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***FLT3* mutations in myelodysplastic syndrome and chronic myelomonocytic leukemia**

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Abstract

FMS-like tyrosine kinase III (*FLT3*) mutations occur in one-third of acute myeloid leukemia (AML) patients and predict poor outcome. The incidence and impact of *FLT3* in myelodysplastic syndrome (MDS) and chronic myelomonocytic leukemia (CMML) is unknown. We conducted a retrospective review to identify WHO MDS and CMML patients with *FLT3* mutations at diagnosis. A total of 2,119 patients with MDS and 466 patients with CMML were evaluated at MD Anderson between 1997 and 2010. Of these, *FLT3* mutation analysis was performed on 1,232 (58%) MDS and 302 (65%) CMML patients. *FLT3* mutations were identified in 12 (0.95%) MDS patients: 9 (75%) had *FLT3-ITD* mutation and 3 had *FLT3*-tyrosine kinase domain (*TKD*) mutation. MDS patients with *FLT3* mutations were younger ($P = 0.02$) and presented as RAEB ($P = 0.03$) more frequently. Median overall survival (OS) for *FLT3*-mutated MDS patients was 19.0 months versus 16.4 months for *FLT3*-nonmutated MDS patients ($P = 0.08$). *FLT3* mutations were identified in 13 (4.3%) CMML patients: 8 had *FLT3-ITD* mutation and 5 had *FLT3-TKD* mutation. There were no significant differences in demographic and disease characteristics among CMML patients with and without *FLT3* mutations. Median OS for *FLT3*-mutated CMML patients was 10.8 months versus 21.3 months for *FLT3*-nonmutated CMML patients ($P = 0.12$). *FLT3* occurs in MDS and CMML at a lower frequency than AML and does not predict poor outcome.

Introduction

FLT3 (FMS-like tyrosine kinase III) is a transmembrane tyrosine kinase that belongs to the Class III family of receptor tyrosine kinases (RTKs; other members of this family include receptors for KIT, FMS, and PDGF) [1]. Signaling via RTKs is frequently deregulated in hematological malignancies [2]. *FLT3* is expressed on the leukemic cells of 70–100% of patients with acute myeloid leukemia (AML) [3]. Additionally, activating mutations in *FLT3* are observed in ~30% of adult AML patients [4]. The two leading types of mutations found in AML include internal tandem duplications in the juxtamembrane domain (ITD, 17–34%)

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and mutations in the tyrosine kinase domain (TKD) activation loop (~7%) [5]. *FLT3* stimulates survival and proliferation of leukemic blasts [6]. Studies suggest that patients with *FLT3*-ITD have significantly elevated peripheral blood white cell counts and increased bone marrow blasts at diagnosis [5,7]. Furthermore, they have a significantly higher induction death rate, increased relapse risk, inferior event-free survival (EFS), and decreased overall survival (OS) [5,7,8]. *FLT3*-TKD mutations have unknown prognostic and predictive significance in AML [9].

The incidence and impact of *FLT3* in myelodysplastic syndrome (MDS) remains poorly defined [9–12]. We conducted a retrospective review at MDACC to identify the incidence, prognostic, and predictive impact of *FLT3* mutations (ITD and TKD) in patients with MDS (per WHO classification) or chronic myelomonocytic leukemia (CMML). We included CMML, because from a practical approach, they are treated as MDS. A higher frequency of *FLT3* mutations in CMML compared to MDS has been previously reported [12].

Methods

We conducted a retrospective review of patients with MDS and CMML evaluated at MDACC between January 1997 and December 2010. The study was conducted following institutional guidelines. A departmental database was used to identify patients with WHO classification MDS or CMML who had documented *FLT3* mutation (either ITD or TKD) at diagnosis.

Variables collected on all patients (*FLT3* mutated and *FLT3* nonmutated) at diagnosis included the following: age, gender, performance status, white blood cell count, absolute neutrophil count (ANC), platelet count, hemoglobin, bone marrow blast percentage, karyotype, and history of a prior malignancy. The IPSS risk score was calculated to determine a patient's risk of leukemic transformation and survival [13].

Detection of *FLT3* mutations

FLT3 analysis has been routinely performed on all patients with MDS and CMML evaluated at MDACC since 2003. However, *FLT3* analysis has also been performed retrospectively on stored MDS and CMML bone marrow specimens at MDACC dating back to 1997. Hence, we were able to include *FLT3* mutation status data on MDS and CMML patients from January 1997 to December 2010.

FLT3 mutations were analyzed in the clinical molecular diagnostic laboratory at MDACC. *FLT3* mutation status was determined in DNA from initial bone marrow aspirate samples. Genomic DNA from bone marrow samples was isolated using the Autopure extractor (QIAGEN/Gentra, Valencia, CA). *FLT3* mutation was analyzed as previously described [14].

Statistical analysis

Differences among variables were evaluated by the χ^2 test and Mann–Whitney *U* test for categorical and continuous variables, respectively. All *P* values were two-sided, and *P* < 0.05 was significant. Survival distributions were estimated using the Kaplan–Meier method,

and the differences were compared using the log-rank test. OS was defined as the time from presentation to the MDACC leukemia service to death from any cause or the last follow-up. Time to progression (TTP) was the time from diagnosis to progression to AML by WHO criteria (i.e., 20% blasts).

Results

There were 2,119 patients with MDS and 466 patients with CMML evaluated at MDACC between January 1997 and December 2010. *FLT3* mutational analysis was performed on 1,232 (58%) of the MDS patients and 302 (65%) of the CMML patients. *FLT3* mutations were identified in 12 (0.95 %) MDS patients and 13 (4.3%) CMML patients.

Patient characteristics

Demographic and disease characteristics were compared between the 12 *FLT3*-mutated MDS patients and 1,220 *FLT3*-nonmutated MDS patients (Table I). *FLT3 ITD* and *FLT3 TKD* mutations were present in 9 (8%) and 3 patients (25%), respectively. The MDS patients with *FLT3* mutations were younger (60 vs. 68 years; $P = 0.02$) and tended to present as RAEB more frequently than MDS patients without *FLT3* mutations ($P = 0.03$). No other significant differences were identified between the two groups. Median white count (WBC), hemoglobin, platelet count, and ANC for the *FLT3*-mutated MDS patients at diagnosis were $3.5 \times 10^9/l$ (range, 1.2–14.5), 9.9 g/l (range, 8.3–11.4), $47 \times 10^9/l$ (range, 15–101), and $1.5 \times 10^9/l$ (range, 0.5–7.2), respectively. Karyotype in *FLT3*-mutated MDS patients was diploid in 9 (75%); $-5/-7$ in 1 (8%), 11q in 1 (8%), and other cytogenetic aberrations in 1 patient (8%). *FLT3*-mutated MDS patients by IPSS: 1 patient had low risk (8%), 6 had intermediate-1 (50%), 4 had intermediate-2 (34%), and 1 had high-risk disease (8%).

Demographic and disease characteristics were compared between the 13 CMML *FLT3*-mutated patients and 289 *FLT3*-nonmutated patients (Table II). *FLT3 ITD* and *FLT3 TKD* mutations were present in 8 (62%) and 5 patients (38%), respectively. There were no significant differences in demographic and disease characteristics among CMML patients with and without *FLT3* mutations. Median WBC, hemoglobin, platelet count, and ANC for the *FLT3*-mutated CMML patients at diagnosis were $31.3 \times 10^9/l$ (range, 2.6–211.8), 10.1 g/l (range, 8.7–12.7), $120 \times 10^9/l$ (range, 23–429), and $13.3 \times 10^9/l$ (range, 0.5–108), respectively. Karyotype in *FLT3*-mutated CMML patient was diploid in 10 (77%), 20q-in 1 (8%), and others in 2 patients (15%).

Outcomes

Median OS for MDS patients with *FLT3* mutation was 19 months compared to 16 months for those without *FLT3* mutation ($P = 0.08$; Fig. 1). Median OS for CMML patients with *FLT3* mutation was 12 months compared to 21 months for those without *FLT3* mutation ($P = 0.12$; Fig. 2). At the time of analysis, 9 of 25 patients had progressed to AML and median TTP was 9 months (range, 1–36).

Discussion

The *FLT3* gene is located on chromosome 13q12 [1]. *FLT3* plays a crucial role in normal hematopoiesis and cellular growth in primitive hematopoietic stem and progenitor cells [15]. *FLT3* is activated following binding of *FLT3* ligand, leading to the activation of downstream signaling pathways including Stat5, RAS, and PI3 kinase [2,6]. Mutations occur in ~30% [4] of adult and pediatric AML cases and are particularly common among cytogenetically normal (44%: 32% with *FLT3-ITD* and 12% with *FLT3-TKD*) [16] or t(15;17) AML (40%) [17]. In the former setting, *FLT3-ITD* is associated with increased blasts, inferior EFS, and OS [5,7,18]. Prognosis is even worse when wild-type *FLT3* allele is lost [8] and *FLT3-ITD* mutations negate the positive influence expressed by NPM1 mutation [19]. The prognostic relevance of *FLT3-TKD* mutations remains controversial [9].

The epidemiologic and clinical features of *FLT3* mutations in MDS and CMML are less known [20]. To date, this is the largest analysis of *FLT3* mutations in MDS and CMML, either as individual diseases or as combined diagnosis. Case series have reported very low frequencies, both in adults and children [10,21,22]. Horiike et al. [10] first reported *FLT3-ITD* mutations in 7 of 92 patients with MDS (3%). Similarly, Shih et al. [12] analyzed 150 patients with MDS (RAEB-T not included) and identified *FLT3-ITD* mutations in only 5 (2.5%) patients [12]. The largest reported series of *FLT3* mutations in MDS was published by Bacher et al. [23] in 2007. Of 367 patients with MDS, *FLT3-ITD* mutations were identified in eight cases (2.2%), all with an underlying diagnosis of RAEB, and *FLT3-TKD* mutation was identified in one patient (0.4%). Interestingly, in the same study, *FLT3-ITD* frequency was 12% in both secondary and therapy-related AML, 22% in de novo AML and up to 27% in relapsed AML [22]. In all three studies, *FLT3* mutations were more frequent among cases progressing to AML and were associated with a trend to worse prognosis and decreased event free and OS. However, in our study, we did not see significant difference in OS in *FLT3*-mutated MDS and CMML patients when compared with those without *FLT3* mutations. On analyzing the groups separately, we noted a trend toward decreased OS in *FLT3*-mutated CMML patients when compared with CMML patients without *FLT3* mutations. Conversely, in MDS, we noted a trend to improve survival in the *FLT3*-mutated group. Advent of hypomethylating agents, improved supportive care, and better transplant options for MDS post-2005 may be responsible for the improved survival noted in the *FLT3*-mutated MDS patients.

The extremely low incidence of *FLT3* mutations in IPSS low and intermediate-1 MDS coupled with increased incidence of *FLT3* mutations in RAEB and AML as noted by Horiike et al. [10] and Bacher et al. [9] led to the suggestion that *FLT3* mutation plays a role in progression from MDS to AML [24]. Two retrospective studies attempted to address this question by performing serial *FLT3* analysis on MDS patients. Shih et al. [12] reviewed 70 patients with MDS that progressed to AML [11]. They identified three patients with *FLT3-ITD* at diagnosis and seven patients that acquired *FLT3-ITD* mutation during AML evolution. They noted that the incidence of *FLT3-ITD* at diagnosis of MDS was significantly lower than that at AML transformation and *FLT3-ITD*-mutated patients progressed to AML more rapidly than *FLT3-ITD* wild-type patients (2.5 ± 0.5 vs. 11.9 ± 1.5 months, $P = 0.114$). *FLT3-ITD*-mutated patients also had a significantly shorter survival than nonmutated

patients (5.6 ± 1.3 vs. 18.0 ± 1.7 months, $P = 0.0008$) [11]. Similar data have been reported by Georgiou et al. [25] in 2006. Our data seem to support this hypothesis. Eleven of 12 of our *FLT3* MDS patients had RAEB. In fact, when we compared disease characteristics of *FLT3*-mutated MDS patients versus nonmutated patients, the only statistically significant difference between *FLT3*-mutated and *FLT3*-nonmutated patients was that MDS patients with *FLT3* mutations were younger and tended to present as RAEB more frequently than MDS patients without *FLT3* mutations. Prospective studies are warranted to confirm this hypothesis.

Finally, interest in this mutation is not only derived from its value as a prognostic biomarker but also because it can serve as a therapeutic target [26,27]. A number of agents with *FLT3* inhibitory activity are being developed [28–31] although experience in MDS is limited.

In conclusion, there was no significant difference in OS in MDS or CMML patients who were *FLT3* mutated versus those without *FLT3* mutations. This would suggest that *FLT3* mutations in MDS and CMML may not carry the same negative prognostic impact as *FLT3* mutations in AML. However, our retrospective analysis is limited by the relatively small number of patients of informative patients. The therapeutic value of *FLT3* inhibitors should be explored in mutated patients.

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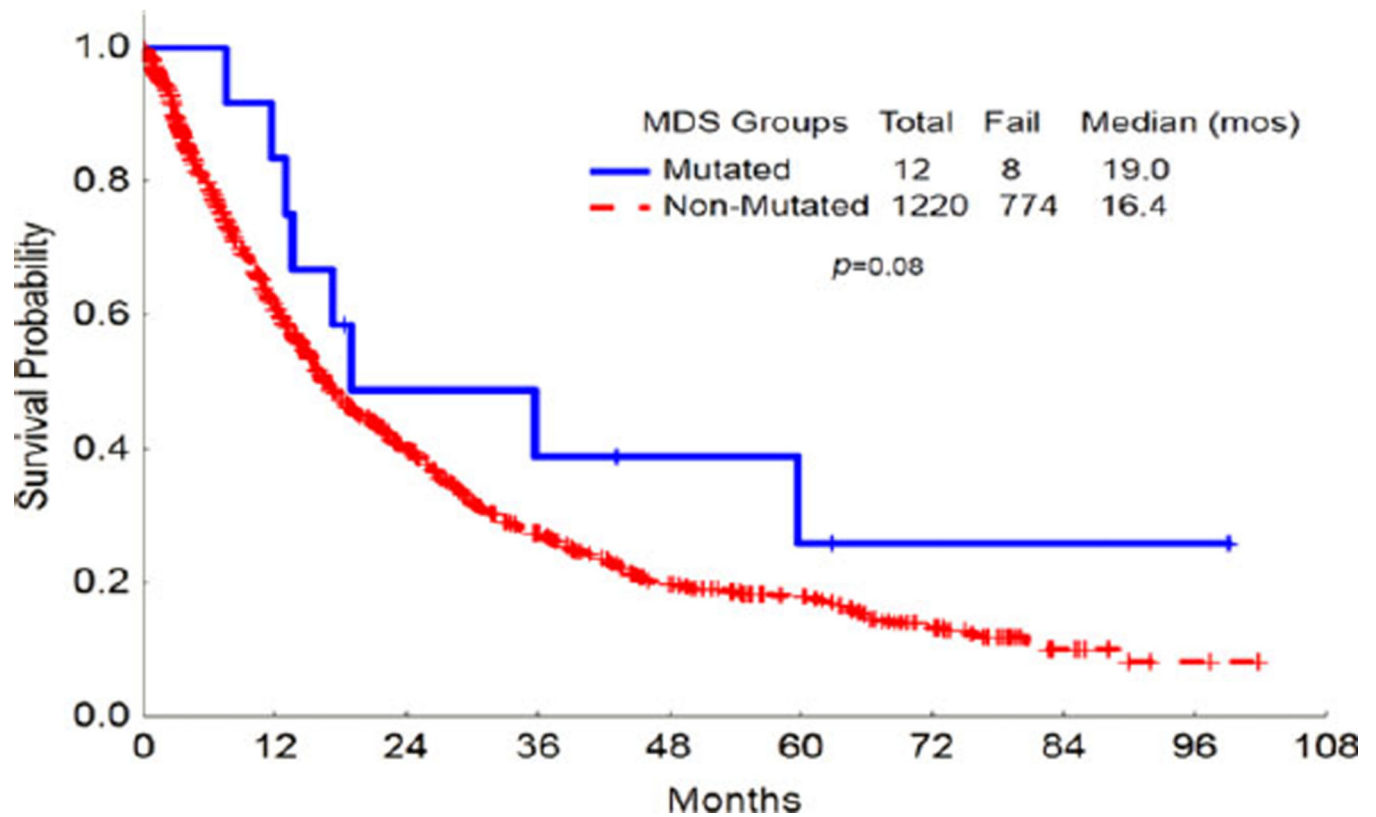


Figure 1. Overall survival of FLT3-mutated MDS patients versus FLT3-nonmutated MDS patients. Kaplan–Meier analysis of overall survival (OS) for FLT3-mutated MDS patients versus FLT3-nonmutated MDS patients. The OS did not differ significantly for FLT3-mutated versus FLT3-nonmutated patients. [Color figure can be viewed in the online issue, which is available at wileyonlinelibrary.com.]

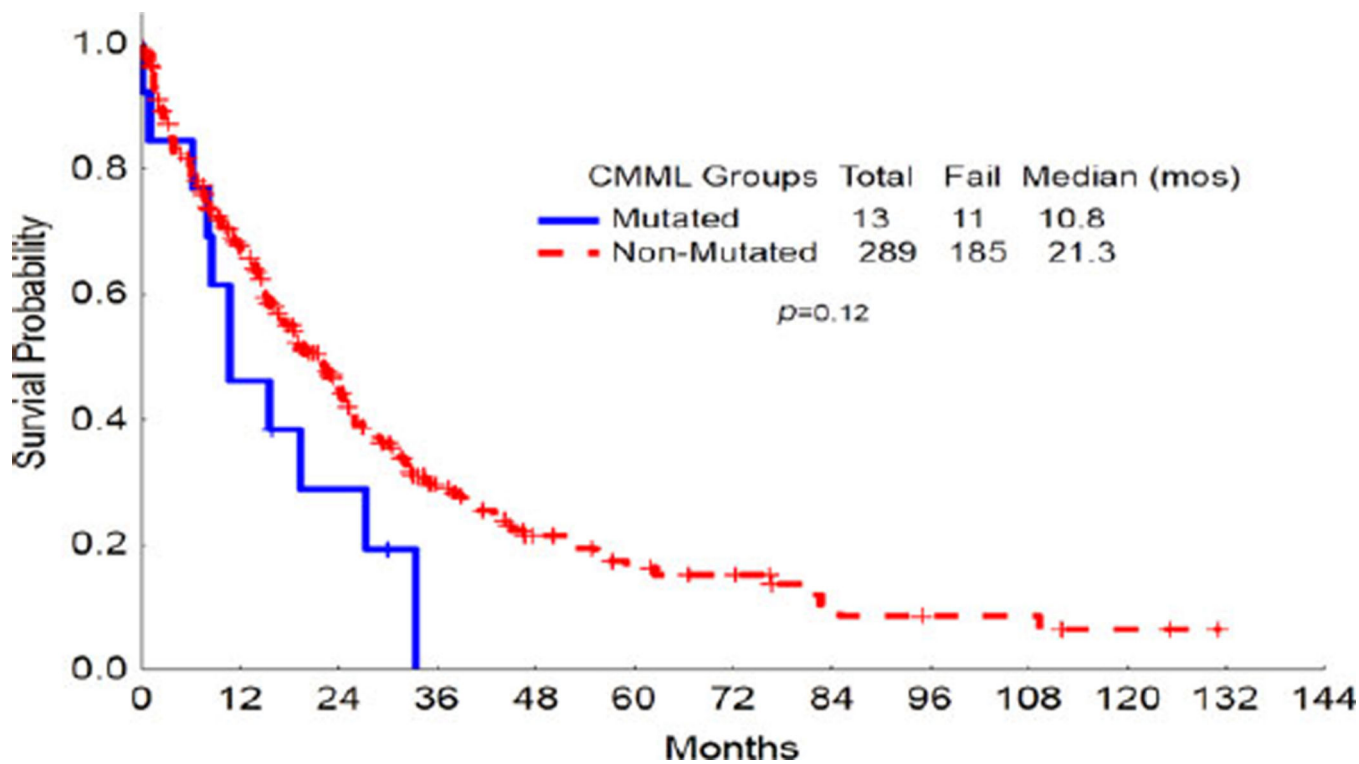


Figure 2. Overall survival of FLT3-mutated MDS patients versus FLT3-nonmutated CMML patients. Kaplan–Meier analysis of overall survival (OS) for FLT3-mutated MDS patients versus FLT3-nonmutated CMML patients. The OS did not differ significantly for FLT3-mutated versus FLT3-nonmutated patients. [Color figure can be viewed in the online issue, which is available at wileyonlinelibrary.com.]

TABLE I

MDS: FLT3-Mutated Versus FLT3-Nonmutated

	FLT3-mutated <i>N</i> (%) / median (range)	FLT3-nonmutated <i>N</i> (%) / median (range)	<i>P</i>
Number	12	1220	
Age (years)	60 [20–74]	68 [16–92]	0.02
Sex			
Female	3 (25%)	432 (35%)	0.45
Male	9 (75%)	788 (65%)	
WBC \leftrightarrow $10^9/L$	3.5 [1.2–14.5]	3.2 [0.3–159]	0.8
Hemoglobin (g/dL)	9.9 [8.3–11.4]	9.8 [4.0–17.5]	0.85
Platelets \leftrightarrow $10^9/L$	47 [15–101]	73 [1–1040]	0.08
ANC \leftrightarrow $10^9/L$	1.5 [0.5–7.2]	1.4 [0–77.4]	0.69
Diagnosis			
RA	1 (8%)	559 (46%)	0.03
RAEB	11 (92%)	640 (52%)	
Deletion 5q	0	21 (2%)	
Cytogenetics			
Diploid, -Y	9 (75%)	583 (48%)	0.26
Deletion 5/7	1 (8%)	323 (26%)	
Other	2 (17%)	251 (21%)	
Indeterminate	0	60 (5%)	
Not done	0	3 (0.2%)	
IPSS score			
High	1 (8%)	110 (9%)	0.71
INT-1	6 (50%)	474 (39%)	
INT-2	4 (34%)	347 (28%)	
Low	1 (8%)	258 (21%)	
Not available	0	31 (3%)	

TABLE II

CMML: FLT3 Mutated Versus FLT3 Nonmutated

	FLT3 mutated <i>N</i> (%)/ median (range)	FLT3 nonmutated <i>N</i> (%)/ median (range)	<i>P</i>
Number	13	289	
Age (years)	65 [55–81]	70 [32–91]	0.4
Sex			0.45
Female	5 (38%)	83 (29%)	
Male	8 (62%)	206 (71%)	
WBC ↔ 10 ⁹ /L	31.3 [2.6–211.8]	13.2 [1.1–149.8]	0.39
Hemoglobin (g/dL)	10.1 [8.7–12.7]	10.6 [5.1–16.4]	0.64
Platelets ↔ 10 ⁹ /L	120 [23–429]	89 [6–820]	0.36
ANC ↔ 10 ⁹ /L	13.3 [0.5–108.0]	6.9 [0.3–6.9]	0.68
Diagnosis			
CMML-1	9 (69%)	199 (69%)	0.98
CMML-2	4 (31%)	90 (31%)	
Cytogenetics			
Diploid, -Y	10 (77%)	206 (72%)	0.73
Deletion 5/7	0	21 (7%)	
Other	3 (23%)	53 (18%)	
Indeterminate	0	4 (1%)	
Not done	0	5 (2%)	