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## *In silico* epitope prediction and 3D model analysis of peste des petits ruminants virus nucleoprotein

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Peste des petits ruminants' virus (PPRV) is an acute, highly contagious viral disease of small ruminants. It is endemic to sub-Saharan Africa, Asia and the Arabian Peninsula. The disease is a major constraint to food security, causing significant economic losses to subsistence farmers in affected areas. The nucleoprotein of morbilliviruses is highly immunogenic and produced in large quantities in virus infected cells. This makes it a suitable target for the host's immune response. In this study, B-cell and T-cell epitopes of PPRV Nig/75/1 nucleoprotein were predicted using a suite of *in silico* tools. 46 T-cell epitopes were predicted, of which 38 were MHC-I binding while 8 were MHC-II binding. Of the 19 B-cell epitopes predicted, 15 were linear epitopes while 4 were discontinuous epitopes. Homology modeling of PPRV-N was done to elucidate the 3D structure of the protein and conformational epitopes. Conservation analysis of the discontinuous epitopes gave an indication into the similarity of the selected epitopes with other isolates of PPRV. Predicted epitopes may form an important starting point for serological screening and diagnostic tools against PPRV. Experimental validation of the predicted epitopes will assist in selection of promising candidates for consideration as antigen-based diagnostic tools. Such diagnostic tools would play a role in the global fight and possible eradication of PPR.

### Biography

Bakang Baloi is currently a PhD candidate in the Department of Biological Sciences at the University of Botswana, Botswana. His interests are in developing low cost vaccines and diagnostics. His current research aims to develop peptide-based veterinary vaccines.

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