

How do novel molecular genetic markers influence treatment decisions in acute myeloid leukemia?

Abstract

Acute myeloid leukemia (AML) is the most common acute leukemia diagnosed in adults, and the majority of patients with AML die from relapsed disease. Although many studies over the past 4 decades have identified disease alleles in AML, recent genome-wide and candidate gene studies have identified additional recurrent somatic mutations in AML patients with biologic, clinical, and therapeutic importance. Herein we review our current understanding of the molecular pathogenesis of AML and discuss how mutational profiling can be used to refine prognostication in AML and to inform therapeutic approaches. We also review the current challenges in translating genomic studies to the clinical setting, which remains a significant challenge and an urgent priority.