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Clinical Relevance of SPRED1 Gene as a Novel Prognostic Biomarker in Acute Myeloid Leukemia

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INTRODUCTION

The Sprouty-related, EVH1 domain-containing protein 1 (SPRED1) is pivotal in the initiation, advancement, and advancement of cancer. Nonetheless, the precise molecular pathways through which SPRED1 contributes to acute myeloid leukemia (AML) are not fully elucidated.

AIM

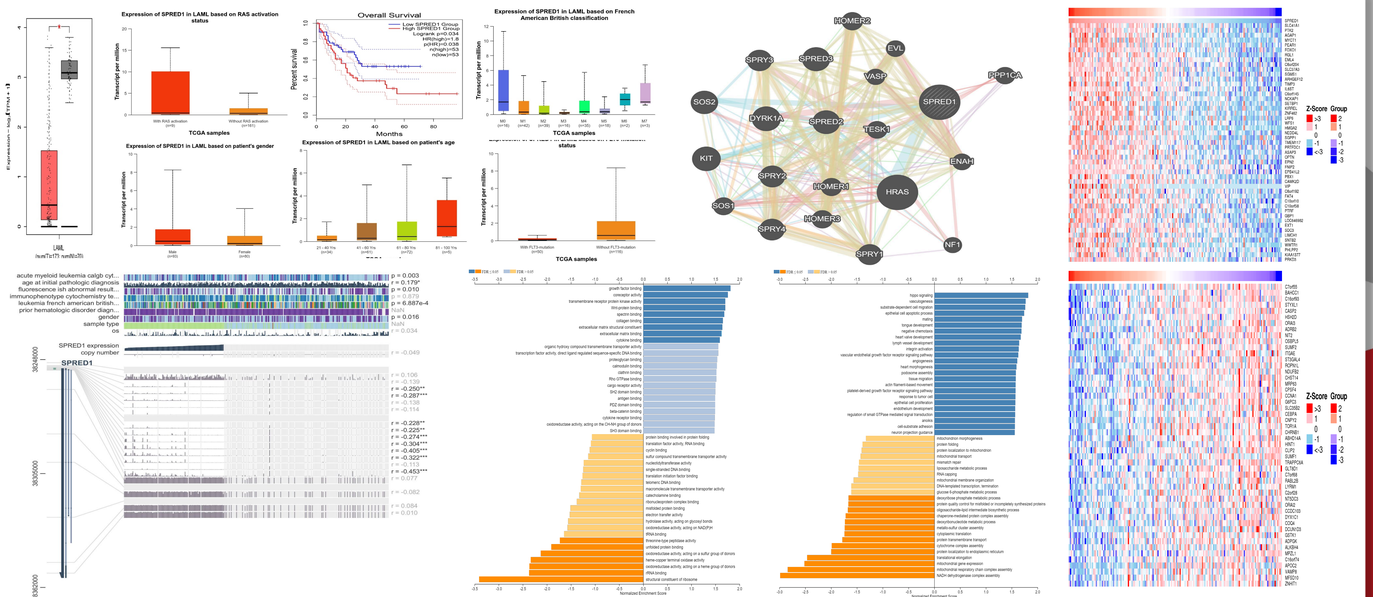
This study aimed to explore the feasibility of utilizing SPRED1 as a diagnostic and prognostic indicator in AML.

METHOD

- Utilizing Gene Expression Profiling Interactive Analysis (GEPIA-2), we evaluated mRNA expression and prognostic significance of SPRED1 in the TCGA-LAML dataset (n=173).
- cBioPortal facilitated screening of SPRED1 expression-related genes and correlation analysis with methylation status.
- Linked Omics database facilitated analysis of SPRED1 and its co-expressed genes, while STRING and Gene MANIA databases constructed a protein–protein interaction (PPI) network.
- Functional enrichment analysis was conducted using Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways, along with Gene Set Enrichment Analysis (GSEA).

RESULTS

In patients with AML (n=173), the expression of the SPRED1 gene was found to be lower compared to healthy individuals (n=70). This reduced SPRED1 expression was significantly associated with mutations in FLT3, fusion with PML-RARA, and poorer clinical outcomes (P<0.05). Additionally, SPRED1 gene expression negatively correlated with methylation levels on the promoter region, patient age, and counts of basophils, lymphocytes, neutrophils, and monocytes, while positively correlating with levels of hemoglobin, platelets, blast cells, leukocytes, and eosinophils (P<0.05). Correlation analysis identified 12,356 positively and 7091 negatively correlated genes, with top positively correlated genes including *SLC41A1, PTK2, AGAP1, MYCT1*, and *PEAR1*, and top negatively correlated genes including *BAHCC1, STYXL1, CASP2, HSH2D*, and *ORA13*, all significantly linked to SPRED1 expression levels in AML (P<0.0001). Furthermore, PPI and enrichment analyses revealed that SPRED1 and its associated genes were predominantly enriched in the regulation of the Hippo, NF-kappa B, and Rap1 signaling pathways. In terms of biological processes, these genes were implicated in substrate-dependent cell migration, vasculogenesis, and epithelial cell apoptotic processes.



CONCLUSIONS

These results suggest that SPRED1 plays a significant role in the progression of AML and holds promise as a potential prognostic biomarker in the disease.

REFERENCES

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