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CONVENTIONAL AND MOLECULAR CYTOGENETIC FEATURES OF MYELODYSPLASTIC SYNDROME IN CHINA

L.-J. Chen[1], J.-Y. Li[1,], Y. Zhu[1], H.-R. Qiu[1], J.-L. Pan[2], R. Wang[1], S.-X. Qian[1], W. Xu[1], Y.-Q. Xue[2]*

[1]*Department of Hematology, The First Affiliated Hospital of Nanjing Medical University, Jiangsu Province Hospital, Nanjing, China*

[2]*The First Affiliated Hospital of Soochow University, Jiangsu Institute of Hematology, Suzhou, China*

Background: **Myelodysplastic syndrome (MDS) constitutes a heterogeneous group of hematopoietic stem cell disorder characterized by peripheral blood cytopenia(s), in the presence of hypercellular bone marrow with features of ineffective hematopoiesis, and susceptibility to acute leukemia (AL). Although the precise pathogenesis of MDS remains to be clarified, cytogenetic abnormalities seem to be involved in its pathogenesis and are considered as an important factor in diagnosis and predicting clinical outcome.** ***Objective:*** **To explore the cytogenetic features of Chinese patients with myelodysplastic syndrome (MDS).** ***Methods:*** **Conventional cytogenetic analysis was performed in 88 MDS patients and among them, 34 cases were studied by interphase fluorescence** in situ **hybridization (I-FISH) with precisely chromosome 8 centromere specific DNA probe and DNA specific probes for 7q32 , 5q31.** ***Results:*** **Of the 88 patients, 45 (51.1%) showed clonal karyotypic abnormalities by CC at diagnosis, including numerical changes (18 cases, 20.5%) , structural changes (12 cases, 13.6%) , and numerical and structural changes simultaneously(15 cases, 17.0%). Trisomy 8, -5/5q-, and -7/ 7q- account for 20.5%, 15.9%, and 5.7% respectively. Complex karyotypes were observed in 17 patients, the incidence being 19.3% in the whole series of cases. Among 34 MDS patients studied by I-FISH, -5/5q-, -7/7q- and trisomy 8 occurring in 4, 2 and 10 cases respectively for CC were confirmed by I-FISH. 5 cases in 30 cases who did not show -5/5q- by CC displayed this abnormality by I-FISH. 3 cases without -7/7q- by CC presented this aberration by I-FISH. 5 cases with trisomy 8 for I-FISH was not identified this change by CC. Conclusions: The frequent abnormalities are trisomy 8, -5/5q- and -7/ 7q-. FISH is very useful in detecting these alterations in MDS and it is an important complement to CC.**

Key Words: **myelodysplastic syndrome, conventional cytogenetics, interphase fluorescence in situ hybridization, -5/5q-, -7/7q-, trisomy 8.**

Chromosome analysis of hematologic malignancies and solid tumors has provided critical insights into the genetic changes that underlie malignant transformation of the cells. Chromosome abnormalities are often specially related to particular subtypes of leukemias and lymphomas. In addition, recurring chromosome alterations are associated with distinct subtypes of leukemia or lymphoma with unique morphologic, immunophenotypic, and clinical features such as response to therapy and prognosis.

Myelodysplastic syndrome (MDS) constitutes a heterogeneous group of hematopoietic stem cell disorder characterized by peripheral blood cytopenia(s), in the presence of hypercellular bone marrow with features of ineffective hematopoiesis, and susceptibility to acute leukemia (AL). Based on the percentage of bone marrow and peripheral blood blasts, the percentage of bone marrow ringed sideroblasts, and the level of circulating monocytes, MDS are classified by the French-American- British (FAB) group into the following groups: refractory anemia (RA), refractory anemia with ringed sideroblasts (RARS), refractory anemia with excess of blasts (RAEB), refractory anemia with excess of blasts in transformation (RAEB-t) and chronic myelomonocytic leukemia (CMML) [1]. Recently, the Word Health Organization (WHO) classification proposed the following groups: RA, RARS, refractory cytopenia with multilineage dysplasia, RAEB, MDS unclassifiable, and MDS associated with isolated del(5q) chromosome abnormality [2]. Some MDS classified in the FAB classification are now classified into acute leukemia using the criteria of the WHO classification. WHO classification improves the predictive value of the FAB classification [3]. Although the precise pathogenesis of MDS remains to be clarified, cytogenetic abnormalities seem to be involved in its pathogenesis and are considered as an important factor in diagnosis and predicting clinical outcome [4, 5]. MDS are not associated with any specific chromosomal abnormality, but the following abnormalities are characteristic of these disorders: deletion 5q, monosomy 7, deletion 7q, and trisomy 8.

Some studies that included large series of patients with MDS and cytogenetic results demonstrated the prognostic influence of cytogenetics. An international study group on MDS proposed a score, the International Prognostic Scoring System (IPSS), to stratify patients according to the percentage of blasts in bone marrow, the number of cytopenias and the karyotype [6]. The IPSS can be used for clinical decision-making in patients with cytogenetic data available. Three categories of karyotype were proposed: group with a good prognosis; group with a poor prognosis; and group with an intermediate prognosis. Bernasconi et al. [7] showed that the WHO classification was associated with a more homogeneous cytogenetic pattern than

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*Correspondence: Fax: 86-25-83781120
E-mail: lijianyonglm@medmail.com.cn

Abbreviations used: AL – acute leukemia; CMML – chronic myelomonocytic leukemia; I-FISH – interphase fluorescence *in situ* hybridization; MDS – myelodysplastic syndrome; RA – refractory anemia; RAEB – refractory anemia with excess of blasts; RAEB-T – refractory anemia with excess of blasts in transformation; RARS – refractory anemia with ringed sideroblasts.

the FAB classification, and WHO classification in combination with IPSS cytogenetic categories were much more effective than IPSS for predicting MDS clinical outcome. In this report, we describe the cytogenetic findings in a series of 88 patients with MDS.

MATERIALS AND METHODS

Patients. From January 2000 to March 2006, 88 consecutive patients with primary MDS were included in this retrospective study. Thorough morphological review and immunophenotype studies were performed and the diagnosis was established according to the FAB criteria. All patients provided informed consent and the University and Institutional Review Boards approved all research studies.

Conventional cytogenetics. Cytogenetic analyses from bone marrow cells were available from 88 patients. Chromosomes were identified by R-banding technique after 24 h culture without stimulation. Karyotypes were classified according to International System for Human Cytogenetic Nomenclature. An abnormal clone was identified as two or more metaphases displaying either the same structural abnormality or the same extra chromosome or at least three cells with the same missing chromosome. Karyotypes were described according to the International System for human Cytogenetic Nomenclature (ISCN 2005) guideline [8]. ⩾ 20 metaphase cells were analyzed in most samples, unless not enough metaphase cells were found on 4 slides in a few samples.

Fluorescence in situ hybridization. Interphase FISH was perform using SpectrumRed directly labeled DNA specific probe for 7q32, 5q31, and chromosome 8 centromere specific DNA probe (gifts from Dr HervéAvet-Loiseau, Laboratoire de Cytogenetique Hematologique, Centre Hospitalier Universitaire de Nantes, France), which were directly labeled by Nick Translation with SpectrumGreen, SpectrumRed, SpectrumRed, respectively.

Slides were made and stored at –70 ˚C for future use. They were thawed and treated with 100 μg/ml RNAse for 30 min at 37 ˚C followed by 2 × SSC washing for 5 min × 2 and treated with 0.005% pepsin for 5 min at 37 ˚C, then washed twice for 5 min each in phosphate buffered saline (PBS) and dehydrated in increasing concentrations of ethanol (70%, 85%, and 100%) at room temperature for 1 min in each solution. The slides were denatured in a 70% formamide solution at 72 ˚C for 2 min, dehydrated in an ethanol series and air-dried. Probes (3 μl) were mixed well with hybridization buffer (5 μl) and denatured at 72 ˚C for 5 min. Probes were applied immediately to slides and hybridized at 37 ˚C overnight. After hybridization, slides were washed at 72 ˚C for 2 min in 0.4 × SSC/0.3% NP-40 and in 2 × SSC/0.1% NP-40 for 1 min at room temperature. Slides were then air-dried and mounted using 10 μl of 4',6-diamidino-2-phenylindole (DAPI II) (Vysis, Downers Grove, USA) counterstain for 1 h.

Fluorescent images were captured with epifluorescence microscope (Leica DRMA2, Germany) equipped with CCD camera (AI company), and using appropriate filters. Five hundred nuclei were analyzed for each probe. The cutoff levels for positive values were defined by adding three standard deviations to the mean of normal control, which determined from samples of 5 cytogenetically normal persons.

Statistical analysis. Age according to FAB subtypes was compared using one factor ANOVA analysis. χ^2 tests were used to compare the percentage of positive cells detected by the two methods: CC and I-FISH.

RESULTS

Patients. Bone marrow samples from 88 patients with MDS were collected from Department of Hematology of the First Affiliated Hospital of Nanjing Medical University and Jiangsu Institute of Hematology during Jan, 2000 to Nov, 2006 period. There were 51 (58.0%) males and 37 (42.0%) females and the median age was 42 years (range: 4 to 74). Of 88 patients, the proportions of patients with FAB subtypes were as follows: 46 (52.3%) cases of RA, 8 (9.1%) cases of RARS, 19 (21.6%) cases of RAEB, 14 (15.9%) cases of RAEB-T, and 1 (1.1%) cases of CMML. The age distribution of the patients according to FAB subtype except CMML has no statistic discrepancy ($P > 0.05$).

Cytogenetic abnormalities in MDS. Of the 88 patients, 45 (51.1%) showed clonal karyotypic abnormalities by CC at diagnosis, including numerical changes (18 cases, 20.5%), structural changes (12 cases, 13.6%), and numerical and structural changes simultaneously (15 cases, 17.0%). Higher incidence of cytogenetic abnormalities was found in RAS (6/8, 75%), RAEB (11/19, 57.9%) and RAEB-T (9/14, 64.3%) patients than that in RA patients (20/46, 43.5%). The frequency of the different chromosomal abnormalities and their relationship with the FAB classification are shown in Table 1.

The most frequent abnormalities were trisomy 8 (18/88, 20.5%), monosomy 5/del(5q) (-5/5q)(14/88, 15.9%), monosomy 7/del(7q) (-7/7q-) (5/88, 5.7%) and del(20q)(5/88, 5.7%). Complex karyotypes were observed in 17 patients, the incidence being 19.3% in the whole series of cases and 37.0% among those patients with abnormal karyotypes.

Fluorescence in situ hybridization. To further pinpoint these chromosome changes, we have performed a detailed I-FISH analysis with precisely chromosome 8 centromere specific DNA probe and DNA specific probes for 7q32, 5q31 in 34 cases with MDS and 5 normal controls. 500 cells were scored for each case. The cut-off point for the identification of these alterations based on the results using these probes in 5 normal controls were set at 3, 6 and 7%.

Among 34 MDS patients, -5/5q-, -7/7q- and trisomy 8 occurring in 4, 2 and 10 cases respectively for CC were confirmed by I-FISH. 5 cases in 30 cases that did not show -5/5q- by CC displayed this abnormality by I-FISH. 3 cases without -7/7q- detected by CC presented this aberration by I-FISH. 5 cases with trisomy 8 by I-FISH was not identified this change by CC. No statistic discrepancy ($P > 0.05$) was found

Number	Sex	Age	FAB	Karyotype
1	F	35	RAEB	47,XX,+8[8]/46,XX[16]
2	M	74	RAS	42,XY,-5,add(6)(p23),dei(8),add(17Xpl2),-18,-19,-20
3	M	26	RAEB	45,XY,-5,-7,-l 1,-13,-17,+marl x2, + mar 2, +mar3[cp] [200
4	M	42	RAS	45,XY,-5[10]
5	M	64	RAS	45,XY,-9,del(l lXq?),-20,+marl [20]
6	M	64	RA	45,XY,t(3 5)(?;?),del(5)(ql3q33),-7,t(17 ;19)(?;?)[cp][20]
7	M	49	RAEBT	46, XY, 7q<q22) [10]/46, XY[10]
8	F	35	RA	46,X,Xq-[12]/46,XX[8]
9	F	23	RAEBT	46,X,-Y,+8?[3]/46,XX[16]
10	F	50	RA	46,XX,20q-p5]/4S,XX[6]
11	F	46	RA	46,XX,20q-[3]/46,XXp9]
12	F	47	RA	46,XX,5q-[19]/46,XX|T]
13	F	64	RA	46,XX,5q-[19]/46,XX[l]
14	F	63	RAS	46,XX,5q-(3/4S,XX,5q-,-18,4marp]/46,XX[15]
15	F	40	RA	46,XX,add(3)(p24),add(9)(p22),4dd(1 4)(q32), add(1 7)(p 1 3)
16	F	44	RAEB	46,XX,delC3)(q?),del(5)(ql3q33),8ddl3) (p 10),+dmin
17	F	16	RAEBT	46,XX,lq+,3q+,7q-, 20q-[6]/46,XX,lq+,3q+,7q-[9]/46, XX, lq+, 3q+, 7q-,9q-, 1 4q+,20q- DQ /47,XX,3q+,7q+,7q-,+21[2]/47^X,lq+,3q+,7q-,+8[l]
18	M	52	RA	46,XY,+21[3]/46,XY[17J
19	F	40	RA	46,XY,+8[18]/46,XY[3]
20	M	65	RAEBT	46,XY,20q-[14]/46,XY[6]
21	M	31	RAS	46,XY,20q-pO]
22	M	56	RAEBT	46,XY,-5,-(€,8q-, -18, +marl[4]/47,XY,-5,+8,+8,8q-[2] /46,X Y,48,8q-,- 1 7 [0 /46,X Y,- 1 7,+marl[l] /48,X Y,-5,+8,8q-,-hnarl, 4mar2[2]/47,XY,-5,+8,8q-, -17, -Hmarl, -Htnar2[l]/46,XY,-hnar2,-17[l)/46,XY,8q-,-9,-18,-hmarl,+rtBr2[ll/46,XY[3]
23	M	56	RAEB	46.X Y,-5,-t€,del(8)(q22),- 1 7,- 1 8,-Hmarl ,-Hmar2 [cp]
24	M	16	RAEBT	46,XY,-5,deK9)(q?),t(9;19)(ql3;pl3), +14,del(16)(pl 1),-17,-18,add(21)(p ?),+22,-Hmar ?t(l $)(?;?)[cp]
25	M	32	RA	46,XY,-7,4xier(l;7)(qlO;plO)[12]
26	M	68	RAEB	46,XY,derC2),del(5)(ql3q33),del(ll)(ql4),der(17),-19,-Hmarl
27	M	38	RAEB	46,XY,lp-,-4p-,-4[14]/46,XY,idem,17p+p]/46,XY[4]
28	M	24	RAEB	46,XY,t(3^(q21H23)pO]
29	F	28	RA	46~49,XX,add(1)(p?),der(2),-4,del(5Xql3q33),del(6)(q?),+8,der(13),-1 7,+r,-Hmarl ,+mar2,+mar3 [cp] PO]
30	F	51	RAEB	47, XX,+8P5]/46,XX[5]
31	F	36	RA	47, XX,+8PQO
32	F	33	RAEB	47,XX,+20PO]
33	F	54	RA	47,XX,+8P5]/46,XX[2]
34	F	58	RAEB	47,XX,+8[8]/46,XX[12]
35	M	52	RA	47,XY,+16[18]/46,XYP]
36	M	41	RA	47,XY,+8 PO]
37	M	32	RA	47,XY,+8[10]/46,XY[10]
38	M	4	RAEBT	47,XY,+8[18]/46,XY[12]
39	M	50	RA	47,XY,+8[3]/46,XY[17]
40	M	34	RAEBT	47,XY,+8[5J/46,XY[15]
41	M	24	RA	47,XY,+8[3/46,XY[ll]
42	M	20	RAEB	47,XY,-5,4S,-Hmarp5]
43	M	41	RAEBT	47,XY,-5,-17,+21,+marl,+inar2pO]
44	F	41	RA	47,XX+8[11]/46,XX[5]
45	M	63	RA	48, XY, +17, -20, -20, marx3pO]/ 46, XY[9]

Table 2. Clinical, cytogenetic and I-FISH data for 34 patients with MDS

Number	Sex	Age	FAB	Karyotype	-5/5q- (%)	-7/7q- (%)	8 trisomy (%)
1	M	49	RAEBT	46, XY, 7q-(q22) [10]/46, XY[10]	7.5	42.5	N3
2	F	39	RAEB	46, XX [20]	7.5	K3.9	NO
3	M	72	RAEE	46,XY[20]	7.5	N4.7	NO
4	F	41	RA	47,XX,-»«[1 1]/46,XX[5]	10	N3.5	65.5
5	F	42	RA	46,XX[20]	13	N 1.0	N 1.0
6	M	41	RAEBT	47,XY,-5,- 1 7,+2 1 ,+marl,-*Biai2pO]	22.5	N4.4	N0.5
7	M	24	RAEB	46,XY,t(3;SXq21;q23)[20]	25	9.5	N2.5
8	M	56	RAEBT	46,XY,-5,+3,8q-, -18, -Hnarl[4]/47,XY,-5,+8,+8,8q-[2] /46,X Y,+8,8q-,- 1 7 |Tj /46,XY,-17,+marl[l]/ 4S,XY,-5,+8,8q-,-Hnarl, • +mar2[2]/47,XY,-5,-t«,8q-, -17, -Unarl, -Hnar2[TJ/46,XY,-Hmsi2,-17|Tj/ 46,XY,8q-,-9,-18,-nnar],-KHiai2[l)/46,XY[3]	71.5	N3.2	7
9	M	20	RAEB	47,XY,-5,+8,-«inar[25]	78	12.7	69.5
10	F	33	RAEB	47,XX,+20[20]	N1.5	N2.0	M 1
11	M	28	RA	46,XY[14]	N1.5	N4.5	19
12	M	24	RA	47,XY,->«[9]/46,XY[l 1]	N2.0	N 1.5	54
13	F	22	RA	46, XX [20]	N2.0	N 1.9	N0.5
14	M	56	RAEBT	46,XY[20]	N2.0	N2.0	Ml
15	M	67	RA	46,XY[27]	N2.0	N2.5	K0.5
16	F	35	RAEB	47,xx,-K3[S]/46,:o£[16]	N2.5	N0.5	34.5
17	F	51	RAEB	47,XX,4«[15]/46,XX[5]	N2.5	N3.2	12
18	M	32	RAS	46,XY[18]	N2.5	10.4	8
19	F	56	RA	46,XX[2Cg	N2.5	N4.4	N3
20	F	54	RA	47,XX,-t« [25] /46,XX [2]	N3	N1.0	75.5
21	F	58	RAEB	47,XX,+6 [8] /46,XX [1 2]	N3	N6.7	28.5
22	M	32	RA	47,XY,-f6 [1 0] /46,XY[1 0]	N3.0	N0.9	17
23	F	44	RAEBT	46, XX [7]	N3.0	N4.3	N3.5
24	M	59	CMML	46,XY[20]	N3.S	K0.5	N 0
25	F	22	RA	46, XX [19]	N3.5	N1.5	N0.5
26	M	34	RAEBT	47,X Y,-t« [5] /46,X Y[l 5]	N3.5	N3.0	52
27	F	34	F&	46, XX [20]	N4	Nl. 1	N
28	F	16	RAEBT	46,XX,lq+,3q+,7q-, 20q-[6]/46,XX,lq+,3q+,7q-[9]/46, XX, lq+, 3q+, 7q-,9q-,14q+,20q-UJ/ 47,XX,3q+,7q+,7q-,+21 [2]/47,XX,lq-*-,3q-«-,7q-,+8[l]	N4.0	41.6	N3
29	M	38	RAEB	46,XY,lp-,-Hp-,-4[l 4] /46,X Y, idem, 1 7p+p] /46,X Y[4]	N4.0	N0.5	7.5
30	F	52	RA	46, XX [20]	N4.5	N2.0	N
31	F	43	RAEB	46, XX [21]	N4.5	N3.6	9
32	M	44	RA	46,XY[19]	N5.5	N3	12
33	M	35	RA	46,XY[18]	N5.S	N4.5	N 1.5
34	F	19	RA	46, XX [30]	N6.0	N5.0	Nl

about these chromosome alterations by χ^2 tests. Seven patients with normal karyotypes revealed -5/5q-(3/7), -7/7q- (1/7) and trisomy 8(4/7).

DISCUSSION

MDS is a highly heterogenous disorder and karyotype analysis is helpful for its diagnosis and prognosis estimation. Acquired clonal chromosomal abnormalities are found in about 30–50% of primary MDS [9]. These abnormalities are predominantly characterized by total/partial chromosomal losses or gains and rarely by balanced structural aberrations. Loss of specific chromosomal regions like 5q-, 7q- and 20q- are usually the secondary cytogenetic abnormalities associated with MDS. Trisomy 8 represents the most common chromosomal gain [10]. In our results, the overall incidence of chromosomal abnormalities was 51.1%, which was similar as reported in the literature [11]. Our study confirmed that RAEB and RAEB-t subtypes had higher frequencies of chromosome abnormalities (57.9% and 64.3%, respectively), and RA the lowest (43.5%). However, it shows that RAS had the highest rate of chromosome abnormalities (75%), which was different from the reported by Chen et al. [12]. We think it maybe the factor of fewer RAS cases.

It was reported that different cytogenetic profiles were present between MDS patients of Chinese and those of Western countries [12]. In Western population, -5/5q- and -7/7q- as single specific karyotype aberrations were more frequently reported (12.8–23.1% and 3.1–19.4%) and applied to IPSS classification. Chinese patients with these aberrations as a single abnormality represented only small subsets of cases and most of them had additional chromosome change. In our study, the frequency of -5/5q- and -7/7q- as a single specific karyotype aberrations were only 2.3% and 1.1% respectively, which demonstrated the results previously reported by Chen et al. [12].

The survival of patients with MDS is strongly affected by chromosomal abnormalities. Cytogenetic abnormalities are important prognostic factor. The presence of del(5q), either as the sole karyotypic abnormality or as part of a more complex karyotype, has distinct clinical implications for MDS. The 5q- syndrome, a subtype of low-risk MDS, is characterized by an isolated 5q deletion and < 5% blasts in the bone marrow and can serve as a useful model for studying the role of 5q deletions in the pathogenesis and prognosis of myeloid malignancies [13]. Complete or partial deletions of the long arm of chromosome 7 (-7/7q-) are nonrandom abnormalities seen in primary and therapy-induced MDS. -7/7q- may denote a dominant mechanism involving loss of critical tumor suppressor gene(s), whose loss of function contribute to leukemic transformation or tumor progression. So it reveals the poor prognostic significance [14]. Complex chromosomal aberrations are present in < or = 30% of patients with primary MDS or acute myeloid leukemia (AML) and are associated with a poor prognosis [15]. Those with normal karyotype, deletion 5q or 20q as a single anomaly, or loss of Y chromosome are good prognosis factors; those with complex karyotypes or chromosome 7 anomalies have poor prognosis; and those with all other abnormalities are intermediate prognosis. In our study, patients with karyotype of good prognosis was 56.8%, and patients with unfavourable karyotype or with karyotype of intermediate prognosis was 21.6% respectively. While unfavourable karyotype, especially complex karyotypes are always involved in RAEB and RAEBT.

CC has some limitations in identification of chromosome alterations. It can only analyze metaphase cells and was affected by the quantity and quality of metaphase spreads. In addition, it is labor- intensive and time-consuming. In order to explore the value of FISH in the detection of total/partial deletion of the long arm of chromosome 5(-5/5q-), 7(-7/7q-) and of gain of chromosome 8 in patients with MDS, I-FISH was performed in 34 cases of 88 MDS patients. 9 were -5/ 5q -positive for I-FISH, of whom 4 were positive and 5 were negative for CC. 5 cases presented -7/7q- aberration by I-FISH, in which 3 cases without -7/7q- for CC. Trisomy 8 was identified in 15 cases by I-FISH, but for CC only 10 occurring in this aberration. Although the difference in the percentage of positive cells detected by the two methods was not statistically significant difference ($P > 0.05$) , I-FISH can detect some aberrations not finding by CC. It is more sensitive than CC for the detection of -5/5q-, 7/7q- and trisomy 8 in MDS.

On comparing the results of FISH and conventional cytogenetics, a superiority of FISH over these karyotypic analysis was detected. FISH is highly sensitive and specific, and it can be performed rapidly [16–18]. Nevertheless, the FISH technique has limitations, detecting only abnormalities specific for the target FISH probe used. Thus, FISH is not a good screening tool for cytogenetically heterogeneous diseases. In clinical practice, conventional cytogenetics continues to be the basic technique for MDS patient evaluation. However, a large number of metaphases, even those of poor quality, must be analyzed in each case. The FISH technique could be considered to be complementary to achieve a more accurate analysis. Our results show that both methods are important in diagnosis of MDS patients. When used together, conventional cytogenetics and FISH can define accurate chromosome abnormalities in MDS patients.

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НЕКОТОРЫЕ ЦИТОГЕНЕТИЧЕСКИЕ ХАРАКТЕРИСТИКИ МИЕЛОДИСПЛАТИЧЕСКОГО СИНДРОМА У БОЛЬНЫХ В КИТАЕ

***Обоснование*: миелодиспластический синдром (МДС) представляет собой гетерогенную группу заболеваний гемопоэтических стволовых клеток, характеризующихся цитопенией периферической крови на фоне гиперклеточности костного мозга с проявлениями неэффективного кроветворения и предрасположенностью к развитию острого лейкоза (ОЛ). Хотя патогенез МДС пока не установлен, считается, что цитогенетические аномалии могут играть роль в развитии заболеваний.Они также могут рассматриваться в качестве необходимого элемента диагностики и прогноза заболевания. *Цель:* исследовать цитогенетические характеристики больных с МДС китайской популяции. *Методы:* у 88 пациентов с МДС проведен стандартный цитогенетический анализ (СЦА). В 34 из 88 случаев применен также метод интерфазной флуоресцентной гибридизации *in situ* (I-FISH) с использование специфичных зондов к центромере хромосом 8 и 7q32 , 5q31. *Результаты:* методами СЦА в 45 (51,1%) из 88 случаев выявлены клональные кариотипические аномалии, в том числе количественные изменения (18 случаев, 20,5%) , структурные изменения (12 случаев, 13,6%) и количественные и структурные изменения одновременно (15 случаев, 17,0%). Трисомия 8, -5/5q-, и -7/7q- выявлена в 20,5, 15,9, и 5,7% случаев соответственно. Комплексные изменения кариотипа отмечали у 17 больных (частота возникновения 19,3% для всей обследованной группы). Из 34 проанализированных случаев -5/5q-, -7/7q-, трисомия 8, выявленные методом СЦА соответственно в 4, 2 и 10 случаях, была подтверждена данными I-FISH. В 5 случаях из 30, в которых методом СЦА -5/5q- не выявлена, методом I-FISH такая аномалия определялась. В 3 случаях, негативных по -7/7q- при анализе СЦА, методом I-FISH выявлена такая аберрация. В 5 случаях с выявленной методом I-FISH трисомией 8, методом СЦА нарушения не установлены. *Выводы:* частыми аномалиями у больных МДС являются трисомия 8, -5/5q- и -7/7q-. Метод FISH эффективен для выявления таких аберраций при МДС и является важным дополнением к СЦА.**

***Ключевые слова:* миелодисплатический синдром, рутинная цитогенетика, интерфазная флуоресцентная гибридизация *in situ*, -5/5q-, -7/7q-, трисомия 8.**

Table 1. Clonal karyotypic abnormalities of myelodisplastic syndrome