DOI: 10.51271/JCHOR-0031

Contributions of ELN2022 update and new genetic analysis tests in the risk assesment and treatment of acute myeloid leukaemia

©Seda Yılmaz, ©Metin Bağcı, ©Abdulkadir Baştürk

Department of Adult Haematology, Konya City Hospital, Konya, Turkiye

Cite this article: Yılmaz S, Bağcı M, Baştürk A. Contributions of ELN2022 update and new genetic analysis tests in the risk assessment and treatment of acute myeloid leukaemia. *J Curr Hematol Oncol Res.* 2024;2(1):22-23.

Corresponding Author: Seda Yılmaz, dr46sedakurtulus@hotmail.com

Received: 10/12/2023 ◆ Accepted: 11/01/2024 ◆ Published: 12/02/2024

Dear Editor,

Acute myeloid leukaemia (AML) is a heterogeneous disease including cytogenetic and molecular abnormalities. ^{1,2} Age, performance status and specific genetic characteristics are important in prognosis. ³⁻⁵ Both directing consolidation treatment and having genetic-based treatment targets have made genetic results even more important. ⁶ The European LeukemiaNet (ELN) 2022 report was published by expanding the genetic mutation profile. ⁷ In order to question what this update has changed in clinical practice, we reviewed the data of patients with acute myeloid leukaemia in whom myeloid panel was studied by Next-Generation Sequencing (NGS).

The data of patients who were followed up in our clinic due to AML and whose myeloid panel was studied by NGS method at the time of diagnosis were analysed. The ELN 2017 and ELN 2022 risk categories of 10 patients were determined.

Among the participants, 30% were female and 70% were male. The median age of the participants was 60±18.41 (25-81) years. According to the ELN2017 AML classification, 20% of the patients were in the good, 50% in the intermediate, 30% in the poor risk group, while according to the ELN2022 AML classification, 20% were in the good, 20% in the intermediate, 60% in the poor risk group. FMSlike tyrosine kinase 3 (FLT3 -ITD) mutation, which can direct the treatment with myeloid panel, was found positive in myeloid panel (NGS) in 2 patients who were found negative with Polymerase Chain Reaction (PCR) method. In addition, EZH2, SF3B1, SRSF2 were found positive in 3 patients and were included in the poor risk group from the intermediate risk group. When the changes in the risk group were analysed, it was observed that 30% of the patients had a change. No statistically significant difference was found between patients with and without changes in risk status with the last ELN report in terms of gender, hemogram parameters at ECOG diagnosis, response to induction regimen and outcome. Targeted agents were added to the treatment of patients with myeloid panel reports (Table). In addition, allogeneic bone marrow transplantation was planned for patients in the high-risk group. A total of 60% of our patients are surviving (Figure).

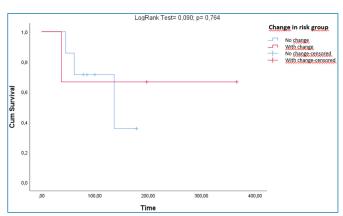


Figure. The relationship between BMI and WCM, BMI and BFP

Table. Genetic risk characteristics of patients and ELN classification				
Patient	Genetic Outcome	ELN 2017	ELN2022	Mutations detected differently between tests
1	SRSF2, EZH2	Intermediate	Poor	
2	SF3B1, SRSF2	Intermediate	Poor	
3	NPM1	Good	Good	
4	t(8;21)	Good	Good	
5	FLT3(PCR)*, NPM1	Intermediate	Intermediate	
6	11q23	Poor	Poor	
7	-10,-12, del(5q), FLT3, U2AF1, ASXL1		Poor	FLT3(PCR) negative
8	EZH2, FLT3	Intermediate	Poor	FLT3(PCR) negative
9	No feature	Intermediate	Intermediate	IDH1
10	-7	Poor	Poor	
*Allelic ratio:0.8				

ELN 2017 is a generally accepted risk classification. The extent to which ELN 2022 recommendations will lead to changes in clinical practice is exciting. The main difference of ELN 2022 risk classification compared to ELN 2017 risk classification is the expansion of somatic gene mutation, definition of variant allele fraction, and removal of FLT3 mutation allele burden. In our study, a change was found in

the risk category of 30% of our patients according to the new risk classification. In addition, while FLT3 was found negative by PCR in 2 patients, it was found positive by myeloid next generation sequencing panel. Again, thanks to this panel, IDH mutation, which is another targeted treatment chance, was detected.

We suggest that genetic risk analyses should be performed with as large a panel and different analysis methods as possible and these tests should be combined and evaluated.

Keywords: Acute myeloid leukemia, classifications, next generation sequencing, polymerase chain reaction

REFERENCES

- 1. Papaemmanuil E, Gerstung M, Bullinger L, et al. Genomic classification and prognosis in acute myeloid leukemia. *N Engl J Med*. 2016;374(23):2209-2221.
- 2. Tyner JW, Tognon CE, Bottomly D, et al. Functional genomic landscape of acute myeloid leukaemia. *Nature*. 2018;562(7728):526-531.
- Sekeres MA, Peterson B, Dodge RK, et al. Differences in prognostic factors and outcomes in African Americans and whites with acute myeloid leukemia. *Blood.* 2004;103(11):4036-4042.
- Olesen LH, Aggerholm A, Andersen BL, et al. Molecular typing of adult acute myeloid leukaemia: significance of translocations, tandem duplications, methylation, and selective gene expression profiling. Br J Haematol. 2005;131(4):457.
- 5. Estey EH. Therapeutic options for acute myelogenous leukemia. *Cancer.* 2001;92(5):1059.
- El Chaer F, Hourigan CS, Zeidan AM. How I treat AML incorporating the updated classifications and guidelines. *Blood*. 2023;141(23):2813-2823.
- Döhner H, Wei AH, Appelbaum FR, et al. Diagnosis and management of AML in adults: 2022 recommendations from an international expert panel on behalf of the ELN. *Blood, J Am Soc Hematol.* 2022;140(12):1345-1377.
- Tallman MS, Wang ES, Altman JK, et al. Acute myeloid leukemia, version 3.2019, NCCN clinical practice guidelines in oncology. J Natl Compr Canc Netw. 2019;17(6):721-749.