Transcriptome Analysis Reveals Role of Long Non-Coding RNA NEAT1 in Dengue Patients

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Abstract : Background: Long non-coding RNAs (lncRNAs) are the important regulators of gene expression and play important role in viral replication and disease progression. The role of lncRNA genes in the pathogenesis of Dengue virus-mediated pathogenesis is currently unknown. Methods: To gain additional insights, we utilized an unbiased RNA sequencing followed by in silico analysis approach to identify the differentially expressed lncRNA and genes that are associated with dengue disease progression. Further, we focused our study on lncRNAs NEAT1 (Nuclear Paraspeckle Assembly Transcript 1) as it was found to be differentially expressed in PBMC of dengue infected patients. Results: The expression of lncRNAs NEAT1, as compared to dengue infection (DI), was significantly down-regulated as the patients developed the complication. Moreover, pairwise analysis on follow up patients confirmed that suppression of NEAT1 expression was associated with rapid fall in platelet count in dengue infected patients. Severe dengue patients (DS) (n=18; platelet count < 20K) when recovered from infection showing high NEAT1 expression as it observed in healthy donors. By co-expression network analysis and subsequent validation, we revealed that coding gene; IFI27 expression was significantly up-regulated in severe dengue cases and negatively correlated with NEAT1 expression. To discriminate DI from dengue severe, receiver operating characteristic (ROC) curve was calculated. It revealed sensitivity and specificity of 100% (95%CI: 85.69 – 97.22) and area under the curve (AUC) = 0.97 for NEAT1. Conclusions: Altogether, our first observations demonstrate that monitoring NEAT1and IFI27 expression in dengue patients could be useful in understanding dengue virus-induced disease progression and may be involved in pathophysiological processes.

Keywords : dengue, lncRNA, NEAT1, transcriptome
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