NAME OF THE THEME: Medical, Health & Pharmaceutical Sciences

Development of B-and T-cell multi-epitope based subunit vaccine for Zika virus by immunoinformatics tools.

Aayushi Mittal[#], Santanu Sasidharan, Shweta Raj, and Prakash Saudagar^{*}

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

*Corresponding Author

Presenting author

Abstract: -The rapidly proliferating Zika virus, through the *Aedes* mosquito is the cause of various birth defects including Microcephaly and it has also been linked to Guillain-Barren Syndrome. As of today, there is no vaccine available for Zika Virus. Therefore, in this study we developed a multi-epitope subunit vaccine for the Zika virus using immunoinformatics approach. The construct was designed using three structural and one non-structural proteins present in Zika Virus. Cytotoxic T-lymphocyte (CTL) [MHC1] and Helper T-lymphocyte (HTL) [MHC2] epitopes were predicted by NetCTL and IEDB online tools respectively and linked along with β defensin with compatible linkers. Further B cell epitope and IFN-y mapping were performed using BCpred and CRDD servers respectively, to confirm the elicitation of humoral immune response. The antigenicity and allergenicity of the designed construct were verified by using AllerTOP and AlgPred online tools. In addition to this, physiochemical parameters were validated thereby marking it safe for utilization in humans. The design construct was then modelled using ITASSER server and the best model was identified using PROCHECK and RAMPAGE servers. Therefore, this developed subunit vaccine may be capable of eliciting an immune response in humans and further experimental studies are required to verify the feasibility of the multi sub-unit construct as a vaccine.

Keywords: - Immunoinformatics, Multi-epitope, Vaccine, Zika Virus

 $oldsymbol{Paper\ ID}$ (To be added by Programme Committee)