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# NEXT-GENERATION SEQUENCING IN ACUTE MYELOID LEUKEMIA: ENHANCING SURVIVAL OUTCOMES AND ASSESSING UTILITY IN RESOURCE-LIMITED SETTINGS

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## INTRODUCTION

Acute myeloid leukemia (AML) represents a complex hematologic malignancy characterized by heterogeneous genetic alterations. Next-generation sequencing (NGS) has revolutionized our understanding of AML pathogenesis, aiding in risk stratification and guiding therapeutic decisions. However, its application and impact on survival outcomes in resource-limited countries remain underexplored.

## AIM

This study aimed to evaluate NGS's clinical effectiveness in predicting outcomes for AML patients in low-income countries, particularly in Lebanon.

## METHOD

**Setting:** The study was conducted at the American University of Beirut Medical Center (AUBMC), a referral center in Lebanon with advanced molecular diagnostic facilities.

**Design**: A retrospective study that analyzed charts of 39 AML patients diagnosed between January 2019 and December 2021 who underwent NGS testing at diagnosis.

**Main Outcome Measures:** All patients underwent NGS profiling at diagnosis using a targeted gene panel covering 54 known AML-associated mutations. Clinical and molecular data were collected, and survival outcomes were assessed.

## RESULTS

The study cohort consisted of 39 patients with AML, with a median age of 57 years (range: 18-82).

Cytogenetic abnormalities were detected in 18 out of 39 patients (46%). FLT3-ITD mutations were identified in 9 out of 39 patients (23%), and NPM1 mutations were present in 8 patients (20.5%). Notably**, 13 out of 39 patients (33.3%) lacked cytogenetic abnormalities**, FLT3, and NPM1 mutations**, however NGS testing proved valuable in identifying mutations in this subgroup**, and the mutations detected by NGS included 4 IDH mutations, 1 ASXL1 mutation, 3 TET2 mutations, 2 DNMT3A mutations, 2 GATA2 mutations, and 2 RUNX1 mutations.

In total, 33 patients received treatment at our institution, with 16 out of 33 (48%) receiving intensive chemotherapy (including patients with high risk mutations detected by NGS). Additionally, 14 patients underwent allo-transplant as part of their treatment strategy.

The 2-year leukemia-free survival (LFS) rate was 67.8% (95% CI: 43.2-83.6).

The 2-year overall survival (OS) rate was 69% (95% CI: 51.0-81.5), demonstrating favorable outcomes in this cohort.

## CONCLUSIONS

This study highlights the feasibility and clinical relevance of NGS even in resource-limited countries, where its implementation can enhance survival outcomes by facilitating targeted interventions and optimizing resource allocation.

## REFERENCES

1. **Dohner H et al.** Diagnosis and management of AML in adults: 2017 ELN recommendations from an international expert panel. Blood. 2017; 129: 424-47
2. **Haferlach T et al.** Landscape of genetic lesions in 944 patients with myelodysplastic syndromes. Leukemia. 2014; 28: 241-7
3. **Papaemmanuil E et al.** Genomic Classification and Prognosis in Acute Myeloid Leukemia. N Engl J Med. 2016 Jun 9;374(23):2209-2221
4. **El Achi H et al.** Biomarkers in Acute Myeloid Leukemia: Leveraging Next Generation Sequencing Data for Optimal Therapeutic Strategies. Front Oncol. 2021 Sep 30;11:748250

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