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RUNX1-Regulated pathways and biomarkers in acute myeloid leukaemia**Hrishika Singh Chauhan**

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Runx1 transcription factor 1 gene (RUNX1), also known as acute myeloid leukaemia 1 protein (AML1), plays a crucial role in the pathogenesis of AML. RUNX1/AML1 is one of the most frequently mutated leukaemias associated with a poor prognosis in AML. Researchers and clinicians can develop personalized medicines and improve diagnosis by identifying the biomarkers associated with mutations. In the current study, we used the genome and transcriptome data from The Cancer Genome Atlas-Acute Myeloid Leukemia (TCGA-AML) cohort. We analysed RUNX1 mutant AML patients compared to non-mutant patients using an integrated multi-omics, multi-database analysis of exome, and transcriptomics data. Finally, we identified the gene signature associated with RUNX1 mutations, including prognostic genes that significantly influenced the overexpression of RUNX1 mutation-associated genes in AML patients. Our results can help to diagnose AML patients with RUNX1 mutations at an early stage.

Biography

Hrishika Singh Chauhan is a distinguished academic and researcher affiliated with the Department of Biotechnology at GITAM (Gandhi Institute of Technology and Management), School of Sciences, Visakhapatnam, India. Her expertise lies in cutting-edge biotechnological research, contributing significantly to the advancement of the field. Based at GITAM (Deemed to be University), she plays a pivotal role in fostering innovation and excellence in education and scientific exploration.