

# Allogeneic hematopoietic stem cell transplantation could overcome the poor prognosis of *DNMT3A*<sup>mut</sup>*NPM1*<sup>mut</sup>*FLT3-ITD*<sup>mut</sup> in acute myeloid leukemia: real-world multicenter analysis in China

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**Abstract** The cooccurrence of *NPM1*, *FLT3-ITD*, and *DNMT3A* mutations (i.e., triple mutation) is related to dismal prognosis in patients with acute myeloid leukemia (AML) receiving chemotherapy alone. In this multicenter retrospective cohort study, we aimed to identify whether allogeneic hematopoietic stem cell transplantation (allo-HSCT) could overcome the poor prognosis of *DNMT3A*<sup>mut</sup>*NPM1*<sup>mut</sup>*FLT3-ITD*<sup>mut</sup> AML across four transplant centers in China. Fifty-three patients with triple-mutated AML receiving allo-HSCT in complete remission were enrolled. The 1.5-year probabilities of relapse, leukemia-free survival, and overall survival after allo-HSCT were 11.9%, 80.3%, and 81.8%, respectively. Multivariate analysis revealed that more than one course of induction chemotherapy and allo-HSCT beyond CR1 were associated with poor survival. To our knowledge, this work is the largest study to explore the up-to-date undefined role of allo-HSCT in patients with triple-mutated AML. Our real-world data suggest that allo-HSCT could overcome the poor prognosis of *DNMT3A*<sup>mut</sup>*NPM1*<sup>mut</sup>*FLT3-ITD*<sup>mut</sup> in AML.

**Keywords** allogeneic hematopoietic stem cell transplantation; acute myeloid leukemia; *DNMT3A* mutation; *NPM1* mutation; *FLT3-ITD* mutation; triple mutation

## Introduction

*NPM1*, *FLT3-ITD*, and *DNMT3A* mutations are the most common genomic lesions in *de novo* acute myeloid leukemia (AML) and play key roles in the pathogenesis

and evolution of the disease, particularly in AML with normal cytogenetics [1–3]. According to limited real-world data, the cooccurrence of these three mutations (i.e., triple-mutated AML) occurs in approximately 5.9%–7% of patients with *de novo* AML [4]. Triple-mutated AML is associated with typical clinical features, such as significantly high white blood cell count and prevalence in young women [4].

Although triple-mutated AML generally has a poor prognosis, it is still categorized as intermediate-risk AML according to the European LeukemiaNet (ELN) 2022 risk classification [5]. The *DNMT3A* mutation is not

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considered a poor prognostic factor in the ELN 2022 risk classification for AML; however, some studies have reported that overlapping *DNMT3A* mutations with *NPM1* or *FLT3*-ITD mutations are associated with a poor prognosis [6,7].

The prognostic effects of individual mutations are often significantly altered by other mutations. Such gene–gene interactions are especially pronounced in *NPM1*-mutated AML [6,8,9]. Triple-mutated AML shows a unique differentiation response to *FLT3* inhibitors [10] and increased sensitivity to ibrutinib [11]. Transcriptomic and immunophenotypic data indicate that triple-mutated blasts are associated with a high frequency of leukemia stem cells and the synergistic upregulation of a specific leukemia stem cell regulator [12]. Specific DNA methylation signatures have been characterized in triple-mutated AML [13]. The genetic interactions among these three mutations have been documented in a mouse model [14] and in humans [6,15,16], further suggesting that triple-mutated AML might represent a distinct entity with poor outcomes.

Large cohort studies identified a poor prognosis for triple-mutated AML [4,6,17–21]. According to a report of 507 consecutive patients with AML from five Brazilian centers, 35 patients were diagnosed with triple-mutated AML; the cumulative incidence of relapse was as high as 85%, and the overall survival (OS) rate was only 4% [4]. *FLT3* inhibitors can improve the clinical outcomes of patients with AML having *FLT3* mutations, but whether they exhibit the same effect on patients with triple-mutated AML remains controversial. Some authors reported that patients with triple-mutated AML may benefit from sorafenib maintenance [19]; however, adding midostaurin to first-line therapy did not improve the clinical outcomes of triple-mutated AML [22].

Allogeneic hematopoietic stem cell transplantation (allo-HSCT) is the most important curative treatment for adult patients with AML. For AML with intermediate- or adverse-risk cytogenetics, the clinical outcomes of patients receiving allo-HSCT are better than those of patients receiving chemotherapy alone [23–25]. However, whether patients with triple-mutated AML could benefit from allo-HSCT remains unknown.

In this multicenter real-world study, we aimed to identify the clinical outcomes of patients with triple-mutated AML who underwent allo-HSCT.

## Materials and methods

### Patients

This multicenter retrospective study was designed by the Peking University Institute of Hematology, the First Affiliated Hospital of Soochow University, Wuhan Tongji Hospital, and Shanghai Ruijin Hospital.

Consecutive patients diagnosed with AML from January 2017 to June 2022 were screened, and the eligibility criteria were as follows: (1) aged  $\geq 16$  years; (2) intermediate-risk *de novo* AML based on ELN 2022 classification [5]; (3) achieved complete remission (CR) before HSCT; and (4) comutation of *DNMT3A*, *NPM1*, and *FLT3*-ITD (*DNMT3A*<sup>mut</sup>*NPM1*<sup>mut</sup>*FLT3*-ITD<sup>mut</sup>). The exclusion criteria were as follows: (1) age < 16 years; (2) patients who did not meet the criteria for intermediate-risk AML as defined by the ELN 2022 classification; (3) therapy-related AML or a previous history of myelodysplasia syndrome; and (4) incomplete medical information. Patients with triple-mutated AML receiving consolidation chemotherapy alone during the same period were also enrolled in the control cohort ( $n = 22$ ), and only six of them achieved CR. Given the small sample size of patients receiving chemotherapy alone, only the allo-HSCT and chemotherapy-based groups were compared using descriptive statistics. The final follow-up was conducted on July 31, 2023. This study was approved by the institutional review board of each participating hospital and conducted in accordance with the *Declaration of Helsinki*. All patients provided written informed consent for the use of their clinical data as part of an ongoing quality improvement program.

### Genotyping

*DNMT3A* mutations were detected as previously reported [26,27]. Next-generation sequencing was performed to detect concurrent mutations. The predominant variants (A, B, and D) within the *NPM1* gene were precisely identified using real-time fluorescence quantitative polymerase chain reaction (PCR) [28] (Supplementary Methods). *FLT3*-ITD mutations were detected using PCR [29] (Supplementary Methods). The allelic ratio for *FLT3*-ITD was determined by calculating the ratio of the area under the curve for the mutant alleles to that of the wild-type alleles (*FLT3*-ITD<sup>mut</sup>/*FLT3*<sup>wt</sup>).

### Transplant regimen

The major preconditioning regimens included cytarabine, busulfan, cyclophosphamide, semustine, and anti-thymocyte globulin [30,31] (Supplementary Methods). The protocol for graft-versus-host disease (GVHD) and infection prophylaxis has been reported previously [32–35] (Supplementary Methods).

### MRD monitoring protocols

MRD status was monitored before allo-HSCT; at 1, 2, 3, 4.5, 6, 9, and 12 months after allo-HSCT; and at 6-month intervals thereafter [3,36,37]. *NPM1* was identified by real-time quantitative PCR according to the ELN MRD

working party. A positive qPCR result was defined as a cycling threshold of  $< 40$  in at least two of three replicates [38]. Multiparameter flow cytometry (MFC) for leukemia-associated aberrant immunophenotypes and/or those different from normal with 0.1% was used as a threshold to distinguish MRD positivity [39].

### Data collection

The investigators at each hospital utilized the institutional electronic medical records and clinical databases. The collected data included information on patient demographics; diagnosis; mutated status of *DNMT3A*, *NPM1*, and *FLT3*-ITD; chemotherapy before allo-HSCT; transplant regimens; MRD status before and after allo-HSCT; maintenance and preemptive therapies; and clinical outcomes. All data were independently reviewed by two physicians with extensive experience in allo-HSCT.

### Definition

Maintenance therapy was defined as patients who were persistently MRD-negative and received therapy for relapse prophylaxis after allo-HSCT. MRD positivity was defined by MFC-MRD or *NPM1*-qPCR positivity. Preemptive therapy was defined as patients who were MRD-positive and received therapy after allo-HSCT to prevent hematologic relapse, including donor lymphocyte infusion [40], interferon- $\alpha$  [41,42], *FLT3* inhibitors, or hypomethylating agents. Relapse was defined as the recurrence of  $> 5\%$  bone marrow blasts, reappearance of blasts in the peripheral blood, development of extramedullary disease, or recurrence of pretransplantation chromosomal abnormalities. Nonrelapse mortality (NRM) was defined as death without disease progression or relapse. Leukemia-free survival (LFS) was defined as survival with continuous CR. OS events were defined as death from any cause.

### Statistical analysis

Data were censored at the time of death or last available follow-up. The primary outcome was the relapse rate. The secondary outcomes included MRD positivity, NRM, EFS, LFS, and OS. Frequencies and percentages were used to describe patient characteristics. The Kaplan–Meier estimator was applied to calculate the probabilities of survival, and the cumulative incidence function was employed to calculate the incidence of relapse and NRM using competing risk analysis. Univariate and multivariate Cox regression analyses were performed to determine the impact of potential prognostic factors on clinical outcomes (Table S1). Two-sided  $P$  values were used. Independent variables with  $P > 0.1$  were sequentially excluded from the model, and  $P < 0.05$  was

considered statistically significant. Statistical analyses were performed with R software 4.2.0 and SPSS 26 (SPSS Inc., IBM, Armonk, NY, USA).

## Results

### Patients' characteristics

Fifty-three patients with intermediate-risk triple-mutated AML receiving allo-HSCT were enrolled, and their characteristics are shown in Table 1. The distribution of other comutant molecular abnormalities is presented in Table S2. Nine patients received maintenance therapy (seven with *FLT3* inhibitors and two with hypomethylating agents) after allo-HSCT. The median follow-up duration was 865 days (range, 775–955) days.

### Engraftment and GVHD

Among the patients, 52 (98.1%) achieved neutrophil engraftment, and the median time from transplantation to neutrophil engraftment was 12.5 days (range, 10–25 days). In addition, 52 patients (98.1%) achieved platelet engraftment, and the median time from transplantation to platelet engraftment was 14 days (range, 8–106 days).

The 100-day cumulative incidences of grades I–IV and III–IV acute GVHD after allo-HSCT were 30.2% (95% CI: 17.7%–42.7%) and 9.4% (95% CI: 1.5%–17.4%), respectively. The 3-year cumulative incidences of total and moderate or severe chronic GVHD after allo-HSCT were 26.4% (95% CI: 13.9%–38.9%) and 6.1% (95% CI: 0%–12.9%), respectively.

### MRD occurrence and relapse

All 53 patients achieved CR before allo-HSCT, among which, 38 (71.7%) and 15 (28.3%) were MRD-negative and MRD-positive, respectively. Seven patients (13.2%) showed MRD positivity after allo-HSCT (MFC positivity alone, one; *NPM1* positivity alone, six), and two of these seven patients showed persistent MRD positivity and relapse after allo-HSCT (Table S2). Five patients achieved MRD negativity: one achieved MRD negativity after preemptive donor lymphocyte infusion, one achieved MRD negativity after sorafenib treatment, and the other three achieved MRD negativity without preemptive interventions.

Eight patients experienced relapse within a median time of 165 days (range, 32–398 days) after allo-HSCT. The 1.5-year cumulative incidence of relapse after allo-HSCT was 11.9% (95% CI: 2.8%–21.0%) and was comparable between the patients who were MRD positive and MRD negative before allo-HSCT (Fig. 1A; Table S3). The cumulative incidence of relapse after allo-HSCT was comparable between the patients with R882 and

**Table 1** Characteristics of patients with triple-mutated AML receiving allo-HSCT

Characteristics	<i>n</i> = 53
Age, <i>n</i> (%)	
16–54 years	43 (81.1)
≥ 55 years	10 (18.9)
Median age at allo-HSCT, years (range)	47 (22–61)
Gender, <i>n</i> (%)	
Male	22 (41.5)
Female	31 (58.5)
Courses of induction chemotherapy before first CR, median (range)	1 (1–4)
Disease status before allo-HSCT, <i>n</i> (%)	
CR1	50 (94.3)
> CR1	3 (5.7)
HCT-CI scores before allo-HSCT, <i>n</i> (%)	
0 (low risk)	38 (71.7)
1–2 (intermediate risk)	11 (20.8)
≥ 3 (high risk)	4 (7.5)
Donor type, <i>n</i> (%)	
Matched sibling donor	14 (26.4)
Haploidentical related donor	37 (69.8)
Unrelated donor	2 (3.8)
Donor/recipient gender matching, <i>n</i> (%)	
Female donor/male recipient combination	7 (13.2)
Others	46 (86.8)
Blood group disparity, <i>n</i> (%)	
Matched	28 (52.8)
Minor mismatched	8 (15.1)
Major mismatched or minor and major mismatched	17 (32.1)
Conditioning regimen, <i>n</i> (%)	
Chemotherapy-based regimen	50 (94.3)
TBI-based regimen	3 (5.7)
Graft type, <i>n</i> (%)	
PB	17 (32.1)
BM + PB	36 (67.9)
MNC counts in graft, median (range, × 10 <sup>8</sup> /kg)	10.9 (3.4–28.7)
CD34 <sup>+</sup> cell counts in graft, median (range, × 10 <sup>6</sup> /kg)	4.8 (1.3–14.9)

Allo-HSCT, allogeneic hematopoietic stem cell transplantation; BM, bone marrow; CR, complete remission; HCT-CI, hematopoietic cell transplantation-specific comorbidity index; MNC, mononuclear cell; PB, peripheral blood; TBI, total body irradiation.

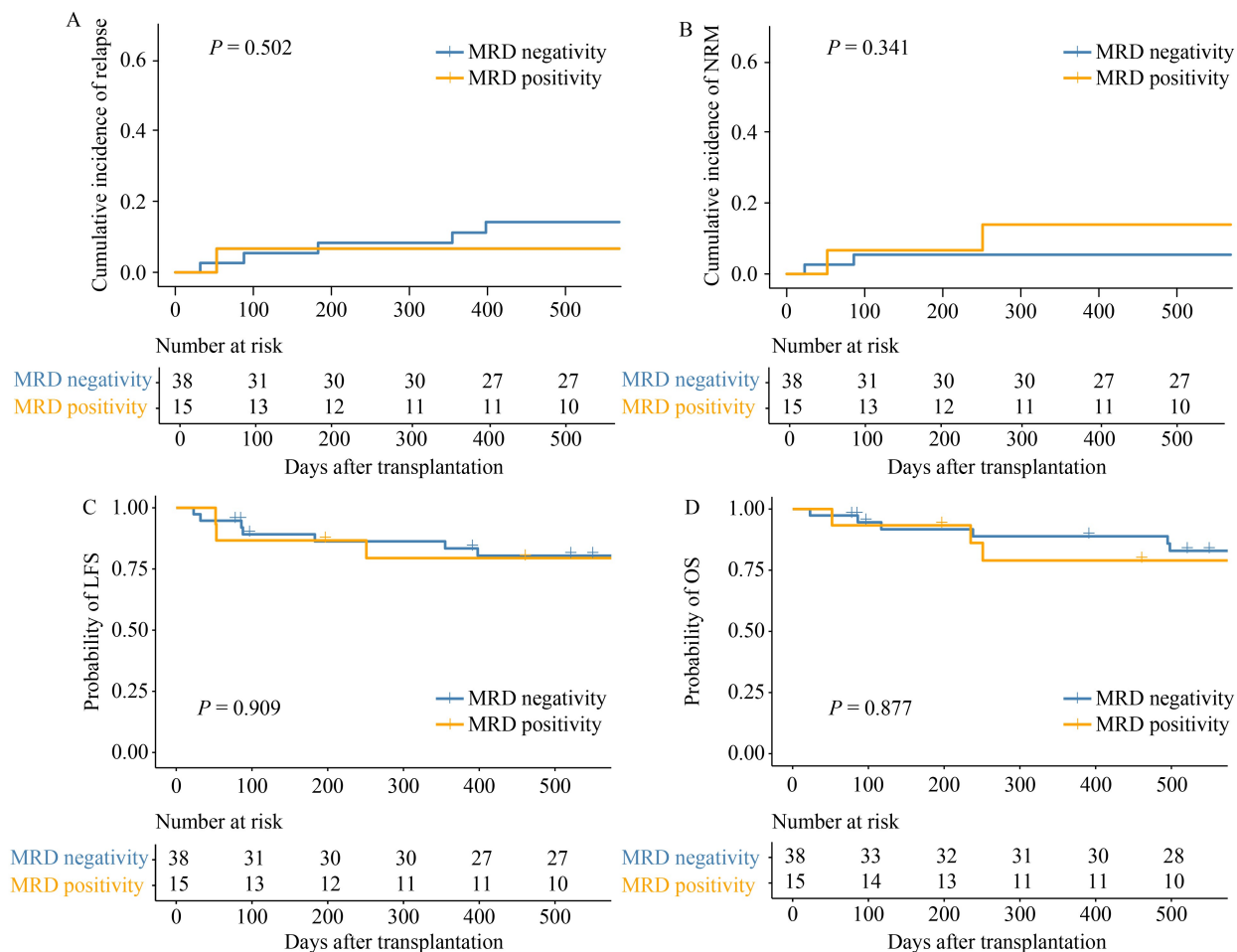
non-R882 mutations (Fig. 2A; Table S4). In addition, the patients who received consolidation chemotherapy alone had a higher cumulative incidence of relapse than those who received allo-HSCT (Fig. 3A; Table S5).

In the multivariate analysis, no risk factors were associated with relapse after allo-HSCT (Table 2).

### NRM, LFS, and OS

Four patients died of NRM (infection, *n* = 3; acute

GVHD, *n* = 1). The 1.5-year cumulative incidence of NRM after allo-HSCT was 7.8% (95% CI, 0.4%–15.2%). The 1.5-year probabilities of LFS and OS after allo-HSCT were 80.3% (95% CI: 70.0%–92.1%) and 81.8% (95% CI, 71.7%–93.3%), respectively. The 1.5-year probabilities of NRM, LFS, and OS were all comparable between the patients who were MRD positive and MRD negative before allo-HSCT (Fig. 1B–1D; Table S3) and between the patients with R882 and non-R882 mutations (Fig. 2B–2D; Table S4). In addition, the patients who



**Fig. 1** 1.5-year clinical outcomes in patients with triple-mutated AML who were positive and negative for MRD before allo-HSCT. (A) relapse, (B) non-relapse mortality, (C) leukemia-free survival, and (D) overall survival.

received consolidation chemotherapy alone had worse LFS and OS than those receiving allo-HSCT (Fig. 3C and 3D; Table S5).

Multivariate analysis revealed that many courses of induction chemotherapy and allo-HSCT beyond CR1 were associated with poor LFS and OS. No risk factors were associated with NRM (Table 2).

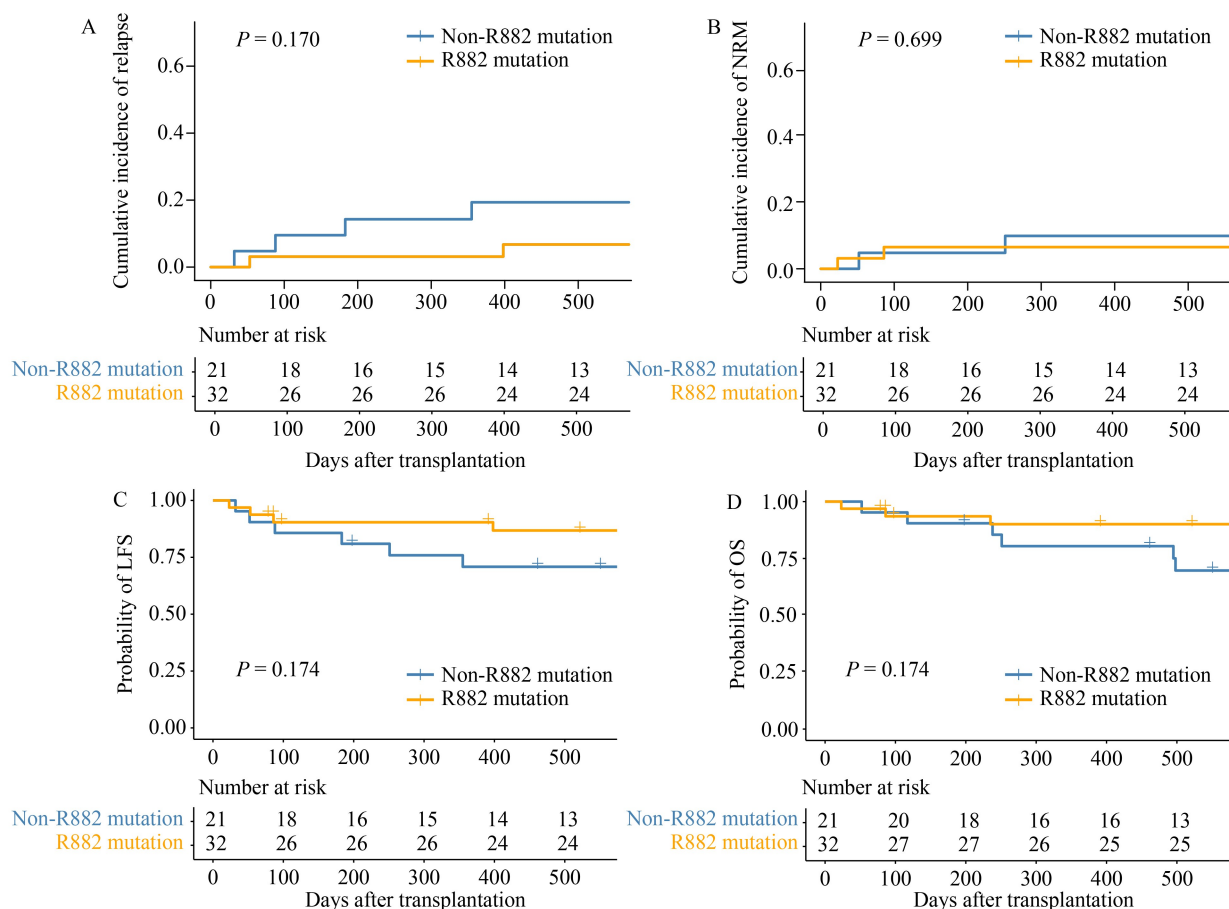
## Discussion

In this study, we observed that the 1.5-year probabilities of relapse, NRM, LFS, and OS after allo-HSCT were 11.9%, 7.8%, 80.3%, and 81.8%, respectively. To our knowledge, this work is the largest study to explore the undefined role of allo-HSCT in patients with triple-mutated AML.

The LFS of triple-mutated AML is poor, and the incidence of relapse could be as high as 70%–85% in patients without allo-HSCT [4, 6]. In the present study, the relapse risk was reduced to 11.9% after allo-HSCT. The EBMT Acute Leukemia Working Party conducted a

large retrospective research on a subgroup of 324 normal-cytogenetic allo-HSCT recipients with *FLT3*-ITD and *NPM1* comutation; the results showed that 244 were triple-positive (75%) and LFS and OS were not significantly different between the patients with and without *DNMT3A* mutation (2-year LFS: 62% vs. 63%, HR: 0.98,  $P = 0.95$ ; 2-year OS: 70% vs. 73%, HR: 1.17,  $P = 0.58$ ) [43]. All these data suggested that allo-HSCT could substantially reduce the relapse risk of triple-mutated AML to the level of intermediate-risk AML.

The maintenance of sorafenib therapy after allo-HSCT could further decrease the incidence of relapse and improve the LFS [19,44] of patients with AML and *FLT3* mutation; however, only seven patients received sorafenib maintenance after allo-HSCT. The 1.5-year probability of relapse was only 11.9%, and the OS rate was as high as 81.8%. This finding suggested that most of the patients in our triple-mutated AML cohort achieved persistent LFS without maintenance. One explanation is that most of the patients (94.3%) were MRD negative before allo-HSCT, and the proportion of women was also high (nearly 60%).



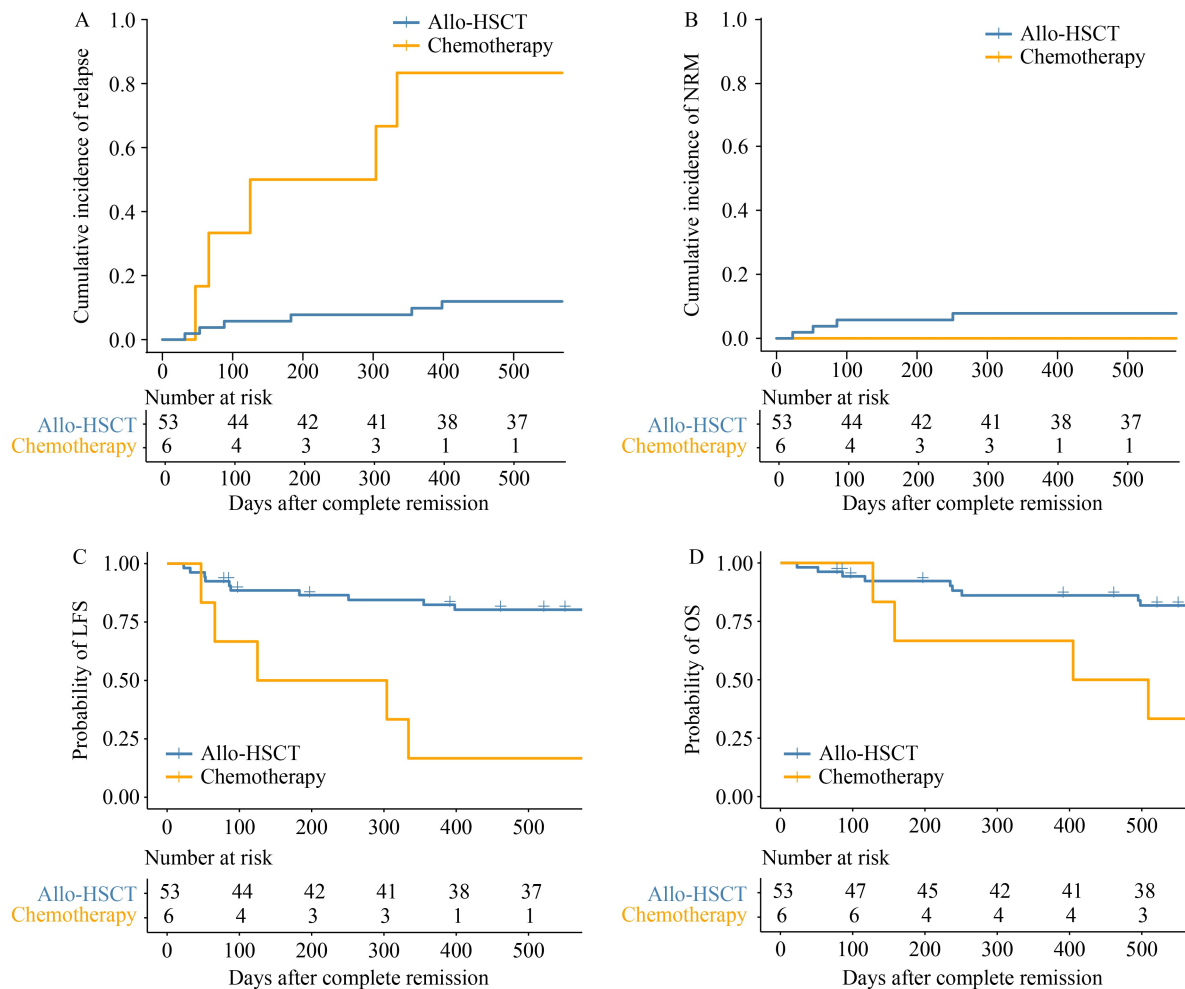
**Fig. 2** 1.5-year clinical outcomes after allo-HSCT in patients with triple-mutated AML and R882 or non-R882 mutations. (A) relapse, (B) non-relapse mortality, (C) leukemia-free survival, and (D) overall survival.

Xuan *et al.* [19] reported that women who were MRD negative before or after allo-HSCT did not benefit from sorafenib maintenance therapy. In the MORPHO study, researchers also observed that the benefits of gilteritinib maintenance were restricted to patients who were MRD positive before allo-HSCT [45]. Zhang *et al.* [46] reported that the clinical outcomes after HID HSCT were comparable between patients with AML with or without FLT3 mutation, suggesting that HID HSCT could partially overcome the poor prognosis of FLT3 mutation. In the present work, more than half of the patients underwent HID HSCT. The patients who received regular MRD monitoring after allo-HSCT and those who were MRD positive all received preemptive therapy, which could also help prevent relapse in the absence of maintenance therapies. Given that the pathogenic mechanism may be different between patients with triple-mutated AML and those with FLT3 mutation alone, the benefit of FLT3 inhibitor maintenance therapy should be verified in patients with triple-mutated AML, particularly in the era of novel FLT3 inhibitors (including quizartinib). However, we could not further identify its efficacy in patients with triple-mutated AML because of

the small number of patients receiving sorafenib maintenance therapy.

Owing to the paucity of patients with triple-mutated AML, our multicenter study was limited by the sample size. Thus, we did not restrict the therapy protocols to induction and consolidation regimens, which might have had an impact on posttransplant outcomes. Nonetheless, 94.3% ( $n = 50$ ) of the patients achieved CR, with 71.7% ( $n = 38$ ) being MRD negative before allo-HSCT. The disease status before allo-HSCT was uniform, which may have partially offset the impact of different induction and consolidation protocols before allo-HSCT.

In conclusion, this large-scale real-world study indicated that patients with triple-mutated AML in CR could benefit from allo-HSCT. The results confirmed the efficacy and safety of allo-HSCT in a disease-specific population of patients with triple-mutated AML. Therefore, sequential allo-HSCT might provide an ideal workflow for this AML subset. Further prospective multicenter randomized controlled trials could help confirm our results. In addition, novel pre- and post-transplant treatments, such as new FLT3 inhibitors, menin inhibitors, and immunomodulation, may further improve



**Fig. 3** 1.5-year clinical outcomes after the first remission in patients with triple-mutated AML who received allo-HSCT or consolidation chemotherapy alone. (A) relapse, (B) nonrelapse mortality, (C) leukemia-free survival, and (D) overall survival.

**Table 2** Multivariable analysis of clinical outcomes following allo-HSCT in patients with triple-mutated AML

Outcomes	HR (95% CI)	<i>P</i>
Treatment failure as defined by leukemia-free survival		
Courses of induction chemotherapy before first CR		
1	1	0.010
> 1	5.77 (1.51–21.97)	
Disease status before allo-HSCT		
CR1	1	0.003
≥ CR1	14.07 (2.51–78.89)	
Treatment failure as defined by overall survival		
Courses of induction chemotherapy before first CR		
1	1	0.012
> 1	5.55 (1.46–21.19)	
Disease status before allo-HSCT		
CR1	1	0.002
≥ CR1	14.45 (2.58–80.95)	

CR, complete remission; HSCT, hematopoietic stem cell transplantation; MRD, minimal residual disease.

the outcomes of patients with triple-mutated AML.

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## Compliance with ethics guidelines

**Conflicts of interest** Wenxuan Huo, Yifan Shen, Jiayu Huang, Yang Yang, Shuang Fan, Xiaosu Zhao, Qi Wen, Luxiang Wang, Chuanhe Jiang, Yang Cao, Xiaodong Mo, Yang Xu, and Xiaoxia Hu declare no competing interests.

The study was approved by the Institutional Review Board of Peking University People's Hospital and the study was performed in accordance with the ethical standards as laid down in the 1964 *Declaration of Helsinki* and its later amendments or comparable ethical standards. Informed consent was obtained from all individual participants or their guardians included in the study.

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## References

1. Cancer Genome Atlas Research Network; Ley TJ, Miller C, Ding L, Raphael BJ, Mungall AJ, Robertson A, Hoadley K, Triche TJ Jr, Laird PW, Baty JD, Fulton LL, Fulton R, Heath SE, Kalicki-Veizer J, Kandoth C, Klco JM, Koboldt DC, Kanchi KL, Kulkarni S, Lamprecht TL, Larson DE, Lin L, Lu C, McLellan MD, McMichael JF, Payton J, Schmidt H, Spencer DH, Tomasson MH, Wallis JW, Wartman LD, Watson MA, Welch J, Wendl MC, Ally A, Balasundaram M, Birol I, Butterfield Y, Chiu R, Chu A, Chuah E, Chun HJ, Corbett R, Dhalla N, Guin R, He A, Hirst C, Hirst M, Holt RA, Jones S, Karsan A, Lee D, Li HI, Marra MA, Mayo M, Moore RA, Mungall K, Parker J, Pleasance E, Plettner P, Schein J, Stoll D, Swanson L, Tam A, Thiessen N, Varhol R, Wye N, Zhao Y, Gabriel S, Getz G, Sougnez C, Zou L, Leiserson MD, Vandin F, Wu HT, Applebaum F, Baylin SB, Akbani R, Broom BM, Chen K, Motter TC, Nguyen K, Weinstein JN, Zhang N, Ferguson ML, Adams C, Black A, Bowen J, Gastier-Foster J, Grossman T, Lichtenberg T, Wise L, Davidsen T, Demchok JA, Shaw KR, Sheth M, Sofia HJ, Yang L, Downing JR, Eley G. Genomic and epigenomic landscapes of adult *de novo* acute myeloid leukemia. *N Engl J Med* 2013; 368(22): 2059–2074
2. Patel JP, Gonen M, Figueroa ME, Fernandez H, Sun Z, Racevskis J, Van Vlierberghe P, Dolgalev I, Thomas S, Aminova O, Huberman K, Cheng J, Viale A, Socci ND, Heguy A, Cherry A, Vance G, Higgins RR, Ketterling RP, Gallagher RE, Litzow M, van den Brink MRM, Lazarus HM, Rowe JM, Luger S, Ferrando A, Paietta E, Tallman MS, Melnick A, Abdel-Wahab O, Levine RL. Prognostic relevance of integrated genetic profiling in acute myeloid leukemia. *N Engl J Med* 2012; 366(12): 1079–1089
3. Di Grazia C, Pozzi S, Geroldi S, Grasso R, Miglino M, Colombo N, Tedone E, Luchetti S, Lamparelli T, Gualandi F, Ibatci A, Bregante S, Van Lint MT, Raiola AM, Dominietto A, Varaldo R, Galaverna F, Ghiso A, Sica S, Bacigalupo A. Wilms tumor 1 expression and pre-emptive immunotherapy in patients with acute myeloid leukemia undergoing an allogeneic hemopoietic stem cell transplantation. *Biol Blood Marrow Transplant* 2016; 22(7): 1242–1246
4. Bezerra MF, Lima AS, Pique-Borras MR, Silveira DR, Coelho-Silva JL, Pereira-Martins DA, Weinhäuser I, Franca-Neto PL, Quek L, Corby A, Oliveira MM, Lima MM, de Assis RA, de Melo Campos P, Duarte BK, Bendit I, Rocha V, Rego EM, Traina F, Saad ST, Beltrão EI, Bezerra MA, Lucena-Araujo AR. Co-occurrence of DNMT3A, NPM1, FLT3 mutations identifies a subset of acute myeloid leukemia with adverse prognosis. *Blood* 2020; 135(11): 870–875
5. Döhner H, Wei AH, Appelbaum FR, Craddock C, DiNardo CD, Dombret H, Ebert BL, Fenaux P, Godley LA, Hasserjian RP, Larson RA, Levine RL, Miyazaki Y, Niederwieser D, Ossenkoppele G, Röhlig C, Sierra J, Stein EM, Tallman MS, Tien HF, Wang J, Wierzbowska A, Löwenberg B. Diagnosis and management of AML in adults: 2022 recommendations from an international expert panel on behalf of the ELN. *Blood* 2022; 140(12): 1345–1377
6. Papaemmanuil E, Gerstung M, Bullinger L, Gaidzik VI, Paschka P, Roberts ND, Potter NE, Heuser M, Thol F, Bolli N, Gundem G, Van Loo P, Martincorena I, Ganly P, Mudie L, McLaren S, O'Meara S, Raine K, Jones DR, Teague JW, Butler AP, Greaves MF, Ganser A, Döhner K, Schlenk RF, Döhner H, Campbell PJ. Genomic classification and prognosis in acute myeloid leukemia. *N Engl J Med* 2016; 374(23): 2209–2221
7. Kihara R, Nagata Y, Kiyoi H, Kato T, Yamamoto E, Suzuki K, Chen F, Asou N, Ohtake S, Miyawaki S, Miyazaki Y, Sakura T, Ozawa Y, Usui N, Kanamori H, Kiguchi T, Imai K, Uike N, Kimura F, Kitamura K, Nakaseko C, Onizuka M, Takeshita A, Ishida F, Suzushima H, Kato Y, Miwa H, Shiraishi Y, Chiba K, Tanaka H, Miyano S, Ogawa S, Naoe T. Comprehensive analysis of genetic alterations and their prognostic impacts in adult acute myeloid leukemia patients. *Leukemia* 2014; 28(8): 1586–1595
8. Eckardt JN, Bill M, Rausch C, Metzeler K, Spiekermann K, Stasik S, Sauer T, Scholl S, Hochhaus A, Crysandt M, Brümmendorf TH, Krug U, Wörmann B, Hiddemann W, Görlich D, Sauerland C, Steffen B, Einsele H, Neubauer A, Burchert A, Schäfer-Eckart K, Berdel WE, Schliemann C, Krause SW, Hänel M, Hanoun M, Kaufmann M, Fransecky L, Braess J, Ruhnke L, Schetelig J, Middeke JM, Serve H, Baldus CD, Platzbecker U, Müller-Tidow C, Bornhäuser M, Herold T, Thiede C, Röhlig C. Secondary-type mutations do not impact outcome in NPM1-mutated acute myeloid leukemia—implications for the European LeukemiaNet risk classification. *Leukemia* 2023; 37(11): 2282–2285

9. Othman J, Meggendorfer M, Tiacci E, Thiede C, Schlenk R, Dillon R, Stasik S, Venanzi A, Bertoli S, Delabesse E, Dumas PY, Pigneux A, Bidet A, Gilkes AF, Thomas I, Voso MT, Rambaldi A, Brunetti L, Perriello VM, Andresen V, Gjertsen BT, Martelli MP, Récher C, Röllig C, Bornhäuser M, Serve H, Müller-Tidow C, Baldus CD, Haferlach T, Russell N, Falini B. Overlapping features of therapy-related and *de novo* NPM1-mutated AML. *Blood* 2023; 141(15): 1846–1857
10. Nybakken GE, Canaani J, Roy D, Morrisette JD, Watt CD, Shah NP, Smith CC, Bagg A, Carroll M, Perl AE. Quizartinib elicits differential responses that correlate with karyotype and genotype of the leukemic clone. *Leukemia* 2016; 30(6): 1422–1425
11. Tyner JW, Tognon CE, Bottomly D, Wilmot B, Kurtz SE, Savage SL, Long N, Schultz AR, Traer E, Abel M, Agarwal A, Blucher A, Borate U, Bryant J, Burke R, Carlos A, Carpenter R, Carroll J, Chang BH, Coblenz C, d'Almeida A, Cook R, Danilov A, Dao KHT, Degnin M, Devine D, Dibb J, Edwards DK, Eide CA, English I, Glover J, Henson R, Ho H, Jemal A, Johnson K, Johnson R, Junio B, Kaempf A, Leonard J, Lin C, Liu SQ, Lo P, Loriaux MM, Luty S, Macey T, MacManiman J, Martinez J, Mori M, Nelson D, Nichols C, Peters J, Ramsdill J, Rofelty A, Schuff R, Searles R, Segerdell E, Smith RL, Spurgeon SE, Sweeney T, Thapa A, Visser C, Wagner J, Watanabe-Smith K, Werth K, Wolf J, White L, Yates A, Zhang H, Cogle CR, Collins RH, Connolly DC, Deininger MW, Drusbosky L, Hourigan CS, Jordan CT, Kropf P, Lin TL, Martinez ME, Medeiros BC, Pallapati RR, Pollyea DA, Swords RT, Watts JM, Weir SJ, Wiest DL, Winters RM, McWeeney SK, Druker BJ. Functional genomic landscape of acute myeloid leukaemia. *Nature* 2018; 562(7728): 526–531
12. Garg S, Reyes-Palomares A, He L, Bergeron A, Lavallee VP, Lemieux S, Gendron P, Rohde C, Xia J, Jagdhane P, Müller-Tidow C, Lipka DB, Imren S, Humphries RK, Waskow C, Vick B, Jeremias I, Richard-Carpentier G, Hébert J, Sauvageau G, Zaugg JB, Barabé F, Pabst C. Hepatic leukemia factor is a novel leukemic stem cell regulator in DNMT3A, NPM1, and FLT3-ITD triple-mutated AML. *Blood* 2019; 134(3): 263–276
13. Yang L, Rodriguez B, Mayle A, Park HJ, Lin X, Luo M, Jeong M, Curry CV, Kim SB, Ruau D, Zhang X, Zhou T, Zhou M, Rebel VI, Challen GA, Göttgens B, Lee JS, Rau R, Li W, Goodell MA. DNMT3A loss drives enhancer hypomethylation in FLT3-ITD-associated leukemias. *Cancer Cell* 2016; 29(6): 922–934
14. Guryanova OA, Shank K, Spitzer B, Luciani L, Koche RP, Garrett-Bakelman FE, Ganzel C, Durham BH, Mohanty A, Hoermann G, Rivera SA, Chramiec AG, Pronier E, Bastian L, Keller MD, Tovbin D, Loizou E, Weinstein AR, Gonzalez AR, Lieu YK, Rowe JM, Pastore F, McKenney AS, Krivtsov AV, Sperr WR, Cross JR, Mason CE, Tallman MS, Arcila ME, Abdel-Wahab O, Armstrong SA, Kubicek S, Staber PB, Gönen M, Paietta EM, Melnick AM, Nimer SD, Mukherjee S, Levine RL. DNMT3A mutations promote anthracycline resistance in acute myeloid leukemia via impaired nucleosome remodeling. *Nat Med* 2016; 22(12): 1488–1495
15. Mardis ER, Ding L, Dooling DJ, Larson DE, McLellan MD, Chen K, Koboldt DC, Fulton RS, Delehaunty KD, McGrath SD, Fulton LA, Locke DP, Magrini VJ, Abbott RM, Vickery TL, Reed JS, Robinson JS, Wylie T, Smith SM, Carmichael L, Eldred JM, Harris CC, Walker J, Peck JB, Du F, Dukes AF, Sanderson GE, Brummett AM, Clark E, McMichael JF, Meyer RJ, Schindler JK, Pohl CS, Wallis JW, Shi X, Lin L, Schmidt H, Tang Y, Haipek C, Wiechert ME, Ivy JV, Kalicki J, Elliott G, Ries RE, Payton JE, Westervelt P, Tomasson MH, Watson MA, Baty J, Heath S, Shannon WD, Nagarajan R, Link DC, Walter MJ, Graubert TA, DiPersio JF, Wilson RK, Ley TJ. Recurring mutations found by sequencing an acute myeloid leukemia genome. *N Engl J Med* 2009; 361(11): 1058–1066
16. Chen M, Zeng Z, Li X, Qin W, Cai X, Chen S, Lu X. Clinical features and prognostic significance of DNMT3A, FLT3, and NPM1 mutations in *de novo* acute myeloid leukemia patients. *Int J Lab Hematol* 2023; 45(6): 899–907
17. Wakita S, Marumo A, Morita K, Kako S, Toya T, Najima Y, Doki N, Kanda J, Kuroda J, Mori S, Satake A, Usuki K, Ueki T, Uoshima N, Kobayashi Y, Kawata E, Nakayama K, Nagao Y, Shono K, Shibusawa M, Tadokoro J, Hagihara M, Uchiyama H, Uchida N, Kubota Y, Kimura S, Nagoshi H, Ichinohe T, Kurosawa S, Motomura S, Hashimoto A, Muto H, Sato E, Ogata M, Mitsuhashi K, Ando J, Tashiro H, Sakaguchi M, Yui S, Arai K, Kitano T, Miyata M, Arai H, Kanda M, Itabashi K, Fukuda T, Kanda Y, Yamaguchi H. Mutational analysis of DNMT3A improves the prognostic stratification of patients with acute myeloid leukemia. *Cancer Sci* 2023; 114(4): 1297–1308
18. Herold T, Rothenberg-Thurley M, Grunwald VV, Janke H, Goerlich D, Sauerland MC, Konstandin NP, Dufour A, Schneider S, Neusser M, Ksienzyk B, Greif PA, Subklewe M, Faldum A, Bohlander SK, Braess J, Wörmann B, Krug U, Berdel WE, Hiddemann W, Spiekermann K, Metzeler KH. Validation and refinement of the revised 2017 European LeukemiaNet genetic risk stratification of acute myeloid leukemia. *Leukemia* 2020; 34(12): 3161–3172
19. Xuan L, Wang Y, Yang K, Shao R, Huang F, Fan Z, Chi P, Xu Y, Xu N, Deng L, Li X, Liang X, Luo X, Shi P, Liu H, Wang Z, Jiang L, Lin R, Chen Y, Tu S, Zhang Y, Sun J, Huang X, Liu Q. Sorafenib maintenance after allogeneic haemopoietic stem-cell transplantation in patients with FLT3-ITD acute myeloid leukaemia: long-term follow-up of an open-label, multicentre, randomised, phase 3 trial. *Lancet Haematol* 2023; 10(8): e600–e611
20. Elrhan H, El-Meligi YM, Elalawi SM. Prognostic impact of concurrent DNMT3A, FLT3 and NPM1 gene mutations in acute myeloid leukemia patients. *Clin Lymphoma Myeloma Leuk* 2021; 21(12): e960–e969
21. Lo MY, Tsai XC, Lin CC, Tien FM, Kuo YY, Lee WH, Peng YL, Liu MC, Tseng MH, Hsu CA, Chen JC, Lin LI, Sun HI, Chuang YK, Ko BS, Tang JL, Yao M, Chou WC, Hou HA, Tien HF. Validation of the prognostic significance of the 2022 European LeukemiaNet risk stratification system in intensive chemotherapy treated aged 18 to 65 years patients with *de novo* acute myeloid leukemia. *Am J Hematol* 2023; 98(5): 760–769
22. Stone RM, Mandrekar SJ, Sanford BL, Laumann K, Geyer S, Bloomfield CD, Thiede C, Prior TW, Döhner K, Marcucci G, Lo-Coco F, Klisovic RB, Wei A, Sierra J, Sanz MA, Brandwein JM, de Witte T, Niederwieser D, Appelbaum FR, Medeiros BC, Tallman MS, Krauter J, Schlenk RF, Ganser A, Serve H, Ehninger G, Amadori S, Larson RA, Döhner H. Midostaurin plus chemotherapy for acute myeloid leukemia with a FLT3 mutation. *N Engl J Med* 2017; 377(5): 454–464
23. Dholaria B, Savani BN, Hamilton BK, Oran B, Liu HD, Tallman MS, Ciurea SO, Holtzman NG, Ii GLP, Devine SM, Mannis G,

- Grunwald MR, Appelbaum F, Rodriguez C, El Chaer F, Shah N, Hashmi SK, Kharfan-Dabaja MA, DeFilipp Z, Aljurf M, AlShaibani AF, Inamoto Y, Jain T, Majhail N, Perales MA, Mohty M, Hamadani M, Carpenter PA, Nagler A. Hematopoietic cell transplantation in the treatment of newly diagnosed adult acute myeloid leukemia: an evidence-based review from the American society of transplantation and cellular therapy. *Transplant Cell Ther* 2021; 27(1): 6–20
24. Lv M, Wang Y, Chang YJ, Zhang XH, Xu LP, Jiang Q, Jiang H, Lu J, Chen H, Han W, Wang FR, Wang JZ, Chen Y, Yan CH, Zhang YY, Sun YQ, Mo XD, Zhu HH, Jia JS, Zhao T, Wang J, Liu KY, Huang XJ. Myeloablative haploidentical transplantation is superior to chemotherapy for patients with intermediate-risk acute myelogenous leukemia in first complete remission. *Clin Cancer Res* 2019; 25(6): 1737–1748
25. Wang L, Zhang C, Fan S, Mo X, Hu X. Treatment options for adult intermediate-risk AML patients in CR1: Allo-HSCT or chemotherapy? *Innovation (Camb)* 2023; 4(4): 100461
26. Shen Y, Zhu YM, Fan X, Shi JY, Wang QR, Yan XJ, Gu ZH, Wang YY, Chen B, Jiang CL, Yan H, Chen FF, Chen HM, Chen Z, Jin J, Chen SJ. Gene mutation patterns and their prognostic impact in a cohort of 1185 patients with acute myeloid leukemia. *Blood* 2011; 118(20): 5593–5603
27. Wang SY, Cheng WY, Mao YF, Zhu YM, Liu FJ, Ma TT, Shen Y. Genetic alteration patterns and clinical outcomes of elderly and secondary acute myeloid leukemia. *Hematol Oncol* 2019; 37(4): 456–463
28. Ruan GR, Li JL, Qin YZ, Li LD, Xie M, Chang Y, Zhang Y, Liu YR, Jiang B, Chen SS, Huang XJ. Nucleophosmin mutations in Chinese adults with acute myelogenous leukemia. *Ann Hematol* 2009; 88(2): 159–166
29. Kiyoi H, Naoe T, Nakano Y, Yokota S, Minami S, Miyawaki S, Asou N, Kuriyama K, Jinnai I, Shimazaki C, Akiyama H, Saito K, Oh H, Motoji T, Omoto E, Saito H, Ohno R, Ueda R. Prognostic implication of FLT3 and N-RAS gene mutations in acute myeloid leukemia. *Blood* 1999; 93(9): 3074–3080
30. Wang Y, Liu QF, Lin R, Yang T, Huang XJ. Optimizing antithymocyte globulin dosing in haploidentical hematopoietic cell transplantation: long-term follow-up of a multicenter, randomized controlled trial. *Sci Bull (Beijing)* 2021; 66(24): 2498–2505
31. Wang Y, Liu QF, Xu LP, Liu KY, Zhang XH, Ma X, Fan ZP, Wu DP, Huang XJ. Haploidentical vs identical-sibling transplant for AML in remission: a multicenter, prospective study. *Blood* 2015; 125(25): 3956–3962
32. Mo XD, Hong SD, Zhao YL, Jiang EL, Chen J, Xu Y, Sun ZM, Zhang WJ, Liu QF, Liu DH, Wan DM, Mo WJ, Ren HY, Yang T, Huang H, Zhang X, Wang XN, Song XM, Gao SJ, Wang X, Chen Y, Xu B, Jiang M, Huang XB, Li X, Zhang HY, Wang HT, Wang Z, Niu T, Wang JS, Xia LH, Liu XD, Li F, Zhou F, Lang T, Hu J, Wu SJ, Huang XJ. Basiliximab for steroid-refractory acute graft-versus-host disease: a real-world analysis. *Am J Hematol* 2022; 97(4): 458–469
33. Shen MZ, Hong SD, Lou R, Chen RZ, Zhang XH, Xu LP, Wang Y, Yan CH, Chen H, Chen YH, Han W, Wang FR, Wang JZ, Liu KY, Huang XJ, Mo XD. A comprehensive model to predict severe acute graft-versus-host disease in acute leukemia patients after haploidentical hematopoietic stem cell transplantation. *Exp Hematol Oncol* 2022; 11(1): 25
34. Fan S, Hong HY, Dong XY, Xu LP, Zhang XH, Wang Y, Yan CH, Chen H, Chen YH, Han W, Wang FR, Wang JZ, Liu KY, Shen MZ, Huang XJ, Hong SD, Mo XD. Machine learning algorithm as a prognostic tool for Epstein–Barr virus reactivation after haploidentical hematopoietic stem cell transplantation. *Blood Sci* 2023; 5(1): 51–59
35. Shen MZ, Hong SD, Wang J, Zhang XH, Xu LP, Wang Y, Yan CH, Chen H, Chen YH, Han W, Wang FR, Wang JZ, Liu KY, Huang XJ, Mo XD. A predicted model for refractory/recurrent cytomegalovirus infection in acute leukemia patients after haploidentical hematopoietic stem cell transplantation. *Front Cell Infect Microbiol.* 2022; 12: 862526
36. Wang Y, Chen H, Chen J, Han M, Hu J, Jiong H, Huang H, Lai Y, Liu D, Liu Q, Liu T, Jiang M, Ren H, Song Y, Sun Z, Wang C, Wang J, Wu D, Xu K, Zhang X, Xu L, Liu K, Huang X. The consensus on the monitoring, treatment, and prevention of leukemia relapse after allogeneic hematopoietic stem cell transplantation in China. *Cancer Lett* 2018; 438: 63–75
37. Laboratory Diagnosis Group, Chinese Society of Hematology, Chinese Medical Association, Wu DP, Huang XJ. Chinese consensus on minimal residual disease detection and interpretation of patients with acute myeloid leukemia (2021). *Chin J Hematol (Zhonghua Xueyexue Zazhi)* 2021; 42(11): 889–97 (in Chinese)
38. Heuser M, Freeman SD, Ossenkoppele GJ, Buccisano F, Hourigan CS, Ngai LL, Tettero JM, Bachas C, Baer C, Béné MC, Bücklein V, Czyz A, Denys B, Dillon R, Feuring-Buske M, Guzman ML, Haferlach T, Han L, Herzig JK, Jorgensen JL, Kern W, Konopleva MY, Lacombe F, Libura M, Majchrzak A, Maurillo L, Ofran Y, Philippe J, Plesa A, Preudhomme C, Ravandi F, Roumier C, Subklewe M, Thol F, van de Loosdrecht AA, van der Reijden BA, Venditti A, Wierzbowska A, Valk PJM, Wood BL, Walter RB, Thiede C, Döhner K, Roboz GJ, Cloos J. 2021 Update on MRD in acute myeloid leukemia: a consensus document from the European LeukemiaNet MRD Working Party. *Blood* 2021; 138(26): 2753–2767
39. Chang YJ, Wang Y, Liu YR, Xu LP, Zhang XH, Chen H, Chen YH, Wang FR, Han W, Sun YQ, Yan CH, Tang FF, Mo XD, Liu KY, Huang XJ. Haploidentical allograft is superior to matched sibling donor allograft in eradicating pre-transplantation minimal residual disease of AML patients as determined by multiparameter flow cytometry: a retrospective and prospective analysis. *J Hematol Oncol* 2017; 10(1): 134
40. Mo XD, Zhang XH, Xu LP, Wang Y, Yan CH, Chen H, Chen YH, Han W, Wang FR, Wang JZ, Liu KY, Huang XJ. Salvage chemotherapy followed by granulocyte colony-stimulating factor-primed donor leukocyte infusion with graft-vs.-host disease control for minimal residual disease in acute leukemia/myelodysplastic syndrome after allogeneic hematopoietic stem cell transplantation: prognostic factors and clinical outcomes. *Eur J Haematol* 2016; 96(3): 297–308
41. Shen MZ, Zhang XH, Xu LP, Wang Y, Yan CH, Chen H, Chen YH, Han W, Wang FR, Wang JZ, Zhao XS, Qin YZ, Chang YJ, Liu KY, Huang XJ, Mo XD. Preemptive interferon- $\alpha$  therapy could protect against relapse and improve survival of acute myeloid leukemia patients after allogeneic hematopoietic stem cell transplantation: long-term results of two registry studies. *Front Immunol.* 2022; 13: 757002
42. Fan S, Pan TZ, Dou LP, Zhao YM, Zhang XH, Xu LP, Wang Y,

- Huang XJ, Mo XD. Preemptive interferon- $\alpha$  therapy could prevent relapse of acute myeloid leukemia following allogeneic hematopoietic stem cell transplantation: a real-world analysis. *Front Immunol.* 2023; 14: 1091014
43. Abou Dalle I, Galimard J-E, Poire X, Huynh A, Wagner Drouet E, Burns D, Mayer J, Kröger N, Eder M, Sanz J, Wu D, Stelljes M, Aljurf M, Nagler A, Esteve J, Ciceri F, Bazarbachi A, Mohty M. The impact of DNMT3A mutation on survival of AML patients receiving allogeneic hematopoietic cell transplantation in first remission depends on the karyotype and co-occurring mutations: on behalf of the EBMT Acute Leukemia Working Party. *Blood* 2023; 142(Supplement 1): 658
44. Xuan L, Wang Y, Huang F, Fan Z, Xu Y, Sun J, Xu N, Deng L, Li X, Liang X, Luo X, Shi P, Liu H, Wang Z, Jiang L, Yu C, Zhou X, Lin R, Chen Y, Tu S, Huang X, Liu Q. Sorafenib maintenance in patients with FLT3-ITD acute myeloid leukaemia undergoing allogeneic haematopoietic stem-cell transplantation: an open-label, multicentre, randomised phase 3 trial. *Lancet Oncol* 2020; 21(9): 1201–1212
45. Levis MJ. BMT-CTN 1506 (MORPHO): a randomized trial of the FLT3 inhibitor gilteritinib as post-transplant maintenance for FLT3-ITD AML. European Hematology Association Congress; 2023 June 8–11; Paris
46. Zhang YY, Mo XD, Zhang XH, Xu LP, Wang Y, Yan CH, Chen H, Chen YH, Han W, Wang FR, Wang JZ, Sun YQ, Liu KY, Huang XJ. FLT3 internal tandem duplication does not impact prognosis after haploidentical allogeneic hematopoietic stem cell transplantation in AML patients. *Bone Marrow Transplant* 2019; 54(9): 1462–1470