Excavating chikungunya genome to design B and T cell multi-epitope subunit vaccine using comprehensive immunoinformatics approach to control chikungunya infection

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Background

Chikungunya virus (CHIKV) is a mosquito borne alphavirus belongs to togaviridae, which affects millions of people living in Africa, Europe Asia and South American continent. Infection caused by this virus in human is characterized by the high fever, rash and arthritis which may persist for the longer duration. Available therapy is not sufficient to eradicate the spread and dynamics and CHIKV infection in human. To prevent the dynamics of CHIKV infection, there is an urgent need to develop an efficient vaccine which can develop a strong humoral as well as cell mediated immune response.

Methods

Here, we have implemented protein structure based strategies to design multi-epitope subunit vaccines against CHIKV. For this study, we took 5 non-structural protein sequences to generate B and T cell epitopes by using T cell (http://margalit.huji.ac.il/Teppred/mhc-bind/index.html) showing MHC class I representation and (PROPRED) for MHC class II representation, B cells (DISCOTOPE and BCEPREDS software) specific software. Later on, isoelectric point, molecular weight was determined and to confirm the localization, proteins were subjected to TARGET P1.1. Further linkers were attached to make final vaccine protein. We performed molecular docking & molecular dynamics against TLR-3 receptor to develop thermostable and most flexible regions of the protein for disulphide engineering by using GROMACS.

Results

Helper and cytotoxic T lymphocytes epitopes were identified and were linked with linker generate a final vaccine molecule. Molecular modelling was performed to get the stable structure of final protein molecule. Ramachandran plot also confirms the stable nature of protein. Finally prepared vaccine has shown good binding scores against TLR-3 ligand during molecular docking experiment. Molecular dynamics experiment also confirms the interaction between multi-epitope vaccine and TLR-3 ligand which also confirms the targeted delivery in host lymphocytes. Finally, we identified multi-epitope protein which was safe and best immunogenic to develop the protection against CHIKV infection.

Conclusions

Vaccination is a well stablished preventive strategy to control the vector borne diseases. We believe that this immunoinformatics based generated vaccine will be able to control the transmission dynamics of CHIKV infection by generating effective immunological memory.