A new look at an old virus: Phylogenetic relationship between an Aleutian mink disease virus from Nova Scotia and global strains

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Infection with Aleutian mink disease virus (AMDV) causes economic losses to the multi-million-dollar mink industry in Nova Scotia (NS). There is no cure or vaccine for the disease and culling seropositive animals has not been effective in permanent eradication of the virus from many farms in NS. It is important to identify the sources of persistent infection or re-contamination of mink farms to develop strategies for controlling the virus. Sequencing of viruses on a farm, and comparing the sequences with existing sequence databases, is the only way to identify the source of contamination. The objective of this study was to find the phylogenetic relationship between one AMDV isolate from Cape Breton Island, NS (NS-CB), which has not been sequenced before, and the global strains. The NS-CB isolate originated from a farm which has been infected by AMDV for over 40 years. DNA was extracted from the spleen of one randomly selected mink from this farm. The entire coding region of the virus, from nucleotides 206 to 4349, was amplified by polymerase chain reaction (PCR) and sequenced by the Sanger sequencing method. NS-CB was compared with 14 global AMDV strains from North America, Europe and Asia, available on Genbank, which had the same sizes as the NS-CB isolate. Pairwise sequence identities were calculated by the Sequence Demarcating Tool (SDT) software, multiple sequence alignment was performed using Muscle program and phylogenetic analysis was performed by Mega7. The NS-CB isolate was the closest to the non-pathogenic AMDV-G, moderately pathogenic SL-3 from Germany and highly pathogenic Utah strain from USA. The four Chinese and four Newfoundland isolates were classified into different branches. It was concluded that the NS-CB isolate is different from the Newfoundland isolates, although they are the closest geographically, and that its pathogenicity could not be predicted from the nucleotide sequence of its entire coding region.

Speaker Biography

P P Rupasinghe has completed her BSc at the University of Peradeniya, Sri Lanka majoring Biology and Chemistry. After moving to Canada, she worked as a Research Assistant at the University of Guelph. During that time she has completed Certificate in Food Science Program of the University of Guelph. She has co-authored four peers-reviewed publications. Currently, she is a part-time Master's student and Research Assistant at Molecular Microbiology laboratory at Dalhousie University.

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