1162

Designing multiepitope subunit vaccine for *Mycobacterium tuberculosis*: Immunoinformatic approach

T. Senbadejo[1,*], T. Ganiyu[2], E.K. Oladipo[3], O. Onile[4]

[1] *Fountain University, Osogbo, Microbiology, Osogbo, Nigeria*
[2] *Fountain University, Osogbo, Osogbo, Nigeria*
[3] *Adeleke University, Ede, Osun State, Nigeria, Microbiology, Ede, Nigeria*
[4] *Elizade University, Ondo, Nigeria*

Background: Tuberculosis is the most common cause of death among adults in the most economically age groups and immune-compromised patients. Increase in transmission of *Mycobacterium tuberculosis* strains with drug resistance has complicated tuberculosis control and continue to pose a challenge to global public health. *Mycobacterium tuberculosis* has recently proved to stimulate strong humoral immunity against adhesin such as hsp70. Vaccination is an effective means of protection and prevention of spread of vaccinable preventable diseases. Bacillus Calmette–Guérin vaccine is the currently the only vaccine used to protect against tuberculosis, hence the need to design more effective vaccines that will protect adults and immunocompromised patients.

Methods and materials: Proteins used in this study were retrieved from the NCBI database. The tools used for the design of the vaccine include AntigenPro server for antigenicity prediction, NETCTL server for CTL epitopes, and IEDB server for HTL epitopes. AAY and GPGPG were used to link both suitable CTL and HTL epitopes respectively while EAAK was used as adjuvants. Protparam server was used to compute the physiochemical parameters of vaccine construct. Allergenicity was predicted using Allertop v2.0. Vaccine 3D model and tertiary structure was predicted using RaptorX server and later refined using the Galaxyrefine server.

Results: The proteins used for the vaccine construct were found to be antigenic as predicted by ANTIGENpro having a score of ≥0.8. A final vaccine construct of 447 amino acids residues was designed using 20 CTL and 10 HTL epitopes. The allergenicity test showed the vaccine protein is non-allergenic in nature and safe for human use. The instability index and aliphatic index were given to be 27.76 and 83.53 respectively which classifies the protein to be thermostable. The estimated half life in mammalian reticulocytes was given as 4.4 h in-vitro.

Conclusion: The designed vaccine construct is stable, immunogenic with high antigenic properties, non allergenic in nature and safe for human use. Designing multiepitope subunit vaccine using Immunoinformatics approach shows that it is feasible to produce effective vaccines against tuberculosis and save millions of lives from being lost every year.

https://doi.org/10.1016/j.ijid.2020.09.1251

1163

Conformational epitopes of thioredoxin as potential vaccines for lymphatic filariasis

M. Jayaprakasam[1,*], P. Prabhu[2], P. Kaliraj[3]

[1] *Indian Council of Medical Research, Division of Epidemiology and Communicable Diseases, New Delhi, New Delhi, India*
[2] *Anna University, Department of Biotechnology, Chennai, India*
[3] *Anna University, Centre for Biotechnology, Chennai, India*

Background: Lymphatic filariasis (LF) is a neglected tropical disease (NTD) that threatens nearly half of the endemic population in India. India accounts for 40% of the world's LF burden. Currently, there may be up to 31 million microfilaraemics, 23 million cases of symptomatic filariasis, and about 500 million individuals at risk of contracting the disease. As per the WHO report, currently, 886 million people in 52 countries are living in areas that require preventive chemotherapy. The national health policy had aimed at eliminating filariasis in India by 2020, which had failed its target. Although vaccines for parasitic diseases like lymphatic filariasis still remains a challenge, new technological advances and computational biology can be exploited to develop and test promising vaccine targets.

Methods and materials: In this study, systematic epitope mapping of key vaccine target thioredoxin using *in-silico* prediction tools identified potential B and T cell epitopes. The conformational epitopes were predicted using computational modelling and confirmed by thioredoxin activity based assay. An array of epitope peptides were synthesized by solid phase peptide synthesis and different constructs were made using combination of conformational epitopes. The peptide constructs were tested for their immunogenicity in mice models for humoral and cellular immunity by various immunoassays. The immunogenic peptides were further tested in Filarial animal model (*Mastomys coucha*) for protection against experimental filariasis.

Results: Two potential B cell epitopes from thioredoxin were identified as conformational epitopes. The combination of these epitopes showed greater immunogenicity in mice and induced a titer of 10,000. The conformational epitope construct induced Th2 cytokines IL4 and IL5 and showed significantly high protection of ~70% protection in Mastomys models compared to controls.

Conclusion: Our results showed that the approach was successful in targeting key conformational epitopes and thus could become a model for other neglected parasitic diseases

https://doi.org/10.1016/j.ijid.2020.09.1252

1164

Intention of receiving nasal spray influenza vaccine among unvaccinated nurses

C.P. Chan*, N.S. Wong, S.S. Lee

The Chinese University of Hong Kong, Stanley Ho Centre for Emerging Infectious Diseases, Hong Kong, China

Background: In preparation for the 2018–2019 influenza season, US Centers for Disease Control and Prevention (CDC) updated its recommendation on the use of a nasal spray vaccine, a live attenuated influenza vaccine (LAIV), for individuals aged 2–49 years. This study aimed at evaluating the intention of previously unvaccinated