Identification of the origin of an unknown Aleutian disease virus in Nova Scotia
A case study

The DNA sequence of a fragment of an Aleutian disease (AD) virus from a ranch in western Nova Scotia was used to identify its origin (let's call this virus AD-X). This virus was isolated from an infected mink on a ranch where clean mink were introduced a few months earlier.

Search of Genbank, the main depository of molecular information in the world, revealed that there were 327 published AD virus sequences (in September 2012). The AD-X overlapped with 111 of these sequences. It did not overlap with 226 sequences in Genbank, including 73 from Newfoundland and 32 from Ontario. The AD-X sequence was also compared with 104 AD viruses from 15 ranches in Nova Scotia. These viruses were sequenced in our laboratory, but the results have not been published yet.

The results showed that:

1- The AD-X sequence was different from most viruses outside North America, including 22 viruses from China (89.8% to 94.9% similarity), 9 from feral and wild mink from Europe (88.4% to 93.9% similarity), 4 viruses from Russia and Japan (87.4% to 91.0% similarity), and10 viruses from Ireland (91.4%-94.2% similarity). Nova Scotia is far from those places and has had little chance of viral transmission for a long time. It was concluded that any virus with less than 95% sequence similarity was not related to the AD-X.

2- The AD-X was not related to any of the 41 AD viruses from Ontario posted in Genbank, because similarities were lower than 95% (88.5% to 93.7%).

3- The AD-X was closest to some of the known viruses from the US and Europe, such as ADV-SL3, a low-pathogenic strain from Germany (98.3% similarity), the pathogenic TH5 (98.3% similarity), the non-pathogenic ADV-G (98.1% similarity), a virus from Finland (97.8% similarity), and the highly pathogenic ADV-TR (97.1% similarity). This virus was not, however, related to the pathogenic ADV-Utah (95.5% similarity) or mildly pathogenic ADV-Pullman (90.7% similarity).

4- The AD-X was most similar to all 104 samples from Western Nova Scotia (97.3% to 99.7%) than to any other virus sequenced to date. More specifically, the AD-X was almost identical (99.1% to 99.7% similarity) to 19 viruses from five ranches in western Nova Scotia (Nova Scotia-19). The AD-X ranch and these 5 ranches are located in very close proximity to each other (the same postal code). AD-X had 97.3% to 98.1% similarity with the other 85 viruses in Nova Scotia (Figure 1).

Conclusions:

Using published information and our sequence database, the origin of the unknown AD virus was pinpointed to an area which is a few square kilometer in size, located in Western Nova Scotia, and having a high ranch density.

Virus DNA profiling is a mature technology that can be used for monitoring the movement of the AD virus among ranches and between wildlife and ranched mink.

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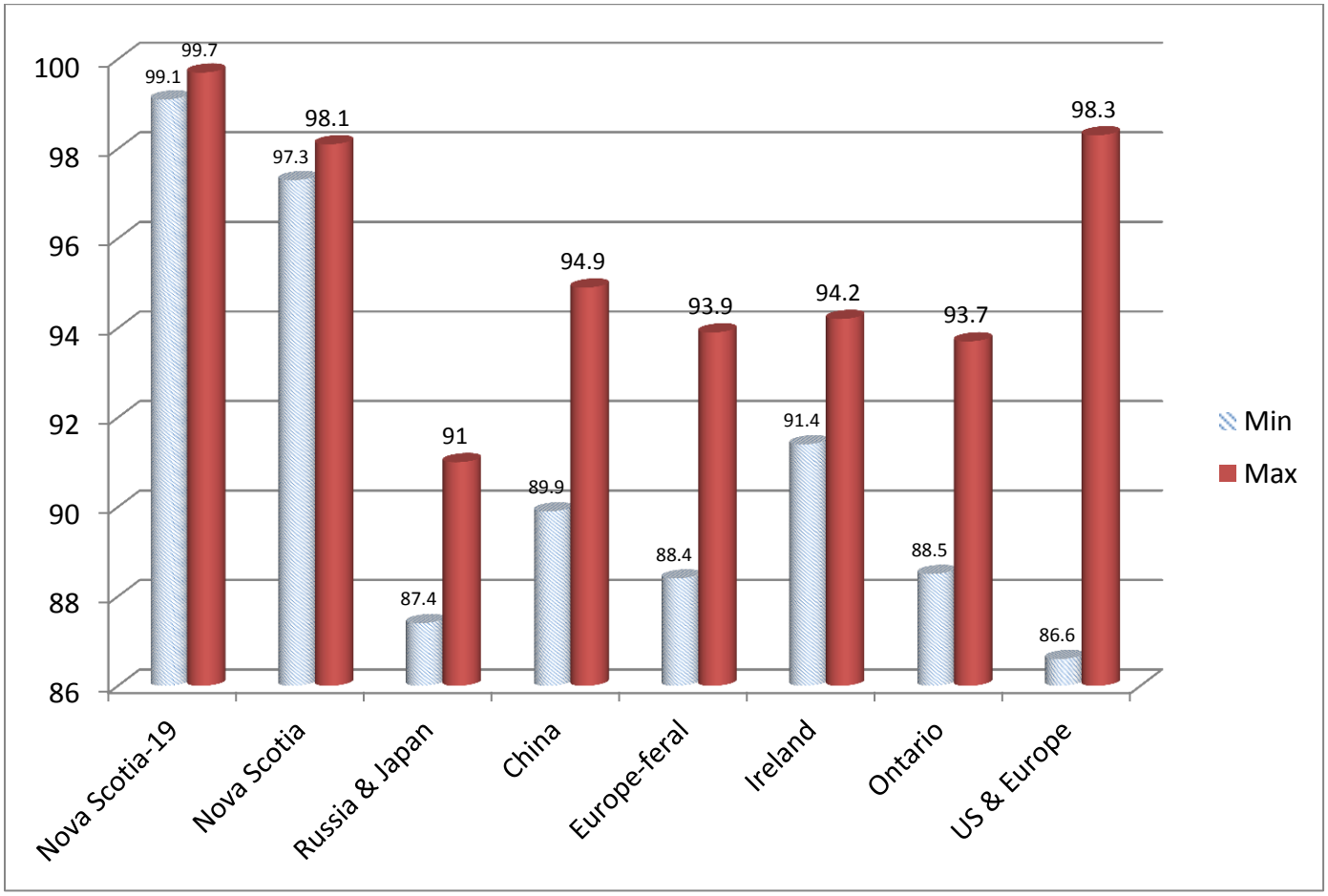

Percent of minimum (Min) and maximum (Max) similarity between the unknown AD virus from Nova Scotia and other AD virus groups