



The 65th ASH Annual Meeting Abstracts

ORAL ABSTRACTS

637.MYELODYSPLASTIC SYNDROMES - CLINICAL AND EPIDEMIOLOGICAL

TP53 Gene allelic State in Myelodysplastic Syndromes (MDS) with Isolated 5q Deletion

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Background & aim: The mutational status of *TP53* gene is a significant prognostic factor in MDS, with two-thirds of patients harboring *TP53* multihit alterations which are associated with poor outcomes. Approximately 20% of patients with MDS with isolated 5q deletion (MDS-del5q) exhibit *TP53* aberrations, though their characteristics and prognostic impact have not been fully elucidated. In this study, we aimed to analyze the characteristics and impact of *TP53* allelic state in patients with MDS-del5q.

Methods: We conducted an international multicenter study in *de novo* MDS-del5q patients according to WHO 2017 classification. Clinical and biological characteristics, including the genetic profile were collected at diagnosis. Genetic profiling included conventional G-banding, *TP53* deletion by FISH and/or SNP-arrays (for *TP53* deletion and copy number neutral loss of heterozygosity). Also, the presence of mutations in myeloid-related genes was assessed by NGS or Sanger. Variant filtering and categorization were performed according to the Spanish Guidelines. Patients were classified as *TP53* wild-type (*TP53*-wt), *TP53*-monoallelic, and *TP53*-multihit as proposed by Bernard *et al.* 2020. Clinical and molecular variables were evaluated for associations with acute myeloid leukemia (AML) evolution and overall survival (OS). In addition, a prognostic model to predict risk of AML evolution was developed using variables selected by the LASSO-cox method with minimum lambda. To calculate the points for each variable, a multivariate competitive risk model (Fine-Gray model) was fitted. Evolution to AML was used as the event and death as the competitive event. Statistical analysis was performed by R (4.2.2).

Results: We included 682 patients with MDS-del5q (Table 1). Median follow-up was 66.8 months (CI95% 61.6-75.2). *TP53* mutations were evaluated by NGS in 92.2% (n=629) and by Sanger in 7.8% (n=53) of patients. Overall, 18.7% (n=128) of MDS-del5q presented *TP53* mutations. After integrating mutational data (FISH and SNP-arrays), 72.7% (n=93) of *TP53*-mutated patients were classified as *TP53*-monoallelic, whereas 27.3% (n=31) as *TP53*-multihit (4.5% of the whole cohort). Other recurrent mutations were *SF3B1* (21%), *DNMT3A* (18%), *TP53* (18%), *TET2* (14%), *ASXL1* (10%), *CSNK1A1* (6%) and *JAK2* (6%). Only bone marrow blasts differ between the *TP53*-wt and *TP53*-mutated groups ($p=0.031$). Furthermore, only gender and VAF were different between *TP53*-monoallelic and *TP53*-multihit, being the number and type of co-occurring mutations similar among all subgroups (Table 1).

Median OS of the whole cohort was 73.8 months (CI95% 63.7-83.4), and 77.3 months (CI95% 66.5-85.3) for MDS-del5q *TP53*-wt and 104 months (CI95% 56.9-89.4) for MDS-del5q *TP53*-mutated ($p=0.3$). Similarly, there was no significant differences in the risk to AML evolution between *TP53*-wt and *TP53*-mutated patients (AML evolution at 60 months of 19.9% and 29.7%, respectively; $p=0.307$). Of note, however, the *TP53*-multihit group presented worse prognosis compared to *TP53*-monoallelic and *TP53*-wt patients (median OS of 55.2, 73.2 and 77.3 months, and AML evolution at 60 months of 40.4%, 25.5% and 19.9% in *TP53*-multihit, *TP53*-monoallelic and *TP53*-wt MDS-del5q) [Figure 1]. Interestingly, *TP53*-monoallelic MDS with a *TP53* VAF >20% showed similar prognosis to *TP53*-multihit patients (median OS of 43.7 and 55.2 months, and AML evolution at 60 months of 36.7% and 40.4%, respectively).

Finally, a risk score (MDS-del5q score) for AML evolution was developed with five variables, each assigned a different weight based on the regression coefficients: additional chromosomal abnormality, 2 points; *TP53*-multihit, 2 points; BM blast >2%, 2 points; platelets $\leq 100 \times 10^9/L$, 3 points, and *SF3B1*-mutation, 1 point. Three risk-groups were defined: Low, intermediate, and high-risk for ≤ 1 , 2, or ≥ 3 points, respectively, with an AML evolution at 60 months of 11.5%, 23.3% and 43.7%, respectively; $p < 0.05$

Conclusions: In contrast to previous findings in MDS without del5q, our series of MDS-del5q, the longest described to date, reveals that multihit *TP53* status is uncommon in MDS-del5q. However, multihit alterations have prognostic significance in this subgroup. Finally, the MDS-del5q score allows to stratify patients into three distinct risk groups for AML evolution. These findings could hold considerable implications for guiding treatment decisions.

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Table 1. Characteristics of MDS-del5q patients, TP53-wt and TP53-mutated MDS, and according to TP53 allelic state.

Variable	Total n=662	TP53-wt (n=554; 83.7%)	TP53-monoallelic (n=128; 19.3%)	TP53-mutated (n=99; 14.9%)	P (TP53-wt vs mutated)	P (monoallelic vs mutated)
Age, years (median)	74 (64-80)	74 (65-80)	73 (66-79)	73 (68-80)	0.729	0.571
Sex, male	29.8%	27.3%	25%	18.2%	0.023	0.003
Hb, g/dL (median)	9.2 (8.1-10.4)	9.2 (8.1-10.3)	9.2 (8.1-10.3)	8.9 (7.9-10.3)	0.808	0.117
Leuk, x10 ⁹ /L (median)	4.04 (3.5-5.1)	4.1 (3.5-5.1)	4.1 (3.5-5.1)	3.9 (3.5-5.4)	0.287	0.021
Neutro, x10 ⁹ /L (median)	2 (1.5-3.3)	2 (1.5-3.3)	2 (1.5-3.3)	1.9 (1.3-3.1)	0.829	0.566
PLT, x10 ⁹ /L (median)	209 (188-247)	209 (179-234)	210 (146-311)	212 (154-314)	0.871	0.211
BM Fibro, % (median)	2 (1-8)	2 (1-5.5)	2 (1-3)	5.5 (3-5.5)	0.001	0.001
PSG-R (Y, & L)	83.7%	89.7%	89.6%	88.7%	0.381	0.778
Isolated del5q abnormality	83.1%	82.5%	85.9%	83.8%	0.348	0.382
WBC, median % (median)	20.4 (9-34.5)	NA	20.4 (9-34.5)	18.9 (7.2-31.4)	NA	<0.001
SF3B1	29.8%	27.3%	15.2%	15.8%	0.702	0.737
DNMT3A	18.4%	18.5%	17.7%	19.0%	0.867	0.540
TET2	14.1%	13.5%	16.5%	15.0%	0.500	0.871
ASXL1	9.8%	10.0%	8.9%	5.5%	0.758	0.480
CSMD1A1	6.3%	7.3%	3.0%	3.0%	0.106	0.607
JAK2	6.6%	6.2%	7.6%	4.8%	0.704	0.059

Figure 1. Risk of evolution to acute myeloid leukemia in MDS-del5q with TP53-wt, TP53-monoallelic and TP53-multihit

