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POSTER ABSTRACTS

723.ALLOGENEIC TRANSPLANTATION: LONG-TERM FOLLOW-UP AND DISEASE RECURRENCE

IPSS-M Predicts Survival Outcomes Significantly Better Than IPSS-R in Patients Undergoing Allogeneic Hematopoietic Stem Cell Transplantation for Myelodysplastic Neoplasms

Tingting Yang¹, Bingqian Jiang¹, Yi Luo¹, Yanmin Zhao¹, Guifang Ouyang², Jian Yu¹, Jianping Lan³, Ying Lu⁴, Xiaoyu Lai¹, Baodong Ye⁵, Yi Chen⁶, Lizhen Liu¹, Yang Xu⁷, Qunyi Guo⁸, Pengfei Shi⁹, Haowen Xiao¹⁰, Huixian Hu¹¹, Huarui Fu¹, Yishan Ye, MD¹, Xinyu Wang¹, Jie Sun¹, Weiyan Zheng, MD¹, Jingsong He¹, Yi Zhao¹, Wenjun Wu¹, Zhen Cai¹, Guoqing Wei¹, He Huang¹, Jimin Shi¹

¹ Bone Marrow Transplantation Center, The First Affiliated Hospital, Zhejiang University School of Medicine, Hangzhou, China

²Department of Hematology, Ningbo First Hospital, Ningbo, China

³Department of Hematology, Zhejiang Provincial People's Hospital, Hangzhou, China

⁴Department of Hematology, Yinzhou People's Hospital, Ningbo, China

⁵Department of Hematology, The First Affiliated Hospital of Zhejiang Chinese Medical University (Zhejiang Provincial Hospital of Chinese Medicine), Hangzhou, China

⁶Department of Hematology, The First Affiliated Hospital of Wenzhou Medical University, Wenzhou, China

⁷The Second Affiliated Hospital, Zhejiang University, School of Medicine, Hangzhou, China

⁸Department of Hematology, Taizhou Hospital of Zhejiang Province, Wenzhou Medical College, Taizhou, China

⁹Department of Hematology, The Affiliated Hangzhou First People's Hospital, Zhejiang University School of Medicine, Hangzhou, China

¹⁰Department of Hematology, Sir Run Run Shaw Hospital, Zhejiang University, School of Medicine, Hangzhou, China

¹¹Department of Hematology, Jinhua Central Hospital, Jinhua, China

Background

The newly published molecular International Prognostic Scoring System (IPSS-M) represents a powerful risk stratification tool for treatment decision-making in myelodysplastic neoplasms (MDS); however, its utility in the context of allogeneic hematopoietic stem cell transplantation (allo-HSCT) remains to be fully explored.

Methods

We retrospectively analyzed a large multicenter cohort of 347 MDS patients who underwent allo-HSCT between January 2017 and October 2022. The prediction accuracy of IPSS-M at diagnosis for 3-year survival outcomes was assessed and compared to that of the conventional revised International Prognostic Scoring System (IPSS-R).

Results

Among the 347 patients, median age at transplant was 48.3 years and 41.2% of patients were female. According to IPSS-M, patients were clustered as very low risk (1.2%), low risk (11.2%), moderately low risk (11.5%), moderately high risk (18.2%), high risk (33.4%), and very high risk (24.5%), resulting in a restratification of 49.3% of the entire cohort when compared with IPSS-R. Of these reclassified patients, 52.6% patients were upstaged and 47.4% were downstaged. Median follow-up time among the survivors was 28.6 (range, 4.7 to 76.6) months. With the IPSS-M model, overall survival (OS) and leukemia-free survival (LFS) discrimination was refined relative to the IPSS-R as evidenced by a 7.0 percentage- and 5.7 percentage-point increase in the concordance index (C-index), which was further supported by the lower Akaike Information Criterion and higher C-indexes in multivariate analyses. Among patients undergoing haploidentical HSCT, IPSS-M model also demonstrated significantly improved prognostic performance for LFS versus IPSS-R (C-index, 0.707 vs 0.604) which was validated by multivariate analyses. When restricting our analyses to younger patients (<49 years) and patients carrying detectable mutations, IPSS-M retained greater prognostic value with respect to OS and LFS; while it failed to stratify individual probability of OS and LFS in their counterparts.

Conclusions

IPSS-M was confirmed to increase prognostic discrimination at the individual level and is applicable to transplant-specific settings, which also had an advantage for subjects carrying mutations and younger patients.

Disclosures No relevant conflicts of interest to declare.

IPSS-R **IPSS-M** Very High (n=85, 24.5%) Very High (n=82, 23.6%) High High (n=116, 33.4%) (n=100, 28.8%) Moderate High Intermediate (n=63, 18.2%) (n=124, 35.7%) Moderate Low (n=40, 11.5%) Low (n=39, 11.2%) Low (n=39, 11.2%) Very Low Very Low (n=4, 1.2%) (n=2, 0.6%)

Figure 1 Sankey diagram comparing IPSS-R and IPSS-M risk categories.



IPSS-R				IPSS-M			
Variable	HR (95% CI)		Р	Variable	HR (95% CI)		Р
OS				OS			
Recipient sex				Recipient sex			
Female	1			Female	1		
Male	1.57 (1.04 - 2.36)		0.030	Male	1.53 (1.02 - 2.29)		0.040
Age at HSCT				Age at HSCT			
< 49	1			< 49	1	1.	
> 49	1.59 (1.08 - 2.34)	h+	0.018	≥ 49	1.50 (1.02 - 2.20)		0,040
IPSS-R				IPSS-M			
Very low low	1			Very low + low	1	200 C	
Intermediate	1.18 (0.59 - 2.39)	-	0.637	Moderate low	1.17 (0.45 - 3.06)	- -	0.751
High	1.47 (0.70 - 3.06)		0.305	Moderate high	1.25 (0.55 - 2.82)	+	0.599
Veryhigh	2 25 (1 08 - 4 67)	1.0	0.030	High	2.03 (0.97 - 4.25)		0.061
AB() match	2.10 (100 100)			Very high	2.82 (1.32 - 6.02)	·	0.007
Match	1			ABO match			
Mismatch	1.40 (0.96 - 2.05)		0.085	Match	1		
Interval from dia	mosis to HSCT		0,000	Mismatch	1.35 (0.92 - 1.99)	+	0.126
21 1 1				Interval from diagn	nosis to HSCT		
~ 7.1	1 (8 (1 12 - 2 52)		0.012	< 7.1	1		
> 7.1 Domainto modulo	1.08 (1.12 - 2.52)		0.012	≥ 7.1	1.78 (1.19 - 2.65)		0.005
Donor to recipien				Donor to recipient			
Female to mate				Female to male	1		
Others	1.11 (0.54 - 2.29)		0.776	Others	1.14 (0.55 - 2.37)	-	0.718
Transfusion dependence				Transfusion dependence			
No	1			No	1		
Yes	1.32 (0.89 - 1.95)	+-	0.164	Yes	1.13 (0.76 - 1.69)	+	0.549
Concordance =	0.627 (sc = 0.030); AIC=1188.	02		Concordance = 0.64	48 (se = 0.028); AIC = 1184.81		3
LFS		4		LFS			-
Recipient sex				Recipient sex			
Female	1			Female	1		
Male	1.62 (1.10 - 2.38)	⊢ ⊷	0.015	Male	1.54 (1.05 - 2.25)	H	0.028
Age at HSCT				Age at HSCT			
< 49	1			<49	1		
≥ 49	1.40 (0.98 - 2.01)	 − −	0.067	\geq 49	1.30 (0.91 - 1.87)	<u>+</u>	0.150
IPSS-R				IPSS-M			
Very low + low	1			Very low + low	1		
Intermediate	1.19 (0.59 - 2.40)		0.632	Moderate low	1.26 (0.50 - 3.20)	· • • • • • • • • • • • • • • • • • • •	0.623
High	1.76 (0.86 - 3.60)	+•	0.124	Moderate high	1.37 (0.62 - 3.05)		0.435
Very high	2.95 (1.45 - 6.03)		0.003	High	2.15 (1.04 - 4.47)	· · · · ·	0.040
ABO match				Very high	3.41 (1.63 - 7.14)		0.001
Match	1			ABO match			
Mismatch	1.37 (0.96 - 1.97)	↓	0.087	Match	1		10.225
Interval from dia	gnosis to HSCT			Mismatch	1.33 (0.92 - 1.91)	+-	0.124
< 7.1	1			Interval from diagn	tosis to HSCT		
> 7.1	1.74 (1.18 - 2.55)		0.005	< 7.1	1		19972
Donor to recipien	it sex		01000	≥7.1	1.73 (1.19 - 2.53)		0,005
Eemsle to male	1			Donor to recipient s	sex		
Others	1 10 /0 56 - 2 16)		0.780	Female to male	1	0.00-00	02/07/07
HSCT type	1.10 (0.00 - 2.10)		0.700	Others	1.16 (0.59 - 2.28)		0.668
moor the	1			HSCT type	121		
MSD	1.4			MSD			
MSD	1.24 (0.75 - 2.06)		0 202			2.	
MSD Haplo	1.24 (0.75 - 2.06)		0.395	Haplo	1.22 (0.74 - 2.02)	+	0.435

Figure 1

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