

Co-Circulation of Highly Diverse Aleutian Mink Disease Virus Strains in Finland

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Aleutian mink disease virus (AMDV) is the causative agent of Aleutian disease (AD) that affects mink of all genotypes and also infects other mustelids like ferrets, martens and badgers. So far, the knowledge of Finnish AMDV strains has been restricted to small parts of virus genome mostly from newly infected farms, and the feral mustelids. Here, we studied the diversity and evolution of Finnish AMDV strains by sequencing complete coding sequences from 31 isolates from mink originating from farms with different history with the virus, as well as from feral mink. The data set was supplemented with partial genomes obtained from 26 isolates. Sequences show that the Finnish AMDV strains have great diversity compared to global strains, and that the virus has been introduced to Finland in multiple events. Mink in the wild carry viruses of high intra-host diversity suggesting that the feral mink tolerate the chronic infections for extended periods of time. Furthermore, we observed frequent recombination events, and variation in the evolutionary rate in different parts of the genome, as well as between different branches of the phylogenetic tree.