

Abstract

The dengue virus (DENV) genome diversity plays an important role in clinical and epidemiology as introduction or replacement of DENV lineages have the potential to create severe dengue outbreak. It is also important in vaccine research as a successful dengue vaccine has to provide protection against all serotypes without causing antibody-dependent enhancement (ADE). In this study, we characterize the genomes of DENVs isolated from a recent outbreak in Jember, East Java, Indonesia. Running the sequenced E gene on NCBI BLAST, we constructed phylogenetic tree using maximum likelihood method (ML) to examine close relatedness of Jember isolates. Further, the presence of positive selection acting on prM and E gene from DENV isolates in Indonesia were examined using various approaches. Finally, to gain a whole genome insight on the virus, next-generation sequencing (NGS) preparation was performed on Jember isolates. The result showed the geographic circulation of DENV in Asia as Jember isolates are shown to be closely related to isolates from Balikpapan and Taiwan. Selection pressure analysis showed the E gene being under more selective pressure compared to prM gene. Both genes experienced episodic positive selection, with some acting on known antigenic sites that might have effect on host immune response and vaccine design while others on sites known to markers for distinguishing between lineages. Taken together, our results showed relationships between Jember isolates and past DENV isolates as well as evolutionary dynamics that may play a part in epidemiology and vaccine design.

Keywords: *Dengue, Dengue epidemiology, Vaccine design, prM protein, E protein, Phylogenetic tree, Positive selection, Illumina sequencing*