ABSTRACT

Introduction: Peste de petits is an acute, highly contagious viral disease of the ruminant caused by ruminant virus (PPRV) which is a morbillivirus it mainly affect sheep, goats and other livestock. This study was aimed at predicting the most immunogenic epitopes- against PPRV using immune-informatics tools from two exterior immunogenic proteins hemagglutinin (H) and fusion (F) proteins The work involved determining the 3D models of PPRV hemagglutinin and fusions proteins and conducting an integrated in silico approach to predict both the B and T-cell epitopes. Epitopes predicted in this study are an important starting point for serological screening and diagnostic tools against PPRV.

Methods: PPRV proteins were retrieved from GenBank of the National Centre for Biotechnology Information (NCBI). Each protein from the retrieved sequences was aligned using the Clustal Omega program for conservancy. Transmembrane domains in the retrieved sequences were further evaluated using TMHMM server and were further evaluated in the SignalP-NN program. B and T cells epitopes were predicted from the retrieved sequences using the Immune Epitope Database (IEDB) analysis resource (http://www.iedb.org/bcell/. The criteria for identifying the B cell epitope was based on surface accessibility, epitope linearity and antigenicity. T cell epitope prediction for MHC class I (MHC1) was made using artificial neural networks (ANNs) based methods such as allele specific NetMHC. Prediction for T cells epitopes was based on the selection of 9mers cow alleles.

Results and Discussion:

The different structure and binding affinities of the two classes of MHC was exploited using different prediction tools to predict epitopes in two immunogenic proteins of PPRV, F and H. Analysis for MHC I epitopes prediction was done using cow alleles BoLA-D18.4, BoLAHD6, BoLA-JSP.1, BoLA-T2a, BoLA-T2b, and BoLA-T2c. H protein predicted more than 20 CTL epitopes but only epitopes that were binding multiple alleles and had strong binding based on the binding threshold (binding threshold <2%) were selected. One epitope was predicted as the best, $_{3}AQRERINAF_{11}$, since it was linked to three out of the four BoLA alleles. It was followed by $_{374}DLQNKGECL_{382}$ and $_{556}RLNFKGNPL_{564}$ with each being linked to two alleles. Fusion (F protein) predicted more than 20 CTL epitopes but only one epitope was predicted as the best, $_{343}ALYPMSPLL_{351}$, since it was linked to all the four BoLA alleles. It was followed by $_{53}KLMPNITA_{I61}$ and $_{161}RLANKETIL_{169}$ with each being linked to two out of the four alleles.

Conclusion:

Keywords: Keywords: *Peste de petits ruminant virus, transmembrane domains, epitope prediction, BoLA alleles*