

12th Asia Pacific Global Summit and Expo on

Vaccines & Vaccination

November 24-25, 2016 Melbourne, Australia

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

Ahmed Hamdi Abu-Haraz¹, Khoubieb Ali Abd-elrahman², Mojahid Salah Ibrahim², Waleed Hassan Hussien², Mohammed Siddig Mohammed¹, Marwan Mustafa Badawi¹ and Mohamed Ahmed Salih¹

¹Africa City of Technology, Sudan

²University of Medical Science and Technology, Sudan

Sudan ebolavirus is single stranded negative sense RNA genome belonging to filovirus Filoviridae family that causes hemorrhagic fever. 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, ETFLQSP 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, FLRATTELRL, FLYDRLAST and FVWVILFQ) 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 Abu-haraz has passed the final exams of his master programm and he is waiting for the discussion of his dissertation.

dr.ahmedabuharaz@gmail.com

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