

# Molecular Epidemiology of Dengue Viruses Co-circulating in Upper Myanmar in 2006

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To understand the molecular epidemiology of circulating dengue viruses (DENV) in Upper Myanmar, DENV isolation was attempted by inoculating the sera of a panel of 110 serum samples onto a C6/36 mosquito cell line. The samples were collected from dengue (DEN) patients admitted at Mandalay Children's Hospital in 2006. Infected culture fluids were subjected to a RT-PCR to detect the DENV genome. Three DENV strains were isolated. This was the first DENV isolation performed either in Mandalay or in Upper Myanmar. One strain belonged to DENV serotype-3 (DENV-3), and two other strains belonged to DENV serotype-4 (DEN-4). The sequence data for the envelope gene of these strains were used in a phylogenetic comparison of DENV-3 and DENV-4 from various countries. Phylogenetic analyses revealed that this DENV-3 strain was clustered within genotype II, and the two DENV-4 strains were clustered within genotype I in each serotype. The Myanmar strains were closely related to strains from the neighboring countries of Thailand and Bangladesh. These results are important for elucidating the trends of recent and future DEN outbreaks in Myanmar.