Higher ASXL1 Expression Is Associated With Improved Overall Survival in TP53-Mutated Acute Myeloid Leukemia

Max Bustillo[1], Sophio Kakabadze[1], Darilis Palacio[2]
[1]Ascension Saint Joseph, Chicago, IL, USA; [2]Independent Researcher, Chicago, IL, USA

INTRODUCTION

TP53-mutated acute myeloid leukemia (AML) has adverse outcomes, but clinically meaningful survival heterogeneity remains. The prognostic significance of ASXL1 expression in TP53-mutated AML is incompletely defined.

AIM

To determine whether higher ASXL1 expression is associated with improved overall survival (OS) in TP53-mutated AML, including chemotherapy-treated patients, and to explore directionality in TCGA-LAML.

METHOD

- Retrospective analysis of publicly available, deidentified genomic, transcriptomic, and clinical data from Beat AML, with exploratory assessment in TCGA-LAML.
- OS according to continuous ASXL1 expression using Cox proportional hazards regression. Multivariable modeling adjusted for DNMT3A expression, secondary AML, and MPN-associated disease. ASXL1 expression was analyzed as log2 RNA-seq RPKM and averaged per patient when multiple samples were available.

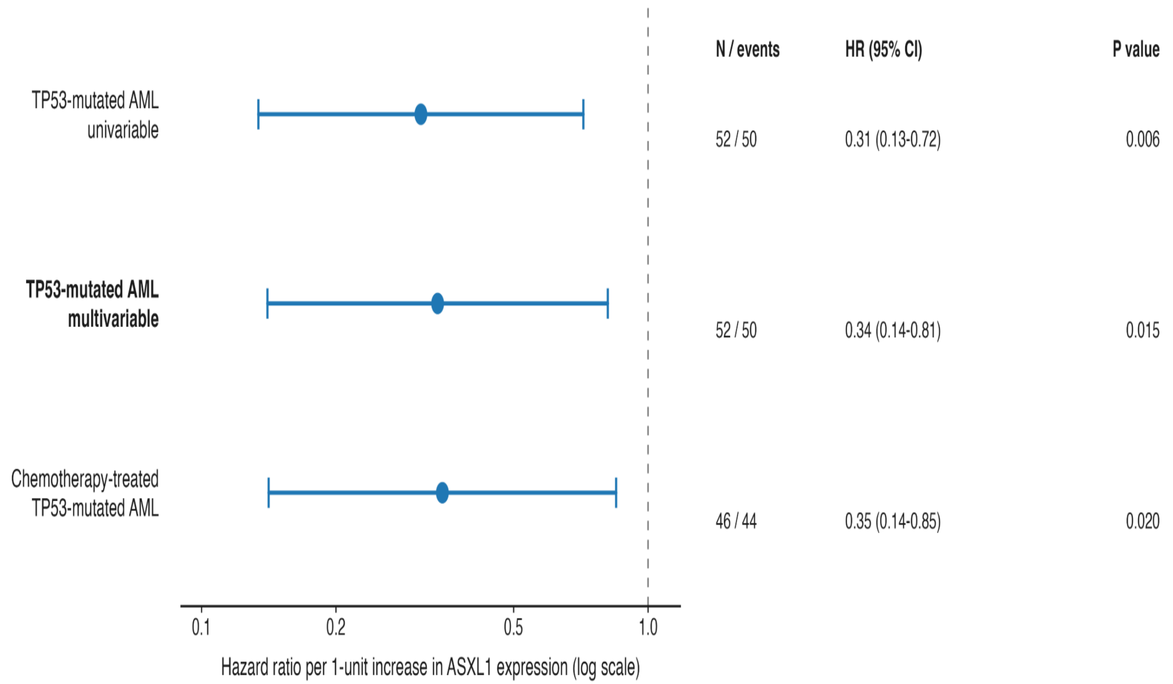
CONCLUSIONS

Higher ASXL1 expression was independently associated with improved OS in TP53-mutated Beat AML, including chemotherapy-treated patients. Exploratory TCGA-LAML results were directionally consistent but underpowered. ASXL1 expression may identify prognostic heterogeneity within TP53-mutated AML and warrants validation in larger independent cohorts.

RESULTS

STUDY COHORT
76 unique TP53-mutated patients identified
↓
52 with ASXL1 expression and OS data
50 deaths
↓
46 chemotherapy-treated patients
44 deaths

KEY RESULT
Higher ASXL1 expression remained independently associated with improved OS after multivariable adjustment.
Adjusted HR 0.34
95% CI 0.14–0.81; P=0.015



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CONTACT INFORMATION

Max Bustillo
Ascension Saint Joseph
Chicago, IL, USA
Email: max.Bustillo@ascension.org

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