

Abstract

Dengue virus is a mosquito-borne viral disease that major health concern in the tropics such as Indonesia, being one of the largest dengue-endemic countries in the world. Pasuruan, despite being among the most vulnerable regions in East Java, lacked molecular data about the virus, making monitoring the dynamics of the virus impossible. The objective of this study is to investigate which antigenically distinct serotypes and genotypes are predominant in Pasuruan.

50 blood samples were obtained from dengue-suspected patients from at from Regional General Hospital dr. R. Soedarsono between May and July 2019. Serotyping was performed using RT and multiplex PCR. Genotyping was performed by constructing a phylogenetic tree using the NJ method. 7 out of 50 samples were successfully isolated (14% isolation rate). All 7 samples are identified as DENV-4. 1 out of the 7 samples were successfully sequenced. The phylogenetic tree suggests that the sequenced sample is DENV-4 Genotype II. The results of this study provide more molecular data of dengue virus for further investigation of the viral dynamics in Pasuruan.

Keywords: *Dengue Virus, Serotype, Genotype, Pasuruan, East Java*