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Prediction of Biomarkers to Detect Severe Dengue in the Acute Stage

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Abstract

Dengue virus infection presents a wide spectrum of manifestations including asymptomatic infections, Dengue Fever (DF), or severe dengue, such as Dengue Haemorrhagic Fever (DHF) and dengue shock syndrome in affected individuals. Our aim was to predict the likelihood of a dengue patient, developing a severe form of the disease at an early stage, for more efficient patient management. Many studies have been carried out in protein assay methods to identify potential biomarkers, but quantitative transcriptomic level studies are rare for dengue. The extracted RNAs from the peripheral blood mononuclear cells of 59 DF patients and 35 DHF patients during the febrile stage of the disease were used to measure the expression levels of selected genes by quantitative polymerase chain reaction. The mRNA expression levels of cytokines IL-06, IL-10, LTF, TGFBR3, UQCRQ, and RASSF5 were analysed by relative quantification using GAPDH as a reference. The study revealed that the mRNA level of IL 06 was upregulated and other five genes such as IL-10, LTF, TGFFBR3, UQCRQ, and RASSF5 were down-regulated in DHF compared to DF patients during the acute phase of dengue infection. Statistically significant differences were found for UQCRQ and RASSF5 gene expression levels in DHF and DF patients. These may be useful as potential biomarkers for the clinical prognosis of severe dengue. Further studies need to be done to confirm the findings.

Keywords: *Dengue, Biomarkers, Real-time Polymerase Chain Reaction*