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Translocation t(7;9)(q22;q34) in therapy-related myelodysplastic syndrome after allogeneic bone marrow transplantation for acute myeloblastic leukemia

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Abstract

Reciprocal translocations involving the long arm of chromosome 7 are relatively rare cytogenetic aberrations in myelodysplastic syndrome (MDS) and acute myeloblastic leukemia (AML). A 44-year-old woman was initially given a diagnosis as *de novo* AML M6A with a normal karyotype. After achieving a complete remission, she received allogeneic bone marrow transplantation from an unrelated male donor. Seven months later, pancytopenia appeared with 14.8% myeloblasts and dysplastic changes of neutrophils and megakaryocytes in the bone marrow. Chromosome analysis demonstrated complex karyotypes including add(7)(q22) and add(9)(q34) detected in all abnormal metaphase spreads. Spectral karyotyping revealed that they were derived from a reciprocal translocation t(7;9)(q22;q34). Fluorescence *in situ* hybridization analyses showed that *D7S486* at 7q31 was translocated to the der(9)t(7;9), and that the *ABL* gene at 9q34 remained on the der(9)t(7;9). Because the same translocation reappeared and sustained for more than eight months after second stem cell transplantation, we thought the diagnosis as therapy-related MDS after allogeneic transplantation. The t(7;9)(q22;q34) was supposed to have a crucial role in the pathogenesis of MDS. Furthermore, considering other two reported cases of AML, t(7;9)(q22;q34) may be a novel recurrent translocation in myeloid malignancies.

1. Introduction

Monosomy 7 and deletions of the long arm of chromosome 7, -7/del(7q), are commonly found in a variety of myeloid malignancies including myelodysplastic syndrome (MDS) and acute myeloblastic leukemia (AML), particularly in therapy-related MDS and AML (t-MDS/t-AML) [1]. These abnormalities are detected as a part of more complex karyotypes in adults, and are generally associated with very poor prognosis. Several conventional cytogenetic and fluorescence *in situ* hybridization (FISH) analyses showed that commonly deleted segments in MDS/AML with del(7q) were located at 7q22 and 7q31-33 [2-4]. Then, 7q22 could be a critical region in the pathogenesis of MDS/AML and the presence of one or more tumor suppressor genes at 7q22 has been suggested. However, a recurring mutation of candidate tumor suppressor genes remains to be identified in MDS/AML with -7/del(7q) [5].

On the other hand, reciprocal translocations involving 7q are relatively rare cytogenetic aberrations; only limited cases with 7q22 translocations have been analyzed in MDS/AML [3, 4, 6]. We describe here a unique case of t-MDS with t(7;9)(q22;q34), which appeared after allogeneic bone marrow transplantation (BMT) for AML.

2. Materials and methods

2.1. Case History

A 44-year-old woman was admitted to our hospital for fever and pancytopenia in November 2004. Peripheral blood showed hemoglobin 7.5 g/dL, platelets $52 \times 10^9/L$ and white blood cells $1.2 \times 10^9/L$ with 16% myeloblasts, 43% segmented neutrophils, 1% eosinophils, 1% monocytes and 39% lymphocytes. One hundred five erythroblasts were also detected among 100 white blood cells. Bone marrow was normocellular with markedly erythroid hyperplasia (Fig. 1A): 10.5% myeloblasts, 1.2% myeloid cells and 84.6% erythroblasts including 1.1% proerythroblasts without apparent dysplastic changes. Surface marker analysis by three-color flow cytometry with CD45 gating revealed that the myeloblasts were positive (more than 20%) for CD4 (23.5%), CD13 (70.4%), CD33 (91.0%) and HLA-DR (81.6%) but negative for CD34 (0.8%). We diagnosed her disease as *de novo* AML M6A in the French-American-British (FAB) classification or erythroleukemia in the World Health Organization (WHO) classification. An induction therapy with idarubicin and cytosine arabinoside was started and she achieved a complete remission (CR). After two courses of consolidation therapy including high-dose cytosine arabinoside, she received allogeneic BMT from a HLA-matched unrelated male donor following the conditioning regimen with cyclophosphamide and total body irradiation (TBI) in May 2005. She obtained complete chimerism according to FISH for sex chromosomes and maintained hematological CR after BMT.

In December 2005, severe pancytopenia appeared: hemoglobin 5.2 g/dL, platelets $17 \times 10^9/L$ and white blood cells $0.9 \times 10^9/L$ with 16% segmented neutrophils, 3% eosinophils, 1% basophils, 2% monocytes and 78% lymphocytes. Bone marrow was normocellular with increased number of megakaryocytes. Differential count was 14.8% myeloblasts, 11.6% myeloid cells, 44.6% lymphocytes and 21.8% erythroblasts (Fig. 1B). Dysplastic changes, such as multi-separated nuclear megakaryocytes and pseudo-Pelger anomaly of neutrophils,

were observed in the bone marrow cells (Fig. 1C and 1D). Surface marker analysis revealed that the myeloblasts were positive for CD13 (52.1%), CD33 (96.8%), CD34 (80.8%) and HLA-DR (74.7%) but negative for CD4 (3.2%). Mixed chimerism with 14.0% recipient type was also shown by FISH in the bone marrow cells. These findings initially suggested the first relapse of *de novo* AML, although we finally made a diagnosis as t-MDS of recipient origin after BMT. Then, she received non-myeloablative cord blood transplantation (CBT) from a HLA-matched unrelated male donor following the conditioning regimen with fludarabine, melphalan and TBI in January 2006. She achieved complete chimerism and second hematological CR after CBT.

However, mild pancytopenia appeared again in April 2006. Peripheral blood showed hemoglobin 8.5 g/dL, platelets $55 \times 10^9/L$ and white blood cells $2.6 \times 10^9/L$ with 32% segmented neutrophils, 7% monocytes, 5% eosinophils and 56% lymphocytes. In spite of repeated bone marrow examinations, hematological relapse after CBT was not apparent by morphological findings. Moreover, mixed chimerism with less than 5% recipient type was shown by FISH, but cytogenetic relapse was actually detected as described in Results. She is now under observation only by discontinuation of an immunosuppressive agent, tacrolimus. Mild pancytopenia in the peripheral blood has continued at a similar level but not progressed for more than eight months.

2.2. Chromosome analyses and spectral karyotyping

Chromosome analyses were performed by the G-banding technique on short-term culture of the cells obtained from bone marrow. Karyotypes were described according to the International System for Human Cytogenetic Nomenclature [7]. Spectral karyotyping (SKY) was carried out with SkyPaint kit (Applied Spectral Imaging, Migdal Ha'Emek, Israel).

2.3. Fluorescence in situ hybridization (FISH) analyses

We used LSI D7S486/CEP 7 Dual Color Probe and LSI BCR/ABL ES Dual Color Translocation Probe (Vysis, Downers Grove, IL, USA) to characterize t(7;9)(q22;q34). The D7S486/CEP 7 Dual Color Probe is a mixture of the approximately 200 kb D7S486 probe labeled with SpectrumOrange at 7q31 and the centromere of chromosome 7 (D7Z1) probe labeled with SpectrumGreen. The LSI ABL probe labeled with SpectrumOrange is approximately 650 kb extending from area centromeric of the *ASS* gene to telomeric of the last *ABL* exon at 9q34. We also used CEP X (DXZ1) SpectrumOrange and CEP Y (DYZ1) SpectrumGreen probes (Vysis) for chimerism analyses in sex-mismatched BMT and CBT (XY-FISH). The cut-off values for false positive of XX cells and XY cells were set at 3.0% and 2.0%, respectively.

3. Results

Chromosome analysis of the bone marrow cells at the initial diagnosis of AML M6A showed 46,XX[20], whereas the karyotypes at the onset of t-MDS after BMT were as follows (Fig. 2):

46,XX,add(2)(q31),add(2)(q?),add(7)(q22),add(9)(q34)[9]/46,XX,add(2)(q11),add(2)(q11),t(6;8)(p11;q22),add(7)(q22),add(9)(q34),del(9)(p?),add(11)(q23),t(12;21)(q14;q22)[5]/46,XY[5]. To clarify these complex cytogenetic aberrations, we performed SKY analysis and revised the karyotypes as follows (Fig. 3):

46,XX,t(2;2)(q24;q35),t(7;9)(q22;q34)[3]/46,XX,t(2;11)(q11;q23),der(2)?ins(2)(2pter->2q11::2?:2q23->2qter),t(6;8)(p11;q22),t(7;9)(q22;q34),del(9)(p?),del(12)(q14?),der(21)t(12;21)(q14;q22)[1]/46,XY[1]. That is, add(7)(q22) and add(9)(q34), detected in all abnormal metaphase spreads, were shown to be derived from a reciprocal translocation t(7;9)(q22;q34).

For further characterization of t(7;9)(q22;q34), we next performed FISH analyses with *D7S486* and *BCR/ABL* probes. As expected, the *D7S486* signal located at 7q31 was translocated to the der(9)t(7;9) and was not deleted (Fig. 4A). The *ABL* signal located at 9q34 remained on the der(9)t(7;9), indicating that the breakpoint at 9q34 was telomeric to the *ABL* gene (Fig. 4B).

Results of G-banding/SKY and XY-FISH analyses during the clinical course are summarized in Table. 1. Complex karyotypes including t(7;9)(q22;q34) appeared again after CBT in approximately 10% of metaphase spreads analyzed. XY-FISH analyses also showed persistent mixed chimerism at cytogenetic relapse after CBT, but XX (recipient) type was detected in only 3.2 to 3.6% of 500 interphase cells.

4. Discussion

We have identified a reciprocal translocation t(7;9)(q22;q34) in a case of t-MDS after BMT. Among the complex karyotypes, only t(7;9)(q22;q34) was detected in all abnormal metaphase spreads, indicating that the translocation had a crucial role in the pathogenesis of t-MDS. As shown in Table 2, four cases of hematological malignancies with t(7;9)(q22;q34) have been described [8-11]. The t(7;9)(q22;q34) in a case of chronic myelogenous leukemia (CML) seems to be derived from a complex variant type of t(9;22)(q34;q11) with *ABL* rearrangement [9]. On the other hand, the diagnoses in other three cases with t(7;9)(q22;q34) were MDS/AML and no *ABL* rearrangement was found in two of three cases [10, 11]. These findings suggest that t(7;9)(q22;q34) is apparently distinct cytogenetic aberration between CML and MDS/AML cases and that t(7;9)(q22;q34) is a novel recurrent translocation in myeloid malignancies.

FISH analyses of several reciprocal translocations involving 7q22, such as t(3;7)(q28;q22) and t(2;7)(p11;q22), have shown the heterogeneity of 7q22 translocation breakpoints in MDS/AML [3, 6]. Tosi *et al.* [4] also reported a case of AML with t(7;7)(p13;q22), in which the region of approximately 500 kb mapped 7q22 was deleted following the translocation. This finding implies that submicroscopic deletions accompanying 7q22 translocations, as well as the possible formation of fusion genes, may be important in the pathogenesis of MDS/AML. Putative tumor suppressor genes at 7q22 could be inactivated by deletion or disruption of their structures after translocations. In the present case, it is unknown whether submicroscopic deletion occurred, but at least *D7S486* at 7q31 was not deleted following t(7;9)(q22;q34). We also demonstrated that the breakpoint at 9q34 in t(7;9)(q22;q34) was telomeric to the *ABL* gene. Some recurrent translocations involving 9q34, other than t(9;22)(q34;q11) with *BCR/ABL*, have been molecularly characterized in acute leukemia [12-15]. Among the genes at 9q34, *CAN* and *NOTCH1* are located telomeric

to the *ABL* gene, suggesting that these genes might be associated with t(7;9)(q22;q34). Furthermore, Poppe *et al.* [16] reported a child with MDS and t(7;9)(p15;q34). The breakpoint at 9q34, mapped distal to *ABL* and proximal to *NOTCH1*, may be close to that in the present case.

When t(7;9)(q22;q34) appeared immediately after BMT, we initially diagnosed the disease as first relapse of *de novo* AML. However, the findings such as no progression after second stem cell transplantation, low percentages of myeloblasts, dysplastic changes of neutrophils and megakaryocytes, and markedly complex karyotypes involving 7q, finally raised the possibility that the diagnosis was t-MDS of recipient origin induced by the first conditioning regimen with TBI and cyclophosphamide. In contrast to the higher frequency of t-MDS after autologous transplantation [17], there have been only a few cases of t-MDS after allogeneic transplantation [18, 19]. Muroi *et al.* [19] reported a case of t-MDS appeared four months after allogeneic BMT following the conditioning regimen with etoposide, cyclophosphamide and TBI for AML. The diagnosis in this case was easily made as t-MDS, because of the low percentage of blasts, evident trilineage dysplasia and complex abnormal karyotypes involving 5q, all of which were the recipient type. On the other hand, in the present case, mixed chimerism with limited percentages of recipient cells has been observed to date. Therefore, because of residual normal donor cells, it is difficult to rule out the possibility that the diagnosis was relapse of AML completely. At present, the disease activity appears to be generally controlled only by graft-versus-leukemia effect for more than eight months. Further observation for the present case will be required to elucidate the clinical features of t-MDS with t(7;9)(q22;q34).

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References

- [1] Pedersen-Bjergaard J, Rowley JD. The balanced and the unbalanced chromosome aberrations of acute myeloid leukemia may develop in different ways and may contribute differently to malignant transformation. *Blood* 1994;83:2780-2786.
- [2] Le Beau MM, Espinosa III R, Davis EM, Eisenbart JD, Larson RA, Green ED. Cytogenetic and molecular delineation of a region of chromosome 7 commonly deleted in malignant myeloid diseases. *Blood* 1996;88:1930-1935.
- [3] Fischer K, Fröhling S, Scherer SW, Brown JM, Scholl C, Stilgenbauer S, Tsui LC, Lichter P, Döhner H. Molecular cytogenetic delineation of deletions and translocations involving chromosome band 7q22 in myeloid leukemias. *Blood* 1997;89:2036-2041.
- [4] Tosi S, Scherer SW, Giudici G, Czepulkowski B, Biondi A, Kearney L. Delineation of multiple deleted regions in 7q in myeloid disorders. *Genes Chromosomes Cancer* 1999;25:384-392.
- [5] Curtiss NP, Bonifas JM, Lauchle JO, Balkman JD, Kratz CP, Emerling BM, Green ED, Le Beau MM, Shannon KM. Isolation and analysis of candidate myeloid tumor suppressor genes from a commonly deleted segment of 7q22. *Genomics* 2005;85:600-607.
- [6] Johnson EJ, Scherer SW, Osborne L, Tsui LC, Oscier D, Mould S, Cotter FE. Molecular definition of a narrow interval at 7q22.1 associated with myelodysplasia. *Blood* 1996;87:3579-3586.
- [7] Mitelman F, editor. *ISCN 1995: an international system for human cytogenetic nomenclature* (1995). Basel: S. Karger, 1995.
- [8] Mitelman F, Johansson B, Mertens F. Mitelman database of chromosome aberrations in cancer. Updated on July 10, 2006. Available at:
<http://cgap.nci.nih.gov/Chromosomes/Mitelman>. Accessed November 20, 2006.
- [9] Johansson B, Fioretos T, Mitelman F. Cytogenetic and molecular genetic evolution of

chronic myeloid leukemia. *Acta Haematol* 2002;107:76-94.

- [10] Marosi C, Köller U, Koller-Weber E, Schwarzingen I, Schneider B, Jäger U, Vahls P, Nowotny H, Pirc-Danoewinata H, Steger G, Kreiner G, Wagner B, Lechner K, Lutz D, Bettelheim P, Haas OA. Prognostic impact of karyotype and immunologic phenotype in 125 adult patients with de novo AML. *Cancer Genet Cytogenet* 1992;61:14-25.
- [11] Reddy KS, Sulcova V. A FISH study of variant Philadelphia rearrangements. *Cancer Genet Cytogenet* 2000;118:121-131.
- [12] von Lindern M, Poustka A, Lerach H, Grosveld G. The (6;9) chromosome translocation, associated with a specific subtype of acute nonlymphocytic leukemia, leads to aberrant transcription of a target gene on 9q34. *Mol Cell Biol* 1990;10:4016-4026.
- [13] von Bergh ARM, Wijers PM, Groot AJ, van Zelderen-Bhola S, Falkenburg JHF, Kluin PM, Schuurin E. Identification of a novel RAS GTPase-activating protein (*RASGAP*) gene at 9q34 as an *MLL* fusion partner in a patient with de novo acute myeloid leukemia. *Genes Chromosomes Cancer* 2004;39:324-334.
- [14] Gervais C, Mauvieux L, Perrusson N, Hélias C, Struski S, Leymarie V, Lioure B, Lessard M. A new translocation t(9;11)(q34;p15) fuses *NUP98* to a novel homeobox partner gene, *PRRX2*, in a therapy-related acute myeloid leukemia. *Leukemia* 2005;19:145-148.
- [15] Ellisen LW, Bird J, West DC, Soreng AL, Reynolds TC, Smith SD, Sklar J. *TAN-1*, the human homolog of the *Drosophila notch* gene, is broken by chromosomal translocations in T lymphoblastic neoplasms. *Cell* 1991;66:649-661.
- [16] Poppe B, Yigit N, De Moerloose B, De Paepe A, Benoit Y, Speleman F. *HOXA* gene cluster rearrangement in a t(7;9)(p15;q34) in a child with MDS. *Cancer Genet Cytogenet* 2005;162:82-84.
- [17] Pedersen-Bjergaard J, Andersen MK, Christiansen DH. Therapy-related acute myeloid leukemia and myelodysplasia after high-dose chemotherapy and autologous stem cell

transplantation. *Blood* 2000;95:3273-3279.

- [18] Au WY, Lie AKW, Ma SK, Leung YH, Siu LLP, Kwong YL. Therapy-related myelodysplastic syndrome of recipient origin after allogeneic bone marrow transplantation for acute lymphoblastic leukaemia. *Br J Haematol* 2001;112:424-426.
- [19] Muroi K, Kawano C, Yokote T, Otsuki T, Kirito K, Komatsu N, Ozawa K. Early myelodysplastic syndrome after allogeneic bone marrow transplantation for acute myeloid leukemia. *Leuk Lymphoma* 2002;43:1493-1496.

Figure legends

Fig. 1. Bone marrow smear at the initial diagnosis of AML M6A (A, x400) and at the onset of t- MDS (B to D, x1000, May-Grünwald-Giemsa staining). (A) Myeloblasts (arrows) and increased number of erythroblasts, (B) myeloblasts, (C) multi-separated nuclear megakaryocytes and (D) pseudo-Pelger anomaly of neutrophils, are shown.

Fig. 2. G-banded karyotype of the bone marrow cells at the onset of t-MDS. The karyotype is as follows:

46,XX,add(2)(q11),add(2)(q11),t(6;8)(p11;q22),add(7)(q22),add(9)(q34),del(9)(p?),add(11)(q23),t(12;21)(q14;q22). Arrows indicate rearranged chromosomes.

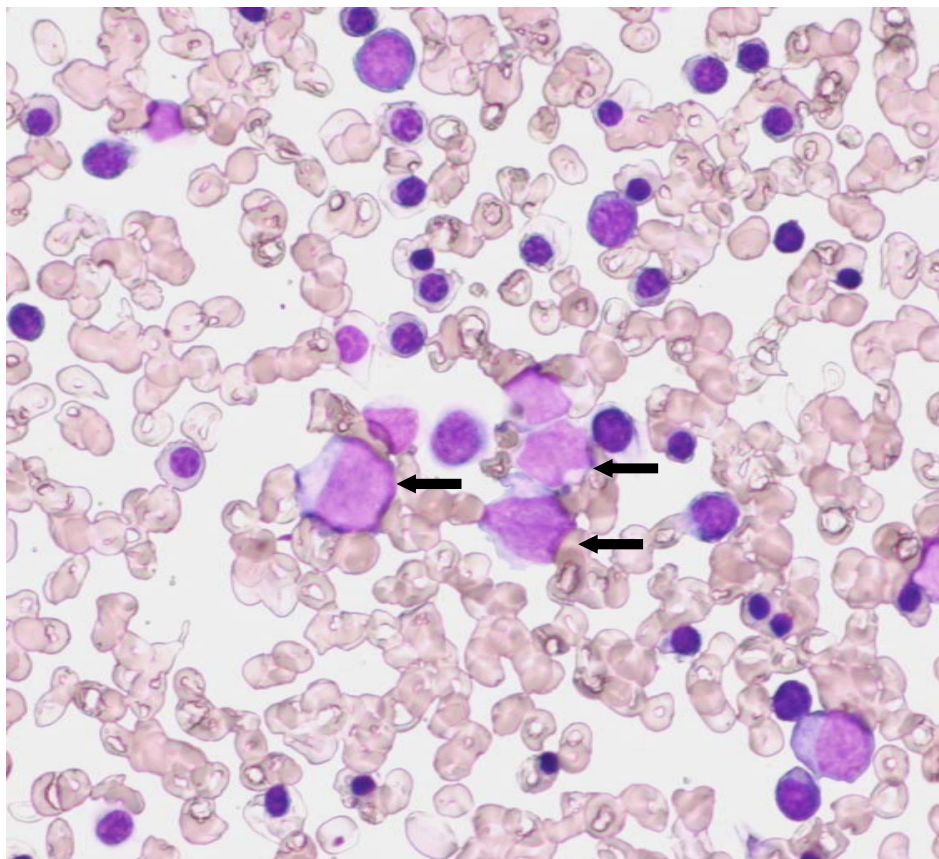
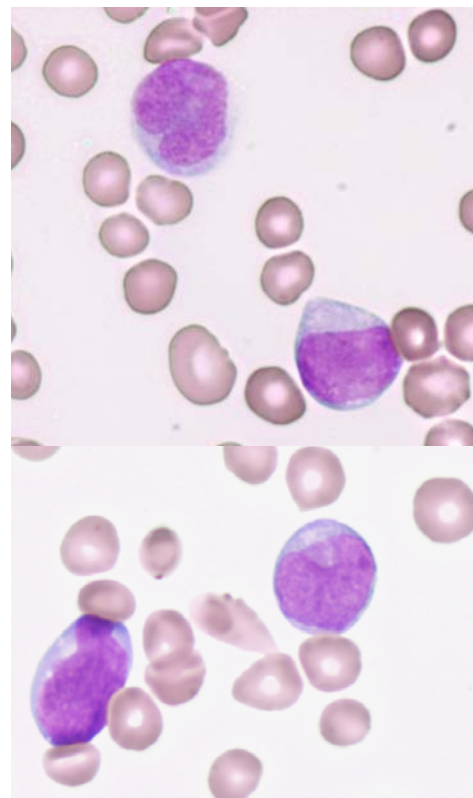
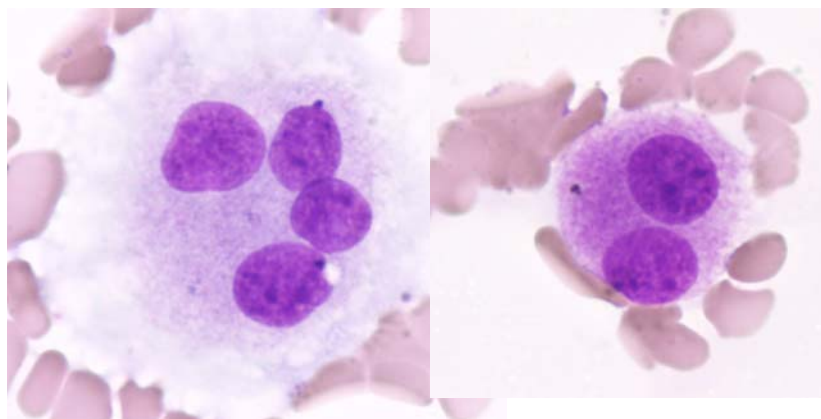
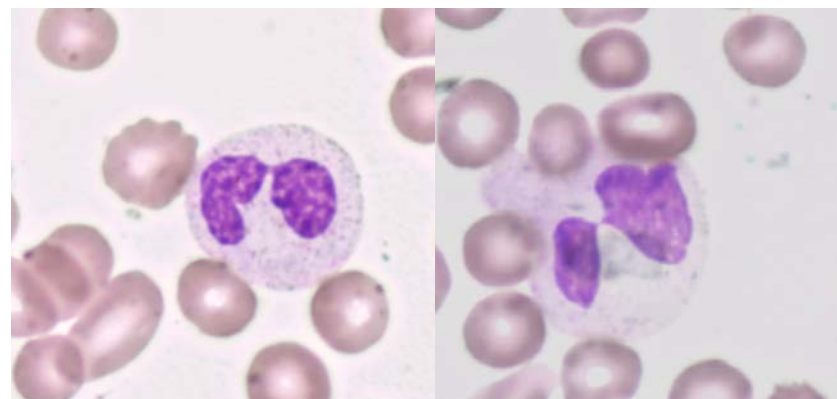
Fig. 3. Spectral karyotyping of the metaphase spread after spectrum-based classification (left side, reverse DAPI; right side, SKY). Chromosomes were assigned a pseudocolor according to the measured spectrum. The karyotype is revised as follows:

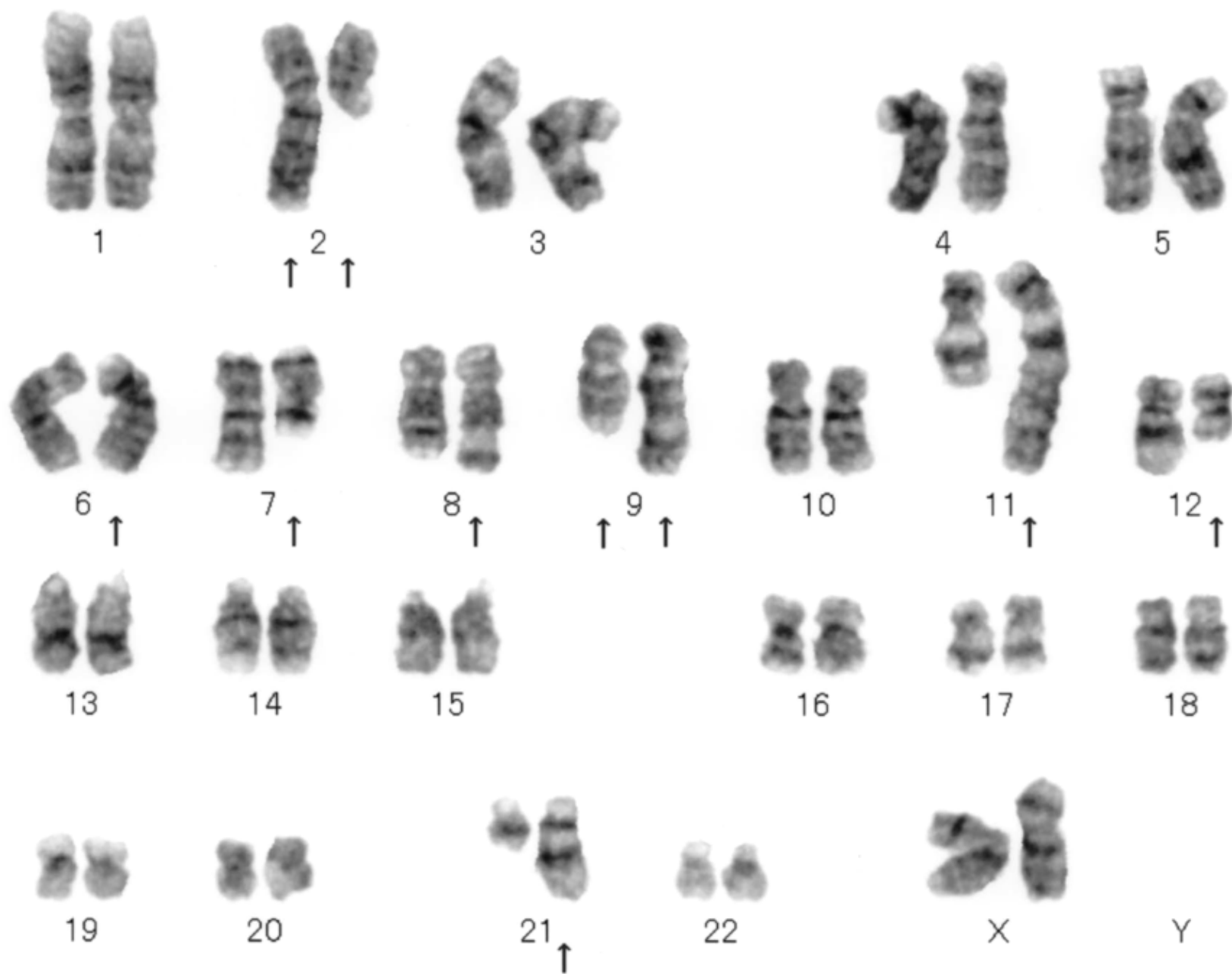
46,XX,t(2;11)(q11;q23),der(2)?ins(2)(2pter->2q11::2?:2q23->2qter),t(6;8)(p11;q22),t(7;9)(q22;q34),del(9)(p?),del(12)(q14?),der(21)t(12;21)(q14;q22). Arrows indicate rearranged chromosomes.

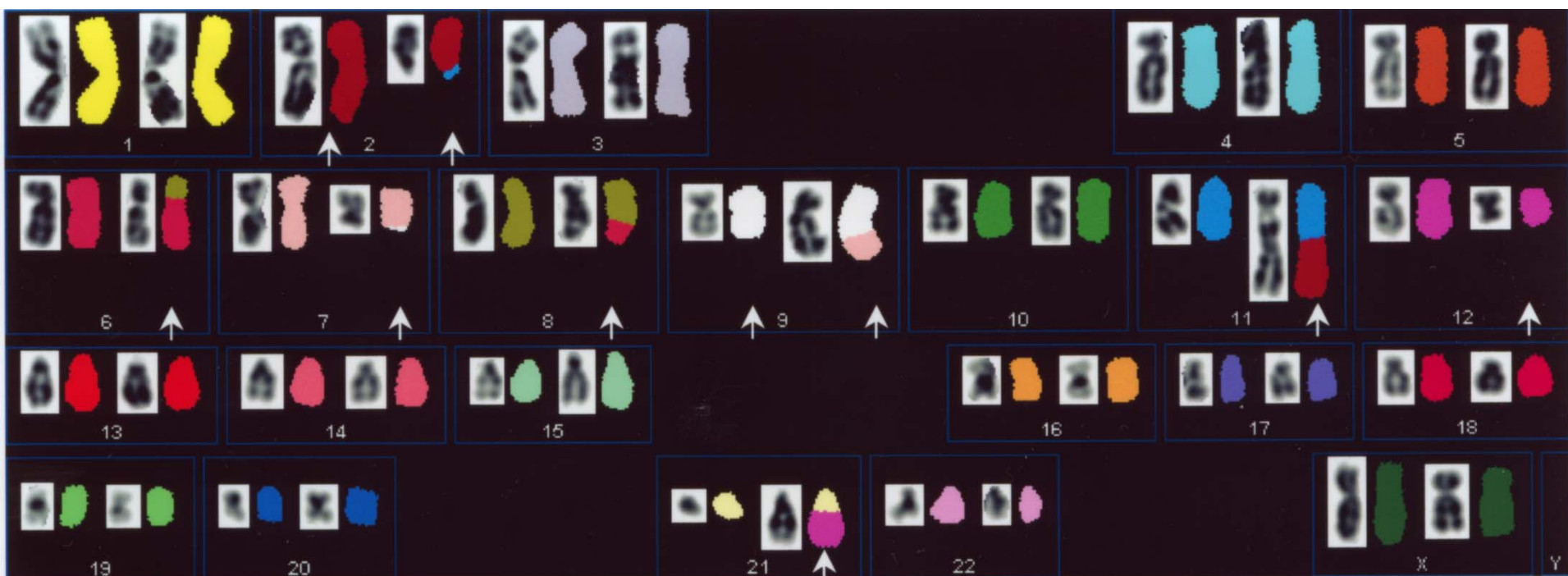
Fig. 4. FISH analyses with (A) *D7S486/CEP7* and (B) *BCR/ABL* probes on metaphase spreads.

(A) Arrows indicate 1) *D7S486* (orange) and *CEP7* (green) signals on normal chromosome 7, 2) *CEP7* signal on the der(7)t(7;9)(q22;q34) and 3) *D7S486* signal on the der(9)t(7;9)(q22;q34). The *D7S486* signal at 7q31 is translocated to the der(9)t(7;9)(q22;q34) as expected.

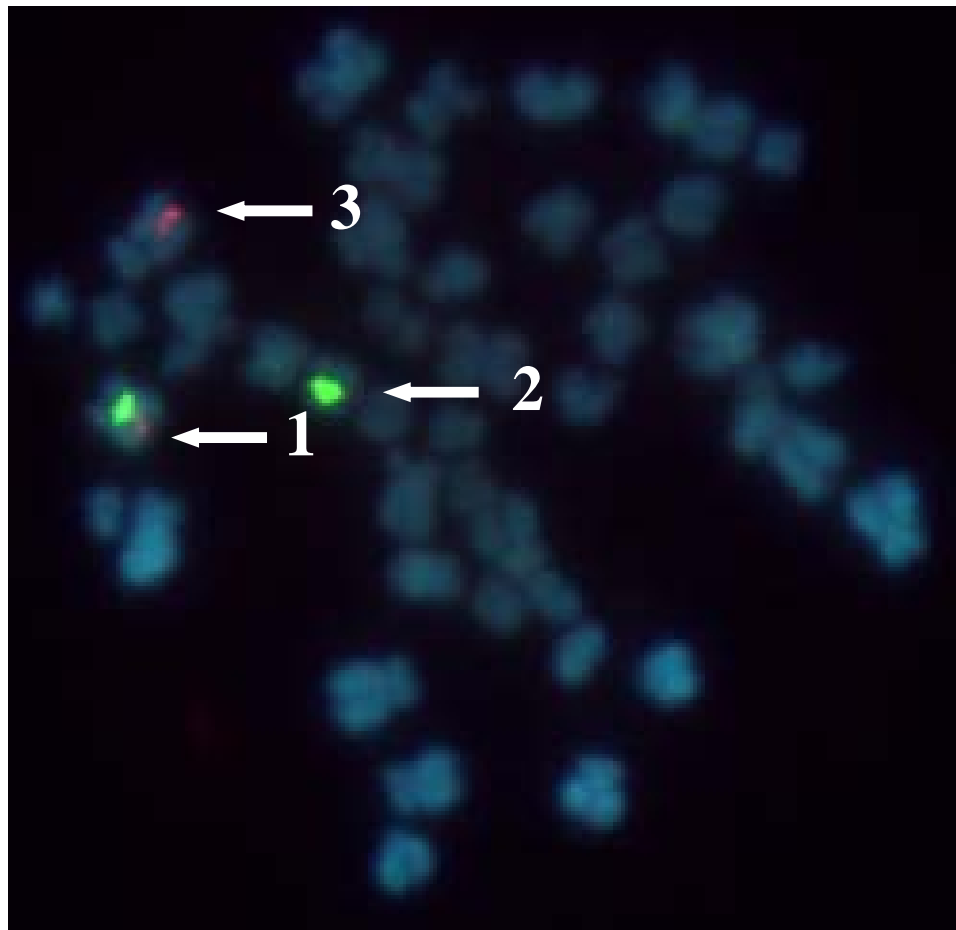
(B) Arrows indicate 1) *BCR* signals on normal chromosomes 22 (green), 2) *ABL* signal on normal chromosome 9 (orange), and 3) *ABL* signal on the der(9)t(7;9)(q22;q34). The *ABL* signal at 9q34 remains on the der(9)t(7;9)(q22;q34).

A**B****C****D**





A



B

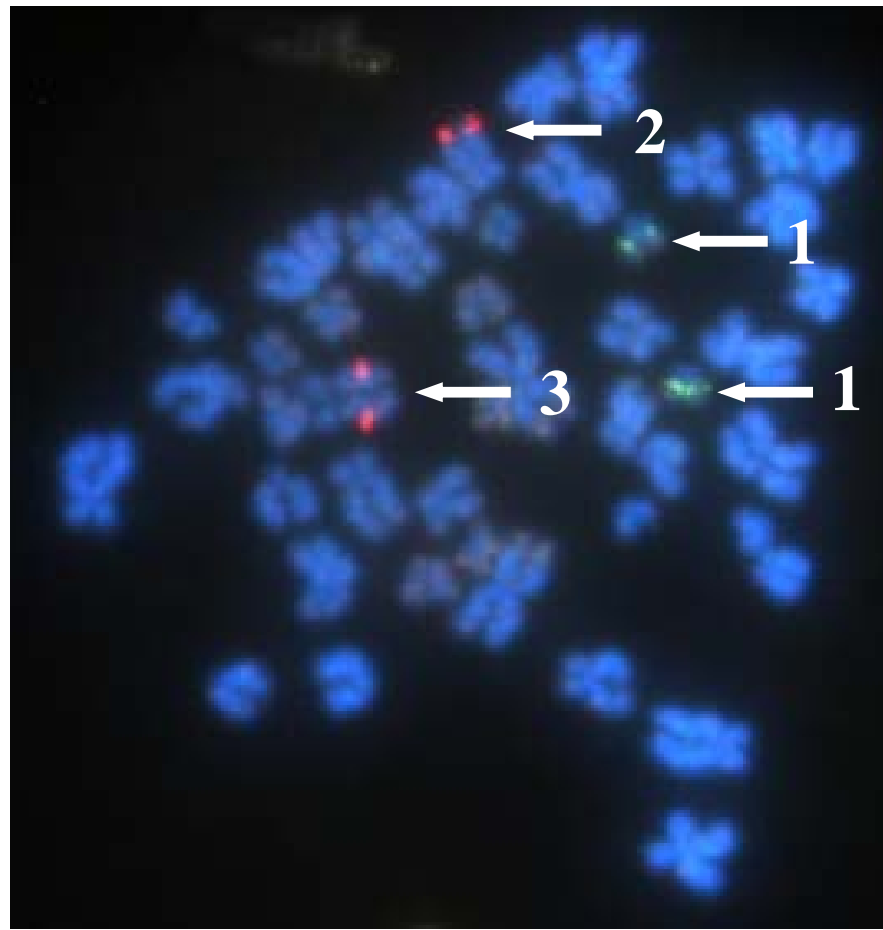


Table 1. Summary of cytogenetic analyses

<i>Date</i>	<i>Disease Status</i>	<i>Karyotypes</i> (by G-banding and SKY)	<i>FISH</i> <i>XX/XY(%)</i>
November 2004	AML M6A	46,XX[20]	ND
January 2005	CR	46,XX[20]	ND
July 2005	CR, after BMT	46,XY[20]	0.4/99.2
October 2005	CR, after BMT	46,XY[20]	2.0/97.4
December 2005	t-MDS, after BMT	46,XX,t(2;2)(q24;q35),t(7;9)(q22;q34)[3]/46,XX,t(2;11)(q11;q23),der(2)?ins(2)(2pter->2q11::2?::2q23->2qter),t(6;8)(p11;q22),t(7;9)(q22;q34),del(9)(p?),del(12)(q14?),der(21)t(12;21)(q14;q22)[1]/46,XY[1]	14.0/86.0
February 2006	CR, after CBT	46,XY[20]	ND
March 2006	CR, after CBT	46,XY[20]	1.4/96.6
April 2006	t-MDS relapse, after CBT	46,XX,t(2;2)(q24;q35),t(7;9)(q22;q34)[2]/46,XY[18]	3.6/95.8
May 2006	t-MDS relapse, after CBT	46,X,add(X)(q11),del(1)(p33),der(2)t(2;11)(q11;q23),add(6)(p11),add(7)(q22),-8,-9,der(11)t(2;11)(q11;q23)add(2)(q37),t(12;21)(q14;q22),+2mar[1]/46,XY[17]	3.2/96.2

July 2006	t-MDS relapse, after CBT	46,XX,add(1)(q32),t(2;11)(q11;q23),add(6)(p11), t(7;9)(q22;q34) ,add(8)(q13),add(9)(p13), der(12)add(12)(p11)add(12)(q22),add(17)(q21),+?add(20)(q11),add(21)(q22),-22[2]/46,XY[16]	3.2/96.2
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Abbreviations: AML, acute myeloblastic leukemia; CR, complete remission; BMT, bone marrow transplantation; t-MDS, therapy-related myelodysplastic syndrome; CBT, cord blood transplantation; SKY, spectral karyotyping; FISH, fluorescence *in situ* hybridization; ND, not done. In karyotypes, t(7;9)(q22;q34) and add(7)(q22) are shown by bold letters. In BMT and CBT, both donors were male (XY), whereas the recipient was female (XX).

Table 2. Reported cases of human malignancies with t(7;9)(q22;q34)

<i>Age/Sex</i>	<i>Diagnosis</i>	<i>Karyotypes</i>	<i>ABL gene</i>	<i>References</i>
76/F	CML CP	46,XX,t(7;9)(q22;q34),t(17;22)(p13;q11)	NE	Johansson <i>et al</i> , 2002 [9]
NA/M	AML M2	45,XY,del(5)(q?),t(7;9)(q22;q34),i(11)(q10),-20	NE	Marosi <i>et al</i> , 1992 [10]
36/M	AML	48,XY,+6,t(7;9)(q22;q34),+8	NR	Reddy and Sulcova, 2000 [11]
44/F	AML M6A-> t-MDS	46,XX,t(2;2)(q24;q35),t(7;9)(q22;q34)	NR	present case

Abbreviations: F, female; M, male; NA, not available; CML CP, chronic myelogenous leukemia chronic phase; AML, acute myeloblastic leukemia; t-MDS, therapy-related myelodysplastic syndrome; NE, not examined; NR, not rearranged shown by fluorescence *in situ* hybridization. In karyotypes, t(7;9)(q22;q34) is shown by bold letters.