

# Genetic Variability of Bovine Viral Diarrhea Virus in Persistently Infected Cattle within Western Canadian Dairy Herds

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Bovine viral diarrhea virus (BVDV) is an economically significant pathogen among dairy herds in Canada. The primary transmitters of BVDV are persistently infected (PI) cattle, which do not produce an immune response towards the persisting strain and constantly shed large amounts of virus. Despite current management programs including vaccination and removal of PI cattle, BVDV continues to circulate in Canadian dairy herds. The current study aimed to identify herds with BVDV infections and collaborate with farmers and veterinarians to eliminate circulation of the virus from these herds. Furthermore, we aimed to describe the strains circulating within Western Canadian dairy herds and assess the role of PIs in the variability and evolution of BVDV.

A total of twenty dairy farms were screened for BVDV resulting in identification of ten PIs. Distribution of BVDV genotypes was consistent with other studies, as BVDV1b was the most prevalent, followed by BVDV1a. Two families of BVDV PIs were identified, enabling us to monitor viral evolution across multiple generations. Genetic analysis of viruses within PI families indicates that novel viral variants arise following transmission from the dam to the fetus. As viral populations diversify from the previous generations, it is possible that they will undergo unpredictable changes in pathogenicity, transmissibility, and response to vaccination.

Management of BVDV infection is dependent on elimination of persistently infected cattle. This study suggests that prolonged unmanaged BVDV infection on farms gives rise to new viral variants. Elucidation of the viral evolution of BVDV persistent infection is essential to develop better strategies to eliminate this impactful viral pathogen and decrease the economic burden on the Canadian dairy industry.