

# Impact of the revised International Prognostic Scoring System, cytogenetics and monosomal karyotype on outcome after allogeneic stem cell transplantation for myelodysplastic syndromes and secondary acute myeloid leukemia evolving from myelodysplastic syndromes: a retrospective multicenter study of the European Society of Blood and Marrow Transplantation

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**Table S1.** Cox regression models for RFS and OS in MDS and sAML patients.

	RFS			OS		
	HR	95% CI	P	HR	95% CI	P
<b>Donor</b> (matched unrelated vs. matched related)	-		-	<b>1.26</b>	1.04-1.54	<b>.022</b>
<b>Age</b>			<b>.004</b>			<b>.003</b>
18-40	1.0		-	1.0		-
40-50*	1.00	0.78-1.27	.975	1.06	0.82-1.37	.666
50-60*	1.20	0.96-1.50	.107	<b>1.30</b>	1.03-1.65	<b>.028</b>
>60*	<b>1.57</b>	1.20-2.05	<b>&lt;.001</b>	<b>1.64</b>	1.23-2.17	<b>.001</b>
<b>Disease status at SCT**</b>			<b>&lt;.001</b>			<b>&lt;.001</b>
RA/RARS/RCMD untreated	1.0		-	1.0		-
RAEB/sAML/CMML in CR*	<b>1.51</b>	1.07-2.13	<b>.020</b>	1.43	1.00-2.05	.051
RAEB/sAML/CMML untreated*	<b>1.71</b>	1.22-2.41	<b>.002</b>	<b>1.62</b>	1.13-2.30	<b>.008</b>
RAEB/sAML/CMML treated, not in CR*	<b>2.57</b>	1.84-3.59	<b>&lt;.001</b>	<b>2.35</b>	1.67-3.32	<b>&lt;.001</b>
<b>Year of SCT</b>	0.98	0.96-0.99	<b>.004</b>	0.97	0.95-0.98	<b>&lt;.001</b>

\*Compared to the first group (reference group) listed in each category

\*\*Patients with missing data for disease status at SCT were kept in the analysis by assigning them to a separate category (HRs not shown).

**Table S2.** Cox regression models with simplified 3-group IPSS cytogenetic classification for RFS and OS in MDS and sAML patients.

	RFS			OS		
	HR	95% CI	P	HR	95% CI	P
<b>Donor</b> (matched unrelated vs. matched related)	-		-	<b>1.25</b>	1.03-1.52	<b>.028</b>
<b>Age</b>			<b>.001</b>			<b>.001</b>
18-40	1.0		-	1.0		-
40-50*	0.99	.078-1.27	.945	1.06	0.82-1.37	.671
50-60*	1.17	0.93-1.46	.179	1.26	1.00-1.60	.051
>60*	<b>1.63</b>	1.25-2.13	<b>&lt;.001</b>	<b>1.71</b>	1.29-2.27	<b>&lt;.001</b>
<b>Disease status at SCT**</b>			<b>&lt;.001</b>			
RA/RARS/RCMD untreated	1.0		-	1.0		-
RAEB/sAML/CMML in CR*	<b>1.57</b>	1.11-2.22	<b>.010</b>	<b>1.47</b>	1.03-2.11	<b>.035</b>
RAEB/sAML/CMML untreated*	<b>1.72</b>	1.22-2.41	<b>.002</b>	<b>1.61</b>	1.13-2.30	<b>.008</b>
RAEB/sAML/CMML treated, not in CR*	<b>2.65</b>	1.90-3.70	<b>&lt;.001</b>	<b>2.40</b>	1.70-3.40	<b>&lt;.001</b>
<b>3-group IPSS-cytogenetics</b>						
Standard <sup>1</sup>	1.0		-	1.0		-
Poor*	<b>1.54</b>	1.28-1.86	<b>&lt;.001</b>	<b>1.57</b>	1.29-1.90	<b>&lt;.001</b>
<b>Year of SCT</b>	0.98	0.96-0.99	<b>.003</b>	0.97	0.95-0.98	<b>&lt;.001</b>

\*Compared to the first group (reference group) listed in each category

<sup>1</sup>Standard=merged good and intermediate risk patients

\*\*Patients with missing data for disease status at SCT were kept in the analysis by assigning them to a separate category (HRs not shown).

**Table S3.** Cox regression models with simplified 5-group IPSS cytogenetic classification and monosomal karyotype for RFS and OS in MDS and sAML patients.

	RFS			OS		
	HR	95% CI	P	HR	95% CI	P
<b>Donor</b> (matched unrelated vs. matched related)	-		-	<b>1.26</b>	1.03-1.54	<b>.022</b>
<b>Age</b>			<b>.002</b>			<b>.003</b>
18-40	1.0		-	1.0		-
40-50*	1.00	0.78-1.27	.972	1.06	0.81-1.37	.686
50-60*	1.14	0.91-1.43	.250	1.24	0.97-1.57	.084
>60*	<b>1.61</b>	1.23-2.12	<b>.001</b>	<b>1.67</b>	1.25-2.23	<b>&lt;.001</b>
<b>Disease status at SCT**</b>			<b>&lt;.001</b>			<b>&lt;.001</b>
RA/RARS/RCMD untreated	1.0		-	1.0		-
RAEB/sAML/CMML in CR*	<b>1.52</b>	1.07-2.15	<b>.018</b>	<b>1.42</b>	0.99-2.04	<b>.057</b>
RAEB/sAML/CMML untreated*	<b>1.69</b>	1.20-2.38	<b>.003</b>	<b>1.59</b>	1.11-2.27	<b>.011</b>
RAEB/sAML/CMML treated, not in CR*	<b>2.50</b>	1.79-3.49	<b>&lt;.001</b>	<b>2.27</b>	1.60-3.21	<b>&lt;.001</b>
<b>Presence of monosomal karyotype</b>	1.07	0.78-1.47	.684	1.08	0.79-1.49	.622
<b>5-group IPSS-cytogenetics</b>			<b>&lt;.001</b>			<b>&lt;.001</b>
Standard <sup>1</sup>	1.0		-	1.0		-
Poor*	<b>1.39</b>	1.13-1.71	<b>.002</b>	<b>1.36</b>	1.10-1.69	<b>.005</b>
Very Poor*	<b>2.18</b>	1.49-3.20	<b>&lt;.001</b>	<b>2.11</b>	1.45-3.09	<b>&lt;.001</b>
<b>Year of SCT</b>	0.98	0.96-0.99	<b>.003</b>	0.97	0.95-0.98	<b>&lt;.001</b>

\*Compared to the first group (reference group) listed in each category

<sup>1</sup>Standard=merged good and intermediate risk patients

\*\*Patients with missing data for disease status at SCT were kept in the analysis by assigning them to a separate category (HRs not shown).