

NAME OF THE THEME: Medical, Health & Pharmaceutical Sciences

Exploring genome of Ebola Virus to construct multi-epitope based subunit vaccine using Bioinformatics approach.

Ajinkya Kadam[#], Santanu Sasidharan, Shweta Raj, Prakash Saudagar^{*}

Department of Biotechnology, National Institute of Technology Warangal, 506004, Telangana, India.

^{*}Corresponding Author

[#] Presenting author

Abstract: - It is assumed that fruit bats of the Pteropodidae family are natural Ebola virus (EBOV) hosts. EBOV causes severe bleeding, organ failure and can lead to death. This investigation depicts the use of the integrated immunoinformatics techniques for development of a multi-epitope subunit vaccine using the structural and non-structural proteins of the EBOV. The designed vaccine consists of Cytotoxic T lymphocyte (MHC-I) and Helper T lymphocyte (MHC-II) epitopes ushered with β -defensin and suitable linkers by NetCTL and IEDB online tools respectively. The existence of humoral immune response specific to B-cell and IFN- γ epitopes were rooted by B-cell mapping among designed vaccine using BCpred and CRDD servers respectively. The constructed vaccine was characterized for its antigenicity, allergenicity and physiochemical factors by using AllerTOP and AlgPred online tools. The results were predicted to be safe and immunogenic in nature. Modelling of the designed construct was performed using ITASSER online tool. Further the generated model was validated using PROCHECK and RAMPAGE servers. Above mentioned techniques results in the multi-epitope subunit vaccine which may have the competence to develop the humoral and also cellular immune response against EBOV. This designed multi-epitope subunit vaccine further requires experimental studies to address its vaccine potentiality.

Keywords: *Ebola virus, Immunoinformatics, Multi-epitope, Vaccine.*

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