Aleutian disease virus types in Nova Scotia- a preliminary report

We have created the largest Aleutian disease virus genome sequence database in the world. This database helped us define relationships among local AD virus types, as well as their relationship to those from other parts of the world

Relative to other viruses, the Aleutian disease (AD) virus is very small. To date, we have sequenced 180 AD viruses from 19 ranches in Nova Scotia. For 104 of these viruses from 15 ranches, we have sequenced 92% of their length. Fragments of such length contain all the regions of the viral genome which are necessary for the virus to infect mink and for its own replication. Our AD virus sequence database is presently the largest of its kind in the world. In fact, it is several times larger than all of the published sequences of the AD viruses combined.

AD virus types in Nova Scotia

The preliminary results of the 104 viruses with 92% genome coverage showed that more than 70% of the viruses were different from each other by at least one nucleotide. This high degree of variability is not surprising because the AD virus changes rapidly as a result of its high mutation rate.

To date, we have identified two groups, 8 types and many sub-types of the AD virus in Nova Scotia. Group 1 viruses are the most common types in Nova Scotia, and Group 2 viruses are 27 nucleotides shorter than the viruses in Group 1. The TR strain of the virus, which caused an outbreak of AD in Utah in the mid-1990s, and resulted in high mortality (a pathogenic strain) is also missing the same 27 nucleotides. This, however, does not mean that Group 2 viruses in Nova Scotia are pathogenic.

Sequence similarities between viruses within each of the 8 types ranged from 98.9% to 100%, indicating that they were very similar to each other. Sequence similarity among members of different types was as low as 96.1%.

On many ranches, more than one viral type was found, particularly on those ranches that have been infected for many years. Viruses on each of the newly infected ranches were similar to each other. It seems that the number of different viral types and sub-types on a ranch is a measure of the history of infection of the ranch.

Some mink were infected with more than one viral type or sub-type. The effects of this condition on the animals' response to infection are not known.

Comparison between local virus types and those in other parts of the world

It is difficult to compare the viral types in Nova Scotia with viral strains in other parts of the world whose DNA sequences have been published. This is because there are only a few AD viruses with complete or almost complete published sequences. Most published sequences are roughly 15% of the full length of this virus.

The following table shows percentage similarities between one virus from Nova Scotia

(from Group 1) and 11 published strains with at least 1900 nucleotides. Utah-1, Danish-K and TR are highly pathogenic, Pullman is moderately pathogenic and ADV-G is non-pathogenic. The Far East strain is from Russia and its virulence has not been reported.

The Nova Scotia virus had the highest similarity (97.5%) with the non-pathogenic ADV-G, and the lowest similarity with the highly pathogenic Danish-K (88.0%). Again, this does not say much about the pathogenicity of local strains.

Note that the similarity among Nova Scotia AD virus types was as low as 96.1%, while similarity between the Nova Scotia AD and several other strains (G, SL3, Utah-1, ZK8, TR) was more than 96.1%. We are trying to identify specific regions of the virus genome that can be used to best differentiate among different viral types and sub-types.

Table 1. Number of nucleotides overlap and percent similarity between one Nova Scotia AD virus sequence and 11 published AD virus sequences.

Strain	Nucleotide overlap	% similarity	Strain	Nucleotide overlap	% similarity
G	4410	97.5	TR	1944	96.8
SL3	4359	97.2	Far East	1941	94.5
Danish-ZK8	3455	96.8	United	2003	93.2
Utah-1	3454	96.7	Pullman	1944	91.3
Utah-1	2003	96.6	Danish-K	2003	88.0
Utah-1	4402	96.1			

Acknowledgements
Technical assistance of Ms. Priyanka Rupsinghe is gratefully acknowledged. The AD Research Program is financially supported by mink industry organizations (Canada Mink Breeders Association, Nova Scotia Mink Breeders Association, Fur Farmers of Canada Marketing Association, American Legend Cooperatives, North American Fur Auctions, American Mink Council, American Mink Farmers Research Foundation), Atlantic Innovation Fund of ACOA, Agriculture and Agri-Food Canada through the CARD Councils of Ontario, British Columbia and Nova Scotia (Agri-Futures Nova Scotia), and the Technology Development Program of the Nova Scotia Department of Agriculture. Constructive comments of Dr. Gordon Finley are greatly appreciated.

Hossain Farid
Department of Plant and Animal Sciences, Faculty of Agriculture, Dalhousie University.
e-mail: ah.farid@dal.ca
November 2012