

Role of 3' UTR and 5' UTR in Phylogenetic Analysis of DENV-2: A Comparative Descriptive Study

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Background/Objective

Current phylogenetic study of dengue virus serotype 2 (DENV-2) uses only whole envelope as the basis of phylogenetic analysis. On the other hand, study conducted by Shurtleff et al supports the potential of using untranslated region (UTR) for this purpose. The aim of this study is to compare the phylogenetic of DENV-2 based on whole envelope, 3' UTR, and 5' UTR.

Method

Three complete genome DENV-2 sequences collected from Laboratory of Microbiology, Faculty of Medicine Universitas Indonesia and additional twenty six complete genome DENV-2 sequences obtained from GenBank were analyzed. Phylogenetic analysis was performed by Genetyx 5.1. Publication from Wu et al was used as the reference to determine genotype.

Result

Envelope-based phylogenetic analysis shows that DENV-2 are grouped into five genotypes. This grouping shares several similarities compared to 5' UTR or 3' UTR-based phylogenetic analysis. However, analysis using 5' UTR was only able to completely distinguish the America and Cosmopolitan genotype. This happens because exclusive mutations occur in both genotype and are not found in the rest of genotype. Analysis based on 3' UTR are able to distinguish genotypes better compared to 5' UTR. However, most genotypes are separated to two or three branches. The presence of highly variable domain I of 3' UTR may explain this phenomenon.

Conclusion

UTR cannot be utilized solely as the basis of phylogenetic analysis of DENV-2. However, the result of this study indicates the possibility of using substructure of UTR such as domain II and domain III of 3' UTR for phylogenetic analysis. Further studies are needed to investigate this.