ORIGINAL ARTICLE

Usefulness of classic cytogenetic testing compared to fluorescence in situ hybridization in genetic diagnosis of 58 patients with myelodysplastic syndromes

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KEY WORDS

chromosome aberrations, classical cytogenetics, fluorescence in situ hybridization, myelodysplastic syndromes

ABSTRACT

INTRODUCTION Myelodysplastic syndromes (MDS) are a heterogeneous group of clonal diseases of pluripotent hematopoietic stem or progenitor cells. MDS are characterized by ineffective hematopoiesis, increased apoptosis, peripheral blood cytopenias, and propensity to evolve into acute myelogenous leukemia.

OBJECTIVES The aim of our investigation was to compare the usefulness of classic cytogenetics and fluorescence in situ hybridization (FISH) to detect chromosome aberrations in myelodysplastic syndromes.

PATIENTS AND METHODS The study was carried out in a group of 58 patients with MDS. G-banding using trypsin and Giemsa (GTG banding) and FISH with a panel of five molecular probes for aberrations with prognostic significance in MDS (cen7/8, 5q31, 7q22/q35, 17p13, 20q13.3) were performed on bone marrow cells.

RESULTS The use of GTG technique allowed to detect chromosome aberrations in 25 (43.1%) subjects. However, the additional use of FISH showed the presence of aberrations also in additional 10 (17.2%) patients, which shifted 11 patients from one cytogenetic category to another.

CONCLUSIONS The use of FISH with MDS probe panel beside classic cytogenetics improves detection of chromosome aberrations, and also stratification of MDS patients to prognostic groups. Both methods should be used simultaneously in every genetically diagnosed MDS patient.

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INTRODUCTION Myelodysplastic syndromes (MDS) are a heterogeneous group of clonal diseases of pluripotent hematopoietic stem or progenitor cells. They are characterized by ineffective hematopoiesis, increased apoptosis, peripheral blood cytopenias, and propensity to evolve into acute myelogenous leukemia (AML).[1-3]

Clonal chromosome aberrations can be detected in 30–60% of primary MDS and 80% of secondary MDS cases. They are most often unbalanced aberrations; losses or gains of the whole chromosomes or their fragments that cause mainly losses of caretaking and gatekeeping genes, or gains of oncogenes or genes related to multidrug resistance.[4-8] The most common aberrations in MDS are: deletion of the long arm of chromosome 5 (del5q = 5q–), monosomy of chromosome 7 (–7), deletion of the long arm of chromosome 7 (del7q = 7q–), trisomy 8 (+8), deletion of the short arm of chromosome 17 (del17p = 17p–) with TP53 gene locus, deletion of the long arm of chromosome 20 (del20q = 20q–).[9]

Detection of chromosome aberrations is useful in differential diagnosis of MDS, myeloproliferative diseases, aplastic anemia or paroxysmal nocturnal hemoglobinuria. It is also useful

in stratification of MDS patients into prognostic subgroups. Moreover, sequential cytogenetic assessment of the patient's bone marrow (BM) at different stages of the disease can provide information about the effectiveness of treatment by monitoring the size of neoplastic aberrant clone.

The aim of our investigation was to compare the usefulness of classic cytogenetics (CC) and fluorescence in situ hybridization (FISH) to detect chromosome aberrations in MDS.

PATIENTS AND METHODS A total of 58 untreated patients, 22 (38%) women and 36 (62%) men, aged 22–89 years (median age = 69 years), with diagnosed MSD established according to French-American-British (FAB) group criteria, were included in the study. The MDS subtypes of patients according to FAB[10,11] and WHO 2001[11,12] are presented in the TABLE. To sum up, there were 25 patients with refractory anemia (RA), 4 with RA with ring sideroblasts (RARS), 16 with RA with excess blasts, 10 with RA with excess blasts in transformation, 2 with chronic myelomonocytic leukemia and 1 with hypoplastic MDS according to FAB, and 20 patients with RA, 2 with RARS, 5 with RA with excess blasts (5–9% blasts), 8 with RA with excess blasts (10–19% blasts), 8 with refractory cytopenia with multilineage dysplasia, 7 with AML, 4 with unclassified MDS, 2 with 5q– syndrome, 2 with hypoplastic MDS, according to World Health Organization. Of all patients, 41 had primary, and 17 secondary MDS. All patients with secondary MDS, and no patient with primary MDS had a previous history of mutagene exposure. The exact dates of cytogenetic examinations are also presented in the TABLE. The patients were diagnosed in the Department of Hematology of Nicolaus Copernicus City Hospital in Toruń between the years 2004 and 2006.

The BM cells obtained by BM biopsy were cultured at 37°C and 5% CO_2 for 24 h without mitogen and for 48 h with addition of granulocyte macrophage colony-stimulating factor. The culture medium was RPMI-1640 (Biomed), supplemented with 20% fetal calf serum (Gibco) and antibiotics.[13-15] The cells were harvested and chromosome slides were made according to routine methods. At least 20 GTG-banded metaphases were analyzed for each patient, according to International System for Human Cytogenetic Nomenclature (ISCN) 2005.[16] The definition of simple (<3 clonal aberrations per cell) and complex (≥3 clonal aberrations per cell) karyotype were used according to ISCN 2005[16] and Southwestern Oncology Group/Eastern Cooperative Oncology Group criteria.[17] Only the patients in whom cell cultures were effective were included in the study.

On the cytogenetic slides FISH with a panel of 5 molecular probes for the most common MDS chromosome aberrations was performed according to the manufacturer protocol. All FISH probes, i.e. cen7/cen8: chromosome α-satellite 7(D7Z1)/8(D8Z1), 5q31/p15: chromosome 5q31(D5S89)/5p15(hTERT), 7q22/q35: chromosome 7q22(MDS1)/7q35(distal CDR), 17p13: chromosome 17p13(p53)/α-satellite 17(D17Z1), 20q13.3: chromosome 20q13.3(AURKA)/α-satellite 20(D20Z1) were produced by Q-Biogene. 1–5 metaphases and 200 interphase nuclei were analyzed for every patient. FISH prehybridization and hybridization procedures were done using the standard methods.[14,18] The analysis of FISH results was performed according to the 2005 ISCN criteria.[16] Cytogenetic and FISH images were registered and analyzed using computer software (Applied Spectral Imaging).

The study complies with the current Polish laws and was approved by the local ethics committee.

RESULTS In all 58 patients, analyzable metaphases were obtained. Using GTG-banded metaphase analysis, chromosome aberrations were found in 25 out of 58 persons (43.1%). The use of FISH technique identified aberrations in additional 10 patients, i.e. in 35 persons (60.3%). Among these 35 patients with chromosome abnormalities, in 6 aberrations detected by GTG and FISH were identical, in 10 chromosome aberrations were shown only by FISH, and in 19 FISH allowed to detect the aberrations additional to those disclosed by GTG. The TABLE presents chromosome aberrations included in MDS panel and detected by GTG and FISH methods.

Classic cytogenetic examinations with GTG banding showed a normal karyotype in 33 patients, a simple karyotype (1-2 aberrations in one clone) in 15 patients, and a complex karyotype in 10 patients. The addition of FISH panel to GTG analysis reduced the number of patients with a normal karyotype from 33 to 23, and increased the number of patients with simple (from 15 to 24) and complex (from 10 to 11) karyotypes. Altogether, 11 patients changed their cytogenetic category. FISH also allowed a better stratification of patients to prognostic categories.

The FIGURE shows the shift of patients with normal, simple, and complex karyotypes from one classification group to another after using FISH panel.

As can be seen in the TABLE, in the group with secondary MDS, which correlated with the

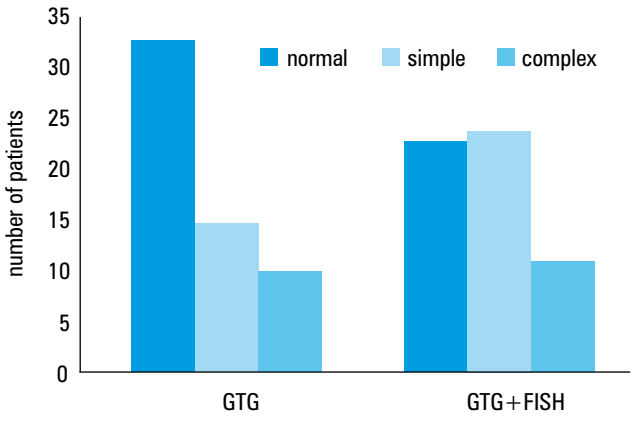

FIGURE Number of patients with normal (black column), simple (white column) and complex karyotype (grey column) depending on cytogenetic methods used: GTG only (3 left-hand columns), and GTG + FISH (3 right-hand columns).

Abbreviations: FISH – fluorescence in situ hybridization

TABLE Selected clinical and hematological data of myelodysplastic syndrome patients and the results of GTG-banded karyotyping and fluorescence in situ hybridization

Patient	Sex/age (year)	Study date (month/year)	FAB cooperative Group subtype	WHO subtype	Primary/ secondary MDS	Type of karyotype	The results of CC and FISH examination						
							the aberration from MDS panel revealed by CC	FISH (the molecular probes used)					
								5q31	7q22	7q35	17p13	cen7	cen8	20q13
1	F/45	08/2004	RAEB	RCMD	P	C	−5 +8 17p−	+	−	−	+	−	+	−
2	F/68	08/2004	RAEB	RCMD	P	S′	5q−	+	−	−	−	−	−	+
3	M/66	10/2004	RARS	U-MDS	P	S′	−	−	−	−	−	−	−	−
4	F/65	11/2004	hypoplastic MDS	hypoplastic MDS	P	C	5q− 7q− +8	+	+	+	−	−	+	−
5	M/71	11/2004	RAEB-t	RCMD	S	C	5q− 7q− 20q−	+	+	+	−	−	−	+
6	M/67	01/2005	RA	RA	P	S′	+8	−	−	−	+	−	+	−
7	M/67	01/2005	RAEB	RCMD	S	C	−	+	+	+	−	+	−	−
8	M/65	02/2005	RARS	U-MDS	P	S′	−	+	+	+	−	+	−	−
9	M/71	04/2005	RAEB	RAEB-2	S	C	+8 5q− 17p−	+	−	−	+	−	+	−
10	F/89	05/2005	RAEB-t	U-MDS	P	S′	+8	−	−	−	−	−	+	−
11	M/79	07/2005	RAEB-t	RAEB-2	S	S′	−7	−	+	+	−	+	−	+
12	F/84	11/2005	RA	RCMD	P	S′	5q−	+	−	−	−	−	−	−
13	M/58	01/2006	RA	RCMD	S	C	7q− 17p−	+	+	+	+	−	−	−
14	M/71	04/2006	RA	RA	S	S′	−	−	−	−	−	−	−	−
15	F/49	08/2006	RA	RA	P	S′	−	+	−	−	−	−	−	−
16	F/76	07/2004	RA	RA	S	N	−	−	−	−	−	−	−	−
17	F/49	04/2004	RA	"5q−"	S	S′	5q−	+	−	−	+	−	−	−
18	M/73	06/2004	RAEB	RAEB-2	P	S′	7q−	−	−	+	−	−	−	−
19	M/69	05/2004	RARS	RARS	P	N	−	−	−	−	−	−	−	−
20	F/72	05/2004	RA	RA	S	N	−	−	−	−	−	−	−	−
21	M/69	05/2004	RAEB-t	AML	S	C	−5 17p−	+	−	−	+	−	−	−
22	M/78	05/2004	RAEB	RAEB-2	P	N	−	−	−	−	−	−	−	−
23	F/55	09/2004	RA	RA	P	N	−	−	−	−	−	−	−	−
24	F/68	10/2004	RAEB	RAEB-1	P	N	−	−	−	−	−	−	−	−
25	M/75	01/2005	RA	RA	S	N	−	−	−	−	−	−	−	−
26	M/78	03/2005	RAEB-t	AML	S	C	5q−	+	+	+	+	+	−	−
27	F/49	03/2005	RAEB	RAEB-2	P	N	−	−	−	−	−	−	−	−
28	M/76	05/2005	RA	RA	P	N	−	−	−	−	−	−	−	−
29	M/68	07/2005	RA	RA	P	S′	−	−	−	−	−	−	−	+
30	M/81	09/2005	RAEB	RAEB-2	P	S′	−	+	−	−	−	−	−	−
31	M/39	09/2005	RA	RA	P	N	−	−	−	−	−	−	−	−
32	F/71	11/2005	RA	RA	P	N	−	−	−	−	−	−	−	−
33	M/74	12/2005	CMML	hypoplastic MDS	P	N	−	−	−	−	−	−	−	−
34	M/79	01/2006	RAEB-t	AML	P	S′	−	−	−	−	−	+	−	−
35	M/72	01/2006	RARS	RARS	P	S′	−	−	+	+	−	+	−	−
36	M/80	02/2005	RA	RA	P	S′	−	−	−	−	+	−	−	−
37	M/80	08/2004	RA	RA	P	N	−	−	−	−	−	−	−	−
38	F/65	03/2006	RA	RA	P	S′	−	−	−	−	+	−	−	−
39	F/76	03/2006	RA	RA	P	S′	−	−	−	−	−	−	−	−
40	M/75	04/2006	RA	RCMD	P	N	−	−	−	−	−	−	−	−
41	M/79	04/2006	RA	RCMD	S	N	−	−	−	−	−	−	−	−
42	M/79	08/2006	RA	RA	S	N	−	−	−	−	−	−	−	−
43	M/77	04/2006	RAEB	RAEB-1	S	S′	+8	−	−	−	+	−	+	−
44	M/71	04/2006	RAEB-t	AML	P	S′	+8	−	−	−	−	−	+	−
45	F/68	06/2006	CMML	U-MDS	P	N	−	−	−	−	−	−	−	−
46	F/47	07/2006	RA	RA	S	N	−	−	−	−	−	−	−	−
47	F/22	08/2006	RA	RA	P	N	−	−	−	−	−	−	−	−
48	M/79	09/2006	RAEB	RAEB-2	P	N	−	−	−	−	−	−	−	−
49	M/68	09/2006	RAEB	RAEB-1	P	C	−5 −20	−	−	−	+	−	−	+
50	M/28	09/2006	RA	RA	P	S′	−	−	−	−	+	−	+	−
51	F/62	01/2005	RAEB-t	AML	P	N	−	−	−	−	−	−	−	−
52	M/73	05/2005	RAEB	RAEB-1	P	S′	−	−	+	+	−	+	−	−
53	F/36	09/2004	RA	RA	P	N	−	−	−	−	−	−	−	−
54	M/69	12/2005	RAEB-t	AML	P	S′	−	−	+	+	−	+	−	−
55	M/68	09/2006	RAEB-t	AML	S	C	5q−	+	−	−	−	−	−	−
56	F/51	09/2006	RAEB	"5q− "	P	S′	5q−	+	−	−	+	−	−	−
57	F/45	09/2006	RAEB	REAB-1	P	C	−20	−	−	−	−	−	−	+
58	M/53	09/2006	RAEB	RAEB-2	P	N	−	−	−	−	−	−	−	−

Abbreviations: −C − complex karyotype, CC − classic cytogenetics, CMML − chronic myelomonocytic leukemia, F − female, FAB − French-American-British, FISH − fluorescence in situ hybridization, M − male, MDS − myelodysplastic syndrome, U-MDS − unclassified MDS, N − normal karyotype, P − primary MDS, p− − deletion of the short arms of chromosome, RA − refractory anemia, RAEB − RA with excess blasts, RAEB-1 − RA with excess blasts (5−9% blasts), RAEB-2 − RA with excess blasts (10−19% blasts), RAEB-t − RA with excess blasts in transformation, RARS − RA with ring sideroblasts, RCMD − refractory cytopenia with multilineage dysplasia, RCMD-RS − refractory cytopenia with multilineage dysplasia with ring sideroblasts, q− − deletion of the long arms of chromosome, S − secondary MDS, S′ − simple karyotype, WHO − World Health Organization, −20 − loss of chromosome 20, +8 − gain of chromosome 8, "5q−" − 5q− syndrome, "−" − aberration not detected, "+" − aberration detected

exposition to mutagens before the onset of MDS, complex karyotypes prevailed. In this group the use of FISH panel did not change cytogenetic category or poor prognosis related to this category. The karyotypes were assessed as complex, both before and after FISH.

To sum up, in 29 out of 35 (82.9%) patients with aberrations after FISH, FISH improved cytogenetic diagnosis. In 10 out of 33 (30.3%) patients without aberrations in GTG banding, FISH allowed a reclassification from normal to a simple karyotype, and in 1 out of 15 (6.6%) patients with simple karyotypes – a reclassification from simple to complex karyotype. However, because both normal and simple karyotypes had a good prognosis, and a complex one had a poor prognosis, only this one patient changed his prognostic category.

Among 24 patients with simple karyotype, some MDS panel aberrations were detected by GTG in 10 (41.7%). The following alterations were identified, 5q– in 4 patients by GTG technique and in 7 by FISH; –7 in 1 subject by GTG technique and in 6 subjects by FISH; 7q– in 1 subject by GTG subjects and in 2 subjects by FISH; +8 in 4 subjects by GTG technique and in 5 subjects by FISH; 17p13/TP53 deletion in none of the subjects by GTG technique and in 7 subjects by FISH; 20q deletion in none of the subjects by GTG technique and in 3 subjects by FISH.

Among 11 patients with a complex karyotype in 10 (91%) some MDS panel aberrations were identified by GTG technique. The following alterations were disclosed: 5q– or –5 in 8 subjects by GTG and in 16 subjects by FISH, –7 in 0 by GTG and in 2 subjects by FISH; 7q– in 3 subjects by GTG and in 5 subjects by FISH; +8 in 3 subjects by GTG and in 3 subjects by FISH; 17p13/TP53 deletion in 4 subjects by GTG and in 6 subjects by FISH; –20 or 20q– in 3 subjects by GTG and in 3 subjects by FISH (TABLE).

DISCUSSION According to the available data, the karyotype analysis is, beside a percentage of BM blasts, number and type of cell lines with dysplasia, and age >65 years, the most important prognostic factor in MDS. It is especially useful in establishing the prognosis in terms of the disease course and transformation to AML, as well as in selecting therapeutic method.[6,19-21]

The addition of FISH with MDS panel probes to CC allows better stratification of MDS patients, which translates into better prognostic categorization. However, FISH does not provide an unequivocal diagnosis of MDS, because the aberrations diagnosed by this panel are characteristic not only of MDS but also of some AML cases, especially the secondary ones.

In our study GTG revealed chromosome aberrations in only 25 out of 58 analyzed patients, i.e. in 43.1%. It is not a high percentage, still we assume that conventional cytogenetics should be a basic tool of cytogenetic analysis in MDS. First, CC deals with proliferating cells, i.e. the cells which are most important in the neoplastic process. Second, the detection of a cytogenetic abnormality may be useful in difficult cases to establish the diagnosis of MDS, or to distinguish between MDS and a benign reactive myeloid hyperplasia or a myeloproliferative neoplasm. Moreover, serial cytogenetic evaluation of the patient's BM can also be informative, particularly when there is a change in the clinical picture. Additional chromosomal aberrations may appear during the course of MDS or an abnormal clone may develop in the BM of patient with previously normal karyotype. During the therapy, the cytogenetic findings can be used to monitor the size of the neoplastic clone in the marrow as an indicator of response. Cytogenetic monitoring should be used in MDS as it is used in AML[22] to control the efficacy of the therapy. The stable panel of MDS FISH probes should be used at diagnosis and in the course of the disease as a complementary technique. If GTG karyotype of BM cells is normal, the use of the panel should identify occult typical aberrations if present. Moreover, if single aberrations are observed by GTG technique, the use of FISH as an additional technique can show the percentage of abnormal cells with each aberration, and help identify other cytogenetic alterations. In a complex karyotype, the use of the FISH panel does not change a cytogenetic category, but enables to detect masked aberrations, which can be useful in choosing a therapy. But, if a very complex karyotype is revealed by GTG, only the use of targeted FISH, chosen according to GTG data, not the FISH panel, together with comparative genomic hybridization or spectral karyotyping will help to explain the nature of complex aberrations and to identify chromosome markers.[23]

In MDS, the presence of normal karyotype is a better prognostic factor than any numerical or structural chromosome change. Thus, the lack of changes in cytogenetic examination may result in a delayed cytostatic therapy or in a less aggressive therapy. However, the lack of aberrations in GTG examination does not always mean that they are absent. The GTG banding technique results are limited by the efficacy of BM cell culture and the quality or spreading of metaphases. It is also possible that an inexperienced cytogeneticist finds the best quality metaphases which are commonly the normal ones, and overlooks the worse ones that may carry aberrations. Moreover, sometimes the percentage of aberrant cells is small, and routine GTG analysis of 20–25 metaphases may not detect any aberration.[24] Generally, GTG karyotyping is underpowered to detect less than 5% of rearranged cell, if less than 50 mitoses are analyzed. Taking into account that a detailed analysis of 50 mitoses in hematologic neoplasms is rarely possible, the chance of detecting small aberrant clone is negligible.

FISH is a more sensitive method than GTG.[7,19,23-27] FISH allows to analyze hundreds of proliferating or interphasal cells, i.e. 10× more

than GTG. But FISH has also its limitations. Classic FISH is a targeted method, which allows only to identify the changes which are indicated by strictly defined molecular probes, complementary to selected genome structures. Thus, simultaneous use of both GTG and FISH is the best solution that allows a more complete and exact search for chromosome aberrations.

In our study, the addition of FISH technique to GTG banding allowed us to find new chromosome aberrations. Thus, it improved the resolution of cytogenetic diagnostics in 29 out of 35 (82.9%) patients with aberrations after GTG and FISH. In 30.3% of patients without aberrations in GTG banding, the cytogenetic diagnosis was changed from normal to simple karyotype after FISH examination.

Rigolin et al. analyzed 101 MDS patients in which classic cytogenetics did not show chromosome aberrations, with FISH molecular probes for aberrations of 5, 7, 8, and 17 chromosomes (–5, 5q–, –7, 7q–, +8, 17p–). They found aberrations in 18 patients (17.8%), that is in a smaller percentage compared to our study (10/33 = 30.3%).[7] This discrepancy may result from technical differences between Rigolin's and our studies (quality of metaphases, number of metaphases analyzed), as well as from ethnic and geographical differences.

Romeo et al. analyzed 40 MDS patients with GTG and FISH with MDS panel probes (5q33–q34/5p15, cen7, cen8, cenY, MLL). The analysis of the results allowed to divide the patients into 3 groups:

1 with aberrations identified by both techniques (10 patients)

2 with aberrations shown only by GTG technique, absent in FISH panel (2 patients)

3 with aberrations observed only by FISH (4 patients).

This showed correlations between GTG and FISH results if good quality metaphases were obtained and limitations of FISH technique when atypical aberrations were present. However, when the poor quality metaphases or no metaphases were present, FISH technique was better than GTG. The authors concluded that both techniques should be used to improve detection of cytogenetic abnormalities in MDS.[23]

In our study and in those of other authors, FISH was able to detect small deletions of 5q31, deletions of 17p13, and monosomy of chromosome 7, omitted by CC. This allowed to place these patients into one of the two categories: "5q–" or "5q– and other aberrations". The finding of 5q31 deletion, precisely observed using FISH alone, is of crucial importance because it distinguishes the group of patients, who can undergo a 5q31(–) specific lenalidomide therapy, which offers patients a complete remission of the disease and prolongation of total survival time.

In 1 out of 15 (6.6%) patients with simple GTG karyotype, the cytogenetic diagnosis after FISH was changed to complex karyotype. However, in our small group of patients this patient was the only one in whom prognostic category of karyotype was changed. In others the category was not altered despite changing the cytogenetic category from normal to simple, because normal and simple karyotypes are included in the same prognostic category. However, the presence of typical MDS aberrations identified by FISH, could be helpful in confirming the clinical diagnosis of MDS. Naturally, the finding of aberrations in patients with complex karyotypes did not change their poor prognostic category, thus it had no clinical importance. The application of MDS panel of FISH probes presented here, together with classical cytogenetics, in studies on larger groups of MDS patients could cause more shifts from one cytogenetic category to another, and what is even more important from the clinical point of view, from one prognostic category to another.

We conclude that CC and FISH with a panel of probes for aberrations having a prognostic significance in MDS should be used simultaneously in order to improve diagnostic efficacy, better categorize patients with regard to prognosis, as well as to select the best, and if possible, genetically tailored treatment options.

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ARTYKUŁ ORYGINALNY

Porównanie przydatności metod cytogenetyki klasycznej i fluorescencyjnej hybrydyzacji *in situ* w genetycznej diagnostyce 58 pacjentów z zespołem mielodysplastycznym

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SŁOWA KLUCZOWE

aberracje chromosomowe, cytogenetyka klasyczna, fluorescencyjna hybrydyzacja *in situ*, zespoły mielodysplastyczne

STRESZCZENIE

WPROWADZENIE Zespoły mielodysplastyczne (*myelodysplastic syndromes* – MDS) stanowią heterogenną grupę klonalnych chorób multipotencjalnych komórek macierzystych lub progenitorowych. MDS charakteryzują się nieefektywną hematopoezą, nasiloną apoptozą, cytopeniami we krwi obwodowej i skłonnością do ewolucji w ostrą białaczkę szpikową.

CELE Celem naszego badania było porównanie przydatności cytogenetyki klasycznej i fluorescencyjnej hybrydyzacji *in situ* (*fluorescence in situ hybridization* – FISH) do wykrywania aberracji chromosomowych w MDS.

PACJENCI I METODY Badania przeprowadzono w grupie 58 pacjentów z MDS. Wykonano badanie komórek szpiku kostnego metodą prążków G (przy użyciu trypsyny i barwienia metodą Giemsy – prążkowanie GTG) i techniką FISH z użyciem panelu pięciu sond molekularnych dla aberracji o znaczeniu prognostycznym w MDS: cen7/8, 5q31, 7q22/q35, 17p13, 20q13.3.

WYNIKI Użycie techniki GTG pozwoliło wykryć aberracje chromosomowe u 25 (43,1%) pacjentów. Jednakże zastosowanie FISH jako dodatkowej metody diagnostycznej pozwoliło na wykrycie aberracji także u kolejnych 10 (17,2%) pacjentów, powodując przesunięcie 11 pacjentów z jednej kategorii cytogenetycznej do innej.

WNIOSKI Użycie FISH z panelem sond MDS obok klasycznej cytogenetyki pozwala na lepszą wykrywalność aberracji chromosomowych, a także lepszą stratyfikację pacjentów z MDS do grup prognostycznych. Obie metody powinny być stosowane równocześnie u każdego genetycznie diagnozowanego pacjenta z MDS.

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