

## MOLECULAR EPIDEMIOLOGY OF DENGUE VIRUSES CO-CIRCULATING IN UPPER MYANMAR IN THE YEAR 2006

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**BACKGROUND:** Myanmar belongs to the disease endemic countries (DEC) for dengue. Dengue outbreaks occurred in Upper Myanmar with special focus on its largest city in the region, Mandalay, which were not extensively studied due to the insufficient laboratory facilities.

**OBJECTIVES:** To understand the dynamics of dengue virus epidemiology in Upper Myanmar, a hospital-based study was conducted in Mandalay Children Hospital in the year 2006.

**METHODS:** A panel of serum samples (110 in number) collected from dengue patients admitted to Mandalay Children Hospital were tested by PanBio Dengue Duo IgM and IgG ELISA tests. These samples were attempted for dengue virus isolation by inoculating the sera into C6/36 mosquito cell line. Infected culture fluids were subjected to reverse transcriptase-polymerase chain reaction (RT-PCR) test to detect the dengue virus genome. Primer extension dideoxy chain termination method was used for direct sequencing of the PCR products obtained covering the complete envelope (E) protein gene. Sequence alignment and phylogenetic analysis were performed using Clustal X vs.2.0.5, Modeltest 3.7 and PAUP software version 4.0b10.

**RESULTS:** Three new dengue virus strains from Mandalay and Upper Myanmar were successfully isolated. These strains included one strain of dengue serotype-3 and two strains of dengue serotype-4. Phynogenetic analyses of these new strains and a vast group of previously published isolates revealed that our dengue-3 strain belongs to genotype II, and the two dengue-4 strains clustered within genotype I. Our sequences clustered together with recent strains from Thailand and Bangladesh which appear to be their closest relatives.

**CONCLUSIONS:** This is the first study presenting the isolation and molecular characterization of DEN viruses in Upper Myanmar. Our findings are important to elucidate the trends of recent and future dengue outbreaks in Myanmar.