Long non-coding RNA NBAT1, TUG1, miRNA-335, and miRNA-21 as potential biomarkers for acute ischemic stroke and their possible correlation to thyroid hormones

Objective:
RNA-based mechanisms of epigenetic modification related to acute ischemic stroke (AIS) have beenwidely studied recently. The currentwork aimed to determine the potential roles of four ncRNAs (TUG1 and its target miR-21, NBAT1, andmiR-335) as promising diagnostic biomarkers in AIS as well as their involvement in the disease pathogenesis.
Methods: The levels of the studied lncRNAs and miRNAs were measured in the serum for two different groups, including patients with AIS (60) and healthy controls (60). All individuals were subjected to a full history investigation and clinical examination. Blood samples were tested for FBS, 2HPP, TAG, HDL, LDL, TSH, T3, and T4 levels.
Results: The serum levels of TUG1 were significantly increased in AIS patients compared to control subjects. It is worthwhile to note that serum TUG1 levels were positively correlated with cholesterol, triglycerides, LDL, carotid IMT (Intima-media thickness), and miR-21, while they were negatively correlated with HDL levels. Our study showed that NBAT1 serum expression levels were elevated in AIS patients compared to controls. NBAT1 expression levels were observed to be positively correlated with triglycerides, TUG1, and miR-21. NBAT1 could distinguish between AIS patients and controls with a sensitivity of 100% and specificity of 100% at a cut-off point of 1.45. Regarding miR-335, we found that its expression levels were downregulated in AIS patients compared with healthy controls. It could distinguish between AIS patients and controls with a sensitivity of 73.3% and a specificity of 100% at a cut-off point of 0.796.
Conclusion: Our results revealed that serum TUG1, miR-21, NBAT1, and miR-335 could be promising molecular diagnostic markers for AIS as these biomarkers could discriminate between AIS patients and healthy controls.