Bangkok during near past three decades. No specific sequence differences distinguished the DF and DHF isolates, suggesting that the E gene alone was not a deter-minant of disease severity. The phylogenetic tree revealed that there is a clear separation within the large Thai group of viruses, with a group virus strains from 1996 onwards being separated from the rest by a branch with 100% bootstrap support, the strains of DEN-3 virus circulating in Bangkok prior to 1996 appear to have disappeared and been replaced by new lineages that have evolved locally, rather than being introduced. However, it remains unclear and requires further study as to whether this replacement represents a selection event, so that strains differ in fitness, or a random population bottleneck. Sequencing of the entire virus genome of selected specimens is underway to ascertain the molecular basis to any differences in fitness among strains.

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MOLECULAR EVOLUTION AND EPIDEMIOLOGY OF DENGUE-3 VIRUSES IN THAILAND

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Sixty dengue-3 (DEN-3) virus isolates from children in Bangkok with varying degrees of clinical dengue severity [dengue fever/dengue hemorrhagic fever/dengue shock syndrome (DF/DHF/DSS)] from 1973 to the present were selected to sequence virus envelope (E) and partial pre-membrane/membrane (preM/M) genes. An analysis of the results was completed to observe potential trends in molecular evolution and the epidemiology of circulating dengue viruses in Thailand. Phylogenetic analysis indicated that only genotype II of the DEN-3 virus serotype circulated in Thailand during the past three decades. There were no diagnostic sequence differences between them, suggesting that E gene alone does not deter-mine disease severity. Comparison of nucleic acid sequences of DEN-3 virus genotype II from Thailand with strains of DEN-3 virus genotype II from GenBank revealed that our 60 DEN-3 isolates share 96.3 – 99.7% nucleic acid sequence homology and 96.6 – 99.8% amino acid sequence homology. The Phylogenetic tree showed that strains of DEN-3 virus circulating in Thailand prior to 1990 appear to have disappeared and have been replaced by new lineages that have evolved locally, rather than being introduced. Sequencing virus entire genome of some selected samples is undertaking for further analysis on selection pressure and recombination.

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