

Sequence and Phylogenetic Analysis of UTR Dengue Virus Serotype-1 Strain Indonesia for Molecular Epidemiology

Paulina Tandijono^{1*}, Beti Dewi¹

¹ Faculty of Medicine University Indonesia

Background/Objective

Similar to other flavivirus, dengue virus (DENV) has untranslated region (UTR) that initiates virus replication through cyclization mechanism. This region supposed to be conserved. However, UTR also prone to mutation. This UTR mutation could be used to describe DENV molecular epidemiology. This research was aimed to describe molecular epidemiology of DENV serotype 1 in Indonesia based on UTR sequences.

Method

This research used 26 strains of DENV-1. Two Indonesian strains (98901518 dan 98901530) were taken from Universitas Indonesia Faculty of Medicine Microbiology Laboratory. Other strains were taken from Genbank. Phylogenetic analysis was done using Genetyx 5.1 program.

Result

Each strain genotype was determined based on envelope. Both Indonesian strains belong to genotype 4. Because there was limited number of strains in Genbank, UTR 5' phylogenetic was created from 58 nucleotides, while UTR 3' was made from 180 nucleotides. In UTR 5', DENV-1 strains arranged randomly and did not match transmission pattern. There were mutations in both Indonesian strains that occur in 79th nucleotide (A → G). Moreover, 89th nucleotide also mutated in Indonesian 98901530 strain. (U → G). While in UTR 3', all strains had been arranged according to their own genotypes. However, kinship between genotypes was different. Both Indonesian strains were located closely to Pacific Islands strains (Nauru Island and French Polynesia).

Conclusion

UTR 3' phylogenetic showed familiarity between Indonesian and Pacific strains, while UTR 5' phylogenetic unusable in describing molecular epidemiology.