

SEQUENCE ANALYSIS OF DENGUE VIRUS TYPE 2 OF THE LARGEST DENGUE OUTBREAK (2001-2) IN TAIWAN SINCE THE WORLD WAR II

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BACKGROUND /AIMS: The four serotypes of dengue viruses (DV1 to DV4) cause the most important arboviral diseases, including the mild dengue fever (DF) and the potentially life-threatening dengue hemorrhagic fever (DHF). To investigate viral determinants associated with severe disease, we examined full genome sequences of DV2 from DF and DHF patients during the 2001-2002 outbreak in Kaohsiung, a metropolis in southern Taiwan.

METHODS: Acute plasma samples from 31 confirmed cases (17 DF and 14 DHF) at two local hospitals (the Yuan General and Huei-Te Hospitals) were subjected to viral RNA extraction and RT as described previously (Wang et al. J Virol 2002;76:4662), followed by PCR of 8 segments and sequencing. The program MEGA was used for sequence and phylogenetic analyses.

RESULTS: Phylogenetic tree revealed that the Kaohsiung viruses, forming two clusters by year, belong to the cosmopolitan genotype. The 2001 cluster was closely related to two Philippines isolates in 2000-2001 with a mean p-distance of 0.29%, suggesting that the Kaohsiung virus probably originates from Philippines. Full genome sequence analysis revealed no consistent nucleotide or amino acid change associated with viruses from DHF patients.

DISCUSSION /CONCLUSIONS: The molecular determinants of DV2 causing DHF could not be identified from this study. Host factors probably play an important role in determining the disease severity. The observation of slower mutation rate of DV2 within the 2002 outbreak, 1×10^{-5} /nt /day, than that between 2001 and 2002 has implication to the evolutionary conservation of dengue virus that replicates alternately between human and mosquito vector.

Keywords: dengue virus, genome sequences, evolution