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(PB2523) MOLECULAR GENETIC PROFILE OF PATIENTS WITH ACUTE MYELOID LEUKEMIA IN THE REPUBLIC OF BELARUS

Topic: 4. Acute myeloid leukemia - Clinical

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Background:

Patients with AML may have a wide range of chromosomal and DNA mitations. Analysis of mutations and their combinations makes it possible to divide patients into risk categories, predict the course and outcomes of AML and include targeted drugs in therapy

Aims:

Study the genetic profile of patients with AML using molecular genetic methods

Methods:

Bone marrow was examined using an automatic MiSeq sequencer (Illumina, USA) and a commercial test system "AmpliSeqTM for Illumina Myeloid Panel" in accordance with the manufacturer's protocol (next-generation sequencing method, NGS). A standard cytogenetic and FISH study of the bone marrow were also performed.

Results:

The study included 39 patients, 40 bone marrow samples were obtained (in 1 patient again when a relapse developed). The group included 17 women (43.6%) and 22 men (56.4%), ranging in age from 18 to 63 years (median 45 years).

The classification options for AML are the following: AML MO-M5 (according to the FAB classification), AML with changes associated with myelodysplasia (according to the 2016 WHO classification), acute leukemia of mixed phenotype, other (no data).

Cytogenetic examination of the bone marrow was performed in 38 patients (97.4%), FISH examination in 25 patients (64.1%). The following mutations were detected (taken into account when dividing patients into risk categories): favorable (t (8;21)); intermediate (normal karyotype, t(15;17), t (7;12), t (11;17), t (11;?), t (19;?), t (2;8), del (7q), marker chromosome, del 3 MLL sections, trisomy 8 (+8), trisomy 11 (+11), monosomy X (-X), absence of Y (-U), hypodiploidy); adverse (monosomy 17 (-17), 11q23 (3 copies of MLL), 11q23 (MLL rearrangement), del(11)(q23), del 5q31 (EGR1)).

A molecular genetic testing was performed in all patients, the following mutations were identified: NPM1 without FLT3-ITD – in 6 patients (15%), CEBPA/bZIP – in 9 patients (22.5%), RUNX1 – in 4 patients (10%), NPM1 with FLT3-ITD – in 3 patients (7.5%), FLT3-ITD without NPM1 – in 10 patients (25%), WT1 – in 3 patients (7.5%), KIT – in 10 patients (25%), TP53 – in 10 patients (25%), ASXL1 – in 1 patient (2.5%), BCOR – in 9 patients (22.5%), EZH2 – in 6 patients (15%), STAG2 – in 1 patient (2.5%), U2AF1 – in 1 patient (2.5%). FLT3-ITD mutation was detected in 13 patients (32.5%) - isolated in 2 patients (5%) and in 11 patients (27.5%) in combination with other mutations.

The spectrum of genetic mutations is shown in Figure 1. Patients are divided into risk categories according to the ELN 2022

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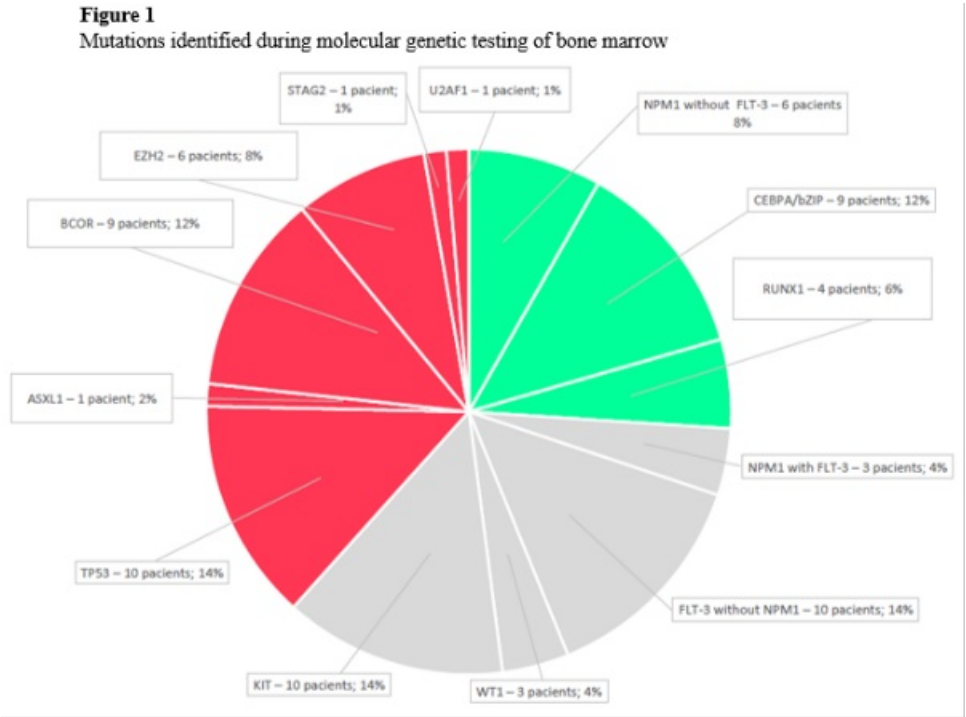
classification (data from cytogenetic and FISH research methods were also taken into account). There were 8 patients (20.5%) in the favorable risk category, 15 patients (38.5%) in the intermediate risk category and 16 patients (41%) in the adverse risk category.

Summary/Conclusion:

The study examined the spectrum of genetic mutations in patients with AML in the Republic of Belarus; patients were stratified into risk categories according to the ELN 2022 classification. The prevalence of FLT3-ITD mutations in patients with AML in the Republic of Belarus suggests the relevance of including a targeted drug of a protein kinase inhibitor (midostaurin) in the treatment regimen.

Figure 1
Mutations identified during molecular genetic testing of bone marrow



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