

Analysis and distribution of CD4⁺ multi-intent epitope candidates against flaviviridae family

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The Flaviviridae are a family of viruses that are primarily spread through arthropod vectors (mainly ticks and mosquitoes). The major diseases caused by the flaviviridae are Dengue fever, Japanese encephalitis, St. Louis encephalitis, Tick-borne encephalitis, West Nile encephalitis, Yellow fever. The current concept discusses the approach of T- lymphocyte epitope based vaccine. In cell mediated immune response, T cells play an important role by targeting internal proteins common to heterologous viral strains. Envelope protein sequences of Flaviviridae family were selected for T-cell epitope prediction. Entropy based analysis of the envelope sequences of Flaviviridae family was done to check the degree of variability of the peptide and to infer the evolutionary stability. In-silico approaches were used to predict and analyze proteome promiscuous Helper T Lymphocytes (HTL) epitopes for Flaviviridae family. The approach of peptide-based vaccine holds several advantages over traditional vaccines, which include the possibility of preparing multi-pathogen vaccine. Population coverage analysis was employed to determine the fraction of individuals expected to respond to a given set of epitopes. The predicted epitopes may provide the support for serodiagnosis or as protective peptide immunogen in novel vaccine design against Flaviviridae family.

Biography

Bhawna Rath has completed her PhD work from SGPGI, Lucknow. She has been into research for 8 years. She has 6 international publications and attended many national and international conferences. Working as Assistant Professor at Amity University, India.

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