Genetic Analysis of Non-structural Protein-1 (NS1) Dengue Virus Serotype 2 Strain Indonesia and Its Comprasion to Strain from Different Geographical Area

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Background/Objective
Studies about genetic characteristic between dengue virus serotype 2 (DENV-2) sequence data is needed to determine its relationship between DENV strain over the world due to limited studies about NS1 DENV gene analysis and its important role during pathogenesis of any stages of DENV infections. The main purpose of this study is to compare between characteristic of sequence data DENV-2 envelope nucleotide and sequence data DENV-2 Non-Structural 1 (NS1) nucleotide, and analyze between amino acid homology in this study and related previous studies.

Method
35 data used for this study are obtained from Laboratory of Microbiology Faculty of Medicine University of Indonesia for data from Indonesia and from GenBank for some data from Indonesia which is obtained from another institutions in Indonesia and from different countries as comparison. Those data are analyzed with software Genetyx 5.1, focused on homology analysis of envelope nucleotide gene, NS1 nucleotide gene, and amino acid gene for   DENV-2.

Result
NS1 sequence data from DENV-2 strain from Indonesia is classified in Cosmpolitan genotype group, which are similar than data analysis from envelope sequence data from same data. Meanwhile in analysis of LX1 epitope, which is considered as typical epitope from NS1, there are any differences in amino acid component at it compared than strain Indonesia data sequences which are included in Cosmopolitan genotype group.

Conclusion
Phylogenetic analysis of NS1 nucleotide gene strain Indonesia is useful for determining the genotypes compared to strain from different geographical area, as it comes possibility that NS1 DENV-2 gene strain Indonesia can be useful for vaccine development. Further studies is needed to explain whether any differences of LX1 epitope give any significant meaning in changes of NS1 DENV conserved area