Journal of Leukemia
ISSN: 2329-6917
OPEN ACCESS Freely available online
Perspective

Emerging Biomarkers in Acute Myeloid Leukemia: Moving Beyond Cytogenetics

Edward Casey*

Department of Hematopathology, King's College London, London, UK

DESCRIPTION

Recent advances in molecular diagnostics have revolutionized our understanding of Acute Myeloid Leukemia (AML), transforming it from a morphologically defined disease into a molecularly heterogeneous spectrum of conditions. While cytogenetic analysis has long served as the cornerstone for AML risk stratification, emerging biomarkers are increasingly demonstrating their critical importance in refining prognostication and guiding therapeutic decisions.

For decades, clinicians have relied primarily on conventional cytogenetics to classify AML patients into favorable, intermediate, or adverse risk groups. This classification has guided treatment intensity decisions, with high-risk patients typically receiving more aggressive therapy, potentially including allogeneic hematopoietic stem cell transplantation in first remission. However, the limitations of cytogenetic analysis have become increasingly apparent, particularly for the substantial proportion of patients classified as having intermediate-risk disease based on a normal karyotype. The advent of Next Generation Sequencing (NGS) has dramatically expanded our capacity to detect genetic alterations in AML, revealing a complex landscape of mutations that influence disease biology, response to therapy, and overall prognosis

Epigenetic modifications represent another frontier in AML biomarker discovery. Alterations in DNA methylation patterns, histone modifications, and chromatin structure contribute significantly to leukemogenesis and have prognostic implications. The identification of mutations in epigenetic regulators such as *DNMT3A*, *TET2*, and *EZH2* has not only provided insights into disease pathogenesis but also opened avenues for targeting these abnormalities therapeutically. Hypomethylating agents like azacitidine and decitabine have shown efficacy in certain AML subsets, particularly in older patients and those with adverse molecular features.

The tumor microenvironment also plays a crucial role in AML pathogenesis and therapy resistance. Interactions between leukemic cells and bone marrow stromal cells can promote leukemic cell survival and protect against chemotherapy-induced apoptosis. Biomarkers reflecting these interactions, such as adhesion molecules, cytokines, and chemokines, may provide valuable prognostic information and identify potential therapeutic targets. For example, high expression of *CXCR4* on leukemic blasts has been associated with poor outcomes and may predict response to *CXCR4* antagonists currently under investigation.

Recent research has highlighted the importance of clonal hematopoiesis and pre-leukemic mutations in AML development and relapse. Mutations in genes such as *DNMT3A*, *ASXL1*, and *TET2* can be detected in seemingly healthy individuals, particularly with advancing age, and may persist after achievement of morphologic remission in AML patients. These persistent pre-leukemic clones can serve as a reservoir for disease recurrence and may influence post-remission treatment decisions. Monitoring these mutations during remission could potentially identify patients at higher risk of relapse who might benefit from preemptive intervention.

The integration of multiple biomarkers into comprehensive risk assessment models represents a promising approach to personalized AML management. Machine learning algorithms incorporating cytogenetics, molecular mutations, gene expression profiles, and clinical variables have demonstrated superior prognostic accuracy compared to conventional risk stratification systems. These computational approaches may eventually enable more precise prediction of treatment outcomes and guide therapeutic decision-making.

Despite these advances, significant challenges remain in biomarker implementation. Technical considerations, including assay standardization, turnaround time, and cost, can limit widespread adoption in clinical practice. Additionally, the interpretation of complex molecular findings requires specialized expertise that may not be available in all treatment centers. Collaborative efforts to establish standardized testing protocols and reporting systems will be essential to ensure equitable access to molecular diagnostics and their benefits.

Correspondence to: Edward Casey, Department of Hematopathology, King's College London, London, UK, E-mail: caseye@gmail.com

Received: 03-Mar-2025, Manuscript No. JLU-25-38097; **Editor assigned:** 05-Mar-2025, PreQC No. JLU-25-38097 (PQ); **Reviewed:** 18-Mar-2025, QC No. JLU-25-38097; **Revised:** 25-Mar-2025, Manuscript No. JLU-25-38097 (R); **Published:** 01-Apr-2025, DOI: 10.35248/2329-6917-25.13.426

Citation: Casey E (2025). Emerging Biomarkers in Acute Myeloid Leukemia: Moving Beyond Cytogenetics. J Leuk. 13:426.

Copyright: © 2025 Casey E. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.