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INSIGHTS INTO THE EPIDEMIOLOGICAL LANDSCAPE OF GENETIC MUTATIONS IN ACUTE MYELOID LEUKEMIA PATIENTS AT AMERICAN UNIVERSITY OF BEIRUT MEDICAL CENTER

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INTRODUCTION

This study evaluated the prevalence of somatic mutations through next-generation sequencing (NGS) in patients diagnosed with acute myeloid leukemia (AML) at American University of Beirut Medical Center. This will provide insights on genomic profiling in the AML population in Lebanon.

AIM

This study aimed to evaluate the frequency and patterns of somatic mutations detected by NGS in the AML population. Also, the association of those mutations with demographics and AML features were examined.

METHOD

- **Design:** This study was a retrospective chart review of AML patients in whom NGS was performed at diagnosis in a primary care center.
- **Patients**: It included patients aged ≥18 years with AML with NGS testing between January 2019 and December 2021.
- **Main Outcomes Measures:** The first outcome measure was mutation prevalence with frequency of each specific mutation detected through NGS.

RESULTS

A total of 39 patients were included in this study. The median age was 58 years (18-82) and 51% of them were males. Most patients (56.4%) were *de novo* AML; 20.5% were secondary from MDS, and 12.8% were therapy related. A total of 18 patients (46.2%) had cytogenetic abnormalities.

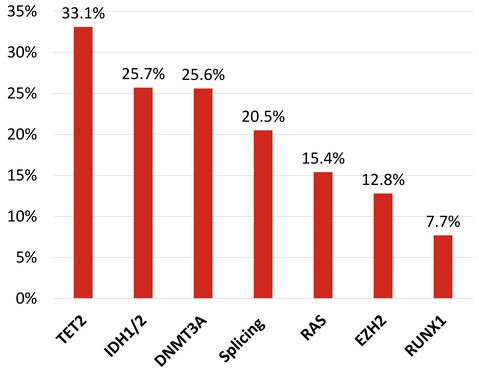
Cytogenetic risk stratification based on ELN 2022 criteria showed 75% were high risk, 10% were intermediate risk, and 15% were favorable risk. Of the 18 patients, 20.5% were *FLT3-ITD* positive and 15.4% were *NPM1* positive by polymerase chain reaction. The median number of mutations detected per patient was 2. The most common mutations detected were *TET2* (33.1%), *IDH1/2* (25.7%), *DNMT3A* (25.6%), splicing mutations (20.5%), *RAS* (15.4%), *EZH2* (12.8%), and *RUNX1* (7.7 %).

Based on ELN 2022 classification by mutations, 58.9% of the total mutations were high risk, 12.8% were intermediate risk, and 2.6% were favorable risk. Patients exhibiting *TET2* were associated with high-risk cytogenetics; however, no statistically significant correlation was found (*P*=0.166). *FLT3* and *NPM1* were statistically significantly associated with female gender (*P*=0.014 and 0.065, respectively). *EZH2* mutation was correlated with male gender (*P*=0.02).

Table 1. Demographic Characteristics

	Value
Total Patients (n)	39
Median Age (years)	58
Percentage of Males (in %)	51%
AML Subtypes (%)	
De novo AML	56.4%
Secondary from MDS	20.5%
Therapy related	12.8%
Patients with Cytogenetic Abnormalities n (%)	18 (46.2%)
Cytogenetic Risk Stratification	
High Risk	75%
Intermediate Risk	10%
Favorable Risk	15%

Figure 1. Percentage of Mutations



CONCLUSIONS

This study showed that frequencies of NPM1 and FLT3 mutations are found to be lower than reported, with a higher prevalence of high-risk mutations.

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