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Transcriptome Analysis for Insights into Disease Progression in Dengue Patients

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Abstract : Dengue virus infection is now considered as one of the most important mosquito-borne infection in human. The virus is known to promote vascular permeability, cerebral edema leading to Dengue hemorrhagic fever (DHF) or Dengue shock syndrome (DSS). Dengue infection has known to be endemic in India for over two centuries as a benign and self-limited disease. In the last couple of years, the disease symptoms have changed, manifesting severe secondary complication. So far, Delhi has experienced 12 outbreaks of dengue virus infection since 1997 with the last reported in 2014-15. Without specific antivirals, the case management of high-risk dengue patients entirely relies on supportive care, involving constant monitoring and timely fluid support to prevent hypovolemic shock. Nonetheless, the diverse clinical spectrum of dengue disease, as well as its initial similarity to other viral febrile illnesses, presents a challenge in the early identification of this high-risk group. WHO recommends the use of warning signs to identify high-risk patients, but warning signs generally appear during, or just one day before the development of severe illness, thus, providing only a narrow window for clinical intervention. The ability to predict which patient may develop DHF and DSS may improve the triage and treatment. With the recent discovery of high throughput RNA sequencing allows us to understand the disease progression at the genomic level. Here, we will collate the results of RNA-Sequencing data obtained recently from PBMC of different categories of dengue patients from India and will discuss the possible role of deregulated genes and long non-coding RNAs NEAT1 for development of disease progression.

Keywords : long non-coding RNA (lncRNA), dengue, peripheral blood mononuclear cell (PBMC), nuclear enriched abundant transcript 1 (NEAT1), dengue hemorrhagic fever (DHF), dengue shock syndrome (DSS)
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