

ABSTRACT

Dengue virus (DENV) poses a global health threat due to the high prevalence, with varying degrees of severity which can escalate to mortality. The disease burden is increased by the genetic diversity, resulting in serotypes and genotypes with different replication rate and clinical severity. This molecular diversity, especially prevalent in endemic regions like Indonesia, underlies the importance of molecular characterization to comprehend transmission dynamics. In addition, phenotypic characterization, for example, using morphological observation of infected cells serves as a valuable tool to explain viral replication behavior. Therefore, this study aims to employ molecular detection techniques, encompassing DENV serotyping and genotyping using Sanger capillary sequencing to characterize the envelope gene of clinical specimens from Bali. To complement that, virus propagation techniques using reference strain-infected Vero cells are performed to gain knowledge and skills on DENV biological characterization for better understanding of transmission dynamics. Using the methods employed, it is revealed that the Bali DENV isolates were dominated by DENV-3 genotype I, followed by DENV-2 genotype Cosmopolitan and DENV-1 genotype I. The isolates had close relationships and highly similar envelope sequences to those from surrounding regions and countries, suggesting both the introduction of viruses from outside Indonesia and the endemic origin of the viruses. This study also found that different strains from the same serotype may induce drastic degrees of cytopathic effect (CPE), requiring further confirmation. This finding may prompt observation of CPE to analyze the damages done by different strains to target cells.

Keyword: Dengue virus; genotyping; viral isolation; phylogeny