

## **Abstract**

**The impact of the underlying diseases that were more commonly seen in adult population than children on disease severity of dengue infections was rarely reported for most of the dengue infected were younger than 15 years old in dengue epidemic areas. We conduct a prospectively observational, hospital-based study on 311 dengue fever (DF) and 94 dengue hemorrhagic fever (DHF) cases in a 2002 Taiwan dengue serotype 2 outbreak. Univariate analyses revealed the significant risk factors associated with DHF cases were patients with diabetes mellitus (DM), Chronic renal insufficiency (CRI), and histories of past dengue infection ( $p=0.037$ ,  $0.025$ ,  $0.003$ , respectively). Multivariate logistic regression analysis revealed past dengue infection was the only significant factor for DHF ( $P=0.008$ ). Nine patients died from DHF. Patients with CRI, DM, or aged more than 65 years old were correlated with higher mortality rate in the results of the univariate analyses. Multivariate logistic regression analysis revealed CRI was the only significant factor for mortality. In summary, prior hetero-serotype dengue infection was the most significant factor of DHF during this outbreak when more than 90% cases were adults. Clinicians should notice dengue infected cases with underlying disease of DM or CRI might have higher possibility of DHF/DSS and that CRI was a significant risk factor for mortality.**

**The comparison of viral load at day 4 and day 5 did not reveal significant difference, however, the number of DHF cases with continuous blood samples is small. Some patient had fever more than 7 days were tested to be PCR positive with quantitative PCR.**

**The sequence of a 240-nucleotide-long region across the envelope/non-structural 1 protein (E/NS1) gene junction of the isolates were determined and analysed. Alignment and comparison of the nucleotide and deduced amino acid sequences of the isolates revealed that nucleotide changes occurred mostly at the third position of a particular codon. Two nucleotide changes resulted in amino acid substitutions. Pairwise comparisons of the nucleotide gave divergence values ranging from 0.4 to 6.6%. Comparison of the nucleotide sequences of the dengue isolates with those of other world revealed that the isolates in 2002 were obvious different from other strains. Phylogenetic tree shows that the isolates in 2002 were belonged to an independent genotype.**

**Keywords : DENGUE ; VIRUS ; TAIWAN**