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Utilizing capsid proteins of Poliovirus to design multi-epitope based subunit vaccine by immunoinformatics approach

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Abstract: - Poliomyelitis, a disease caused by a poliovirus which has already disabled millions of people across the globe by walking. The vaccines used for polio are live attenuated oral polio vaccine (OPV) and inactivated polio vaccine (IPV). Recently, In India the relapse of virulence was observed in attenuated viruses resulting in adverse effects, development of multi-epitope subunit vaccine can be an alternative to overcome this drawback. Therefore, this study illustrates the use of computational and immunoinformatics approach to design a multi-epitope based subunit vaccine. Capsid proteins of all the three types of polio strains were utilized to predict major histocompatibility complex (MHC) class-1 as well as class-2 epitopes using NetCTL and IEDB online tools respectively. The subunit vaccine was designed with β-defensin at N-terminal followed by cytotoxic T-lymphocytes (CTL) epitopes and helper T-lymphocytes (HTL) epitopes connected by compatible linkers. B-cell and IFN-γ epitopes were then predicted from the constructed vaccine using BCpred and CRDD servers respectively. Allergenicity, antigenicity and physiochemical parameters were checked and the design was found to be safe for use. The construct was then modelled using ITASSER online tool and validated using PROCHECK and RAMPAGE servers. This designed multi-epitope subunit vaccine may have the potential to replace live attenuated vaccines. Further experimental investigation and immunogenic studies will help us understand the feasibility of this multi-epitope subunit vaccine.

Keywords: - *Immunoinformatics, Multi-epitope, Poliovirus, Vaccine.*

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