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Multi epitope peptide vaccine prediction against Sudan ebolavirus using immuno-informatics approaches

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Cudan ebolavirus is single stranded negative sense RNA genome belonging to filovirus Filoviridae family that causes hemorrhagic Ofever. There is no treatment or vaccine for it, thus the aim of this study is to design a peptide vaccine using immunoinformatics approaches to analyze the glycoprotein of the all strain of SUDV, to determine the conserved region which is further studied to predict all possible epitopes that can be used as a peptide vaccine. A total of 21 Sudan ebolavirus glycoprotein retrieved from NCBI database were aligned to determine the conservancy and to predict the epitopes using IEDB analysis resource. Three epitopes predicted as a peptide vaccine for B-cell (PPPPDGVR, ETFLQSPP and LQSPPIRE). For T-cell four epitopes showed high affinity to MHC class-I (FLYDRLAST, IIIAIIALL, MHNQNALVC and RTYTILNRK) and high coverage against Sudan and the whole world population. Also in MHC class-II, Four epitopes that interact with most frequent MHC class-II alleles (FAEGVIAFL, FLRATTELR, FLYDRLAST and FVWVIILFQ) with high coverage against Sudan and the whole world population. We recommend in vivo and in vitro study to prove the effectiveness of these predicted epitopes as a peptide vaccine.

Biography

Ahmed Hamdi Merghani Elmahadi Abu-Haraz has completed his Bachelor of Pharmacy from Elrazi University and Master's degree from Sudan Academy of Science, Africa City of Technology, Department of Industrial Biotechnology, He is a responsible Pharmacist at Hamdi Abu-Haraz Pharmacy.

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