A Prospective Study to Evaluate the Prognostic Implications of PRDM16 Gene in Acute Myeloid Leukemia

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Background

Acute myeloid leukemia (AML) is a complex hematologic malignancy distinguished by the accumulation of abnormally differentiated and uncontrolled proliferation of immature myeloid cells in the bone marrow induced due to diverse genetic alterations with recurrent cytogenetic abnormalities [1-3]. PR domain-containing 16 (PRDM16) is a transcriptional coregulatory encodes for zinc finger transcription factor crucial for both normal and malignant hematopoiesis and essential for hematopoietic stem cells (HSCs) maintenance [4]. However, to our knowledge, the molecular interaction, biological and immunological role as well as its clinical diagnostic and prognostic value in AML is still incompletely known.

Objective

This study aimed to characterize the potential role and molecular functions of PRDM16 in AML.

Materials & Methods

In this study, PRDM16 expression level was studied using GEPIA2 database. Kaplan–Meier survival investigation was performed to estimate the prognostic significance of PRDM16 using UALCAN platforms. We explore the molecular mechanisms of PRDM16 in AML, its correlation, and biological function analysis by performing Gene set enrichment analysis (GSEA) and Linked Omics database. The relationship of PRDM16 expression with immune infiltration level was analyzed using TIMER 2.0 and CIBERSORT database.

Results

In our analyses, PRDM16 mRNA was significantly overexpressed in TCGA-LAML cohorts and closely associated with a worse prognosis in TCGA-LAML cohorts (P<0.05). Enrichment analysis revealed that PRDM16 was involved in tumor immunity. Notably, the PRDM16 mRNA expression was negatively linked with the infiltration of immune cells and stromal cells.

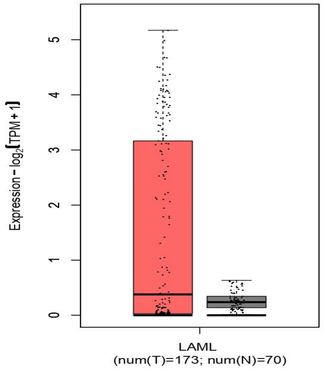


Fig 1 . PRDM16 Gene Expression in AML

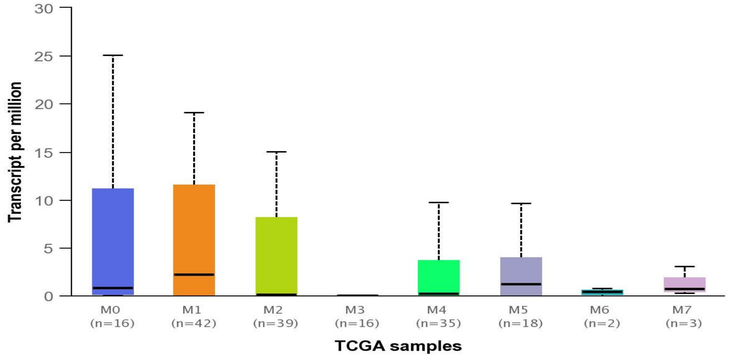


Fig 2 . PRDM16 Gene Expression in AML based on FAB Classification

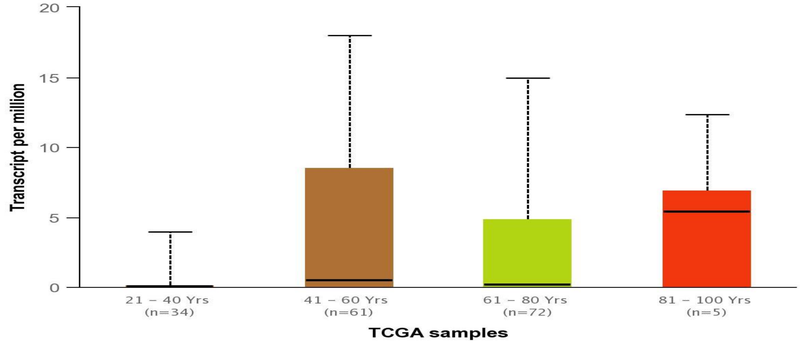


Fig 3 . PRDM16 Gene Expression in AML based on Patients" Age

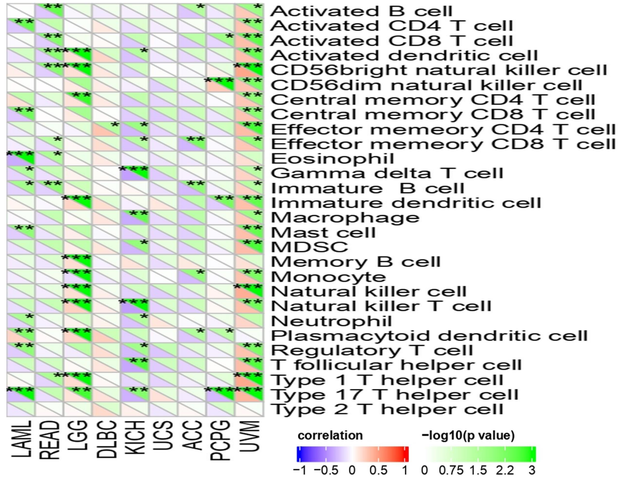


Fig 4 . PRDM16 Gene Expression based on Immune Checkpoints

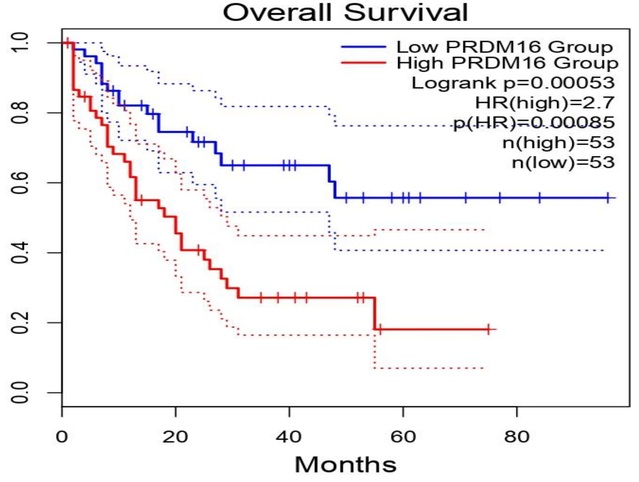


Fig 5 . PRDM16 Survival in AML

Conclusion

In this study, we found that PRDM16 plays a significant role in AML progression and may serve as a potential prognostic biomarker and therapeutic target for the effective management of AML.

References

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Acknowledgement

I am thankful to the the Society of Hematologic Oncology (SOHO) for selecting me for the **Young Investigator Program Grant (YIP).**