PHYLDYNAMICS OF DENGUE VIRUS IN MALAYSIA

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Background:
Dengue is a serious public health threat in Malaysia. The disease is caused by a mosquito-borne flavivirus, dengue virus (DENV). All four DENV genotypes (formerly referred to as serotypes) are endemic in Malaysia. These viruses have circulated in Malaysia for more than 50 years. We undertook a study to examine the phylodynamics of dengue and DENV in Malaysia and established an Integrated Dengue Virus Genome Sequence Information Database (I-DenSeID). We have completed full-genome sequencing of over one thousand DENV isolated over the last 30 years at the University of Malaya Medical Center. The DENV genome database together with the built-in integrated Global Information System (GIS) data will serve as an essential platform for scientists to design mathematical models for the prediction of future dengue outbreaks and the development of candidate dengue vaccines.