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A Novel Epitope Prediction for Vaccine Designing against Ebola Viral Envelope Proteins

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Abstract : Viral proteins of Ebola viruses belong to one of the best studied viruses; however no effective prevention against EBOV has been developed. Epitope-based vaccines provide a new strategy for prophylactic and therapeutic application of pathogen-specific immunity. A critical requirement of this strategy is the identification and selection of T-cell epitopes that act as vaccine targets. This study describes current methodologies for the selection process, with Ebola virus as a model system. Hence great challenge in the field of ebola virus research is to design universal vaccine. A combination of publicly available bioinformatics algorithms and computational tools are used to screen and select antigen sequences as potential T-cell epitopes of supertypes Human Leukocyte Antigen (HLA) alleles. MUSCLE and MOTIF tools were used to find out most conserved peptide sequences of viral proteins. Immunoinformatics tools were used for prediction of immunogenic peptides of viral proteins in zaire strains of Ebola virus. Putative epitopes for viral proteins (VP) were predicted from conserved peptide sequences of VP. Three tools NetCTL 1.2, BIMAS and Syfpeithi were used to predict the Class I putative epitopes while three tools, ProPred, IEDB-SMM-align and NetMHCII 2.2 were used to predict the Class II putative epitopes. B cell epitopes were predicted by BCPREDS 1.0. Immunogenic peptides were identified and selected manually by putative epitopes predicted from online tools individually for both MHC classes. Finally sequences of predicted peptides for both MHC classes were looked for common region which was selected as common immunogenic peptide. The immunogenic peptides were found for viral proteins of Ebola virus: epitopes FLESGAVKY, SSLAKHGEY. These predicted peptides could be promising candidates to be used as target for vaccine design.

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