ABSTRACT

Streptococcus pneumoniae is thriving as a major health problem even after the use of different vaccines. The need of the hour is to develop such vaccines that can efficiently stimulate protective immune response and decreases the disease burden. Reverse vaccinology (In-silico computer-aided technique) was used to screened hypothetical proteins to identify the novel protein-based vaccine candidates against *Streptococcus pneumoniae*. The 351 hypothetical proteins of *Streptococcus pneumoniae* D39 strain obtained from the NCBI server were analyzed. Nine of these proteins showed the good results and were predicted to be efficient candidates for the vaccine. Five proteins were predicted to possess conserved domain regions. These conserved domains can effectively elaborate the function of these proteins. Function prediction was also performed using other tools such as HHpred. Function predicted by HHpred was similar to the conserved domain predicted using CDD. Physicochemical analysis of selected proteins was performed due to their hypothetical nature. Selected proteins also presented to both classes of MHC (I and II). All the proteins were bound with several alleles of both classes of MHC (II and II). Virulence analysis was performed that revealed that all the selected proteins were the virulence factor of bacteria. Conservancy analysis was also performed to select the vaccine candidates conserved across most of the strains if not all to overcome the vaccine limitation associated with serotype specificity. Finally 5 proteins WP_010976578.1, WP_000829085.1, WP_000694288.1, WP_000266233.1 and WP_000781030.1 predicted to serve as potential vaccine candidates. Another method of peptide-based vaccine candidate identification was also used. A strict criteria of the peptide-based vaccine such as B-cell epitopes prediction and then T-cell epitopes from predicted B-cell epitopes and allergenicity, immunogenicity and TAP binding affinity analysis was performed. Good water solubility and other good experimental properties were also checked. Finally, two epitopes were selected and their docking simulation was performed. These two epitopes and 5 proteins possess ideal characteristics such as being extracellular or transmembrane in nature, antigenicity and being non-homologous to human proteins and non-allergic proteins. These peptides and proteins were predicted as probable vaccine candidates to improve existing vaccines either by replacing existing vaccines or became the part of them.