عنوان مقاله:

POLYTOPE VACCINE DESIGN AGAINST STREPTOCOCCUS PNEUMONIAE AND INFLUENZA VIRUS: AN IN SILICO APPROACH

محل انتشار:

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خلاصه مقاله:

Background and Aim:Based on limitations about current vaccines for respiratory pathogens: Streptococcus pneumoniae and Influenza virus, more effective, conserved, cost-affordable and population-specific vaccination approaches are needed. Methods: Several virulence proteins were chosen from Influenza virus and pneumococcus based on their function and role during infection. Their amino acid sequences were retrieved from UniProtKB database, then were exploited to epitope prediction. For prediction of linear B-cell epitopes Kolaskar and Tongaonkar antigenicity method in IEDB server was applied. T-cell epitopes were determined among MHC I and II binding predicted peptides with higher scores for selected mice MHC alleles. Chosen epitopes were linked together with proper linkers. SOLpro was used to determine solubility of constructs upon overexpression in E. coli. Their antigenicity and allergenicity was estimated by ANTIGENpro and AlgPred predictors. Secondary structures were predicted with PSIPRED program. Tertiary structures prediction was done by Swiss-model and Phyer2 servers. Cluspro2.0, the protein-protein docking web server, was applied for study of the interactions between epitopes and MHC molecules.Results:Based on various bioinformatics servers it is shown that the polypeptide constructs have ideal features to be cloned and expressed in a proper E. coli host and then used as a vaccine in animal experiments. Designed polytopes are immunogenic antigens and are not allergens; and are soluble upon overexpression. Results from Cluspro2.0 server, demonstrated the high binding affinity (docking scores) between epitopes and MHC molecules. Conclusion: By help of immunoinformatics tools, we have designed two polytope constructs which can be .used together as bivalent intranasal vaccine against two mentioned serious pathogens

کلمات کلیدی:

Streptococcus pneumoniae, Influenza virus, Vaccine, Immunoinformatics

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