Chromosomal Aberrations and Prognostic Analysis of Secondary Acute Myeloid Leukemia-A Retrospective Study (#77114)

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Chromosomal Aberrations and Prognostic Analysis of Secondary Acute Myeloid Leukemia-A Retrospective Study

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Background Secondary Acute Myeloid Leukemia (S-AML) patients generally have a poor prognosis, but the chromosomal aberrations of S-AML have been rarely reported. We aimed to explore the chromosomal aberrations and clinical significance in patients with S-AML. **Patients and methods** The clinical characteristics and karyotypes of 26 patients with S-AML were retrospectively analyzed. The overall survival (OS) was measured from the time of the patients' transition to AML (i.e., at S-AML diagnosis). **Results** The study included 26 S-AML patients (13 males and 13 females), with a median age of 63 years (range, 20-77 years). They transformed from various hematologic malignancies or solid tumors; most of them were secondary to myelodysplastic syndrome (MDS). About 62% of the S-AML patients showed chromosomal aberrations. The serum lactate dehydrogenase (LDH) level in S-AML patients with abnormal karyotype was higher than those with normal karyotype. Apart from the differences in treatment regimens, S-AML patients with chromosomal aberrations had shorter OS (P<0.05). **Conclusion** S-AML patients with abnormal karyotype have higher LDH levels and shorter OS than normal karyotype patients, and the OS of hypodiploidy was much shorter than hyperdiploid.

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Abstract

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Patients and methods The clinical characteristics and karyotypes of 26 patients with S-AML were retrospectively analyzed. The overall survival (OS) was measured from the time of the patients' transition to AML (i.e., at S-AML diagnosis).

Results The study included 26 S-AML patients (13 males and 13 females), with a median age of 63 years (range, 20-77 years). They transformed from various hematologic malignancies or solid tumors; most of them were secondary to myelodysplastic syndrome (MDS). About 62% of the S-AML patients showed chromosomal aberrations. The serum lactate dehydrogenase (LDH) level in S-AML patients with abnormal karyotype was higher than those with normal karyotype. Apart from the differences in treatment regimens, S-AML patients with chromosomal aberrations had shorter OS ($P<0.05$).

Conclusion S-AML patients with abnormal karyotype have higher LDH levels and shorter OS than normal karyotype patients, and the OS of hypodiploidy was much shorter than hyperdiploid.

Keywords secondary acute myeloid leukemia, chromosomal aberrations, karyotype, survival, lactate dehydrogenase

Introduction

Secondary acute myeloid leukemia (S-AML) refers to AML developing either after a prior hematologic disorder, usually myelodysplastic syndrome (MDS), myeloproliferative neoplasms (MPN), or MDS/MPN.[1,2] Compared with newly diagnosed primary AML (P-AML), S-AML has a poorer prognosis, lower remission rates, and shorter OS.[3,4] S-AML is usually common in elderly patients, which may be related to the high incidence of MDS and other malignant tumors in the elderly population. Although intensive chemotherapy regimens are adopted, S-AML patients prognosis is still poor, especially in elderly patients.[5]

Recent advances in cytogenetic analysis have revealed that many chromosomal aberrations are associated with the onset and recurrence of AML.[6] The recognition and understanding of chromosomal aberrations for the diagnosis and treatment of AML patients is of great significance.[7] Chromosomal aberrations are likely to be associated with disease progression in S-AML.[8]

Some major clinical features are poor prognostic factors for AML. For instance, high WBC and/or LDH levels were identified as significant predictive features for OS.[9,10] Here, we analyzed the clinical and cytogenetic characteristics of 26 S-AML patients to explore the possible pathogenesis of S-AML patients further.

Materials & Methods

Patients

A total of 26 S-AML patients diagnosed or treated in the Second Affiliated Hospital of Anhui Medical University from January 2009 to January 2020 were collected. All the newly diagnosed S-AML patients met the 2008 or 2016 WHO criteria.[11,12] Clinical characteristics of all the patients were obtained from medical records. The study was performed in accordance with the principles expressed in the Declaration of Helsinki. The Institutional Review Board of the Second Affiliated Hospital of Anhui Medical University approved this study, and the approval number was PJ-YX2019-008 (F2).

Karyotype analysis

Of the 26 S-AML patients, 25 had a cytogenetic analysis performed at the time of progression to AML (i.e., at S-AML diagnosis). All cytogenetic analyses were carried out in a standardized fashion at the Chromosome Laboratory, Department of Hematology. Bone marrow specimens were prepared by the short-term culture method and the G-banding method. Twenty (20) metaphase spreads were examined per patient, if available. The International System for Human Cytogenetic Nomenclature (ISCN) was used for karyotyping.[13] The S-AML patients were then divided into two groups: normal karyotype (NK) (chromosome number and structure were normal) and abnormal karyotype (number or structure abnormalities). According to the number of chromosomes, the abnormal karyotype group was further subdivided into diploid (46 chromosomes), subdiploid (<46 chromosomes), and hyperdiploid (>46 chromosomes).

Laboratory examination

The differences of some laboratory examination between the normal karyotype and abnormal karyotype were compared. Laboratory examination were obtained from medical records, including red blood cell (RBC) counts, white blood cell (WBC) counts, platelet counts (PLT),

lymphocyte counts (LYM), mononuclear cell counts (MO), neutrophil counts (NEUT), hemoglobin (Hb), hypersensitive c-reactive protein (Hs-CRP) and lactate dehydrogenase (LDH), using the fully automated hematology analyzer Sysmex XE-2100 (Sysmex Corporation, Japan) and the fully automated biochemical analyzer AU5831 (Beckman Coulter, America).

Follow up

Patients were followed till death, loss to follow-up, or the end of the study follow-up period on July 20, 2020. OS was calculated from the time of S-AML diagnosis to the date of death or last follow-up. Medical record retrieval and telephone follow-up were performed during the study period.

Statistical analysis

The student's t-test was used to test the differences between the two groups for quantitative and normally distributed variables; the Mann-Whitney U test was used for non-parametric variables. Kaplan-Meier survival curves were used to estimate OS. Statistical analyses were performed with the IBM SPSS 25.0. Results were considered significant at $p<0.05$.

Results

Patient characteristics

26 S-AML patients were enrolled in the study, and the median age was 63 years old (range, 20-77 years old). Of these, half of the patients were men. 57.7% of S-AML patients were secondary to MDS (one of them was secondary to MDS, but coexisted with chronic lymphocytic anemia (CLL)), the rest of the patients were secondary to myelodysplastic-myeloproliferative neoplasms (MDS/MPN), chronic myeloid leukemia (CML), chronic myelomonocytic leukemia (CMML), primary myelofibrosis (PMF), gastric diffuse large B cell lymphoma and rectal cancer. The basic characteristics of 26 S-AML patients was shown in Table1. Other clinical features were also collected, such as treatment, which is an important determinant of OS, as well as factors that are closely related to patient prognosis.

It is of great significance to choose the appropriate chemotherapy regimen to manage patients with AML effectively. In clinical practice, an individualized treatment regimen is often tailored to the patient's tolerance and other specific conditions. In our study, many patients were

treated with decitabine in combination with other regimens. Decitabine is a demethylation agent that is effective and safe in older patients with AML; its combination with other regimens (e.g., CAG (Ara-C, Aclarubicin, and G-CSF), retinoic acid) results in a higher OS rate than decitabine alone.[14] However, other optional regimens such as azacytidine, IA/IAG regimen, and intrathecal injection have also been used to treat patients, depending on the patient's condition. The detailed therapeutic regimen of 26 S-AML patients is shown in Table 2.

Karyotype test results

More than half of the S-AML patients had chromosomal aberrations (16/26), the majority (10/16) had detectable aberrations on chromosome 5 or 7. Chromosomal aberrations showed numerical and structural abnormalities in most chromosomes. Hypodiploidy and hyperdiploidy are two common genetic abnormalities of AML. In our study, hypodiploid karyotype was found in 5 patients and hyperdiploid karyotype in 7 patients. The observed abnormalities included: addition (add), insertion (ins), deletion (del), marker chromosome (mar), incomplete karyotype (inc), derived chromosome (der), inversion (inv), isochromosome (i), ring chromosome (r), etc. Karyotypes from the 26 patients with clonal aberrations were listed in Table 3.

Karyotypes and laboratory examination

The S-AML patients were divided into two groups; normal and abnormal karyotypes. The Mann-Whitney U test was used to compare the two groups. The results showed that LDH level was statistically higher in patients with S-AML with chromosomal aberrations ($P<0.05$). The scatter diagram for the LDH levels between the 2 groups is shown in (Fig. 1). RBC, WBC, PLT, and other laboratory examination results showed no significant difference between the normal and abnormal karyotype groups (Table 4).

Overall survival (OS)

The normal karyotype group's median OS was 212 days, while patients with abnormal karyotypes were 162 days. The outcome of S-AML patients with normal karyotype was: 2 died, 3 survived, and 5 lost to follow-up. The abnormal karyotype group's outcome was: 12 died, 1 survived, and 3 lost to follow-up. What is more, all five patients with hypodiploid karyotype died, with a median survival time of 62 days. Of the 7 patients with hyperdiploid karyotype, 5 died, 1 still alive, and 1 lost to follow-up, with a median survival time of 211 days. The Kaplan-Meier survival curve results showed that the OS of S-AML patients with abnormal karyotypes was shorter than those with normal karyotypes ($P=0.038$) (Fig. 2). Also, compared with normal

karyotypes, the OS of hyperdiploid was shorter, while the OS of hypodiploidy was much shorter (P=0.038) (Fig. 3).

Discussion

S-AML is a heterogeneous disease; its incidence increases with age, but therapy remains a challenge.[15] Myelodysplastic syndrome (MDS) is characterized by cytopenia, osteomyelodysplasia, hematopoietic dysfunction, and a high risk of transition to AML.[16] More than half of the S-AML patients reported in this study transformed from MDS to AML. Compared with primary AML patients (P-AML), S-AML patients have a worse clinical prognosis regarding complete remission rate (CR), recurrence-free survival rate, and OS rate.[17] Many factors can cause the poor curative effect, poor prognosis, and short survival time of S-AML patients. Our previous study showed that abnormally increased peripheral blood regulatory T cells (Treg) might cause an imbalance in the immune status of S-AML patients, which might be relevant to the poor chemotherapy response and short survival time of S-AML patients.[18] There is growing evidence that chromosomal aberrations represent a common genomic imbalance of cancer and are associated with cancer prognosis and response to chemotherapy and immunotherapy.[19] It has been reported that there are tumor suppressor genes on chromosome 6q, 7p, 10p, 11q, 14q, and 20q, which is essential for the transformation from MDS to AML.[20] Chromosomal aberrations are common in hematological malignancies. Larson et al [21] have shown that the characteristics of cytogenetic abnormalities in S-AML are similar to those in P-AML. However, compared with P-AML, S-AML patients' prognosis is worse; S-AML patients also have a higher frequency of adverse and moderate risk chromosomal aberrations.

Chromosomal aberrations are associated with progression to S-AML and deserved further study. The purpose of this study was to analyze the chromosomal aberrations of S-AML patients and further explore the factors connected with the survival and prognosis of S-AML in combination with relevant laboratory examinations. Our results indicated that most S-AML patients had abnormal karyotypes, including autosomal and sex chromosome aberrations. Abnormal changes in autosomal karyotypes were more common in S-AML patients and were closely related to survival and prognosis. Studies have demonstrated an increased incidence of abnormalities on chromosomes 5 and 7 in patients with S-AML.[22,23] In our study, 62.5% (10/16) abnormal karyotypes had aberrations on chromosomes 5 and 7. Admittedly, our sample size and

the data were limited; we could not get much information based on the results of the 26 S-AML patients. Abnormal changes of sex chromosomes have been rarely reported in myeloid malignancies.[24] We found an extra sex chromosome (X chromosome) in an elderly woman (65 years old) with FAB-M4 who transformed from MDS; the abnormal karyotypes were: 48,XXX,del(20)(q13),+X,+marker.[8]/48,XX,del(20)(q13),+14,+marker.[3]. The patient was alive at the end of the study follow-up period. Recently, a report associated the X chromosome loss with a better prognosis in female AML patients with t (8;21).[25] We also detected Y chromosome deletion in an elderly male (61 years old) patient who progressed from MDS; the abnormal karyotype was: 43,X,t(5;19)(q21;q13),7q+,-7,-12,-20,-Y,+marker.[7]/44,XY,5q-,7q+,-12,-18,-20,+marker1,+marker2.[13]. Unfortunately, the patient was lost to follow-up, and we do not know whether the patient is alive or not. Some studies have suggested that Y chromosome loss is an age-related phenomenon with no prognostic significance.[26] Another study also indicated that Y chromosome loss increases with age, but it reduces the risk of transformation from MDS to leukemia.[27] In contrast, the loss of Y chromosome was associated with a high recurrence/relapse rate in AML male patients with t (8:21).[25] The relationship between sex chromosome aberrations and survival in S-AML patients needs to be further explored on larger cohorts.

LDH not only plays a vital role in the early diagnosis and prognosis of many solid tumors but also plays a crucial role in evaluating the severity of leukemia patients.[28,29] LDH positively correlated with tumor burden and is an independent prognostic factor for early death in hyperleukocytic AML.[30] Our results showed a significantly increased LDH level in the abnormal karyotype group than the normal group. It suggests that the higher the LDH level in S-AML patients, the greater the tumor burden, the greater the possibility of karyotype abnormality, and the worse the OS rate. LDH is a valuable enzyme among many biochemical parameters and can be easily detected routinely in many clinical laboratories. In brief, abnormalities of LDH and karyotypes are closely related to the severity, survival, and prognosis of S-AML patients that can be a very valuable indicator for further risk stratification of S-AML in the future. Most AML patients with chromosome number abnormalities may manifest with an increase of 1-2 chromosomes (47-48 chromosomes), known as low hyperdiploid, or rare high hyperdiploidy (49-65 chromosomes), both of which are associated with poor outcome in AML.[31-33] Holmfeldt et al[34] reported no difference in 5-year OS and EFS (event-free survival) between AML patients

with non-hyperdiploid and hyperdiploid karyotypes (48-65 chromosomes). Hypodiploidy (<46 chromosomes) has been reported mostly in acute lymphoblastic leukemia (ALL) but rarely in AML.[35-37] However, there is a current lack of further research on the prognosis and survival in S-AML patients with hyperdiploidy or hypodiploidy. In addition to other factors affecting OS, such as various treatment regimens, our research found that karyotypes were closely related to S-AML patients' survival; patients with abnormal karyotypes demonstrated inferior OS compared with those with normal karyotype. What is more, S-AML patients with hypodiploidy showed worse outcomes than those with hyperdiploidy.

There are some limitations to our study. Firstly, the abnormality of sex chromosomes may relate to the survival and prognosis of S-AML, but no definite conclusion could be drawn because of the small number of sex chromosome aberrations in our study. Apart from this, the accurate information of all patients could not be obtained through telephone follow-up in this study, which may interfere with the experimental results. Additionally, this study is a single-center retrospective study; the number of included cases was relatively small, so further study expanding the sample size is needed to validate our results. Moreover, with the heterogeneity of the individualized treatment among AML patients, the treatment regimens could constitute an important source of limitation, which may have influenced the results.

Conclusions

In conclusion, our research highlights chromosomes and LDH contributions to the poor prognosis of S-AML patients. Also, the abnormality of sex chromosomes may be associated with the survival and prognosis of S-AML patients. Understanding the multifactorial contributions will lead to more precise risk classification and treatment strategies. More factors related to the survival and prognosis of S-AML need to be explored, which may contribute to monitoring the progression of the disease, early diagnosis, and improved treatment.

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ADDITIONAL INFORMATION AND DECLARATIONS

Authors' contributions

Qianling Ye and Zhimin Zhai designed the study. Tun Zhang, Huiping Wang, and Hao Xiao collected patients' data. Dongdong Yang was responsible for chromosome analysis. Mingzhu Song prepared the figures and drafted the manuscript. All authors reviewed and revised the manuscript and read and approved the final version.

Data availability

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

Compliance with ethical standards

Conflicts of interest The authors declare no potential conflict of interest.

Ethic's approval and consent to participate The study was performed in accordance with the principles expressed in the Declaration of Helsinki.

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Figure legend

Table 1 The basic characteristics of 26 S-AML patients.

Table 2 The detailed therapeutic regimen of 26 S-AML patients

Table 3 Chromosome karyotypes of the 26 S-AML patients.

Table 4 Laboratory examination in normal and abnormal chromosome karyotypes.

Fig.1 LDH level in normal and abnormal chromosome karyotypes.

Fig.2 OS in normal and abnormal chromosome karyotypes of S-AML patients.

Fig.3 OS in normal, hyperdiploid and hypodiploidy chromosome karyotypes of S-AML patients.

Figure 1

LDH level in normal and abnormal chromosome karyotypes

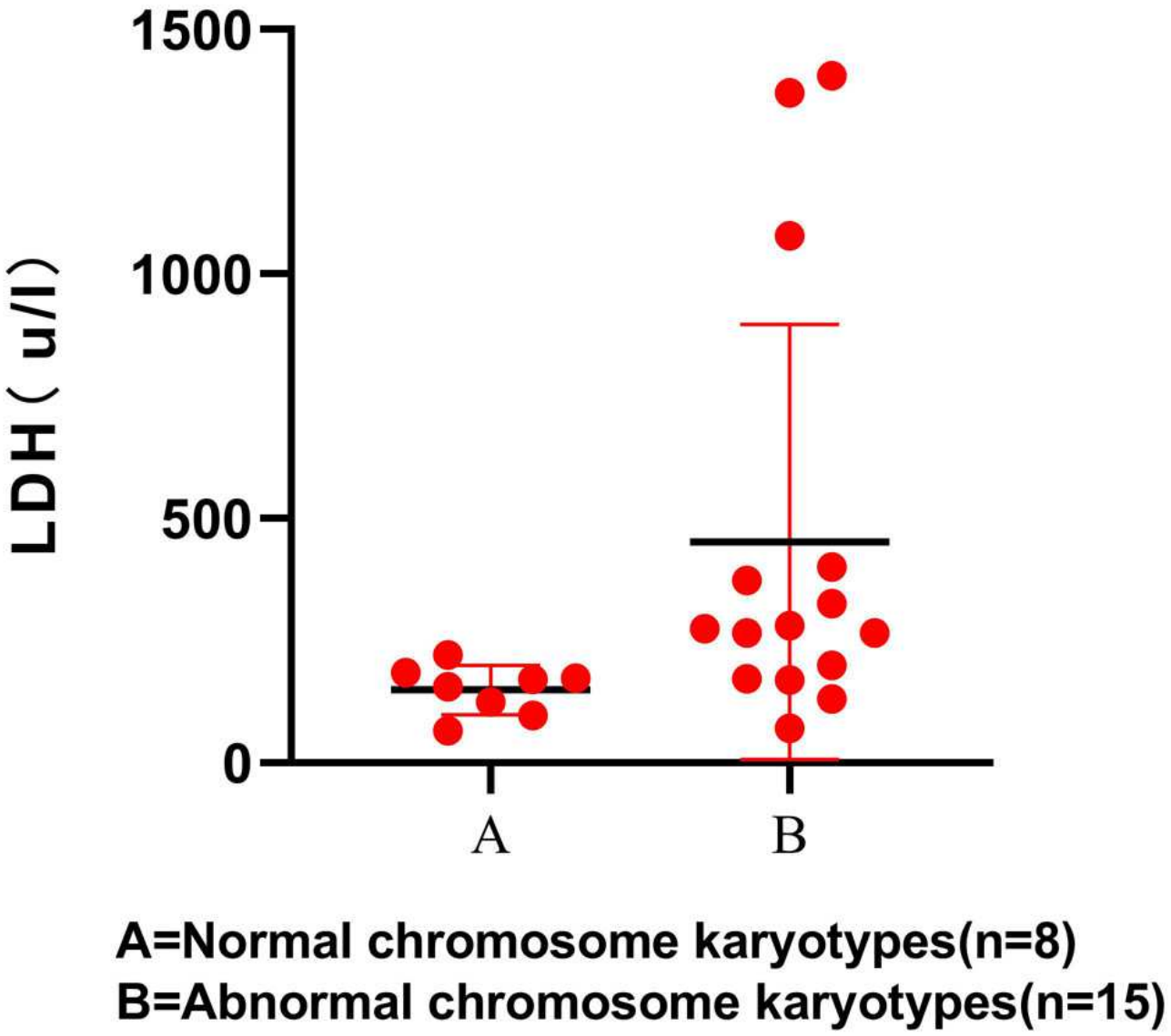

Figure 2

OS in normal and abnormal chromosome karyotypes of S-AML patients.

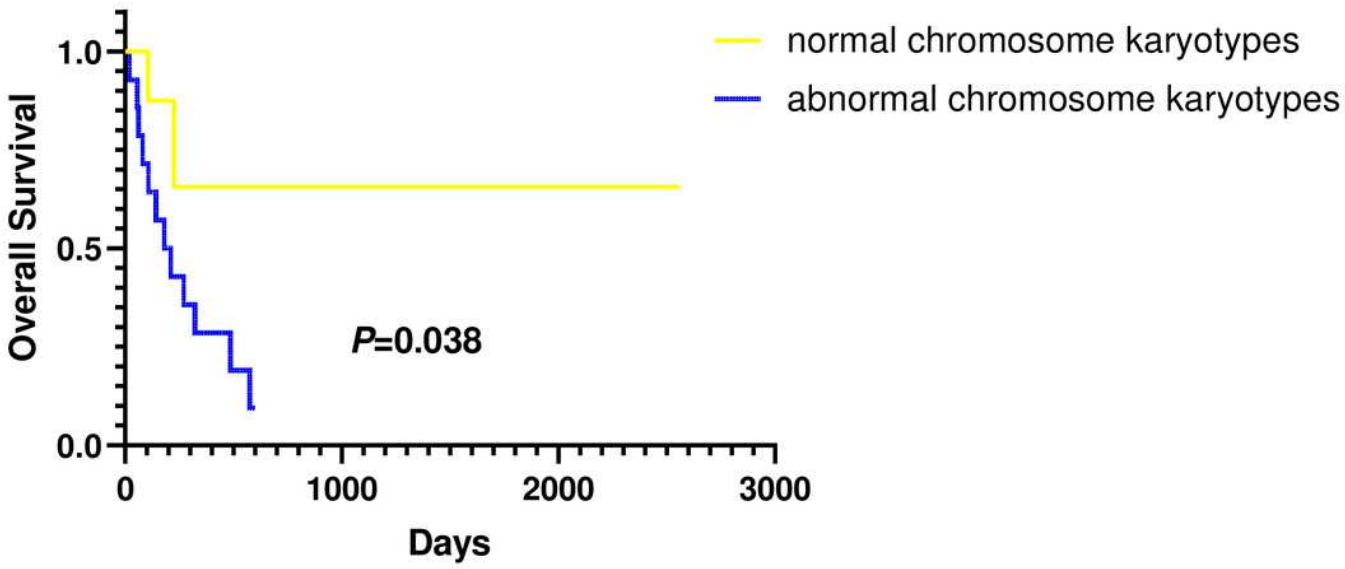

Figure 3

OS in normal, hyperdiploid and hypodiploidy chromosome karyotypes of S-AML patients.

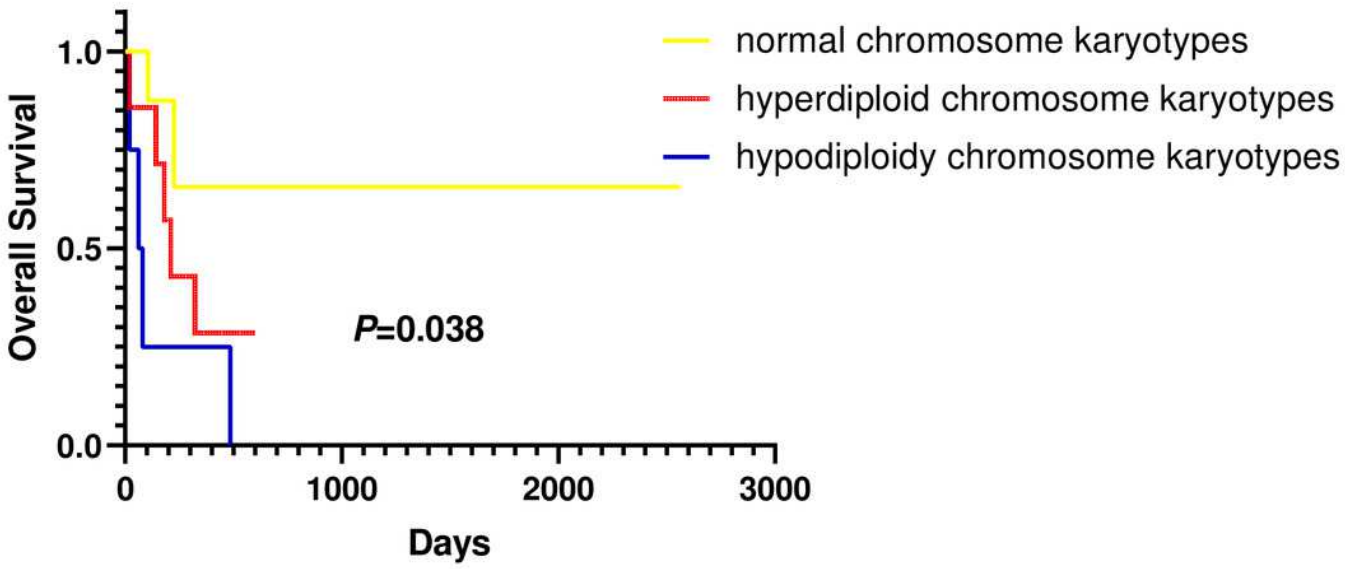

Table 1(on next page)

The basic characteristics of 26 S-AML patients.

1 **Table1. The basic characteristics of 26 S-AML patients**

Characteristics	Patients (N=26)
Median age (range)	63 (20-77)
Gender	
Male	13 (50.0%)
Female	13 (50.0%)
FAB subtype	
M2	11 (42.3%)
M3	1 (3.8%)
M4	2 (7.7%)
M5	1 (3.8%)
M7	1 (3.8%)
unclassified	10 (38.5%)
Diagnosis prior to AML	
MDS	15 (57.7%)
MDS/MPN	1 (3.8%)
CML	3 (11.5%)
CMML	2 (7.7%)
PMF	2 (7.7%)
rectal cancer	2 (7.7%)
gastric diffuse large B cell lymphom	1 (3.8%)

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Table 2(on next page)

The detailed therapeutic regimen of 26 S-AML patients

Table2. The detailed therapeutic regimen of 26 S-AML patients

No	Gender	Age	Original diagnosis	AML	Treatment (after the time of S-AML diagnosis)	Outcome (until July 20, 2020)	OS (Days)
1	Male	72	MDS	M7	Decitabine alone	death	80
2	Female	56	MDS	M2	Decitabine+CAG(Ara-C, Aclarubicin, and G-CSF), HAAG(Homoharringtonine, Ara-C, Aclarubicin, and G-CSF)	death	211
3	Male	76	MDS	M2	Decitabine+CAG(Ara-C, Aclarubicin, and G-CSF)+ATO	death	575
4	Female	65	MDS	M4	No, and we don't know if the patient was treated at any other hospital	survival	600
5	Female	66	MDS	AML（unclassified）	No, and we don't know if the patient was treated at any other hospital	death	485
6	Female	62	MDS	AML（unclassified）	CAG(low dose Cytarabine, Aclarubicin, and G-CSF)+ATO+EPO	death	55
7	Female	65	MDS	M2	IAG（idarubicin+Ara-C+G-CSF)+ DA（Daunorubicin+Ara-C） Azacitidine+HAG（Homoharringtonine, Ara-C, and G-CSF） intrathecal injection（MTX, DXM, and Ara-C） Decitabine, thalidomide, ubenimex, Lenalidomide, Tretinoin, TPO	death	108
8	Male	61	MDS	AML（unclassified）	Decitabine+CAG(Ara-C, Aclarubicin, and G-CSF)	loss to follow-up	10
9	Male	70	MDS	AML（unclassified）	low dose Decitabine+EAG（epirubicin , Ara-C, and G-CSF） Decitabine+MAG（mitoxantrone, Ara-C, and G-CSF） Decitabine+CMG（Ara-C, mitoxantrone, and G-CSF） Thalidomide	death	105
10	Male	61	MDS	AML（unclassified）	Decitabine+HAG（homoharringtonine, Ara-C, and G-CSF） ubenimex, Tretinoin, azacitidine	survival	210

11	Female	77	MDS	M2	Tretinoin+ATO+decitabine+HAG（homoharringtonine, Ara-C, and G-CSF）+EAG（epirubicin , Ara-C, and G-CSF）+MAG(mitoxantrone , Ara-C, and G-CSF)	loss to follow-up	213
12	Female	20	MDS	M2	IA（Idarubicin, Ara-C） Decitabine+CAG(Ara-C, Aclarubicin, and G-CSF)+ATO Decitabine+CHG(Ara-C, Homoharringtonine, and G-CSF)+ATO	loss to follow-up	150
13	Female	66	MDS	AML（unclassified）	No	loss to follow-up	60
14	Male	69	MDS/MPN	M2	Low dose Ara-C, interferon, and dasatinib	loss to follow-up	60
15	Female	64	MDS	M2	CAG(Ara-C, Aclarubicin, and G-CSF)+decitabine	death	226
16	Female	30	gastric diffuse large B cell lymphom	M3	Tretinoin+ATO+intrathecal injection（MTX, DXM, and Ara-C）	survival	1305
17	Male	46	CML	AML（unclassified）	DA（Daunorubicin+Ara-C）+Idarubicin HAG（Homoharringtonine, Ara-C, and G-CSF） Dasatinib+Imatinib(Oral administration of dasatinib and imatinib was subsequently discontinued because of the T325I mutation, which suggested resistance to all tyrosine kinases), Hydroxycarbamide, etoposide, and ATO.	death	180
18	Male	61	CMML	M2	IA（Idarubicin, Ara-C） Decitabine+CAG(Ara-C, Aclarubicin, and G-CSF) Decitabine+HAG（homoharringtonine, Ara-C, and G-CSF）+Tretinoin+ATO Stanozolol, etoposide, ubenimex, and thalidomide Dorubicin liposomes and hexadecadrol Low dose methotrexate, and azacitidine	death	323

19	Female	55	PMF	M2	Decitabine+IA（Idarubicin, Ara-C） Hematopoietic stem cell microtransplantation DAE (Doxorubicin+Ara-C+Etoposide)	death	143
20	Male	61	MDS（coexist with CLL）	AML（unclassified）	ATO+VP-16+Ara-C+G-CSF	death	62
21	Female	66	CMML	M4	Decitabine+HAG（homoharringtonine, Ara-C, and G-CSF） Low dose Decitabine+ATO+DAG(Daunorubicin+Ara-C+G-CSF) Etoposide, Ara-C, and azacitidine	loss to follow-up	328
22	Male	38	PMF	M5	ME (Mitoxantrone, Etoposide), homoharringtonine, Ara-C, ATO	loss to follow-up	450
23	Male	72	rectal cancer	M2	Decitabine+CAG(Ara-C, Aclarubicin, and G-CSF) CTK cell infusion G-CSF, Ara-C, ATO Decitabine+darubicin or Pirarubicin +Ara-C	survival	2560
24	Female	67	rectal cancer	AML（unclassified）	Decitabine+Ara-C	death	21
25	Male	32	CML	AML（unclassified）	MA(Mitoxantrone, and Ara-C) CAG(Ara-C, Aclarubicin, and G-CSF) Dasatinib, methotrexate intrathecal injection（MTX, DXM, and Ara-C）	death	270
26	Male	44	CML	M2	No	loss to follow-up	5

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Table 3(on next page)

Chromosome karyotypes of the 26 S-AML patients.

Table3. Chromosome karyotypes of the 26 S-AML patients

Karyotypes (N)		Chromosome of S-AML
Normal (10)	Diploid (10)	46,XY
		46,XY,-7,+marker.[10]
	Diploid *# (7)	46,XX[3]/46，XX,+der(8)del(q22),del(12)(p11),-2,-5,-7,-11,-17,+22,+marker*3[17]
		46,XY,del(5)q(23),add(17)p(12),-9,12,20,marker×3.[5]
		46,XY,t(9;22)(q34;q11),t(2;12;15),(p13;q13;p11),+8.[20]
		↟46,XY,t(9;22)(q34;q11)[8]/46,XY,t(9;22)(q34;q11),ins(3;3)(q25;q21q25)[5]
		45,XY,add(3)(q29),del(5)(q23),add(12)(p15),-7.[20]
		# 43-46,XX.-2,-3,?add(3)(q11),del(5)(q13q31),del(7)(q31),add(11)(p15),-15,-17,add(17)(p13),-18,add(19)(p13),add(22)(q13)+mar,inc[cp20].
	hypodiploid* (5)	43,X,t(5;19)(q21;q13),7q+,-7,-12,-20,-Y,+marker.[7]/44,XY,5q-,7q+,-12,-18,-20,+marker1,+marker2.[13]
Abnormal (16)		45,XY,-5,-9,+mar[7]/45,XY,del(5)(q15),-9,add(11)(q25)[4]/44,XY,add(5)(p15),del(5)(q15),del(7)(q11),der(12)del(12)(p12)add(12)(p12),-13,-19,-21,+mar[5]
		* 40-48 XX，add(1)(p36),add(2)(q37),del(5)(q15),add(12)(p13),-8,-9,-11,-22,+marker×3.inc.[cp15]
		47,XX,+8.[20]
		48,XXX,del(20)(q13),+X,+marker.[8]/48,XX,del(20)(q13),+14,+marker.[3]
	hyperdiploid* (7)	48,XY,inv(3)(q21q26),+8,t(9;22)(q34;q11),i(17)(q11),+der(22)t(9;22)(q34;q11)[20]
		48,XY,20q-,+8,+13.[5]
		48,XX,t(1;?)(q21;?),+der(1)t(1;?)(p32;?),-6,-7,+14,+19,+r.[8]/48,XX,t(1;?)(q21;?),+der(1)t(1;?)(p32;?),-6,-7,+14,+19,+marker.[2]
		47,XY,5q-,+8.[15]

↟the chromosome of the patient was collected at primary diagnosis (2 months ago); *the chromosome contains in all the three kinds of abnormal karyotypes of chromosome ; #the chromosome contains in both diploid and hypodiploid of abnormal karyotypes of chromosome.

Table 4(on next page)

Laboratory examination in normal and abnormal chromosome karyotypes.

Table4. Laboratory examination in normal and abnormal chromosome karyotypes

laboratory examination	Normal chromosome karyotypes (n=10) median (range)	Abnormal chromosome karyotypes (n=16) median (range)	*P*
RBC （×10^12/L）	2.16（1.47-3.94）	1.98（1.38-5.49）	0.551
WBC（×10^9/L）	1.96（0.3-11.13）	3.28（0.33-47.17）	0.391
PLT（×10^9/L）	13.5（3-269）	28.5（5-207）	0.262
LYM（×10^9/L）	1.09（0.27-2.82）	0.82（0.14-22.08）	0.816
MO（×10^9/L）	0.14（0-2.09）	0.41（0-15.89）	0.165
NEUT （×10^9/L）	0.34（0-9.35）	1.72（0.02-36.62）	0.182
Hb（g/L）	66.5（44-121）	64（49-152）	0.363
hsCRP（mg/L）	61（0.3-87.2）[a]	39（1.5-193.7）	0.452
LDH（U/L）	163.5（65-220）[b]	274（71-1406）[c]	**0.008**

[a] n=9; [b] n=8; [c] n=15