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## Ovine herpesvirus 2 (OvHV-2), the causative agent of sheep-associated malignant catarrhal fever

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Ovhv-2), is the causative agent of sheep-associated malignant catarrhal fever (SA-MCF), a generally fatal disease of cattle and other captive wild ruminants. Information on the Ovhv-2 strains circulating in South Africa (SA) and other African countries with regard to genetic structure and diversity, and pattern of distribution is not available. This study aimed to characterize the Ovhv-2 strains circulating in SA using selected genes encoding glycoproteins and tegument proteins. To establish the genetic diversity of Ovhv-2 strains, four genes, Ov 7, Ov 8 ex2, ORF 27 and ORF 73 were selected for analysis by PCR and DNA sequencing. Nucleotide and amino acid multiple sequence analyses revealed two genotypes for ORF 27 and ORF 73, and three genotypes for Ov 7 and Ov 8 ex2, randomly distributed throughout the regions. Ov 7 and ORF 27 nucleotide sequence analysis revealed variations that distinguished SA genotypes from those of reference Ovhv-2 strains. Epitope mapping analysis showed that mutations identified from the investigated genes are not likely to affect the functions of the gene products, particularly those responsible for antibody binding activities associated with B-cell epitopes. Knowledge of the extent of genetic diversity existing among Ovhv-2 strains has provided an understanding on the distribution patterns of Ovhv-2 strains or genotypes across the regions of South Africa. This can facilitate the management of SA-MCF in SA, in terms of introduction of control measures or safe practices to monitor and control Ovhv-2 infection. The products encoded by the Ov 7, Ov 8 ex2 and ORF 27 genes are recommended for evaluation of their coded proteins as possible antigens in the development of an Ovhv-2 specific serodiagnostic assay.

## **Biography**

Fulufhelo Amanda Doboro is currently working in Agricultural Research Council, South Africa

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