

IL-8, IL-1 β and MMP-9 RELATED GENE EXPRESSION IN THE PERIPHERAL BLOOD AND SEVERITY OF DENGUE VIRUS INFECTION

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Context: Previous studies have suggested an involvement of immune response mediators in the severity of dengue infection. The pathogenesis of dengue hemorrhagic fever (DHF) and dengue shock syndrome is thought to be mediated by various host factors, particularly cytokine-related gene expression.

Objectives: To elucidate the cellular gene responsive to dengue viral infection at the transcriptional level, expression levels of IL-8, IL-1 β and MMP-9 and to correlate their expression levels with disease activity and/or clinical manifestation.

Design, Setting, and Patients: Pediatric patients were enrolled at King Chulalongkorn Memorial Hospital. Whole blood mRNA from children with dengue infection was analyzed on the day of defervescence. Expression levels of IL-8, IL-1 β , and MMP-9 in peripheral blood leukocytes (PBMC) were assayed in 30 children with DF, 19 children with DHF and 10 controls by real-time RT-PCR. Definite diagnosis was based on antibody captured ELISA and/or serotype-specific RT-PCR assays. The analysis utilized Mann-Whitney *U* test and Q-gene software.

Main Outcome Measures: Demographic data, clinical information, including symptoms, severity of illness and mRNA expression pattern of IL-8, IL-1 β and MMP-9

Results: There was no significant different among characteristics of children with dengue infection at the time of admission, except for white blood cell count and Hct which were significant higher among children with DHF ($P < 0.05$). Regarding gene expression pattern of Dengue infection, mRNA levels analyzed on the day of defervescence showed that IL-8 and IL-1 β mRNA levels were not significantly different between children with DF and DHF, but those with DHF had significantly higher levels of MMP-9 mRNA.

Conclusions: MMP-9 might have an important role in dengue pathogenesis. To gain further insight into the pathogenesis of DF and DHF, serial transcription profiling of additional selected genes should be monitored and compared. The expression pattern of these genes in PBMC might serve as a predictor of dengue infection and disease activity.

Keywords: dengue infection, gene expression, disease severity