The circulating serotypes of dengue in Sabah, Malaysian Borneo

ABSTRACT

Background: Dengue is a mosquito borne arbovirus affecting humans and dengue infection has become a major public health problem in Asia Pacific countries. The virus is a positive sense, single-stranded enveloped RNA virus of the genus flavivirus. Malaysia is a dengue endemic country where all four dengue serotypes (DENV-1,-2,-3 and -4) have been reported but serotype data of Sabah is lacking. The aim of this study was to determine the circulating serotypes and other risk factors for dengue patients in Sabah. Methods: This was a cross sectional study, conducted during 2013–2015. A total 579 NS1- positive serum samples obtained from dengue patients were included from Public Health Laboratory of Sabah. All the samples had previously been tested for NS1 dengue using SD Bioline kit. Dengue viral RNA was extracted from NS1positive serum using QIAmp Viral RNA Mini Kit (Qiagen, Hilden, Germany) according to the manufacturer's instructions. The NS1Aq positive samples were tested further by real time polymerase chain reaction (PCR) and reverse transcriptase PCR (RTPCR). Results: From 579 examined samples, 58% were from male patients and 42% were from females. Regarding circulating serotypes in the year 2013, DEN-4 was the predominant serotype at 84.54%, followed by DEN-1 (37.24%), DEN2 (18.12%) and DEN-3 (15.10%). In the year 2014, DEN1 was predominant (89.64%) followed by DEN-2 (31.22%), DEN-4 (10.75%) and DEN-3 (9.7%). Interestingly, in the year 2015, DEN-2 (45%) was predominant followed by DEN-1 (27%), DEN-4 (16%) and DEN-3 (12%). The number of patients with multiple serotype co-infections has seen increased in 2015. Conclusions: Our results show that the circulating serotypes is changing within different years. Therefore, early detection of circulating serotypes could be an important approach to prevent severe clinical outcomes during dengue outbreaks. It will be interesting to examine molecular characteristics and phylogenetic analysis of dengue in this geographical area.