

Characterization of the 2013 dengue epidemic in Myanmar with dengue virus 1 as the dominant serotype

Mya Myat Ngwe Tun^a, Aung Kyaw Kyaw^{a,b}, Nader Makki^a, Rohitha Muthugala^a, Takeshi Nabeshima^a, Shingo Inoue^a, Daisuke Hayasaka^a, Meng Ling Moi^a, Corazon C. Buerano^a, Saw Myat Thwe^b, Kyaw Zin Thant^b, Kouichi Morita^a

^aDepartment of Virology, Institute of Tropical Medicine, Leading Graduate School Program, Nagasaki University, Japan

^b Virology Research Division, Department of Medical Research, Myanmar

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In 2013 in Myanmar, dengue epidemic occurred with 20,255 cases including 84 deaths. This study aimed to determine the serological and molecular characteristics of dengue virus (DENV) infection among children with clinical diagnosis of dengue hemorrhagic fever (DHF) or dengue shock syndrome (DSS) during this period. Single acute serum samples were collected from 300 children in Mandalay Children Hospital, Mandalay, Myanmar. Out of the 300 children, 175 (58.3%) and 183 (61%) were positive for anti-dengue IgM and anti-dengue IgG, respectively. Among the IgM positives, 41 (23.4%) had primary DENV infection. Thirty-nine DENV strains (23 DENV-1, 10 DENV-2 and 6 DENV-4) were successfully isolated after inoculation of the patient serum samples onto C6/36 cells. DENV 1 was the dominant serotype in the 2013 epidemic. There was no correlation between the infecting serotypes and clinical severities. The DENV-1 strains belonged to three lineages of the genotype 1; the DENV-2 strains were of the Asian I genotype and were separated into two lineages; and DENV-4 strains belonged to the same lineage of genotype I. It is of interest to note the diversity of DENV-1 and -2 circulating in the same location during June–August 2013. These DENV isolates were genetically close (98%–100%) to the other previously reported isolates from Myanmar and its neighboring countries, namely China, Thailand, Sri Lanka, Cambodia and Vietnam. Primary DENV infection was still high among the severe dengue cases. Different serotypes of DENV were co-circulating in 2013, however, genotype shift was not observed. Additionally, amino acid mutations were detected in the study strains not seen in the previously reported strains from other countries and Myanmar. This paper provided information on the circulating serotypes for the last 15 years and the recent dengue situation in Mandalay, Myanmar after 2006.