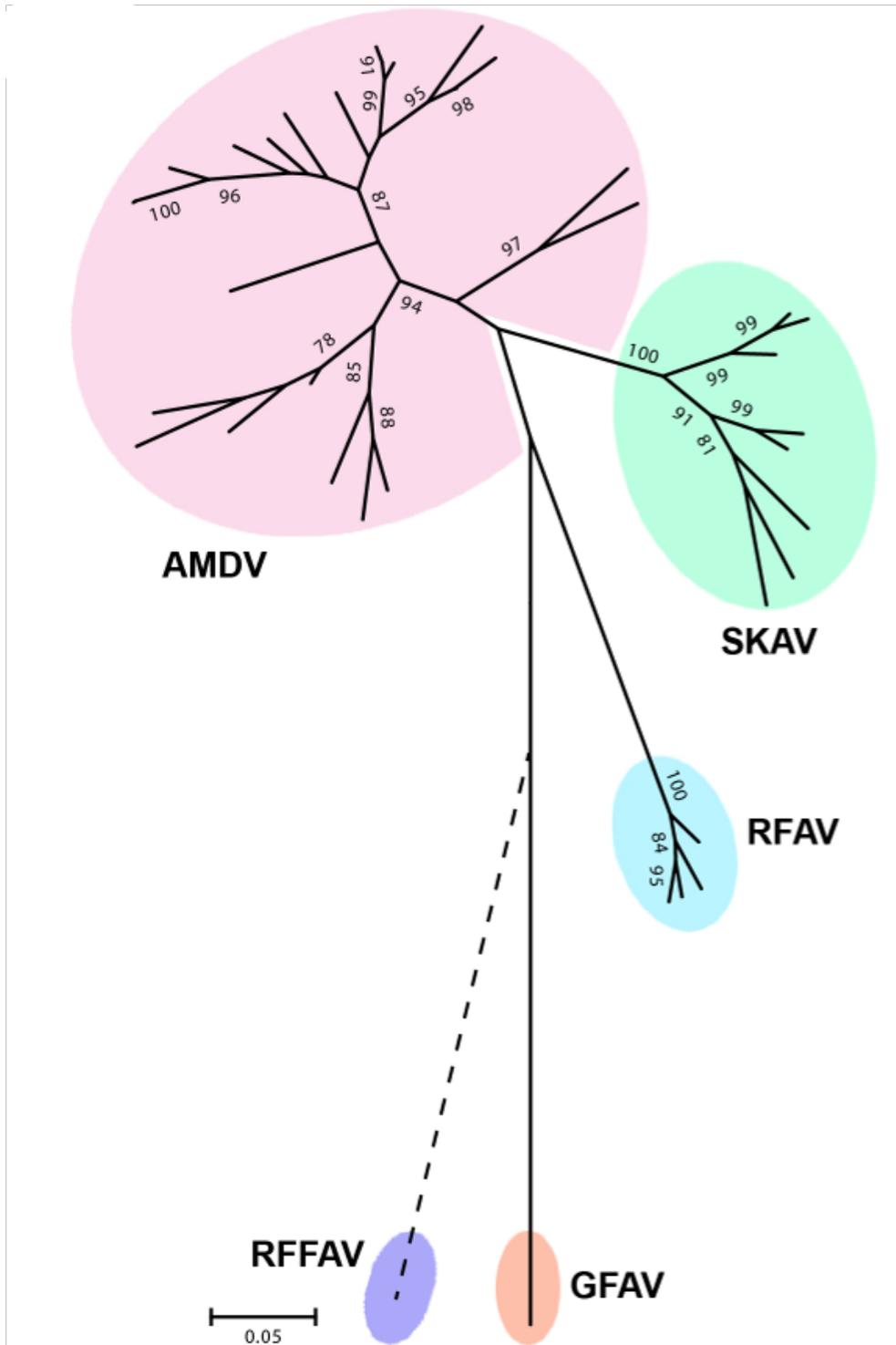
Forty-four viruses from samples collected from in and around Vancouver were characterized, and the complete genomic sequence was obtained from 8 of these viruses. Our results showed that these skunk AMDV-like viruses are clearly separate from AMDV and they form a novel viral species, which we named Skunk Amdoparvovirus (SKAV, Figure 1). The epidemiological investigation highlighted the presence of 2 different viral types and several subtypes, and the occurrence of double-infections and recombination. Furthermore, we found evidences for these viruses in Ontario and California, underlining how this novel species is widespread in other parts of North America. Finally, we found evidence for SKAV infection in mink from Ontario, showing how previously unknown viruses could represent a threat to wild and farmed mink and highlighting the need for a strict viral surveillance, especially if animals are exchanged between farms and across various provinces.

## **2. Mink**

Fifty samples from 4 different farms were received from British Columbia, along with 1 sample collected from a wild mink. Twelve samples from farmed animals were AMDV-positive and sequencing of the complete NS1 gene revealed that those samples are related to some of the sequences identified in NL. However, the complete genomic sequence of the virus identified in the wild animals was clearly separated from all other AMDV sequences, showing that the whole spectrum of mink AMDV is currently not known and how yet-to-be-discovered types could represent a potential danger to wild and farmed animals.

## **3. Raccoons**

Fourteen racoon samples positive for viruses closely related to Mink enteritis virus were received from British Columbia. Preliminary investigations showed the presence of 3 distinct variants among the 13 sequenced viruses. The complete genome sequencing of 5 of these viruses will be part of future research.



**Figure 1.** Phylogenetic tree of skunk amdoparvoviruses (SKAVs) identified in striped skunks in British Columbia compared to other viral species of the genus *Amdoparvovirus* (AMDV: Aleutian mink disease virus; RFAV: raccoon dog and fox amdoparvovirus; GFAV: gray fox amdoparvovirus; RFFAV: red fox fecal amdoparvovirus).

## **Scientific accomplishments associated with the funding**

### **1. Scientific publications**

Canuti M, Doyle HE, Britton A, Lang AS. 2017. Full genetic characterization and epidemiology of a novel amdoparvovirus in striped skunk (*Mephitis mephitis*). *Emerging Microbes and Infections*; In press, accepted for publication 23 January 2017

### **2. Conference/meeting presentations**

Canuti, M. Parvoviruses in Canadian fur-bearing (and other) animals. Newfoundland and Labrador Fur Breeders' Association Annual Information Workshop; Oral presentation; Gander, January 23-24, 2017

Doyle HE, Canuti M, Britton A, Lang AS. Molecular characterization of the Aleutian disease virus in the urban striped skunk (*Mephitis mephitis*) population of British Columbia. Science Atlantic Aquaculture & Fisheries and Biology Conference 2016; Oral presentation; Halifax, March 11-13, 2016

Doyle HE, Canuti M, Britton A, Lang AS. Molecular characterization of the Aleutian disease virus in the urban striped skunk (*Mephitis mephitis*) population of British Columbia. Canadian Society of Microbiologists 2016 Conference; Poster presentation; Toronto, June 12-15, 2016

### **3. Student theses**

Doyle HE. Molecular characterization of the Aleutian disease virus in the urban striped skunk (*Mephitis mephitis*) population of British Columbia. Biology Department Honours Thesis, 2016

### **4. Supported researchers**

Dr. Marta Canuti, Post-doctoral Fellow

Hillary Doyle, Undergraduate Honours Student and Research Assistant