

Source of the Aleutian mink disease virus outbreak in Nova Scotia

Aleutian mink disease virus (AD virus) is endemic in Nova Scotia, yet many ranchers have managed to keep their premises free of the virus by implementing strict biosecurity measures. Virus-free ranches are important sources of clean breeding stock for other ranches in the province.

Several virus-free ranches in central and western Nova Scotia became infected with the AD virus between December 2012 and March 2013 and most of them suffered high animal mortality. To identify source of the virus, two segments of the AD virus genome; one of 1040 nucleotides in the left side of the virus genome and one of 980 nucleotides in the right side of the virus, were sequenced in two mink from each of the nine infected ranches in central and western Nova Scotia. These two regions covered 42.1% of the entire length of the virus genome. All 18 samples were found to have exactly the same sequences in both regions of the virus genome, except one sample which was different by one nucleotide in the left side of the genome. The results strongly suggested that contamination of these nine ranches originated from a single source.

The sequences were compared with published AD virus sequences and with 80 previously sequenced virus isolates from western Nova Scotia. The source of contamination was pinpointed to five ranches which are located in a small region (same postal code) in western Nova Scotia. Sequences of these viruses, which were called NOVA-OB1, NOVA-OB2 and NOVA-OB3, are published in Genbank

public database (<http://www.ncbi.nlm.nih.gov/nucleotide/>) with the accession numbers KM494943, KM494944 and KM494945.

In addition to sequencing of the virus, post mortem examination and histopathology were performed on 32 carcasses from five of the ranches. No gross abnormalities characteristic of AD was observed on any of the organs of the mink examined. Microscopic examination of the kidney, liver and lung of these animals showed that all had histopathological lesions suggestive of AD, confirming that the virus strain was pathogenic.

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