SEQUENCE ANALYSIS OF E/NS1 GENE JUNCTION OF DENGUE VIRUS TYPE 2 ISOLATED IN BRUNEI

Osmali Osman¹, Mun Yik Fong² and Shamala Devi¹

¹Department of Medical Microbiology, ²Department of Parasitology, Faculty of Medicine, University of Malaya, Kuala Lumpur, Malaysia

Abstract. A preliminary study of dengue infection in Brunei between 2005 and 2006 showed that dengue 2 was the predominant serotype. A total of five DEN-2 isolates were isolated and maintained in the mosquito cell-line, albopictus C6/36. The sequence spanning the envelope and non-structural protein 1 (E/NS1) junction (positions 2311 to 2550) of the isolates were determined and analysed at the amino acid and nucleotide levels. Alignment of the 240 nucleotide sequences among the five isolates showed changes occurring at 7 positions (2.9%) of the region. All but one nucleotide substitution (position 2319, amino acid 742 V→F) were found at the 3rd position of the codons and were silent mutations. Amino acid homology ranged from 98% to 100%. Sequence divergence of the Brunei isolates varied from 5% to 6.6% compared with dengue-2 prototype New Guinea C strain. Comparison of the Brunei DEN-2 isolates with sixty-five other strains placed them in a cluster containing Indonesian strains isolated in 1973, 1978 and 2004 and Malaysian strains isolated in 1996, 1998 and 1999 in genotype group IV.

Correspondence: Shamala Devi, Department of Medical Microbiology, Faculty of Medicine, University of Malaya, Kuala Lumpur 50603, Malaysia. Tel: +60 3 79675759; Fax: +60 3 79584844

E-mail: shamalamy@yahoo.com