# Abstract: PB2378

# Title: EXPRESSION ANALYSIS, CLINICAL SIGNIFICANCE AND POTENTIAL FUNCTION OF ALOX5AP IN ACUTE MYELOID LEUKEMIA

**Abstract Type: Publication Only**

**Topic: Acute myeloid leukemia - Biology & translational research**

**Background:**

Acute myeloid leukemia (AML) is a group of hematologic malignancies with diverse biological characteristics and clinical manifestations that may lead to blocked differentiation and uncontrolled proliferation of leukemic primitive cells. Arachidonate 5-Lipoxygenase-activating protein (ALOX5AP) has been recognized as an oncogene that has been linked to several facets of carcinogenesis, including leukocyte activation. However, its function in AML has not been investigated

**Aims:**

In this work, we examined the clinical and prognostic importance of the ALOX5AP gene in patients with AML by determining its expression, methylation patterns, and molecular mechanism.

**Methods:**

We examined the ALOX5AP gene's expression and DNA methylation state in 173 AML patients and 70 control cases. The Kaplan–Meier survival estimation method was employed to assess the predictive importance of SLC40A1 using Kaplan Meier plotter. Moreover, we also estimate the correlations between ALOX5AP gene expression and functional states in AML single-cell datasets. Further, we also performed correlation analysis to identify the potentially associated gene linked with the ALOX5AP gene based on their expression levels using the Linked Omics database. Finally, we investigated the molecular mechanisms of ALOX5AP in AML using gene set enrichment analysis (GSEA).

**Results:**

Our findings showed that ALOX5AP was significantly overexpressed and the methylation level of the ALOX5AP gene was lower in AML (n=173) cohorts compared to normal cases (n=70) ($p < 0.05$). However, SLC40A1 gene expression was negatively correlated with lower ALOX5AP gene methylation ($p < 0.0342$) and was associated with poor overall survival (OS) in AML patients (p 0.0024). ALOX5AP expression was shown to be significantly greater in M5 subtypes, older AML cases, and AML patients with FLT3-ITD mutations. ALOX5AP gene expression is positively associated with metastasis, differentiation, proliferation, inflammation, and angiogenesis functional states in AML single-cell datasets. In correlation analysis ALOX5AP gene was positively correlated with the NCF1 gene, followed by SIRPB1, IL1RN, ITGBP genes while negatively correlated with UBFD1, KDM5B, ZMYM3, and POLR3D ($p < 0.001$). Gene enrichment analysis revealed ALOX5AP gene was enriched in various biological processes including granulocyte activation, phagocytosis, interleukin-1 production, neutrophil-mediated immunity, and regulation of innate immune response, while in molecular function SLC40A1 gene was enriched in cytokine binding, pattern recognition receptor activity. Furthermore, ALOX5AP gene was enriched in the Chemokine signalling pathway, Toll receptor signalling pathway, and Ras pathway activation in KEGG pathway enrichment.

**Summary/Conclusion:** ALOX5AP is crucial to the development of AML and may be used as a prognostic biomarker and therapeutic target for efficient treatment AML

**Keywords:** Acute myeloid leukemia, Leukemia, Acute leukemia, Myeloid leukemia