

Genetic Analyses of the Dengue 2 Outbreak in 2001-2003, Kaohsiung, Taiwan.

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Background/Objective

Dengue hemorrhagic fever (DHF) is one of the most essential mosquito-borne diseases caused by dengue virus (DENV). While the outbreak of DENV1 in 2014 result in more than 15000 dengue hemorrhagic fever (DF) cases, to a largest ever number in a single outbreak, the outbreak of DENV2 in 2002 in Kaohsiung brought about more DHF patients. Since DF has not become endemic in Taiwan, and most DF/DHF cases in previous epidemics were cased by DENV2 strains, it' s important to gain greater insight into the virus evolution, epidemiological properties and temporal-spatial transmission pattern of the virus.

Method

During 2001-2003, 123 sequences from patients in addition with 10 sequences from imported cases of DENV2 E protein were collected. Demographic and clinical data were also recorded in this period. Both phylogenetic and geographic analyses were conducted to study the viral transmission.

Result

Based on the phylogenetic analysis on E protein with strains isolated in 2001-2003, five DEN-2 viruses isolated in 2002 – 1185, 1252, 1275, 1375 and 1615 – closely clustered with a clade formed by viruses isolated in 2001. Further investigation showed that these “2001-like” viruses appeared in the early stage of 2002 epidemic period, and no virus classified as 2001-like group was found after mid-state (30th week) of epidemic. These results again exhibited DEN-2 viruses in 2001 may contribute to the epidemic in 2002, co-circulating with new variants of DEN-2 viruses emerged in the 2002.

Conclusion

Genetic variations among these DENV-2 viruses were also found in the same epidemic in Kaohsiung, although its role in virology and epidemiology remained unclear. In the future, we will focus on both epidemiological and virological information for the better interpretation on viral strain variations.