

Contribution of Revised International Prognostic Scoring System Cytogenetics to Predict Outcome After Allogeneic Stem Cell Transplantation for Myelodysplastic Syndromes

A Study From the French Society of Bone Marrow Transplantation and Cellular Therapy

Jordan Gauthier,^{1,2} Gandhi Damaj,³ Carole Langlois,⁴ Marie Robin,⁵ Mauricette Michallet,⁶ Patrice Chevallier,⁷ Yves Beguin,⁸ Stéphanie N'guyen,⁹ Pierre Bories,¹⁰ Didier Blaise,¹¹ Jérôme Cornillon,¹² Aline Clavert,¹³ Mohamad Mohty,¹⁴ Anne Huynh,¹⁵ Anne Thiébaut-Bertrand,¹⁶ Stéphane Vigouroux,¹⁷ Alain Duhamel,⁴ and Ibrahim Yakoub-Agha^{1,2}

Background. The prognosis of myelodysplastic syndromes (MDS) after allogeneic stem cell transplantation is critically determined by cytogenetic abnormalities, as previously defined by International Prognostic Scoring System (IPSS) cytogenetics. It has been shown that a new cytogenetic classification, included in the IPSS-R (cytogenetic-IPSS-R [C-IPSS-R]), can better predict the outcome of untreated MDS patients. **Methods.** In this study, we assessed the impact of the IPSS-R cytogenetic score (C-IPSS-R) on the outcome of 367 MDS patients transplanted from HLA-identical siblings or HLA allele-matched unrelated donors. **Results.** According to the C-IPSS-R, 178 patients (48%) fell in the good risk, 102 (28%) in the intermediate risk, 77 (21%) in the poor risk, and 10 (3%) in the very poor risk group. In multivariate analysis, after a median follow-up of 4 years, the poor and very poor-risk categories correlated with shorter overall survival (OS) (4-year OS, 32%; hazard ratio [HR], 1.59; P = 0.009 and OS, 10%; HR, 3.18; P = 0.002, respectively) and higher cumulative incidence of relapse (CIR) (CIR, 52%; HR, 1.82; P = 0.004 and CIR, 60%; HR, 2.44; P = 0.060, respectively). **Conclusions.** Overall, the C-IPSS-R changed the IPSS cytogenetic risk only in 8% of cases but identified a new risk group, the very poor C-IPSS-R category, with dismal outcome after allogeneic stem cell transplantation (10% 4-year OS, 60% 4-year CIR). Posttransplantation maintenance therapy should be investigated in prospective trials for patients with high-risk C-IPSS-R karyotypes.

(Transplantation 2015;99: 1672-1680)

yelodysplastic syndromes form a heterogeneous group of myeloid neoplasms with varying outcomes, mainly influenced by the cytogenetic abnormalities borne by the

Received 7 September 2014. Revision requested 5 November 2014.

Accepted 31 October 2014.

- ¹ CHRU Lille, Pôle Spécialités Médicales et Gérontologie, Service des Maladies du Sang, Secteur Allogreffe de Cellules Souches Hématopoïétiques, F59037, Lille, France.
- ² Université de Lille, UFR Médecine F59000, Lille, France.
- ³ Hematology Department, Caen University Hospital, Amiens, France.
- ⁴ Department of Biostatistics, Lille University Hospital, Lille, France.
- ⁵ Hematology Department and Hematopoietic Stem Cell Transplantation Unit, Saint-Louis Hospital, Paris, France.
- ⁶ Hematology Department, Lyon-Sud Hospital, Lyon, France.
- ⁷ Hematology Department, Nantes, France.
- ⁸ Hematology Department CH-Liège, Liège, Belgium.
- ⁹ Hematology Department, Pitié-Salpêtrière Hospital, Paris, France.
- ¹⁰ Hematology Department, Strasbourg University Hospital, Strasbourg, France.
- ¹¹ Hematopoietic Stem Cell Transplantation Unit, Paoli Calmettes Institute, Marseille, France.
- ¹² Hematology Department, Loire Oncology Institute (ICL), Saint Priest en Jarez, France.
- ¹³ Hematology Department, Nantes University Hospital, Nantes, France.

malignant clone. Common management of myelodysplastic syndrome (MDS) patients comprises best supportive care, hypomethylating agents (HMAs) or induction-type chemotherapy,

- ¹⁶ Hematology Department, Grenoble University Hospital, Grenoble, France.
- ¹⁷ Hematology Department, Bordeaux University Hospital, Bordeaux, France.
- The authors declare no conflict of interest.

Correspondence: Ibrahim Yakoub-Agha, MD, PhD, UAM allogreffes de CSH, CHRU Lille, F-59037 Lille CEDEX, France. (Ibrahim.yakoub-agha@chru-lille.fr)

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¹⁴ Hematology Department, Saint-Antoine Hospital, Paris, France.

¹⁵ Hematology Department, Toulouse University Hospital, Toulouse, France.

This study was presented, in part at the French Society of Bone Marrow Transplantation and Cell Therapy (SFGM-TC) annual meeting, November 8–11, 2013, Lyon, France and at the European Bone Marrow Transplantation Congress, April 1–3, 2014, Milan, Italy.

J.G. participated in research design, in the writing of the paper and in data analysis. G.D. participated in the writing of the paper and in data analysis. C.L. participated in data analysis, M.R., M.M., P.C. Y.B., S.N., P.B., D.B., J.C., A.C., M.M., A.H., A.T.-B., S.V., and A.D. participated in the writing of the paper and in the performance of the research. I.Y.-A. participated in the research design, in the writing of the paper and in the performance of the research.

although none of those treatments will prevent ineluctable progression or relapse. Because of its curative potential, allogeneic stem cell transplantation (allo-SCT) remains the best treatment option for MDS patients.¹⁻⁴ The International Prognostic Scoring System (IPSS),⁵ the revised IPSS (IPSS-R),⁶ and the World Health Organization (WHO) classification-based scoring system (WPSS)⁷ are presently in use by clinicians to help risk stratification. Besides bone marrow blasts, cytopenias and transfusion requirement for the WHO classification-based scoring system, cytogenetic abnormalities make for the most adverse item in all the aforementioned scores. Several retrospective studies observed a sustained impact of IPSS-poor risk cytogenetics after allo-SCT, isolating patients with an increased risk of relapse.⁸ Karyotypic prognostication of MDS patients has been recently refined into a 5-group classification⁹ and included in the IPSS-R (C-IPSS-R).⁶ In a large retrospective study, Deeg et al¹⁰ observed a more discriminating effect of this new C-IPSS-R classification compared to IPSS cytogenetics to predict poor prognosis after allo-ST. Additionally, the presence of a monosomal karyotype (MK) was associated with poorer outcome, which was also observed in another study carried out by the European Society for Blood and Marrow Transplantation group.¹¹ Monosomal karyotypes were included as well in a transplantation-risk index recently published by Della Porta et al.¹²

In this retrospective, multicenter study, we evaluated the impact of the C-IPSS-R classification on the outcome of a large cohort of MDS patients undergoing allo-SCT from HLAidentical siblings or 10/10 HLA allele-matched unrelated donors. Moreover, we assessed its contribution when compared to stratification by IPSS cytogenetics and according to the presence of an MK.

MATERIALS AND METHODS

This study was approved by the French Society of Bone Marrow Transplantation and Cell Therapies (SFGM-TC) board and conducted according to the declaration of Helsinki.

Patient and Donor Characteristics

We analyzed 367 consecutive patients with MDS who underwent allo-SCT in 23 French and Belgian centers between January 1999 and December 2009. Morphological classification, according to French-American-British¹³ and WHO classifications¹⁴ was documented as a separate variable at initial diagnosis and at time of transplantation. Prior progression was defined as a change of WHO/French-American-British category, regardless of treatment, between diagnosis and transplant. Disease status at transplant was defined by 2 categories: "active disease" and "responders." The "active disease" group was attributed in the following cases: stable disease, relapse after complete or partial remission, response failure or progressive disease after treatment according to International Working Group 2006 criteria.¹⁵ In addition, patients who received best supportive care only before transplantation were also included in the "active disease" group. When complete or partial remission International Working Group 2006 criteria were observed at transplant, patients were classified as "responders." Patient characteristics at diagnosis and at transplant are summarized in Table 1 and Table 2, respectively.

Transplantation and Follow-Up Modalities

Transplantation modalities were made as homogenous as possible using the following inclusion/exclusion criteria: (i) Patients older than 18 years referred for first allo-SCT. (ii) Source of stem cell was marrow or blood from either a sibling or an HLA-A, -B, -Cw, -DR, and -DQ identical unrelated donor at allele level (so-called 10/10). Patients who received allo-SCT from an HLA-mismatched donor, cord blood, or T-cell-depleted graft, and patients with chronic myelo-monocytic leukemia were excluded. The participating centers were asked to verify the data recorded for each patient in the French Bone Marrow Transplantation Registry and to provide additional information. Quality of the data was controlled using a computerized search for discrepancy errors and vigorous on-site data verification of each file.

TABLE 1.

Baseline characteristics of patients at diagnosis

Patients characteristics		%	C-IPSS-R categories								
	Total (n = 367)		Good		Intermediate		Poor		Very poor		
			n	%	n	%	n	%	n	%	
Sex											
Male	230	63	122	68	54	53	50	65	4	40	
Female	137	37	56	32	48	47	27	35	6	60	
FAB/WHO											
RA/RARS/RCMD/5q-	114	31	50	28	41	40	22	29	1	10	
RAEB-1	102	28	49	28	32	31	18	23	3	30	
RAEB-2	134	36	70	39	27	27	32	42	5	50	
RAEB-t/AML	17	5	9	5	2	2	5	6	1	10	
IPSS cytogenetics											
Good	176	48	176	98	0	0	0	0	0	0	
Intermediate	96	26	2	2	90	88	4	5	0	0	
Poor	95	26	0	0	12	12	73	95	10	100	
Monosomal karyotype											
No	304	83	177	99	94	92	31	40	2	20	
Yes	63	17	1	1	8	8	46	60	8	80	

RARS, RA with ringed sideroblasts; RAEB-T/AML, RAEB in transformation/ acute myeloid leukemia

TABLE 2.

Baseline characteristics of patients at transplantation

			C-IPSS-R categories								
	No. patients (n = 367)	%	Go	od	Intermediate		Poor		Very poor		
Characteristics at transplant			n	%	n	%	n	%	Ν	%	
Patient age, y											
< 54	184	50	85	48	49	48	44	57	6	60	
> 54	183	50	93	52	53	52	33	43	4	40	
Previous progression											
No	249	68	120	67	70	69	53	69	6	60	
Yes	118	32	58	33	32	31	24	31	4	40	
Previous treatment											
Best supportive care	146	40	66	37	40	39	37	48	3	30	
HMA	42	11	19	11	.0	9	12	16	2	20	
ITC	151	41	81	45	40	39	25	32	5	50	
HMA + ITC	14	4	8	5	5	5	1	1	0	0	
Missing data	14	4	4	2	8	8	2	3	0	0	
Hb a/dl			I	2	0	0	2	0	0	0	
> 9 7	180	49	83	47	48	47	44	57	5	50	
< 9.7	177	48	00 Q1	51	-10 50	40	32	42	4	40	
< 5.7 Missing data	10	40 2	1	2	1	40	1	1	1	10	
Platolote C/I	10	0	т	2	7	-	I	I	I	10	
	170	40	20	50	51	50	22	12	6	60	
< 72	179	49	09	10	47	16	12	43 56	2	20	
< 7.5 Missing data	10	40	00	40	47	40	40	1	1	10	
	10	3	4	2	4	4	I	I	I	10	
	100	50	96	10	50	EO	24	15	0	20	
≥ 2.9	102	10	00	40 50	29	20	34 40	40	3	30	
< 2.9 Missing data	1/0	40	00	00	39	30	42	04 1	1	10	
IVIISSII IY Uala	10	Z	4	Z	4	4	I	I	I	10	
Time to transplantation, mo	104	50	70	40	50	50	45	50	10	100	
< 10	184	50	100	43	53	52	40	28	10	100	
≥ 10	183	50	102	57	49	48	32	42	0	0	
Marrow Diasts, %	000		100	50	01	00	10	50	4	40	
< 5	208	57	103	58	61	60	40	52	4	40	
≥ 5	159	43	75	42	41	40	37	48	6	60	
Disease status"	450	10	07	10			07	05	_	50	
Responders	158	43	87	49	39	38	27	35	5	50	
Active disease	209	57	91	51	63	62	50	65	5	50	
Sex mismatch ²							. –				
Yes	84	23	54	30	14	14	15	19	1	10	
No	283	//	124	70	88	86	62	81	9	90	
Donor type									_		
Sibling	229	62	105	59	69	68	48	62	7	70	
HLA-matched unrelated	138	38	73	41	33	32	29	38	3	30	
Stem cell source											
Marrow	117	32	58	33	29	28	28	36	2	20	
PBSC	250	68	120	67	73	72	49	64	8	80	
Conditioning											
MAC	141	38	63	35	42	41	32	42	4	40	
RIC/NMA	226	62	115	65	60	59	45	58	6	60	
ATG											
No	207	56	98	55	60	59	41	53	8	80	
Yes	160	44	80	45	42	41	36	47	2	20	
TBI											
No	236	64	111	62	67	66	53	69	5	50	
Yes	131	36	67	38	35	34	24	31	5	50	

^a Disease status at transplant was defined by two categories: "active disease" and "responders". The "active disease" group was attributed in the following cases: stable disease, relapse after complete or partial remission, response failure or progressive disease after treatment according to IWG 2006 criteria. ^b Sex mismatch is defined as male patient who received graft from a female donor.

PBSC, peripheral blood stem cells; RIC/NMA, reduced intensity conditioning/nonmyeloablative; ATG, antithymocyte globulin; TBI, total body irradiation; ITC, induction-type chemotherapy.

The HLA matching was crosschecked with the data of the French Bone Marrow Donor Registry as previously described.¹⁶ Predonation work-ups in donors¹⁷ and follow-up after transplantation¹⁸⁻²⁰ were conducted according to the SFGM-TC guidelines.²¹

Cytogenetics

Cytogenetic analysis at diagnosis was performed using conventional procedures and documented with respect to the International System for Human Cytogenetic Nomenclature. Cytogenetic abnormalities were classified according to the C-IPSS-R classification designed by Shantz et al⁵ as well as the IPSS cytogenetic classification. The presence of an MK was also assessed and defined as the combination of 2 monosomies or 1 structural abnormality associated with 1 monosomy.²² Three patients who fell in the very good risk category were removed from the analysis, and 49 patients were excluded because their files lacked or provided incomplete cytogenetic data.

Statistical Analysis

The analysis was performed on the reference date of April 1, 2011. Overall survival (OS) was defined as the interval from allo-SCT to death, regardless of the cause of death. Relapse was defined as the presence of more than 5% marrow blasts and/or reappearance of major myelodysplastic features associated with cytopenia and evidence of autologous reconstitution when chimerism was available. Nonrelapse mortality (NRM) was defined as death resulting from the graft procedure without evidence of relapse. All censored criteria were calculated from the time of transplantation. Distributions over time were estimated by the Kaplan-Meier product limit method. The log-rank test was used to determine the prognostic value of patient characteristics at transplant on OS. The occurrence of relapse and NRM was studied using a competing risk methodology. For the event of relapse, NRM was considered as the competing event. For NRM, the competing event was relapse. The cumulative incidence of each event was estimated using the Kalbfleish and Prentice method. The individual prognostic value of each variable was assessed by the Gray test (comparison of cumulative incidence curves using bivariate analyses). Variables having a significance level of P less than 0.15 in univariate analysis were introduced in a multivariable Cox regression model for OS, in a Fine and Gray model for relapse and NRM, with backward selection at level P less than 0.15. Adjusted hazard ratios and 95% confidence intervals (95% CI) were computed, and a P value of 0.05 or less was considered statistically significant. Statistical analyses were performed using the SAS and R software programs. The R package "cmprsk" was used for the Fine and Gray model.

RESULTS

Patient Characteristics

At diagnosis, 114 (31%) of the 367 patients had refractory anemia (RA), RA with ringed sideroblasts or refractory cytopenia with multilineage dysplasia, 102 patients (28%) had RA with excess of blasts (RAEB-1 < 10%), 134 patients (36%) had RA with excess of blasts ranging from 10% to 19% (RAEB-2), and 17 patients (5%) had RAEB in transformation/ acute myeloid leukemia with marrow blasts between 20% and 30% (Tables 1 and 2).

We analyzed 230 males (63%) and 137 females (37%)with a median age of 54 years (range, 20-70) at allo-SCT. The donor was an HLA-matched sibling in 229 cases (62%) and an HLA-matched unrelated donor in 138 (38%). The conditioning regimen was myeloablative conditioning (MAC) in 141 patients (38%) and reduced intensity conditioning/ nonmyeloablative in 226 patients (62%).²³ Peripheral blood stem cell was used in 68% and bone marrow stem cells in 32% of our patients. An excess of blasts in the marrow was observed in 159 patients (43%) of our patients. Overall, 118 of the 367 patients (32%) had progressed to more advanced disease before transplantation. A best supportive care approach had been offered to 146 patients (40%), whereas 237 patients (56%) had received either an HMA and/or induction-type chemotherapy. Median time to transplantation was 10 months and median follow-up after transplantation was 4 years (range, 3-142 months). In the poor IPSS karyotypes and intermediate risk C-IPSS-R subsets, median follow-up was of 69 months (range, 18-124) and 53 months (range, 3-134), respectively. The whole estimate for OS was of 45%, whereas cumulative incidence of relapse (CIR) and NRM were of 37% and 24%, respectively. Median time for neutrophil engraftment was of 17 days (range, 0-100). Grade 2 to 4 acute Graft Versus Host Disease (GVHD) was diagnosed in 142 patients (39%) and grade 3 to 4 acute GVHD in 66 patients (18%). Among the 322 patients alive after day 100, we observed chronic GVHD in 176 patients (55%) and extensive GVHD in 67 patients (33%).

Cytogenetic Subgroups

Cytogenetic risk was, according to the C-IPSS-R, good, intermediate, poor, or very poor in 178 (48%), 102 (28%), 77 (21%), and 10 (3%) patients, respectively. The IPSS cytogenetic good risk group coincided completely with the C-IPSS-R good risk group (175 patients). Three patients in the IPSS intermediate risk group were classified as good risk by the C-IPSS-R classification and in those patients the following abnormalities were found: del 12p, del 5q with monosomy 11, del 5q with trisomy 21. Four patients with intermediate IPSS karyotypes fell in the C-IPSS-R poor risk group (all 4 patients carried chromosome 3 abnormalities). The IPSS high-risk patients were split into the IPSS-R intermediate (12 patients with del 7q), poor (73 patients), and very poor risk group (10 patients with complex karyotypes including more than 3 abnormalities). Overall, a change in the cytogenetic risk was only observed in 29 patients (8%).

We observed a MK in 63 (17%) patients. Considering C-IPSS-R, MKs were present in 1 (1%), 8 (8%), 46 (60%), and 8 (80%) patients within the good, intermediate, poor, and very poor risk groups, respectively. Among patients without an MK (n = 304) 177 (58%) fell in the good risk, 94 (31%) in the intermediate risk, 31 (10%) in the poor risk, and 2 (0.6%) in the very poor risk C-IPSS-R category. In those 2 patients, a complex karyotype with more than 3 abnormalities was found but without any monosomy. The following MKs were identified in patients with intermediate risk by C-IPSS-R (n = 8): monosomy 5 and trisomy 21, del 11q and monosomy 20, monosomy 5 and t(X;1), monosomy 5 and trisomy 8 in 2 patients, monosomy 9 and monosomy 11, monosomy 2 and trisomy 17, monosomy 5 and monosomy 11.

TABLE 3.

Univariate analysis

Patient characteristics367% P^a % P^b %Patient age at transplantation, y< 54 ≥ 54 18343Sex	P ^b 0.431 0.270
Patient age at transplantation, y < 54 184 47 0.345 31 0.019 26 ≥ 54 183 43 41 22 Sex Sex 22	0.431 0.270
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	0.431 0.270
≥ 54 183 43 41 22	0.270
Sex Sex	0.270
	0.270
Male 230 43 0,294 36 0,923 26	
Female 137 48 37 20	
FAB/WHO at diagnosis	
BA/BABS/BCMD/5g- 114 50 0.54 33 0.287 24	0.518
BAFB-1 102 41 33 29	01010
BAEB-2 134 44 42 19	
BAER-t/AMI 17 41 35 24	
RIPSS cytogenetics at diagnosis	
Good 178 53 0.004 32 0.001 21	0 163
Intermediate 102 44 30 31	0.100
Pror 77 32 52 10	
Very noor $10 10 60 30$	
IPSS cutorenetics at diagnosis	
Good 176 52 0.015 32 0.004 21	0 1 3 9
Intermediate 06 45 31 31	0.100
Pror 95 32 50 21	
Monosomal kanvotune at diagnosis	
No 304 48 0.006 32 <0.001 25	0 235
V_{ac} 63 20 60 17	0.200
Pravious progression	
No 2/Q /7 0.027 35 0.220 22	0316
V_{ac} 118 40 40 26	0.010
Pravious treatment	
Rest supportive care $1/6$ 46 0.207 36 0.206 12	0.058
HMA 42 57 41 22	0.000
TTC 151 42 36 20	
HMA \pm ITC 14 43 34 26	
Missing data 1/	
Missing data 14	
< 5 208 50 0.012 31 0.013 24	0.834
> 5 150 38 1/1 0.013 24	0,004
\geq 0 100 00 \pm 24	
Responders 158 51 0.003 36 0.859 18	0.040
Active disease 200 40 37 28	0.040
Sex mismatch ^d	
Ves 84 46 0.835 33 0.467 26	0.616
No 283 44 37 23	0.010
Sibling 229 47 0.075 39 0.371 21	0.046
HI A-matched unrelated 138 41 33 29	0.040
Stem cell source	
Marrow 117 38 0.210 37 0.531 30	0.060
PBSC 250 48 36 21	0.000
Conditioning	
MAC 1/1 /2 0/13 30 0.006 33	~0.001
RIC 226 /7 /1 10	~0,00T
ΔTG	
No 207 39 0.088 35 0.158 20	0.005
Yee 160 52 30 16	0.000

Continued next page

TABLE 3. (Continued)

	No. patients	4	-y OS	4	-y CIR	4-y NRM	
Patient characteristics	367	%	Pa	%	P ^b	%	P ^b
TBI							
No	236	51	0.006	35	0.505	20	0.066
Yes	131	34		40		30	
Hb at transplantation, g/dL							
≥ 9.7	180	49	0.125	37	0.781	27	0.166
< 9.7	177	41		35		19	
Missing data	10						
Platelets at transplantation, G/L							
≥ 73	179	52	0.002	37	0.635	28	0.072
< 73	178	39		35		19	
Missing data	10						
Leukocytes at transplantation, G/L							
≥ 2.9	182	49	0.111	35	0.810	26	0.303
< 2.9	175	42		37		21	
Missing data	10						

^a Log-Rank.

^b Gray test (cumulative incidence).

^c Disease status at transplant was defined by two categories: "active disease" and "responders". The "active disease" group was attributed in the following cases: stable disease, relapse after complete or partial remission, response failure or progressive disease after treatment according to International Working Group 2006 criteria.

^d Sex mismatch is defined as male patient who received graft from a female donor

RCMD, refractory cytopenia with multilineage dysplasia.

Univariate Analysis

As shown in Table 3, classification by C-IPSS-R, IPSS cytogenetics and MKs significantly impacted OS and relapse. The OS and CIR according to C-IPSS-R categories are represented in Figure 1.

Overall Survival

The C-IPSS-R (P = 0.004), the IPSS (P = 0.015) cytogenetic classification, and the presence of an MK (P = 0.006) were associated with shorter survival. Previous progression (P = 0.037), marrow blasts that are 5% or higher (P = 0.012), total body irradiation (P = 0.006), and platelet count of 73G/L or less at transplant (P = 0.002) also adversely impacted OS.

Cumulative Incidence of Relapse

Patient age (P = 0.019), C-IPSS-R (P = 0.001), IPSS cytogenetics (P = 0.004), MKs (P < 0.001), marrow blasts that are 5% or higher (P = 0.013) and reduced intensity conditioning/nonmyeloablative (P = 0.006) were associated with higher CIR.

Nonrelapse Mortality

Higher NRM was observed in patients with active disease at transplantation (P = 0.040) and in those allografted from

an unrelated donor (P = 0.046). The MAC (P < 0.001) and antithymocyte globulin (P = 0.005) were also associated with higher NRM.

Subgroups Univariate Analysis

To evaluate the contribution of the C-IPSS-R, we applied this new classification to 95 patients with poor risk IPSS karyotypes and identified 2 groups with different outcomes. As displayed in Figure 2, CIR was significantly lower in patients with intermediate risk C-IPSS-R, compared to a group including both poor and very poor risk C-IPSS-R groups with relapse rates of 17% and 55%, respectively (P = 0.025). The C-IPSS-R reclassified a very few patients previously categorized as intermediate risk by IPSS cytogenetics. In this subgroup, 3 patients fell in the good risk category and 4 patients in the poor risk group. No difference was observed regarding relapse rates (n = 96, P = 0.402).

As shown in Figure 3, among 102 patients classified as C-IPSS-R intermediate risk, patients with MKs relapsed more often (63% vs 28%; P = 0.006) but had similar OS rates (29% vs 45%; P = 0.282). A trend toward higher relapse rates was also observed in C-IPSS-R poor risk patients with MKs (n = 77) but this did not reach statistical significance (61% vs 39%; P = 0.091, data not shown).



FIGURE 1. Outcome after transplantation according to the C-IPSS-R.

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FIGURE 2. Relapse in poor IPSS karyotypes reclassified by the C-IPSS-R.

Multivariate Analysis

Poor and very poor C-IPSS-R groups were independent risk factors for shorter OS (hazard ratio [HR], 1.56; 95% CI, 1.10-2.20; P = 0.012 and HR, 2.67; 95% CI, 1.33-5.35; P = 0.006, respectively), and higher CIR (HR, 1.82; 95% CI, 1.20-2.72; P = 0.004 and HR, 2.44; 95% CI, 0.93-5.27; P = 0.060, respectively). Marrow blasts at transplant that are 5% or higher was an independent risk factor for shorter OS (HR, 1.33; 95% CI, 1.00-1.75, P = 0.049) and higher CIR (HR, 1.46; 95% CI, 1.04-2.07; P = 0.034). Previous progression was associated with shorter OS but without reaching statistical significance (HR, 1.30; 95% CI, 0.97-1.74; P = 0.081). Patients who received total body irradiation had significantly shorter OS (HR, 1.38; P = 0.010). The MAC was associated with lower relapse rates (HR, 0.59; 95% CI, 0.40-0.85; P =0.004, respectively). Two independent risk factors for higher NRM were identified: HLA-matched unrelated donors (HR, 1.57; 95% CI, 1.03-2.40; P = 0.035) and MAC regimens (HR, 2.17; 95% CI, 1.40-3.33, *P* < 0.001) (Table 4).

DISCUSSION

Allo-SCT remains today the only therapeutic option to potentially cure patients suffering from MDS. However, highrisk cytogenetics strongly hinders the procedure. Because the IPSS-R cytogenetic classification was based on analysis of nontransplanted MDS patients, we wished to determine its contribution once compared to other cytogenetic classifications, such as IPSS cytogenetics and MKs. Pretransplant tumor burden, reflected by the percentage of marrow blasts, has been previously linked to adverse outcome^{3,24} and was also in our study an independent risk factor for relapse. We took into account that previous therapy influenced the percentage of marrow blasts at transplant and hence considered cytogenetics and marrow blasts separately, as opposed to other authors who studied the IPSS-R as a whole.¹² Although the IPSS-R seems to help the risk-stratification of MDS patients at diagnosis, we find it challenging to use this new classification at the time of allo-SCT. As a matter of fact, the percentage of marrow blasts and cytopenias cannot be interpreted with accuracy at the time of transplant because the alteration of those parameters can result from either the efficacy or toxicity of the treatment administered before transplantation. Indeed, this prognostic tool relies on variables unmodified by therapy and determined specifically at diagnosis.6

Because clonal evolution is common in MDS during the course of the disease, cytogenetic evaluation before allo-SCT

would be more appropriate. However, only cytogenetic evaluation at diagnosis was considered in our study because of the missing data. Of note, we observed similar results when analyzing cytogenetics at transplant despite the smaller number of patients (data not shown).

The main findings in our study were that patients classified at diagnosis in the C-IPSS-R high-risk categories (poor and very poor risk) experienced higher relapse rates and shorter OS after allo-SCT. These findings are in line with aforementioned studies.^{10,12} As expected, we also found an independent impact of poor risk IPSS cytogenetics and MKs on posttransplantation outcomes (data not shown), which has already been reported by others.^{8,11}

Because many clinicians still commonly use the IPSS, we investigated how the C-IPSS-R could contribute to more accurate prognostication by changing the cytogenetic risk of our patients. Considering their former IPSS cytogenetic group, a change in prognostic category after applying C-IPSS-R was only observed in 8% of cases. In a study reported by the Seattle group, this percentage was higher (about 17%), in contrast with our study.¹⁰ At first glance, cytogenetic risk only seems to be modified in a small number of patients. Consequently, we took a closer look at the outcome and the specific chromosomal abnormalities observed in these subsets. In patients labeled poor risk according to IPSS cytogenetics, the C-IPSS-R classification distinguished 13 intermediate risk patients with significantly lower relapse rates (Figure 2). Indeed, IPSS cytogenetics overlook the better prognosis associated with isolated del(7q), which was identified in all these IPSS-R intermediate/IPSS poor cytogenetic risk patients. Interestingly, patients with chromosome 3 abnormalities (n = 4), which were previously considered as intermediate risk by IPSS, were moved to the poor risk C-IPSS-R group. Besides these observations, a change of cytogenetic risk category after applying the C-IPSS-R was only observed in about 8% of patients compared to their previous IPSS cytogenetic risk. If cytogenetic risk only changed in a few patients, the C-IPSS-R defined a group of patients with very poor outcome, represented by the very poor risk category, with a 60% cumulative incidence of relapse and 10% OS. Unlike what has been previously described,^{10,12} a limited number of patients (n = 10) was included in the very poor risk group in our study. The study design could be responsible for this low percentage because we systematically excluded allo-SCT from donor with HLA mismatch. Given the urgent need for



FIGURE 3. Impact of MKs on relapse in the C-IPSS-R intermediate risk group.

TABLE 4.

Multivariate analysis

	4-y 0S				4-y CIR		4-y NRM			
Characteristics	HR	95% CI	Р	HR	95% CI	Р	HR	95% CI	Р	
C-IPSS-R										
Good	1			1						
Intermediate	1.34	0.95-1.87	0.091	0.96	0.61-1.47	0.85				
Poor	1.56	1.10-2.20	0.012	1.82	1.20-2.72	0.004				
Very poor	2.67	1.33-5.35	0.006	2.44	0.93-5.27	0.060				
Previous progression										
No	1	0.97-1.74	0.081							
Yes	1.30									
Marrow blasts at transplantation										
< 5%	1	1.00-1.75	0.049	1	1.04-2.07	0.034				
$\geq 5\%$	1.33			1.46						
TBI										
No	1	1.09-1.92	0.010							
Yes	1.45									
Donor type										
Sibling	1	1.03-2.40	0.035							
HLA-matched unrelated	1.57									
Conditioning										
RIC/NMA				1	0.40-0.85	0.004	1	1.40-3.33	< 0.001	
MAC				0.59			2.17			

allo-SCT, most patients with very complex karyotypes are more likely to receive such grafts.

In accordance with other studies,^{10-12,25} MKs were in our patients a strong risk factor for adverse outcome after allo-SCT. Two independent studies called into question the prognostic value of MKs in cohorts of nontransplanted MDS patients.^{26,27} Recently, Kelaidi et al²⁸ reported similar findings in 98 MDS patients undergoing allo-SCT. They argued that the additional karyotypic abnormalities frequently associated with MKs (such as complex and very complex karyotypes), and not MKs themselves, account for their negative influence on outcome. After multivariate analysis taking into account karyotype complexity, they concluded that MKs do not affect outcome independently. In line with these findings, 86% of MKs (n = 54) in our study were already considered as poor or very poor risk by the C-IPSS-R. Nonetheless, we observed MKs in a small number of patients (n = 8) classified as intermediate risk by the C-IPSS-R, which were at higher risk for relapse (Figure 3) but did not experience significantly shorter survival. We conclude that if MKs are unlikely to refine classification by the C-IPSS-R, their prognostic impact within intermediate IPSS-R karyotypes remains to be investigated in a larger cohort.

Overall, our study confirms the prognostic value of the C-IPSS-R classification in patients with MDS undergoing allo-SCT. Particularly in patients with poor IPSS cytogenetics, this classification is more discriminant and distinguishes a very poor risk group with dismal outcome. How should we manage patients with very poor C-IPSS-R risk? In 2 recent studies published under the aegis of the SFGM-TC group, Damaj et al^{16,29} concluded that the absence of cytoreductive therapy (intensive chemotherapy or azacytidine) did not alter outcome after allo-SCT. In addition, Itzykson et al³⁰ reported that patients with complex karyotypes respond poorly and

transiently to azacytidine. In patients fit for the procedure, we therefore encourage early and upfront allo-SCT in patients with very poor C-IPSS-R karyotypes.³¹ This approach could be followed by posttransplant preventive strategies, such as HMAs^{32,33} and/or donor lymphocyte infusions.³⁴

ACKNOWLEDGMENTS

The authors would like to thank Mor Sény Gueye for collecting and checking data on site. Special thanks go to Nicole Raus, the SFGM-TC data manager. Ibrahim Yakoub-Agha would like to thank the "Association Capucine" for their support in his research.

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