Chimeric multi-epitope vaccine against Mayaro virus: An immunoinformatic approach

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ABSTRACT

Mayaro virus is a mosquito-borne zoonotic pathogen endemic. The virus can cause an acute, self-limited dengue-like illness of 3-5 days. It comes under the family of Togaviridae in the genus of Alphavirus. This virus has similarities with the agents of other more prominent disease like dengue, Zika (*Flaviviridae*), chikunguniya (Togaviridae). A reverse vaccinology strategy was applied to the core proteins to identify the antigenic proteins. The two antigenic proteins were nonstructural polyprotein and togavirin. VaxiJen v2.0 server was used to predict the antigenicity of these proteins. The antigenic proteins were screened for B cell epitopes using ABCpred server. Potential MHC 1 and MHC 2 epitopes were analyzed using NetMHC and NetMHC2 servers. The screened epitopes were analyzed for allergeneicity using Algpred server and Toxicity of the peptides were analyzed using Toxinpred server. The screened peptides were screened for their signal peptide cleavage sites using SignalP 4.1 Server and transmembrane helices using TMHMM Server v. 2.0. The shortlisted peptide candidate was then checked for their parameters using ProtParam tool in Expasy server. Solubility was estimated using Solpro server. 3D structure of peptide was designed, validated and refined to obtain high quality structure. From the selected peptides, a chimeric vaccine was developed by linking the peptides with GPGPG linker to cholera toxin B subunit. The vaccine was modelled by I-Tasser and refined by Galaxy refine server and validated using Ramachandran plot. The properties of the chimeric vaccine was also analyzed. Reverse translation was carried out using JCAT tool for expression in E.coli.

Keywords: Mayaro virus, Immunoinformatics, peptide, vaccine, epitope mapping

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