Molecular epidemiology of dengue virus in Manado, North Sulawesi, Indonesia, 2012

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Background: Dengue infection is one of the most important arthropod-borne viral diseases with large global burden especially in tropical and subtropical countries. The disease is caused by dengue virus (DENV) with four distinct serotypes; DENV-1, -2, -3, -4. As RNA viruses, DENV undergo diverse genetic characteristics as shown by the presence of various genotypes within serotype. Up to now, dengue has caused major public problem in all 33 provinces in Indonesian with periodic major outbreak. While dengue is endemic in Indonesia, only limited information of DENV genotype is available. Among 33 provinces, Manado the capital city of North Sulawesi province reported major outbreak throughout 2012. Therefore we conducted study to investigate the distribution of DENV genotype in Manado, North Sulawesi, Indonesia, in 2012.

Methods & Materials: Serum samples were collected from patients suspected of dengue infection in Manado. The serum samples were tested for DENV using RT-PCR. Positive serum samples were cultured in the C6/36 mosquito cell line for further envelope gene sequencing. The full-length envelope gene was obtained using gene sequencing. The phylogenetic analyses were performed by Neighbor Joining using MEGA 4.0 with 1000 replicates. Known genotype sequence of DENV-1, DENV-2, DENV-3 and DENV-4 from Indonesia and other countries obtained from GenBank were included in the analyses for references.

Results: Of 227 serum samples studied, 107 (47%) were positive DENV by RT-PCR. DENV-2 was predominant followed by DENV-3, DENV-1 and DENV-4 serotype. Twelve out of 28 DENV isolates were successfully sequenced for their envelope genes. Seven of these isolates were DENV-2, three DENV-3 isolates, one DENV-1 and one DENV-4 isolates. Phylogenetic analyses revealed that DENV-2 fall into cosmopolitan genotype, while DENV-3 were clustered together in genotype I. The DENV-1 and DENV-4 were grouped in genotype I and II, respectively. All of the viruses isolated from Manado in 2012 were clustered within genotypes that have been circulating in Indonesia for at least 30 years.

Conclusion: This study found that all four DENV serotypes circulated in Manado were clustered with genotypes that have been circulating in Indonesia for at least 30 years.

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