Controlling the Chikungunya Virus Disease in Dengue Endemic Areas through the Development of a Peptide Vaccine

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The Chikungunya and Dengue viruses are arboviruses transmitted by the mosquitoes Aedes aegypti and Aedes albopictus. Co-circulation of Dengue and the Chikungunya virus (CHIKV) make it difficult to distinguish between the two diseases. As both cause febrile symptoms in the initial stages of infection, CHIKV is often masked and misdiagnosed as Dengue in Dengue endemic areas. This misdiagnosis affects how the symptoms of each disease are treated. This study targets the non-structural protein 2, nsP2, of CHIKV which has peptidase and helicase functions. nsP2 plays an important role in viral replication, the cleavage of the viral non-structural polyprotein, and inhibiting the protective immune response in the host cell. Thus, epitopes in nsP2 are ideal for a peptide vaccine. In this study, potential cytotoxic (CD8) T cell epitopes in nsP2 that will elicit an immune response are determined through an immuno-informatics approach. To test the accuracy of the procedure, the structural polyprotein of the Ross River virus, an alphavirus like CHIKV, is used as a control. Out of the top 82 CD8 T cell epitopes identified, three novel epitopes are selected. These epitopes are highly immunogenic, show maximum binding to MHC Class I alleles, and are conserved in 99 strains. For the first time, a population coverage analysis is done on these epitopes by analyzing their binding ability to 1,089 MHC Class I alleles. The development of a vaccine for Dengue is difficult because of its multiple serotypes and antibody-dependent enhancement of infection. As far as is currently known, all strains of Chikungunya belong to a single serotype. Therefore, an effective vaccine against CHIKV can help clinical management in CHIKV and Dengue endemic areas.

Awards Won:

Third Award of $1,000