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T-Cell Epitope Prediction Of Dengue Virus (DENV) Non-Structural-1 (NS1) Gene Using RANKPEP Prediction Tools

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Structured Abstract

Background: Dengue virus (DENV) is a mosquito transmitted *flavivirus*, which remains a major health risk to the population especially in the southeast of Asia. The four serotypes of DENV 1 to 4 make the task of developing a vaccine more complicated since there is no cross serotype immunity.NS1 is a non-structural protein and play an important role in viral replication and immune modulation. Therefore, NS1 is an excellent target of development of T-cell based vaccines. It is important to determine conserved T-cell epitopes in all dengue serotypes hence designing a highly protective anti-dengue vaccine.

Methods: In this analysis, the immunoinformatics methodology was used in predicting T-cell epitopes based on the NS1 protein of DENV 1 to DENV 4. Protein sequences of NS1 were obtained in FASTA format and analysed by the RANKPEP prediction tool to recognise the possible major histocompatibility complex (MHC) Class I and Class II epitopes. The selected human leukocyte antigen (HLA) alleles analysed were specific to Southeast Asia which is Malaysia, Myanmar, Thailand, Indonesia, Philippines and Vietnam. Epitopes that were predicted were ranked according to RANKPEP scores with only high sequence conservancy of 80 to 100% being selected to proceed with further analysis and WebLogo 3.0 was used to visualise the sequence conservation.

Results: A total of 48 NS1 protein sequences from DENV 1 to DENV 4 were successfully retrieved from the databases. The number of these epitopes suggested high sequence conservation between DENV 1 and DENV 4 and were linked to several HLA alleles. WebLogo analysis established that there was a good preservation of amino acid residues in the chosen epitopes and this means that they can be recognised by cells in all strains of dengue.

Conclusion: To summarize, this paper was able to identified conserved T-cell epitopes that may cause cross serotype immune response. These results justify the possibility of the identified epitopes of T-cell based on dengue vaccine and are a basis to further experimental validation and population coverage.

Keywords: Dengue Virus, Reverse vaccinology, NS1 protein, T-cell Epitopes.

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