IPRC/24/205 Science, Technology, Mathematics & Medicine

Salivary miR-150-5p as a Thymus-influenced early non-invasive prognostic marker for severe dengue: A bioinformatics analysis

N. Ambanpola[1], T. Manilgama[1], K.N. Seneviratne[1], and N. Jayathilaka[*]

[1]Department of Chemistry, Faculty of Science, University of Kelaniya, Kelaniya 11600, Sri Lanka

MicroRNAs play important roles in regulating gene expression and cellular functions during viral infections, including dengue fever. While miR-150-5p has been identified as a circulating biomarker in blood, its potential in saliva as an early, non-invasive prognostic marker for severe dengue (SD) has yet to be explored. We analyzed multiple NCBI GEO datasets (GSE150623, GSE190749, GSE123336, GSE209670, and GSE139242) to examine miR-150-5p expression across bio-fluids. Differentially expressed genes and miRNAs were determined according to a threshold log2 fold change (logFC) > 1 and adjusted p-value (adj. p) < 0.05. We utilized mirDIP, miRDB, and TargetScanHuman to predict miR-150-5p target genes, which were cross-verified with human genes interacting with Dengue viral proteins using the DenHunt Database. The KEGG pathway analysis was performed in the NetworkAnalyst platform. Overlapping genes identified through Venn diagrams were considered as the candidate thymus-specific proteins potentially involved in dengue viral interactions. We observed significant upregulation of miR-150-5p plasma samples from SD patients compared to dengue fever patients, with logFC = 1.214798 and adj. p = 0.0368. In non-dengue samples, we found high expression in saliva compared to serum with logFC = 2.349937 and adj. P = 6.30E-05, and plasma with logFC = 2.036475 and adj. P = 0.0014. We identified 15 Specific Dengue-Related Genes (SDRGs) as miR-150-5p targets, 7 of which directly interact with dengue proteins: ANKRD12, CCNT1, CD38, CTNNB1, PDIA6, STAT1, and TNF. KEGG analysis revealed enrichment in immune pathways, such as T-cell receptor signaling, implicating miR-150-5p in the immune response to dengue. Differential expression of SDRGs revealed STAT1, overexpressed in CD4+ and CD8+ thymic T-cells. The results implicate the interplay between miR-150-5p, thymic activity, and immune response during dengue infection. These findings suggest that salivary miR-150-5p, through its regulation of immune-related genes and thymic activity, may serve as a reliable early prognostic marker for SD, warranting further clinical validation.

Keywords: Differential gene expression, microRNA, NCBI GEO, KEGG, Lymphoid organ.

[*]njayathi@kln.ac.lk
ORCiD ID: https://orcid.org/0009-0007-1506-2158