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Original Article

Clinical characteristics of t(8;21) acute myeloid leukemia with AML1/ETO fusion in a single center in China

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Abstract: Acute myeloid leukemia (AML) is a heterogeneous disease and shows different clinical features among different races, and great diversity in prognosis. In order to under the relationship between clinical characteristics and prognosis, 92 patients with t(8;21) AML in a single centre of China were retrospectively analyzed, and clinical characteristics such as peripheral blood, morphological type of blast cells, molecular detection and cytogenetics, optimal treatments, and outcomes are summarized. Among all 92 t(8;21) AML patients, 80 (87.0%) presented with AML-M2. Moreover, 80 (52.29%) cases of AML1/ETO-positive were identified among 153 patients diagnosed with AML-M2. AML1/ETO-positive patient groups are significantly younger than negative ones (34 *vs* 49 years old; *P<0.001*). The most common accompanying mutation of t(8;21) AML patients was stem cell factor receptor (c-KIT) mutation (47.22%). In addition to ectopic t(8;21), the most common chromosomal abnormality was sex chromosome deletions (38.18%). Patients with c-KIT mutation had lower haemoglobin (*P*=0.044) and complete remission (CR) rates (*P*=0.026) and shorter overall survival (OS) (*P*=0.004) than c-KIT-negative groups. Unexpectedly, the 3-year OS rate was not higher for patients treated with hematopoietic stem-cell transplantation (HSCT) than with only chemotherapy (53.83% vs 64.44%; *P*=0.740). AML1/ETO-positive patients showed a higher CR rate and longer OS than AML1/ETO-negative patients. However, neither difference was statistically significant (*P*=0.250 and *P*=0.675 respectively). These findings indicate that retrospective analysis of Chinese patients can provide critical information in the optimal treatment of t(8;21) AML patients with AML1/ETO. C-kit is a poor prognostic factor, and HSCT is not the best choice for t(8;21) AML patients.

Keywords: t(8;21) AML, AML1/ETO fusion, China, c-kit mutation, optimal treatment

Introduction

Acute myeloid leukemia (AML) is a heterogeneous haematologic malignancy characterized by the clonal expansion of myeloid blasts in peripheral blood, bone marrow, and/or other tissues, and it is the most common form of acute leukemia among adults [1]. The recurrent translocation t(8;21) represents approximately 12% of adult and approximately 30% of paediatric AML cases [2, 3], and it involves the AML1 gene on chromosome 21 and the ETO gene on chromosome 8, which generates an AML1-ETO fusion protein [4]. Previous studies have shown that t(8;21) AML with AML1-ETO fusion is closely associated with the AML-M2 subtype (French-American-British Classification; FAB) (18-40%) and has a high complete remission (CR) rate with standard chemotherapy and a prolonged survival when sequential high-dose cytarabine is administered [3, 5, 6].

A Cancer and Leukemia Group B study showed that race is an important predictor for t(8;21) AML, suggesting that direct adoption of treatment strategies based on clinical studies comparing Whites and non-Whites may not be advisable [7]. Recent studies from China have focused mainly on the clinical impact of cytogenetics [8, 9]. Information on clinical characteristics, and optimal treatments, such as the clinical impact of hematopoietic stem-cell transplantation (HSCT), thus remains unavailable for Chinese patients.

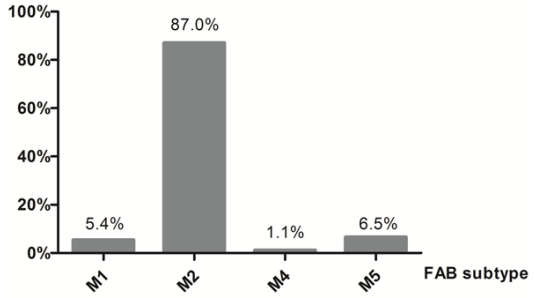

Figure 1. FAB subtype among t(8;21) AML patients.

To establish optimal therapeutic strategies applicable to Chinese patients, clarifying clinical characteristics and prognosis of AML1/ETO in Chinese patients with t(8;21) AML is crucial. The present retrospective single-centre study was conducted to investigate the clinical characteristics of AML1/ETO in Chinese patients with t(8;21) AML.

Materials and methods

Patients and treatments

From January 2008 to December 2017, 92 Chinese adult patients (≥13 years old) who were newly diagnosed with de novo t(8;21)(q22;q22) AML according to WHO classifications were consecutively enrolled. Diagnosis of t(8;21) AML was established based on chromosomal analysis and/or detection of AML1/ETO fusion gene by real-time reverse transcription-polymerase chain reaction. Cytomorphologic findings of 153 AML (FAB: M2) adult patients (≥13 years old) were documented in a standardized manner. All patients were selected from the Tongji Hospital haematological clinicopathologic database, which contains information on patients newly diagnosed with haematological conditions and their subsequent treatment.

Patients were treated with induction therapy consisting of administration of idarubicin (8-12 mg/m^2/day × 3)/daunorubicin (60 mg/m^2/day × 3)/mitoxantrone (10 mg/m^2/day × 3) and cytarabine (100 mg/m^2/day × 7). Once complete remission (CR) was achieved, consolidation therapy was begun, consisting of intermediate/high-dose cytarabine (1.5-2 g/m^2/12 hours on days 1-3) or standard-dose cytarabine-based chemotherapy (idarubicin/daunorubicin/mitoxantrone and cytarabine). Allogeneic and autologous hematopoietic stem-cell transplantations (HSCT) were performed in a risk-adapted and priority-based manner.

Morphological analysis

Sampling: Drawing from the posterior or autoposterior superior iliac spine bone marrow at the time of diagnosis of *de novo* AML, we extracted 0.2 ml bone marrow liquid for morphological and cytochemical staining. Furthermore, 3-5 ml of EDTA anticoagulation was used for molecular biological detection, and 3-5 ml of heparin anticoagulant was used for karyotype analysis and FISH detection.

Smear staining: Two dry smears were taken. The bone marrow smear was stained by Wright's staining for approximately 10~15 minutes and analysed morphologically by two experts who were blinded to patients' diagnosis and their cytomorphologic status. The experts counted 500 nucleated cells and performed calculations for various cells, including cells from bone marrow smear staining.

Classification criteria: Morphological diagnosis and classification were based on the French-American-British (FAB) cooperative criteria. Close attention was paid to the presence of morphological features considered to be suggestive of t(8;21).

Cytogenetic and molecular genetic analysis

Cytogenetic studies on bone marrow or unstimulated peripheral blood samples obtained prior to induction therapy were performed using standard G-banding with trypsin-Giemsa or trypsin-Wright's staining in our centre. Karyotypes were interpreted using International System for Cytogenetic Nomenclature (2013) criteria [10]. Studies were considered normal diploid if no clonal abnormalities were detected in a minimum of 20 mitotic cells examined. Central review of karyotypes for t(8;21) AML patients was performed by at least 3 members of the experts in our centre. Genomic DNA and total RNA were extracted as described previously [11]. To improve the accuracy of cytogenetic diagnosis, all specimens were also analysed by fluorescence in situ hybridization (FISH) using a comprehensive DNA probe set allowing for the detection of the most relevant AML-associated genomic aberrations [12]. FISH

Table 1. Clinical characteristics of patients with t(8;21) AML

	M2	Non-M2	*P* value
Number	80	12	
Gender			0.447
Male (number, %)	44 (55.0%)	8 (66.7%)	
Female (number, %)	36 (45.0%)	4 (33.3%)	
Age (years, median, range)	33.50 (13-70)	32.00 (14-69)	0.754
WBC (× 10^9/L) (mean, SD)	11.46 (11.51)	13.93(10.29)	0.363
Median, range	7.45 (0.77-64.86)	13.72 (1.62-29.30)	
Hemoglobin (g/L) (mean, SD)	68.36 (25.02)	67.07 (16.99)	0.706
Median, range	64.50 (1.38-129.00)	69.55 (32.00-103.00)	
Platelets (× 10^9/L) (mean, SD)	39.32 (66.67)	36.04 (24.19)	0.451
Median, range	23.50 (2.20-564.00)	28.50 (9.00-88.00)	

Table 2. Cytogenetic abnormalities and gene mutations associated with t(8;21) AML

Mutations	Frequency, no./total (%)
Cytogenetic abnormalities	
X in female patients	6/26 (23.08%)
Y in male patients	15/29 (51.72%)
Del (9q)	3/55 (5.45%)
Trisomy 4	3/55 (5.45%)
Others	28/55 (50.90%)
Molecular genetic mutations	
FLT3-length mutation: FLT3/ITD	1/38 (2.63%)
c-KIT	17/36 (47.22%)

and real-time quantitative PCR (RQ-PCR) were further used to analyze AML1/ETO fusion as previously described [13, 14].

In addition, diagnostic samples from some patients were analysed for mutations in the AML1/ETO, c-KIT, FLT3/ITD, NPM1, IDH1, DNMT3A and CEBPA genes by reverse transcription polymerase chain reaction (RT-PCR) [15-20].

Statistical analysis

Complete remission (CR) was defined as recovery of morphologically normal bone marrow and normal peripheral blood cell count (absolute neutrophil count >1,000/mm^3 and platelet count >100,000/mm^3) and no signs or symptoms of the disease or evidence of central nervous system leukemia or other extramedullary infiltration within the first three chemotherapy cycles [21]. Overall survival (OS) was measured from the beginning of treatment until date of death or last follow-up. Data, including AML1/ETO expression, c-KIT mutation status, white blood count, haemoglobin concentration, platelet count, bone marrow blasts and age, were collected at the time of treatment.

Categorical variables were described based on the count and relative frequency (%) of subjects in each category. Numerical variables between groups were compared using the non-parametric Mann-Whitney test. The distributions of categorical variables in different groups were compared by X^2 test (unordered categorical variable). Survival curves were generated using the Kaplan-Meier method, and the log-rank test was used to compare survival between groups. Statistical analysis was performed using SPSS 22 software. The best discriminator threshold was detected using the minimal *P* value approach (a method aimed at minimizing the identification of rare classes of subjects). A *P* value of less than 0.05 was chosen as a threshold for statistical significance.

Results

M2 was the most common FAB subtype in t(8;21) AML patients

A total of 92 t(8;21) AML patients were examined, including 80 (87.0%) M2, 5 (5.4%) M1, 1 (1.1%) M4 and 6 (6.5%) M5 cases (**Figure 1**). Clearly, M2 was the most common FAB subtype among t(8;21) AML patients.

Table 1 shows basic clinical information pertaining to the 92 cases of t(8;21) AML. The gender ratio was 52:40 (M:F), and the median age was 33.5 years old (13-70 years old). Peripheral

Table 3. Clinical characteristics of patients with c-KIT mutation

	c-KIT positive	c-KIT negative	*P* value
Number	17	19	
Gender			0.095
Male (number, %)	6 (35.3%)	12 (63.2%)	
Female (number, %)	11 (64.7%)	7 (36.8%)	
Age (years, median, range)	38 (14-58)	27 (14-56)	0.260
WBC (× 10^9/L) (mean, SD)	11.96 (7.45)	9.00 (8.02)	0.079
Median, range	9.24 (2.52-28.21)	6.10 (0.77-26.20)	
Hemoglobin (g/L) (mean, SD)	55.30 (22.62)	71.02 (20.09)	0.044
Median, range	55.00 (1.38-97.00)	68.20 (35.00-105.00)	
Platelets (× 10^9/L) (mean, SD)	35.78 (43.92)	35.50 (24.00)	0.401
Median, range	22.00 (2.20-189.00)	23.00 (10.00-88.00)	
AML FAB subtype			0.797
M2 (number, %)	14 (82.4%)	15 (78.9%)	
Non-M2 (number, %)	3 (17.6%)	4 (21.1%)	
CR (number, %)	3/8 (37.5%)	11/13 (84.6%)	0.026

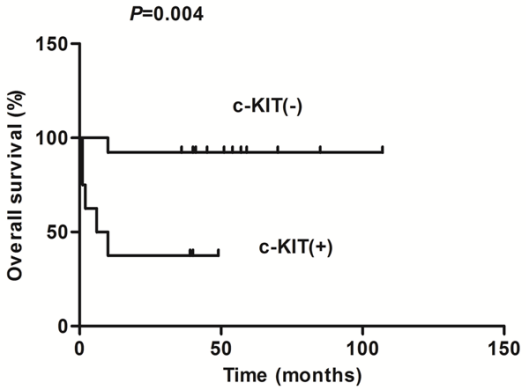

Figure 2. Survival analysis of patients with and without c-KIT mutation.

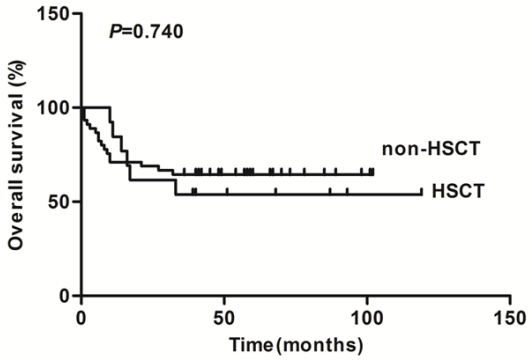

Figure 3. Survival analysis of patients with and without hematopoietic stem-cell transplantation (HSCT).

blood features, age and gender tended to show no differences between the M2 and non-M2 groups under various conditions (P>0.05).

The most frequent additional chromosomal abnormality and mutation among t(8;21) AML patients were sex chromosome loss and stem cell factor receptor (c-KIT)

As shown in **Table 2**, 15 (51.72%) male t(8;21) AML patients lack the Y chromosome and 6 (23.08%) female t(8;21) AML patients lack the X chromosome. Furthermore, trisomy 4 and chromosome 9 deletion were associated with t(8;21) AML (**Table 2**). In addition to cytogenetic abnormalities, mutations of growth factor receptors and transcription factors were also identified in t(8;21) AML patients, including 17 (47.22%) stem cell factor receptor (c-KIT) mutations and 1 (2.63%) FMS-related tyrosine kinase 3 (FLT3) mutation (**Table 2**). These statistics suggest that the loss of sex chromosome and c-KIT were the most frequent additional chromosomal abnormality and mutation among t(8;21) AML patients.

c-KIT mutation predicts unfavorable outcomes in patients with t(8;21) AML

Analysis of c-KIT mutation was performed in 36 t(8;21) AML patients, 17 of whom were c-KIT-positive. Haemoglobin was lower among c-KIT-positive patients than among c-KIT-negative patients (55.30 *vs* 71.02 g/L; *P*=0.044), while other peripheral blood features tended to show no significant differences (**Table 3**).

Table 4. Clinical characteristics of patients with AML-M2

	AML1/ETO-positive	*AML1/ETO*-negative	*P* value
Number	80	73	
Gender			0.121
Male (number, %)	44 (55.0%)	31 (42.5%)	
Female (number, %)	36 (45.0%)	42 (57.5%)	
Age (years, median, range)	33.5 (13-70)	49 (19-93)	<0.001
WBC (× 10^9/L) (mean, SD)	11.46 (11.513)	24.04 (52.896)	0.281
Median, range	7.45 (0.77-64.86)	5.32 (334.00-0.22)	
Hemoglobin (g/L) (mean, SD)	68.36 (25.03)	76.29 (19.66)	0.015
Median, range	64.50 (1.38-129.00)	75.00 (42.00-133.00)	
Platelets (× 10^9/L) (mean, SD)	39.32 (66.67)	69.95 (86.78)	<0.001
Median, range	23.50 (2.20-564.00)	47.00 (3.40-516.00)	
Bone marrow blasts (%) (mean, SD)	43.27 (17.94)	43.60 (16.38)	0.798
Median, range	41.70 (4.00-93.00)	44.00 (19.00-84.00)	

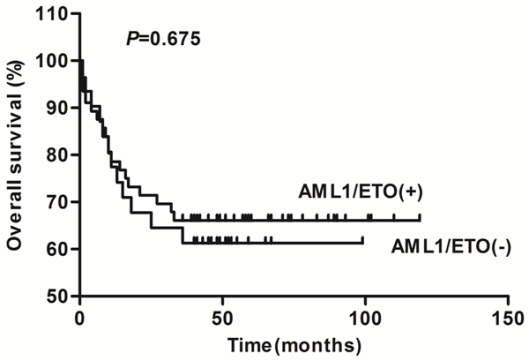

Figure 4. Survival analysis of patients with AML-M2 between AML1/ETO-positive group and AML1/ETO-negative group.

From January 2008 to December 2014, 21 patients with c-KIT mutation were included. The complete remission (CR) rate of the entire group was 14/21 (66.67%); the CR rate of the c-KIT-positive group was 3/8 (37.50%), while that of the negative group was 11/13 (84.60%). The CR rate was significantly higher in the negative group (*P*=0.026). With a median follow-up time of 41 months (1-107 months), the actuarial 3-year overall survival (OS) rate was significantly higher for c-KIT-negative patients than for c-KIT-positive patients (92.30% *vs* 37.50%, *P*=0.004) (**Figure 2**).

Hematopoietic stem-cell transplantation (HSCT) does not significantly improve prognosis in patients with t(8;21) AML

From January 2008 to December 2014, among the 58 patients included, 45 patients were treated with only chemotherapy and 13 underwent hematopoietic stem-cell transplantation (HSCT). With a median follow-up time of 43.5 months (1-119 months), the actuarial 3-year OS rate was lower for patients treated with HSCT than for those treated with only chemotherapy (53.83% *vs* 64.44%; *P*=0.740) (**Figure 3**).

AML1/ETO expression was common among AML-M2 patients

A total of 153 patients diagnosed with AML-M2 who underwent FISH studies on their bone marrow were evaluated by two physicians in this research. These included 80 (52.29%) AML1/ETO-positive AML-M2 patients. **Table 4** shows the basic clinical information pertaining the 153 cases of AML-M2. There were significant differences in age between the AML1/ETO-positive group and AML1/ETO-negative group, which we included as quantitative measures. Patients in the AML1/ETO-positive patient group were significantly younger (34 *vs* 49 years old; *P<0.001*). While the white blood cell (WBC) count and bone marrow blasts tended to show no differences between the AML1/ETO-positive group and AML1/ETO-negative group under various conditions, haemoglobin and platelets were lower in AML1/ETO-positive patients than in AML1/ETO-negative patients (68.36 *vs* 76.29 g/L; *P*=0.015 and 39.32 *vs* 69.95 × 10^9/L; *P<0.001*, respectively).

Expression of AML1/ETO predicts favourable outcomes in patients with AML-M2

From January 2008 to December 2014, 98 AML-M2 patients were included. The CR rate of the entire group was 60/87 (68.97%), whereas

the AML1/ETO-positive group showed a CR rate of 41/56 (73.21%), while the negative group showed a CR rate of 19/31 (61.29%). The CR rate was higher in the positive group, but the difference was not significant (P=0.250). With a median follow-up time of 46 months (1-119 months), the 3-year OS was higher for AML1/ETO-positive patients than for AML1/ETO-negative patients (66.07% *vs* 61.29%; P=0.675) (**Figure 4**). However, the difference was not statistically significant.

Discussion

Acute myeloid leukemia (AML) is a heterogeneous disease that is classified based on the presence of specific cytogenetic abnormalities as well as the French-American-British (FAB) classification of leukemic cells and immunophenotype. One of the common translocations identified in leukemia is that between chromosome 8q22 and chromosome 21q22 [22]. In this study, we found that 87% of t(8;21) AML patients showed FAB-M2 AML, 5.4% M1, 1.1% M4 and 6.5% M5, which is consistent with results reported in previous studies [23, 24]. M2 was clearly the most common FAB subtype among t(8;21) AML patients.

The prevalence of t(8;21) (q22;q22) fused the *AML1* (also known as *RUNX1*) and *ETO* (otherwise *RUNX1T1* or *MTG8*) genes and resulted in expression of the AML1/ETO chimeric protein [24]. A total of 153 patients diagnosed with AML-M2 were included in this study, among whom 80 (52.29%) were AML1/ETO-positive. Mutation of AML1/ETO was frequent among AML-M2 patients. AML1/ETO-positive patients were significantly younger than AML1/ETO-negative patients (34 *vs* 49 years old; p<0.000 by SPSS) but showed lower haemoglobin and platelets (68.36 *vs* 76.29 g/L; p<0.05 by SPSS and 39.32 *vs* 69.95 × 10^9/L; p<0.000 by SPSS). Moreover, the AML1/ETO mutation was a favorable prognostic factor associated with a higher CR and a superior OS in AML-M2 patients, which was consistent with the results of previous studies [1, 25, 26].

However, significant differences in CR or OS between AML1/ETO-positive and AML1/ETO-negative patients were not found. Among 73 AML1/ETO-negative AML-M2 patients, 9 cases harboured FLT3/ITD mutation, 10 NPM1, 5 IDH1 and DNMT3A, and 13 CEBPA. Previous studies suggested that FLT3/ITDs were associated with leukocytosis and unfavourable outcomes in patients with karyotypically normal AML [27, 28]. Konstanze [29] showed that NPM1 mutations were identified in 48% of young AML patients. NPM1 mutations predicted a better response to induction therapy and favourable OS only in the absence of FLT3/ITD [29]. In this study, 10 AML1/ETO-negative patients harboured mutant NPM1, and 8 (80%) showed no FLT3/ITD mutation; however, no AML1/ETO-negative patients showed NPM1 mutation. Mutations in CCAAT/enhancer binding protein alpha (CEBPA) have been observed in 5% to 14% of AML cases [30]. A previous study suggested that CEBPA (double-mut) were associated with a unique gene expression profile and favourable overall and event-free survival, while CEBPA (single-mut) AMLs did not express a discriminating signature and could not be distinguished from wild-type cases with respect to clinical outcome [30]. Among 13 AML1/ETO-negative patients with mutant CEBPA in our study, 6 cases showed CEBPA double allele mutations, which indicates a superior OS. DNMT3A mutations are highly recurrent in patients with *de novo* AML with an intermediate-risk cytogenetic profile and are independently associated with a poor outcome [19]. IDH1/2, which encodes the enzyme isocitrate dehydrogenase, was recently shown to be mutated in approximately 16% of all AML cases and strongly associated with normal cytogenetic status [31]. In our cohort, only 5/73 (6.85%) of AML1/ETO-negative patients showed IDH1 and DNMT3A mutations.

While t(8;21) AML has a relatively good prognosis, relapse rates of approximately 30%-40% have been observed for unknown reasons [32-35]. Certain reports have suggested that the number of AML1/ETO transcripts could serve as an indicator for relapse, as higher AML1/ETO transcript at diagnosis and a limited reduction of AML1/ETO transcript at the time of achieving complete remission predict a higher risk of relapse [14, 36]. In this study, at diagnosis, the ratios of AML1-ETO copies in AML-M2 patients ranged between 9.31 × 10^{-2} and 27.83 × 10^0 with a median of 1.30 × 10^0, higher than the values reported in previous studies [14, 36].

Moreover, a high frequency of c-KIT mutation (47.22%) was detected in patients with t(8;21) AML. c-KIT, also known as CD117, is a tyrosine-

protein kinase that functions as a cell-surface receptor and plays a critical role in regulating cell survival and proliferation, stem-cell maintenance, haematopoiesis, gametogenesis, mast cell development, migration and function, and melanogenesis [37, 38]. Mutations and high expressions of c-KIT in AML1/ETO patients have been discussed in numerous studies. Approximately 12.8%-46.8% of t(8;21) AML cases and approximately 33.3%-45% of inv (16) AML cases involve c-KIT point mutations. c-KIT was expressed significantly higher in 81.3% of patients with t(8;21) AML than in patients with other leukemias [39]. Furthermore, induced expression of AML1/ETO in U937-AE cells significantly up-regulated mRNA and protein levels of c-KIT. It was suggested that t(8;21) AML follows a stepwise model in leukemogenesis, i.e., AML1/ETO represents the first, fundamental genetic hit for initiating the disease, whereas activation of the c-KIT pathway may be a second but also crucial hit for the development of a full-blown leukemia [39].

In this study, we identified c-KIT mutation as an adverse prognostic factor associated with a lower CR and an inferior OS in t(8;21) AML patients. A multicenter retrospective study in China suggested that c-KIT mutation is a poor prognostic factor in t(8;21) AML patients [40]. Gao [15] showed that c-KIT-associated inferior prognosis in AML1/ETO-positive AML patients is c-KIT mutation-independent because the predictive capability of c-KIT for both OS and event-free survival was further improved in the subgroup of patients carrying AML1/ETO and wt c-KIT. The use of receptor tyrosine kinase inhibitors of VEGFRs, PDGFRs and c-KIT, such as pazopanib and SU5416, which remove the endothelial cell protection of AML cells and enhance AML cell sensitivity to cytarabine, may serve as promising therapeutic strategy for AML patients with c-KIT mutation [41, 42]. One patient in our study was treated with dasatinib and acquired CR until the end of follow-up. Dasatinib (BMS-354825) is an aminothiazole analogue that is an orally administered (p.o.) protein tyrosine kinase (PTK) inhibitor and has specificity toward five kinases/kinase families (BCRABL, c-SRc, c-KIT, PDGFβ receptor, and EPHA2) [43]. Heo SK [44] demonstrated that dasatinib treatment played a potential role in anti-leukemic therapy in c-KIT-positive AML cells.

It has been suggested that AML1/ETO blocks differentiation and induces self-renewal in hematopoietic progenitor cells, but expression of AML1/ETO alone is not sufficient to induce a leukemia-like disease in mouse models [45, 46]. Thus, these studies show that AML1-ETO is critical in causing myeloid leukemia, which requires one or more additional mutations for leukemogenesis [46]. Additional cytogenetic abnormalities such as the loss of one of the sex chromosomes demonstrate the nature of additional mutations in patients associated with AML1-ETO-mediated leukemogenesis [47]. In this study, 15 (51.72%) male t(8;21) AML patients lacked the Y chromosome and 6 (23.08%) female t(8;21) AML patients lacked the X chromosome. Thus, missing sex chromosomes is a rather common phenomenon and occurs at the highest frequency in t(8;21) AML patients with other abnormal chromosomes. Further study showed that loss of sex chromosomes tends to occur at a younger age in patients with t(8;21) AML than in the general population (median age 31 years *vs* 34 years, P>0.05). Groups showing loss of a sex chromosome have been suggested to exhibit poorer outcomes [48].

AML patients with t(8;21) aberration often have favourable outcomes; however, relapse still occurs in 30%-40% patients, with only 50%-60% of patients with t(8;21) AML cured with regimens involving high-dose cytarabine (HD-Ara-C) [49]. Hematopoietic stem-cell transplantation (HSCT) exhibits the strongest anti-leukemia effects. Zhu [50] demonstrated that allogeneic-HSCT (allo-HSCT) could reduce relapse and improve survival compared with chemotherapy/autologous-HSCT (auto-HSCT) for high-risk t(8;21) AML patients, and chemotherapy/auto-HSCT achieved a low relapse rate and high survival for low-risk patients. Thus, allo-HSCT benefited high-risk patients but impaired the survival of low-risk patients. In this single-center prospective cohort study, OS was lower for t(8;21) AML patients treated with HSCT than for those treated with chemotherapy alone (53.83% *vs* 64.44%). It was not necessary to treat t(8;21) AML patients with HSCT for long-term survival. However, our study has some limitations. Among the patients examined in this study, 22.41% (13/58 underwent HSCT, which made it difficult to divide patients into groups and compare the outcomes of treatment according to patients' different risk sta-

tus and transplantation approach. A larger survey sample is needed in future studies.

Despite providing novel and useful information about AML1/ETO among Chinese patients with t(8;21) AML, some issues remain to be addressed. First, specific mutations often associated with t(8;21), such as N-Ras, PU.1 and AML1, were not included in the present study. Second, detailed information about certain t(8;21) AML patients, including gene and karyotype at diagnosis and treatment outcome, was not available in the present study. Those require to be investigated in future studies.

Conclusions

In summary, the clinical characteristics of AML1/ETO in t(8;21) AML might differ between patients from China and those from Western countries. c-kit is a poor prognostic factor, and HSCT is not the best choice for t(8;21) AML patients. Clinicians should be alert to potential clinical differences among races, thus correctly evaluating the prognosis and choosing optimal treatment.

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Disclosure of conflict of interest

None.

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