

Determining Vaccine Protection Potential for Dengue Virus Serotype 1: A Comparative Descriptive Study of Non Structural Protein I

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Background/Objective

In the last two decades, numerous researches have been conducted to identify non structural 1 (NS1) protein epitopes of dengue virus (DENV) as potential vaccine targets. However, most of the studies analyze only some limited number of strains thus it can not represent the true distribution of the identified epitopes on the field. This study aims to compare whether the identified epitopes are still conserved within various strains collected from different genotypes and geographical areas.

Method

Twenty nine representative samples were analyzed in this study. Twenty two complete genome of DENV-1 nucleotide sequences were collected from GenBank with 5 additional samples were obtained from Goncalvez et al. as genotype reference and 2 more samples collected from Laboratory of Microbiology, Faculty of Medicine, Universitas Indonesia. All of the nucleotide sequences were converted to amino acid sequences and homologized at 11 identified epitopes using Genetyx 5.1.

Result

From 11 epitopes identified, four of them having in average of 6 samples with substituted amino acid sequences while the 7 remaining epitopes stay conserved in all of the 29 samples. If the genotypes were rank due to the numbers of substituted samples they contain, genotypes I will be the first which contains most of the substituted samples, followed by genotype V, genotype IV, and genotypes II being the least.

Conclusion

Most of the identified NS1 DENV-1 epitopes are still conserved within various strains from different genotypes. Thus, vaccines that targets these conserved epitopes are able to protect different strains from various genotypes. However, substituted epitopes deserved further investigation whether these epitopes are still effective as vaccine targets.