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Molecular epidemiology of Aleutian mink disease virus in China

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Aleutian mink disease virus (AMDV) is a parvovirus that causes an immune complex mediated disease in farmed minks worldwide. To obtain a more detailed understanding of the molecular epidemiology of mink AMDV in China, 18 of the 280 positive samples were randomly selected and analyzed. Samples were collected from 5 farms in 5 provinces in China. Near full length genome of AMDV from all the samples were amplified and sequenced. Phylogenetic tree based on full length *VP2* gene with 11 reference-isolates shows that AMDV strains formed five groups. While phylogenetic tree based on 328 bp partial NS1 gene with 128 reference-isolates shows that AMDV strains formed three groups. There are some unique Chinese amino acids. The molecular clock is not applicable to ADV, a number of recombination sites were detected in *NS1* gene. The results of the analysis suggested that both indigenous AMDV and imported AMDV were prevalent in the primary mink production areas in China.

Biography

Zhanglei has completed her PhD from Jilin University Heping Campus. She is currently an Associate Professor and Postgraduate Tutor of Institute of Special Wild Economic Animals and Plants, Chinese Academy of Agricultural Sciences. She is mainly engaged in fur animal disease including molecular epidemiological investigation and diagnosis products research work.

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