Identification of strains of mink Aleutian disease virus in Nova Scotia

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Aleutian disease (AD) is a serious health problem for the mink industry in Nova Scotia. The 4801 bp long Aleutian disease virus (ADV) genome displays a high degree of genetic variability, which has resulted in a proliferation of strains of ADV causing varying degrees of severity of the disease. To identify ADV strains, DNA was extracted from frozen tissues of mink that were positive according to Counter-immune electrophoresis. A 631 bp fragment of the highly variable portion of the viral genome that codes for the nonstructural NS1 protein was amplified by the polymerase chain reaction (PCR). PCR products from 22 mink from three neighboring ranches were bi-directionally sequenced. Two viral strains (ADV types I and II) were identified, which differed from each other at three positions on the PCR product, indicating 99.5% sequence similarity. These strains showed 96% sequence similarity with the highly pathogenic ADV-Utah, moderately pathogenic ADV-SL3, and the non-pathogenic ADV-G strain, but showed lower levels of similarity with the highly pathogenic ADV-United and Danish ADV-K strains (88.5% and 87.4% sequence similarity, respectively). These results show that the portion of the virus that was sequenced in this study is not a good indicator of the degree of virus pathogenicity. ADV type I was detected on ranches 2 (10 samples) and 3 (5 samples) while type II was detected only on ranch 1 (7 samples). Ranches 1 and 3 were infected in 1999, while ranch 2 was infected in 2001. It may be concluded that ranch 1 was not the source of virus on ranch 2, instead the origin of ADV on ranch 2 was other ranches, feral mink or other wild mammals. The results also suggest that viral strain identification is a powerful tool for epidemiology of the ADV on mink ranches.