

POSTER SYMPOSIUM – P6

Phylogenetic Analysis of Dengue Virus Isolated in Brunei from June 2015 to July 2016

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BACKGROUND

Dengue is an emerging mosquito-borne viral infection with well-known endemicity in Southeast Asia, including Brunei Darussalam. There are four serotypes of dengue virus (DENV-1 to DENV-4), each of which is further subdivided into distinct genotypes. There is a lack of available information regarding the genotypes of dengue virus strains circulating in Brunei. Therefore, we conducted an investigation of dengue infections throughout Brunei using samples collected from June 2015 to July 2016 in order to describe the genotype pattern of dengue viruses in Brunei.

MATERIALS AND METHODS

A total of 115 serum samples confirmed as NS1 dengue positive through serology testing were selected. Real time-polymerase chain reaction was performed on extracted viral RNA of the samples to obtain the serotypes. Additionally, these serum samples were sent to Environmental Health Institute, National Environment Agency, Singapore for genotype analysis and data shared on UNITEDengue platform.

RESULTS

Serotyping showed that all four serotypes were present during this time period with DENV-1 as the dominant serotype. A total of 35 sequences were obtained from the sample population (28 of DENV-1, 2 of DENV-2 and 5 of DENV-3). The DENV-1 isolates were grouped into Genotype I and II, DENV-2 into Cosmopolitan clade I and DENV-3 into Genotype I and III with DENV-1 Genotype I as the most predominant strain.

CONCLUSION

Phylogenetic analysis revealed that the DENV-1 isolates were most closely related to viruses isolated in Singapore and Malaysia since 2013 and associated with the 2005 Singapore outbreak.

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