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Expression Analysis, Clinical Significance, and Potential Function of ALOX5AP in Acute Myeloid Leukemia

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INTRODUCTION

Acute myeloid leukemia (AML) presents as a heterogeneous group of hematologic malignancies characterized by dysregulated proliferation and differentiation of leukemic primitive cells. Arachidonate 5-lipoxygenase-activating protein (ALOX5AP) has been implicated in carcinogenesis, yet its role in AML remains under-studied.

AIM

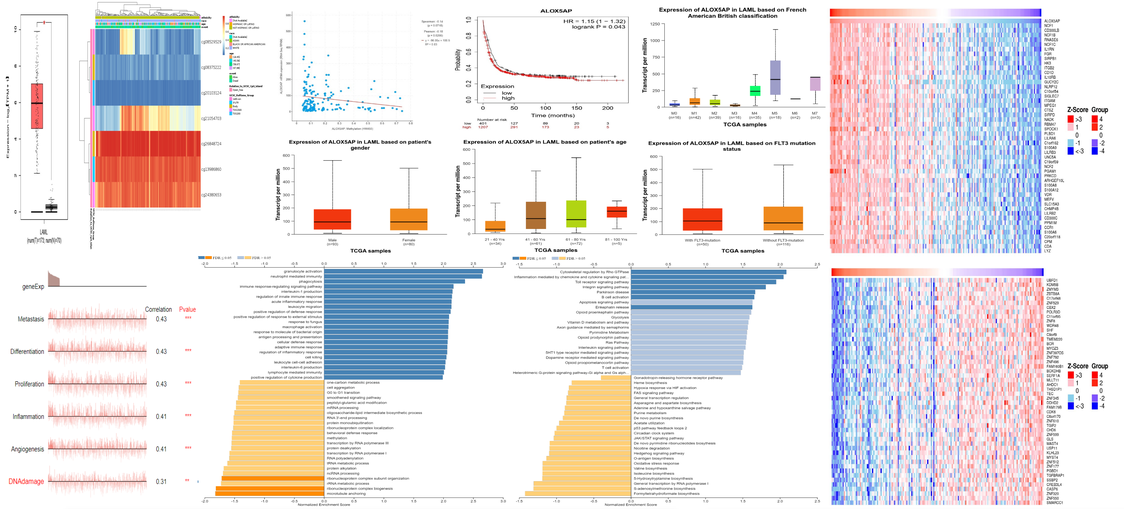
This work aimed to investigate the clinical and prognostic significance of the ALOX5AP gene in AML through analysis of its expression, methylation patterns, and molecular mechanisms.

METHOD

A total of 173 AML patients and 70 control cases were assessed for ALOX5AP gene expression and DNA methylation status. Kaplan–Meier survival estimation was employed to evaluate ALOX5AP's predictive importance. Correlations between ALOX5AP expression and functional states in AML single-cell datasets were estimated. Additionally, correlation analysis identified associated genes using the Linked Omics database, while gene set enrichment analysis (GSEA) elucidated molecular mechanisms of ALOX5AP in AML.

RESULTS

ALOX5AP was significantly overexpressed and exhibited lower methylation levels in AML cohorts compared to controls (P<0.05). Notably, *SLC40A1* gene expression negatively correlated with lower ALOX5AP gene methylation (P<0.0342) and was associated with poor overall survival in AML patients (P 0.0024). ALOX5AP expression was higher in M5 subtypes, females, older AML patients, and those with *FLT3*-ITD mutations. Furthermore, ALOX5AP expression correlated positively with metastasis, differentiation, proliferation, inflammation, and angiogenesis in AML single-cell datasets. Correlation analysis identified positive associations with genes like *NCF1, SIRPB1*, and *IL1RN*, while negative correlations were found with *UBFD1* and *KDM5B* (P<0.001). Gene enrichment analysis revealed ALOX5AP involvement in granulocyte activation, cytokine binding, and chemokine signaling pathways.



CONCLUSIONS

ALOX5AP emerges as a critical factor in AML development, offering potential as a prognostic biomarker and therapeutic target. Its overexpression and methylation patterns correlate with clinical outcomes and molecular subtypes, underscoring its importance in AML pathogenesis. These findings highlight ALOX5AP's multifaceted role in AML and its potential for guiding personalized treatment strategies in the future.

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