

POSTER SYMPOSIUM – P7

Brunei Dengue Virus Characterisation Study from August 2016 to June 2017

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BACKGROUND

Dengue infection has always been a major public health threat globally including Brunei Darussalam. The re-emergence of dengue is increasingly associated with a shift in epidemiology. Dengue fever can be caused by any of four (DENV-1 to DENV-4) genetically related but antigenically distinct dengue virus (DENV) serotypes. Dengue virus characterization has been shown to be very important in determining the origin, evolution and geographic distribution of the dengue viruses via serotyping and genotyping study. In this study, we characterise the dengue virus isolated in Brunei from the period of August 2016 to June 2017.

MATERIALS & METHODS

A total of 100 serum samples from suspected dengue patients (NS1 antigen or IgM positive) were collected from August 2016 to June 2017. Molecular analysis of dengue virus serotype and dengue virus nucleotide sequences, followed by sequence alignment and phylogenetic analysis of the dengue virus envelope (E) protein were performed and data submitted to UNITE Dengue.

RESULTS

The serotype pattern fluctuated between October 2016 and February 2017. DENV-1 continued to drive the dengue transmission in subsequent months and accounted for 74.3% of the total serotyped cases (March to May 2017). Within DENV-1 population, genotype Ia continues as the dominant strain (77.3%). Identical sequences (at E gene level) were observed in different districts - Muara, Temburong & Belait. DENV-1 genotype Ia in Brunei is genetically distinguishable from genotype Ia strains reported in Malaysia and Singapore.

CONCLUSION

DENV-1 continued as the dominant strain within the population during the first half of 2017 in the country.

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