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GENETIC ABNORMALITIES IN A REAL-WORLD COHORT OF MULTIPLE MYELOMA (MM) PATIENTS, AND THEIR IMPACT ON OUTCOMES: SINGLE-CENTER EXPERIENCE

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INTRODUCTION

MM is a plasma cell malignancy with a highly heterogeneous risk. 2 decades ago, the risk was assessed mainly on the basis of features reflecting the disease burden; more recently, genetic changes have been considered as the most important determinants of MM risk. Single nucleotide polymorphisms (SNPs) microarray molecular karyotyping allows a very detailed assessment of chromosomal aberrations. The use of SNPs for the testing of myeloma patients as a standard of care was introduced at our center in 2017. Most of the published data on myeloma patients' genetic aberrations comes from patients participating in clinical trials. We present data from a real-world cohort of patients.

OBJECTIVE

To assess the prevalence and impact on prognosis of genetic aberrations detected by SNPs in a real-world cohort of patients.

METHODS

This retrospective study included real-world data from MM patients (≥18 years) diagnosed in 2017 or later, who underwent autologous stem cell transplantation (ASCT) between 2017 and 2021 at Vilnius University Hospital Santaros Klinikos.

Patients were categorized by karyotype abnormalities:

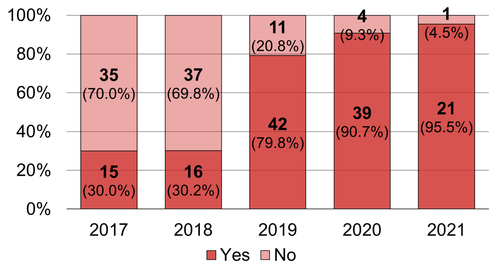
- large hyperdiploidy (>50 chromosomes),
- mild hyperdiploidy (47-50 chromosomes),
- non-hyperdiploidy (pseudodiploidy (46 chromosomes with one trisomy and one monosomy), normal and hypodiploidy (<46 chromosomes).

Overall survival (OS) and progression-free survival (PFS) were estimated using the Kaplan-Meier method.

RESULTS

221 patients underwent ASCT: in 133 (60.2%) patients SNPs testing were performed*

In the group of SNPs performed median age was 60 years (range: 38-76)

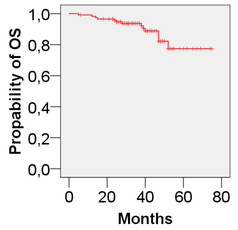


Scheme 1. *SNPs performed rate by year of diagnosis.*

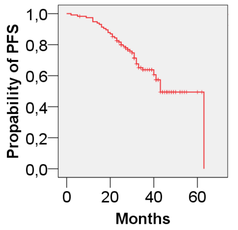
**In our clinical practice after ASCT majority of the patients didn't receive any maintenance. treatment*

Variable	n (%)
Gender	
Female	75 (56.4)
Male	58 (43.6)
Karyotype	
large hyperdiploidy	23 (17.3)
mild hyperdiploidy	44 (33.1)
non-hyperdiploidy	66 (49.6)
+1q	37 (27,8)
del(17p)	12 (9,0)
SCT type and number	
First ASCT	116 (87.2)
Second ASCT	14 (10.5)
ASCT+allogeneic SCT	3 (0.02)

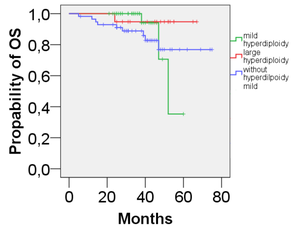
Table 1. *SNPs performed group characteristics.*



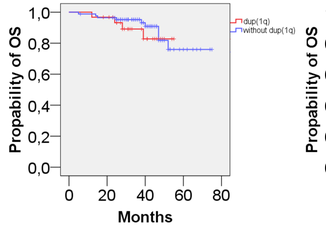
Scheme 2. *In the first ASCT group median OS was not reached (5-year – 77%).*



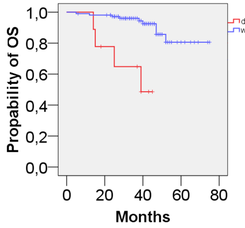
Scheme 3. *In the first ASCT group median PFS was 43 months (95% CI: 38.6–47.4; 5-year survival without event – 49%)*



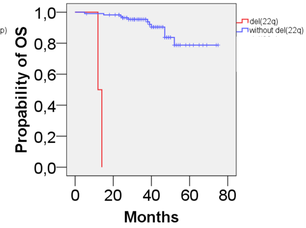
Scheme 4. *In the first ASCT group patients with large, mild or non-hyperdiploidy had no significant difference.*



Scheme 5. *In the first ASCT group patients with dup(1q) had similar OS as without dup(1q) group.*



Scheme 6. *In the first ASCT group patients with del(17p) had significantly shorter OS (P=0.001).*



Scheme 7. *In the first ASCT group patients with del(22q) had significantly shorter OS (P=0.001).*

Patients groups	PFS		OS	
	months, median (95% CI)	P value	months, median (95% CI)	P value
Large vs mild vs non- hyperdiploidy	not reached vs 41 (28.22-53.78) vs 43 (36.55-49.45)	0.247	not reached vs 52 (44.49-59.51) vs not reached	0.282
with dup(1q) vs without	not reached vs 43 (37.78-48.21)	0.741	Both not reached	0.624
with del(17p) vs without	16 (13.08-18.92) vs 43 (39.38-47.62)	0.112	39 (-) vs not reached	0.001
with del(22q) vs without	2 (-) vs 63 (-)	0.001	12 (-) vs not reached	0.001

Table 2. *Comparing PFS and OS in the first ASCT group, there were no significant differences between large, mild, and non- hyperdiploidy.. In the first ASCT group, patients with del(17q) and del(22q) had significantly shorter OS and PFS (both P=0.001).*

CONCLUSIONS

In real-world data cohort from MM patients, del(17p) and del(22q) abnormalities detected by SNPs are poor prognosis factors for OS and PFS.

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