ORIGINAL RESEARCH ARTICLE

WILEY

Genetic alteration patterns and clinical outcomes of elderly and secondary acute myeloid leukemia

Shi-Yang Wang | Wen-Yan Cheng | Yuan-Fei Mao | Yong-Mei Zhu | Fu-Jia Liu | Ting-Ting Ma | Yang Shen

Shanghai Institute of Hematology, Department of Hematology, Ruijin Hospital Affiliated to Shanghai Jiao Tong University School of Medicine, Shanghai, China

Correspondence

Yang Shen, No.197 Ruijin Er Road, Ruijin Hospital, Shanghai, China. Email: shen_yang@126.com

Funding information

National Key R&D Program of China, Grant/ Award Number: 2016YFE0202800; National Natural Science Foundation of China, Grant/ Award Number: 81770141; Shanghai Municipal Education Commission-Gaofeng Clinical Medicine Grant Support, Grant/Award Number: 20161406

Peer Review

The peer review history for this article is available at https://publons.com/publon/10. 1002/hon.2656

Abstract

To illustrate the clinical and genetic features of elderly and secondary acute myeloid leukemia (AML) patients, we compared 145 elderly AML (e-AML) and 55 secondary AML (s-AML) patients with 451 young de novo AML patients. Both e-AML and s-AML patients showed lower white blood cell (WBC) and bone marrow (BM) blasts at diagnosis. NPM1, DNMT3A, and IDH2 mutations were more common while biallelic CEBPA and IDH1 mutations were less seen in e-AML patients. s-AML patients carried a higher frequency of KMT2A-AF9. In treatment response and survival, e/s-AML conferred a lower complete remission (CR) rate and shorter duration of event-free survival (EFS) and overall survival (OS) compared with young patients. In multivariate analysis, s-AML was an independent risk factor for OS but not EFS in the whole cohort. Importantly, intensive therapy tended to improve the survival of e/s-AML patients without increasing the risk of early death, and hematopoietic stem cell transplantation (HSCT) could rescue the prognosis of s-AML, which should be recommended for the treatment of fit patients.

KEYWORDS

acute myeloid leukemia, elderly, genetic, prognosis, secondary

1 | INTRODUCTION

Acute myeloid leukemia (AML) is a group of biological and clinical heterogeneous hematologic malignancies, whose prognosis is strongly associated with underlying genetic alterations and clinical factors, especially the history of antecedent hematological diseases or cytotoxic treatment, which is called secondary acute myeloid leukemia (s - AML). In addition, age is another important clinical feature, which exerts negative effect on the disease. More importantly, AML is increasingly considered as a senile disease, which was reported of a median age of 66 in the United States¹ and 71 in Sweden.² With the

development of high dose chemotherapy, hematopoietic stem cell transplantation (HSCT) and even tailored therapy, the treatment outcome of AML has improved significantly in the last decades; however, the prognosis of elderly AML (e-AML) and s-AML remains dismal. Both elderly and secondary AML (e/s-AML) patients present with increased age, poor performance status, more comorbidities, depleted hematopoietic reserves, and more importantly, the disease-associated factors, such as unfavorable cytogenetic and molecular abnormalities, leading to insufficient treatment and poor treatment outcome.³⁻⁵ It was reported that e/s-AML patients harbored less favorable cytogenetics such as *CBF*-rearrangements but more unfavorable cytogenetics especially abnormalities involving 5 or 7 chromosome at diagnosis.^{2,6} Genetic landscape of AML has been widely studied in the

Shi-Yang Wang, Wen-Yan Cheng, and Yuan-Fei Mao contributed equally to this work.

This is an open access article under the terms of the Creative Commons Attribution License, which permits use, distribution and reproduction in any medium, provided the original work is properly cited.

© 2019 The Authors. Hematological Oncology published by John Wiley & Sons Ltd

past decades, however, most of previous studies focused on de novo AML especially those patients with young age, ^{7,8} while reports regarding genetic alterations and their prognostic significance in e/s-AML are still rare.

More importantly, the treatment of e/s-AML remains controversial. Various modalities, such as hypomethylation agents as exemplified as decitabine and azacitidine, and low doses chemotherapy were tried in this group of patients; however, no therapeutic regimen was proved to be significantly superior to traditional chemotherapy. To some extent, the treatment decision was strongly dependent on the fitness of AML patients.

In this study, we examined genetic alterations and post-treatment minimal residual diseases (MRD) in order to illustrate their distribution and prognostic impact in e/s-AML and to provide treatment recommendations for those patients.

2 | METHODS

2.1 | Patients

From January 2013 to December 2017, a total of 651 adult patients (18 years old or above) with newly diagnosed non-M3 AML at Shanghai Institute of Hematology (SIH) were executively enrolled in this study, among which, 55 patients were diagnosed as s-AML (34 patients had an antecedent hematological disease [AHD-AML] and 21 patients were diagnosed as therapy-related AML [t-AML]). Cytogenetic risk stratification was based on 2017 European LeukmiaNet (ELN) recommendations.

This study was approved by the ethic committee of Ruijin Hospital. All patients had given informed consent for both treatment and cryopreservation of bone marrow (BM) and peripheral blood according to the Declaration of Helsinki.

2.2 | Treatment protocols

For young de novo patients (younger than 60 years old), standard intensive "3 + 7" induction regimens (idarubicin $10-12 \text{ mg/m}^2$ or daunorubicin $45-60 \text{ mg/m}^2$, D1-3; cytarabine 100 mg/m^2 D1-7) were given as the initial induction therapy. If CR was achieved, four cycles of high-dose cytarabine (2 g/m^2) was given as consolidation. For e-AML (60 years and older) and s-AML patients, the treatment was mainly decided by the physician in consideration of the fitness of patients and risk of disease. Fit patients received treatment similar to young patients but reduced cycles of consolidation to 2 cycles of high-dose cytarabine; unfit patients received "3 + 7" regimens with reduced dose, hypomethylation treatment or palliative treatment according to the physician's decision.

2.3 | Molecular events and MRD

Genetic alterations including FLT3-ITD/TKD, KMT2A-PTD, NPM1, NRAS, CKIT, CEBPA, DNMT3A, IDH1, IDH2, RUNX1-RUNXT1T1, CBF β -MYH11, KMT2A rearrangements were detected as previously

reported.¹⁰ Bone marrow aspirate samples were processed according to the standard procedure of our institution as previously reported.¹¹ Detection of MRD after induction therapy was based on leukemia-associated immunophenotype (LAIP) at diagnosis and performed by ten-color multiparametric flow cytometry. MRD was considered positive when leukemia cells were greater than or equal to 0.01%.

2.4 | Statistical analyses

Complete remission (CR) was defined by the criteria of the International Working Group. 12 Early death (ED) was defined as death within 30 days after diagnosis. Overall survival (OS) was measured from the date of disease diagnosis to death from any cause, and patients alive at last follow-up were censored. Event-free survival (EFS) was defined as the time from diagnosis to the date of relapse (if achieved CR) or death from any cause, whichever occurred first, with patients still alive censored at the date of last follow-up. Patients who received HSCT were censored at the time of HSCT to eliminate its impact on EFS and OS. The Kaplan-Meier method was used to calculate the distribution of OS and EFS. A log-rank test was performed to compare the difference in survival time. Multivariate analyses were conducted by using binary logistic regression for CR and ED, and Cox proportional hazard model for OS and EFS. All of the above statistical procedures were carried out by using the SPSS Version 24.0 statistical software package.

3 | RESULTS

3.1 | Characteristics of patients

The baseline characteristics of patients were shown in Table 1. Patients with s-AML presented female predominance (P = .041), most of whom had a previous history of breast carcinoma (43%). Older age (P < .001), lower white blood cell (WBC) count (P = .031), hemoglobin (HB, P = .004), and BM blasts (P < .001) were observed in s-AML as compared with young patients. Similarly, elderly patients showed lower WBC (P = .036) and BM blasts (P = .009) at diagnosis. In WHO subtype distribution, higher frequency of pure erythroid leukemia was seen in s-AML (P = .013). Both e-AML and s-AML patients received less intensive induction, but more hypomethylation treatment and palliative treatment than younger patients (all P < .001).

3.2 | Cytogenetic and genetic alterations

In cytogenetic classification, elderly patients had a significantly higher proportion of intermediate risk cytogenetics (P = .011). Favorable cytogenetic alterations were less frequent in both elderly and secondary patients (P = .008 and .014, respectively) as compared with young patients.

With regard to genetic abnormalities, the incidence of CBF leukemia was significantly lower in e/s-AML patients as compared with young patients (7.1% vs 14.7%, P = .013 for RUNX1-RUNX1TI and 2.6% vs 7.4%, P = .038 for $CBF\beta-MYH11$). A higher frequency of

TABLE 1 Clinical characteristics of AML patients

			de novo AML		
Factor	s-AML, N = 55	P ^a	Young, N = 451	Elderly, N = 145	P ^a
Age, y		<.001			<.00
Median	57		43	65	
Range	21-77		18-59	60-81	
Male gender, n (%)	22 (40.0)	.041	246 (54.5)	76 (52.4)	.65
WBC count, ×10 ⁹ /L		.031			.03
Median	6.8		16.83	10.56	
Range	0.8-144.1		0.77-419.9	0.5-241.94	
HB, g/L		.004			.33
Median	69		85	82	
Range	34-143		30-171	15-142	
PLT count, ×10 ⁹ /L		.074			.09
Median	60		41	44	
Range	3-752		2-1726	3-512	
BM blasts, %		<.001			.00
Median	39.5		69	60.5	
Range	16.5-95		7-98.5	17.5-96.5	
WHO category, n (%)					
AML with recurrent genetic abnormalities					
AML with t(8;21)(q22;q22.1); RUNX1-RUNX1T1	2(3.6)	.042	59(13.1)	10(6.9)	.0.
AML with inv(16)(p13.1q22) or t(16;16)(p13.1;q22); CBFB-MYH11	O(O)	.112	28(6.2)	4(2.8)	.10
AML with t(9;11)(p21.3;q23.3); MLLT3-KMT2A	4(7.3)	.013	6(1.3)	1(0.7)	.8.
AML with inv(3)(q21.3q26.2) or t(3;3)(q21.3;q26.2); GATA2, MECOM	O(O)	1	1(0.2)	1(0.7)	.4:
Provisional entity: AML with BCR-ABL1	O(O)	1	1(0.2)	O(O)	1
AML with mutated NPM1	7(12.7)	.436	76(16.9)	39(26.9)	.0
AML with biallelic mutations of CEBPA	3(5.5)	.048	69(15.3)	11(7.6)	.0
AML, NOS					
AML without maturation	O(O)	1	1(0.2)	2(1.4)	.1
AML with maturation	O(O)	.45	12(2.7)	6(4.1)	.5
Acute myelomonocytic leukemia	9(16.4)	.837	69(15.3)	18(12.4)	.3'
Acute monoblastic/monocytic leukemia	6(10.9)	.387	69(15.3)	25(17.2)	.5
Pure erythroid leukemia	4(7.3)	.013	6(1.3)	2(1.4)	1
Not classified	20(36.4)	<.001	54(12.0)	26(17.9)	.0
Therapy					
Intensive induction	23 (41.8)	<.001	422 (93.6)	79 (54.5)	<.0
Hypomethylation	12 (21.8)	<.001	5 (1.1)	15 (10.3)	<.0
Palliative treatment	20 (36.4)	<.001	24 (5.3)	51 (35.2)	<.0

Abbreviation: AML, acute myeloid leukemia; BM, bone marrow; HB, hemoglobin; NOS, not otherwise specified; PLT, platelet; WBC, white blood cell; WHO, The World Health Organization.

NPM1 (P = .003), *DNMT3A* (P = .015), and *IDH2* (P = .004) mutations, but lower frequency of biallelic *CEBPA* (Bi*CEBPA*, P = .029) and *IDH1* (P = .038) mutations were observed in elderly patients. In addition, s-AML patients carried *KMT2A*-AF9 (P = .007) more frequently when compared with young de novo patients (Table 2).

As for the association between genetic abnormalities and clinical features, NPM1 mutations were associated with higher WBC in elderly patients (P = .037). Moreover, s-AML patients with KMT2A-AF9 were prone to having higher BM blasts (P = .068) (Table S1).

^aAll compared with young patients.

TABLE 2 Cytogenetic and genetic alteration patterns of acute myeloid leukemia (AML) patients

			de novo AML		
Variable Number/Total (%)	s-AML, N = 55	P ^a	Young, N = 451	Elderly, N = 145	P ^a
Cytogenetics					
Favorable	3/49 (6.1)	.014	84/404 (20.8)	13/126 (10.3)	.008
Intermediate	38/49 (77.6)	.076	262/404 (64.9)	97/126 (77.0)	.011
Unfavorable	8/49 (16.3)	.712	58/404 (14.4)	16/126 (12.7)	.639
Genetic Alterations					
RUNX1-RUNX1T1	2/46 (4.3)	.052	59/401 (14.7)	10/122 (8.2)	.063
CBFβ-MYH11	0/37 (0)	.170	28/378 (7.4)	4/114 (3.5)	.139
FLT3-ITD	4/44 (9.1)	.416	54/402 (13.4)	18/124 (14.5)	.759
FLT3-TKD	3/44 (6.8)	.932	21/400 (5.2)	6/124 (4.8)	.856
KMT2A-fusion	5/44 (11.4)	.193	21/400 (5.2)	6/123 (4.9)	.870
KMT2A-AF9	4/44 (9.1)	.007	6/400 (1.5)	1/123 (0.8)	.896
KMT2A-PTD	2/44 (4.5)	.956	24/399 (6.0)	9/123 (7.3)	.604
NPM1	7/44 (15.9)	.618	76/400 (19.0)	39/123 (31.7)	.003
CKIT	2/41 (4.9)	.354	42/387 (10.9)	10/118 (8.5)	.457
NRAS	7/44 (15.9)	.669	54/398 (13.6)	18/124 (14.5)	.789
BiCEBPA	3/45 (6.7)	.070	69/403 (17.1)	11/122 (9.0)	.029
DNMT3A	7/46 (15.2)	.373	43/397 (10.8)	24/125 (19.2)	.015
IDH1	2/23 (8.7)	.971	28/314 (8.9)	2/87 (2.3)	.038
IDH2	1/22 (4.5)	.996	22/314 (7.0)	15/87 (17.2)	.004

^aAll compared with young patients.

3.2.1 | Treatment responses

In total cohort, CR rate and ED rate were 76.1% and 10.5%, respectively. Both s-AML and e-AML patients conferred reduced CR rate as compared with young patients (s-AML vs young: 58% vs 83%, P < .001; e-AML vs young, 60.7% vs 83%, P < .001). Additionally, a higher frequency of ED (e-AML vs young: 16.6% vs 8%, P = .003) was observed in e-AML (Table 3). In order to find significant factors that

can independently predict ED and CR, we conducted univariate and multivariate analyses (Tables S1 and 4).

Among patients achieving CR, 258 young, 56 elderly, and 23 secondary AML patients had a definite LAIP feature before treatment, and the MRD of whom could be monitored. The frequency of positive MRD was higher in s-AML than in young patients (P = .039, Table 3). When e-AML and s-AML patients were put together, those who were treated with intensive therapy had a higher CR rate (74.2% vs 44.3%,

TABLE 3 Treatment responses

			de novo AML		
Factor	s-AML, N = 55	P ^a	Young, N = 451	Elderly, N = 145	P ^a
CR status		<.001			<.001
CR, % (n)	58 (29)		83 (356)	60.7 (82)	
Missing/unknown	5		22	10	
Early death		.172			.003
Yes, % (n)	14.5 (8)		8 (36)	16.6 (24)	
Missing/unknown	0		2	0	
MRD		.039			.819
<0.01%, % (n)	17.4 (4)		39.1 (101)	37.5 (21)	
Missing/unknown	32		193	89	

Abbreviation: AML, acute myeloid leukemia; CR, complete remission; MRD, minimal residual disease.

^aAll compared with young patients.

P < .001) and tended to have a lower incidence of positive MRD (60.8% vs 82.1%, P = .051) than those treated with other therapy categories. In addition, e/s-AML patients receiving intensive therapy tended to have a lower ED rate than those who were treated with palliative treatment (12.7% vs 22.5%, P = .090).

3.3 | Impact of prognostic factors on survival

The median follow-up in all patients was 27 months (range, 0-66 months). Generally, e/s-AML patients had inferior EFS and OS compared with young patients (elderly vs young: 9 vs 18 months for EFS, P < .001, and 12 vs 44 months for OS, P < .001; s-AML vs young: 7 vs 18 months for EFS, P < .001, and 11 vs 44 months for OS, P < .001, respectively) (Figure 1A,B). In the stratification of patients who received intensive therapy, e/s-AML patients also conferred shorter EFS and OS than young patients (elderly vs young: 12 vs 20 months for EFS, P < .001, and 15 vs 44 months for OS, P < .001; s-AML vs young: 9 vs 20 months for EFS, P = .022, and 14 vs 44 months for OS, P = .026, respectively) (Figure 1C,D). However, there was no difference in EFS and OS between young and e/s-AML patients who received less intensive therapy (Figure 1E,F). In elderly patients, the median EFS and OS were significantly longer in patients who received intensive therapy, as compared with other treatment modalities (12 vs 6 months for EFS, P = .025, and 15 vs 6 months for OS, P = .04, respectively). A similar tendency was observed in s-AML (9 vs 5 months for EFS, P = .35 and 14 vs 5 months for OS, P = .149). Combining e-AML and s-AML patients together, patients receiving intensive therapy were prone to having a longer EFS and OS than those treated with decitabine-based hypomethylation therapy (10 vs 6 months for EFS, P = .093, and 15 vs 7 months for OS, P = .067, respectively) and palliative treatment (10 vs 6 months for EFS, P = .048, and 15 vs 6 months for OS, P = .057, respectively) (Figure 1G,H). Univariate analysis for EFS and OS was shown in Table S3. In order to explore the prognostic significance of increased age and s-AML after accounting for other recognized prognostic factors, we conducted multivariate analysis (Table 4). In whole cohort, s-AML relative to de novo AML was an independent risk factor for OS (P = .009), while it was not associated with EFS. Notably, the independent prognostic impact of s-AML on OS was lost when HSCT was not regarded as a censored event, suggesting that HSCT may abrogate the adverse impact of s-AML on survival to a certain extent (Table S4).

4 | DISCUSSION

Acute myeloid leukemia is a hematologic malignancy with a relative high incidence rate especially in high Human Development Index (HDI) countries.¹³ The incidence of AML increases with age, which makes AML a tumor of the elderly population.¹ As a separate type of AML, s-AML becomes more and more common due to the aging population and the increasing use of leukemogenic cytotoxic therapy.¹⁴

Our study demonstrated that e/s-AML patients have distinct clinical features compared with young de novo AML patents, such as lower WBC and BM blasts at diagnosis, which indicate that both elderly and secondary AML are less proliferative diseases, partly because they may have either transformed from MDS or experienced an undetected MDS period. Consistently, R. Coleman Lindsley et al¹⁵ reported that one third elderly de novo AML and t-AML patients carried "secondary-type" mutations and showed clinical characteristics indistinguishable from AHD-AML, indicating that a large proportion of elderly de novo AML and t-AML patients may transit through unconscious myelodysplastic disease.

The genetic and molecular heterogeneity of AML have been widely acknowledged and integrated to optimize the prediction of

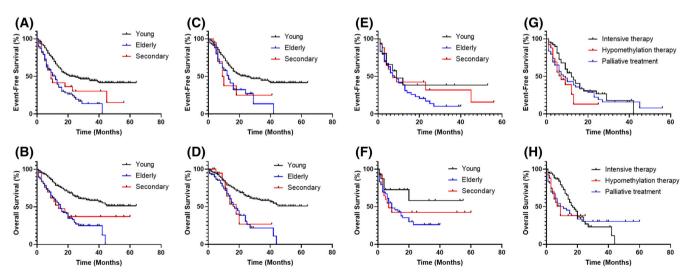


FIGURE 1 Kaplan-Meier curves for probability of event-free survival and overall survival. A,B, Event-free survival and overall survival for all young, elderly, and secondary acute myeloid leukemia (AML) patients. C,D, Event-free survival and overall survival for young elderly and secondary AML patients treated with intensive therapy. E,F, Event-free survival and overall survival for young, elderly, and secondary AML patients treated with less intensive therapy. G,H Event-free survival and overall survival for patients received intensive therapy, hypomethylation therapy and palliative treatment in elderly and secondary AML group

TABLE 4 Multivariate analyses for CR, ED, EFS, and OS^a

	క		ED		EFS		OS	
Covariate	OR (95% CI)	١	OR (95% CI)	۵	HR (95% CI)	Ь	HR (95% CI)	۵
Total								
Age (y)	0.945 (0.926-0.963)	<.001	1.061 (1.031-1.093)	<.001	1.040 (1.029-1.052)	<.001	1.042 (1.030-1.055)	<.001
WBC ($\times 10^9$ /L)		NS		NS	1.004 (1.002-1.007)	<.001	1.005 (1.003-1.008)	<.001
Cytogenetics ^b	0.328 (0.177-0.607)	<.001		NS	3.074 (2.159-4.377)	<.001	3.441 (2.371-4.994)	<.001
s-AML vs de novo AML		NS		NS		NS	2.023 (1.195-3.426)	600:
FLT3-ITD	0.433 (0.224-0.837)	.013		NS	1.669 (1.134-2.458)	600.	1.957 (1.297-2.955)	.001
KMT2A-PTD	0.330 (0.131-0.830)	.018		NS		NS	1.780 (1.000-3.167)	.05
NRAS		NS	3.010 (1.368-6.620)	900:		NS		NS
BiCEBPA	7.004 (1.647-29.782)	800:		NS	0.435 (0.274-0.689)	<.001	0.333 (0.183-0.606)	<.001
Elderly								
BM blasts (%)		NS	1.050 (1.016-1.085)	.004		NS	1.015 (1.000-1.030)	.051
WBC (×10 ⁹ /L)		NS		NS	1.009 (1.002-1.016)	.01	1.008 (1.001-1.016)	.033
Cytogenetics ^b		NS		NS	3.370 (1.642-6.916)	.001	2.693 (1.241-5.844)	.012
CBFβ-MYH11		NS	49.197 (3.050-793.497)	900:	4.171 (1.444-12.048)	800.	6.441 (2.097-19.783)	.001
KMT2A-PTD	0.233 (0.055-0.987)	.048		NS		NS		NS
IDH1		NS		NS	6.918 (1.559-30.698)	.011		NS
Secondary								
Age (y)	0.927 (0.870-0.987)	.018		NS	1.073 (1.020-1.129)	.007		NS
HB (g/L)	1.032 (1.004-1.061)	.027		NS		NS		NS
WBC (×10° /L)		NS		SN	1.018 (1.005-1.031)	900:	1.014 (1.003-1.026)	.017
Cytogenetics ^b		NS		NS	5.455 (1.621-18.354)	900:	5.547 (1.789-17.193)	.003
NRAS		NS	13.125 (1.662-103.673)	.015	7.321 (1.700-31.521)	900.	4.104 (1.096-15.368)	.036

Abbreviation: AML, acute myeloid leukemia; BM, bone marrow; CR, complete remission; ED, early death; EFS, event-free survival; HB, hemoglobin; HR, hazard ratio; OR, odds ratio; OS, overall survival; WBC, white blood cell.

 $^{^{\}text{a}}\textsc{Patients}$ who received HSCT were censored at the time of HSCT. $^{\text{b}}\textsc{Unfavorable}$ vs others.

clinical outcomes for AML patients. Previous studies demonstrated that FLT3-ITD, TP53, RUNX1, ASXL1 aberrations, and KMT2A rearrangements are associated with adverse prognosis, while patients with biCEBPA mutations. RUNX1-RUNXT1T1. and CBFβ-MYH11 seem to have a relatively good outcome. 10,16-22 However, our knowledge concerning distribution and prognostic significance of gene alterations in e/s-AML patients remains scarce. Our study indicated that elderly and secondary patients carried more inferior molecular events such as KMT2A-AF9 and DNMT3A mutations and less favorable ones including RUNX1-RUNXT1T1, CBFβ-MYH11, and biallelic CEBPA. Furthermore, genetic aberrations including NRAS, DNMT3A, IDH1 mutations, and CBFβ-MYH11 conveyed prognostic information independently in e-AML or s-AML patients. However, some significant genetic alterations such as TP53, TET2, ASXL1, and RUNX1 mutations were not routinely tested in our center and accordingly not available in this retrospective study. Tsai et al²² reported that the e-AML harbored more mutations concerning PTPN11, NPM1, RUNX1, ASXL1, TET2, DNMT3A, and TP53 genes, but had less WT1 mutations. In addition. DNMT3A and TP53 mutations were independent adverse prognostic factors for elderly patients. Other studies 10,23-25 showed epigenetic modifier genes (EMGs) including DNMT3A. ASXL1. and TET2 were more frequent in e-AML patients, which was thought to be associated with age-related clonal hematopoiesis and inferior survival. S-AML patients were reported to carry less NPM1 mutations and FLT3-ITD.^{26,27} Besides, patients with AML secondary to MDS and CMML carried more ASXL1 and NRAS mutations.²⁷ Currently, a prospective study including more molecular events is performed in our center, which will provide more integrated results concerning the distribution and prognostic significance of molecular alterations in e/s-AML

Consistent with previous studies, 3,6,24,28 we observed that both e-AML and s-AML were associated with lower CR rate and a short duration of EFS and OS. Although some new therapeutic agents were applied to these high-risk AML patients, the treatment of e/s-AML remains a challenge, and there is no consensus on this controversial issue. Some studies indicated that because of remarkable improvement in supportive care, intensive therapy leads to a better survival without increasing early death rate in e/s-AML patients. 3,6,29,30 Canadian Consensus Guidelines recommended that patients under the age of 80 should be treated with intensive therapy, except for those with major comorbidities or adverse risk cytogenetics who are not candidates for HSCT.31 However, other studies including MD Anderson reported that patients receiving less intensive therapy such as hypomethylation drugs had superior prognosis compared with those receiving intensive induction.^{28,32,33} Our study showed that e/s-AML patients treated with intensive therapy had a higher CR rate and tended to have a lower frequency of positive MRD. More importantly, a tendency of a longer EFS and OS was observed in intensively treated patients compared with those who received hypomethylation therapy or palliative treatment. These results may partially be because patients receiving intensive therapy have better performance status and fewer comorbidities, and our prospective study will provide more convincing evidence.

Recently, a study reported that CPX-351 could improve the response rates and survival of patients aged 60 to 75 with s-AML compared with standard 3 + 7 treatment.³⁴ The Food and Drug Administration (FDA) approved glasdegib and venetoclax for the treatment of patients over 75 years old, or young patients who have comorbidities that are not suitable for intensive induction chemotherapy.^{35,36} We expect that the frontline use of these new drugs may improve the outcomes of e/s-AML individuals, which need to be compared with traditional intensive therapy in prospective research.

In summary, the incidence of e/s-AML is increasing and will be more common in the future, which merits our attention. Both elderly and secondary AML presented with distinct clinical, cytogenetic, and molecular features, whose prognosis remains dismal compared with young de novo patients, with a significant shorter EFS and OS. Intensive therapy could improve the prognosis of e/s-AML patients to a certain degree and should be recommended for patients as long as the conditions are appropriate. HSCT could abrogate the adverse prognostic impact of s-AML and should be considered for the treatment of fit s-AML patients. More importantly, prospective clinical trials with new drugs are warranted in this special group of patients.

ACKNOWLEDGEMENTS

This work was supported in part by the National Key R&D Program of China (no. 2016YFE0202800), the National Natural Science Foundation of China (no. 81770141), and Shanghai Municipal Education Commission-Gaofeng Clinical Medicine Grant Support (no. 20161406).

CONFLICT OF INTEREST

The authors declare no conflict of interest.

ORCID

Shi-Yang Wang https://orcid.org/0000-0002-9649-7407

REFERENCES

- Dores GM, Devesa SS, Curtis RE, Linet MS, Morton LM. Acute leukemia incidence and patient survival among children and adults in the United States, 2001-2007. *Blood*. 2012;119(1):34-43.
- Lazarevic V, Horstedt AS, Johansson B, et al. Incidence and prognostic significance of karyotypic subgroups in older patients with acute myeloid leukemia: the Swedish population-based experience. *Blood Cancer* J. 2014;4(2):e188.
- Juliusson G, Antunovic P, Derolf A, et al. Age and acute myeloid leukemia: real world data on decision to treat and outcomes from the Swedish Acute Leukemia Registry. *Blood*. 2009;113(18):4179-4187.
- Granfeldt Ostgard LS, Medeiros BC, Sengelov H, et al. Epidemiology and clinical significance of secondary and therapy-related acute myeloid leukemia: a national population-based cohort study. J Clin Oncol Off J Am Soc Clin Oncol. 2015;33(31):3641-3649.
- Xu XQ, Wang JM, Gao L, et al. Characteristics of acute myeloid leukemia with myelodysplasia-related changes: a retrospective analysis in a cohort of Chinese patients. Am J Hematol. 2014;89(9):874-881.

- Hulegardh E, Nilsson C, Lazarevic V, et al. Characterization and prognostic features of secondary acute myeloid leukemia in a populationbased setting: a report from the Swedish Acute Leukemia Registry. Am J Hematol. 2015;90(3):208-214.
- Papaemmanuil E, Gerstung M, Bullinger L, et al. Genomic classification and prognosis in acute myeloid leukemia. N Engl J Med. 2016; 374(23):2209-2221.
- Ley TJ, Miller C, Ding L, et al. Genomic and epigenomic landscapes of adult de novo acute myeloid leukemia. N Engl J Med. 2013;368(22): 2059-2074.
- Dohner H, Estey E, Grimwade D, et al. Diagnosis and management of AML in adults: 2017 ELN recommendations from an international expert panel. *Blood*. 2017;129(4):424-447.
- Shen Y, Zhu YM, Fan X, et al. Gene mutation patterns and their prognostic impact in a cohort of 1185 patients with acute myeloid leukemia. *Blood*. 2011;118(20):5593-5603.
- Weng XQ, Shen Y, Sheng Y, et al. Prognostic significance of monitoring leukemia-associated immunophenotypes by eight-color flow cytometry in adult B-acute lymphoblastic leukemia. *Blood Cancer J.* 2013; 3(8):e133.
- Cheson BD, Bennett JM, Kopecky KJ, et al. Revised recommendations of the International Working Group for Diagnosis, Standardization of Response Criteria, Treatment Outcomes, and Reporting Standards for Therapeutic Trials in acute myeloid leukemia. *J Clin Oncol Off J Am Soc Clin Oncol*. 2003;21(24):4642-4649.
- Miranda-Filho A, Pineros M, Ferlay J, Soerjomataram I, Monnereau A, Bray F. Epidemiological patterns of leukaemia in 184 countries: a population-based study. *The Lancet Haematology*. 2018;5(1):e14-e24.
- Morton LM, Dores GM, Tucker MA, et al. Evolving risk of therapyrelated acute myeloid leukemia following cancer chemotherapy among adults in the United States, 1975-2008. *Blood*. 2013;121(15): 2996-3004.
- Lindsley RC, Mar BG, Mazzola E, et al. Acute myeloid leukemia ontogeny is defined by distinct somatic mutations. *Blood*. 2015;125(9): 1367-1376
- Taskesen E, Bullinger L, Corbacioglu A, et al. Prognostic impact, concurrent genetic mutations, and gene expression features of AML with CEBPA mutations in a cohort of 1182 cytogenetically normal AML patients: further evidence for CEBPA double mutant AML as a distinctive disease entity. Blood. 2011;117(8):2469-2475.
- Fröhling S, Schlenk RF, Breitruck J, et al. Prognostic significance of activating FLT3 mutations in younger adults (16 to 60 years) with acute myeloid leukemia and normal cytogenetics: a study of the AML Study Group Ulm. *Blood*. 2002;100(13):4372-4380.
- Stengel A, Kern W, Haferlach T, Meggendorfer M, Fasan A, Haferlach C. The impact of TP53 mutations and TP53 deletions on survival varies between AML, ALL, MDS and CLL: an analysis of 3307 cases. *Leukemia*. 2017;31(3):705-711.
- Tang JL, Hou HA, Chen CY, et al. AML1/RUNX1 mutations in 470 adult patients with de novo acute myeloid leukemia: prognostic implication and interaction with other gene alterations. *Blood*. 2009; 114(26):5352-5361.
- Metzeler KH, Becker H, Maharry K, et al. ASXL1 mutations identify a high-risk subgroup of older patients with primary cytogenetically normal AML within the ELN Favorable genetic category. *Blood*. 2011; 118(26):6920-6929.
- Muñoz L, Nomdedéu JF, Villamor N, et al. Acute myeloid leukemia with MLL rearrangements: clinicobiological features, prognostic impact and value of flow cytometry in the detection of residual leukemic cells. *Leukemia*. 2003;17(1):76-82.
- Tsai CH, Hou HA, Tang JL, et al. Genetic alterations and their clinical implications in older patients with acute myeloid leukemia. *Leukemia*. 2016;30(7):1485-1492.

- Jaiswal S, Fontanillas P, Flannick J, et al. Age-related clonal hematopoiesis associated with adverse outcomes. N Engl J Med. 2014; 371(26):2488-2498.
- 24. Appelbaum FR, Gundacker H, Head DR, et al. Age and acute myeloid leukemia. *Blood.* 2006;107(9):3481-3485.
- 25. Park SH, Chi HS, Cho YU, Jang S, Park CJ. Evaluation of prognostic factors in patients with therapy-related acute myeloid leukemia. *Blood Research*. 2013;48(3):185-192.
- Kayser S, Dohner K, Krauter J, et al. The impact of therapy-related acute myeloid leukemia (AML) on outcome in 2853 adult patients with newly diagnosed AML. *Blood*. 2011;117(7):2137-2145.
- Fernandez-Mercado M, Yip BH, Pellagatti A, et al. Mutation patterns of 16 genes in primary and secondary acute myeloid leukemia (AML) with normal cytogenetics. PLoS ONE. 2012;7(8):e42334.
- Boddu PC, Kantarjian HM, Ravandi F, et al. Characteristics and outcomes of older patients with secondary acute myeloid leukemia according to treatment approach. *Cancer*. 2017;123(16): 3050-3060.
- Sorror ML, Storer BE, Elsawy M, et al. Impact of comorbidities at diagnosis of acute myeloid leukemia on one-year mortality. *Blood*. 2015; 126:532-532.
- Othus M, Kantarjian H, Petersdorf S, et al. Declining rates of treatment-related mortality in patients with newly diagnosed AML given 'intense' induction regimens: a report from SWOG and MD Anderson. Leukemia. 2014;28(2):289-292.
- 31. Brandwein JM, Zhu N, Kumar R, et al. Treatment of older patients with acute myeloid leukemia (AML): revised Canadian consensus guidelines. American Journal of Blood Research. 2017;7(4):30-40.
- Quintás-Cardama A, Ravandi F, Liu-Dumlao T, et al. Epigenetic therapy is associated with similar survival compared with intensive chemotherapy in older patients with newly diagnosed acute myeloid leukemia. *Blood.* 2012;120(24):4840-4845.
- 33. Kantarjian H, Ravandi F, O'Brien S, et al. Intensive chemotherapy does not benefit most older patients (age 70 years or older) with acute myeloid leukemia. *Blood*. 2010;116(22):4422-4429.
- Kim M, Williams S. Daunorubicin and cytarabine liposome in newly diagnosed therapy-related acute myeloid leukemia (AML) or AML with myelodysplasia-related changes. *Ann Pharmacother*. 2018;52(8): 792-800.
- DiNardo CD, Pratz K, Pullarkat V, et al. Venetoclax combined with decitabine or azacitidine in treatment-naive, elderly patients with acute myeloid leukemia. *Blood*. 2019;133(1):7-17.
- Cortes JE, Heidel FH, Hellmann A, et al. Randomized comparison of low dose cytarabine with or without glasdegib in patients with newly diagnosed acute myeloid leukemia or high-risk myelodysplastic syndrome. *Leukemia*. 2019;33(2):379-389.

SUPPORTING INFORMATION

Additional supporting information may be found online in the Supporting Information section at the end of this article.

How to cite this article: Wang S, Cheng W, Mao Y, et al. Genetic alteration patterns and clinical outcomes of elderly and secondary acute myeloid leukemia. *Hematological Oncology*. 2019;37:456–463. https://doi.org/10.1002/hon.2656