Title
Acute myeloid leukemia with NUP98::RARG rearrangement: a case report and review of the relevant literature

Author(s)
Inamura Junki / TAKETANI Takeshi / Mochida Miho / Goto Tsukimi / SUZUKI Ritsuro / Igarashi Sho / Tsukada Nodoka / Yamamoto Masayo / Shindo Motohiro / Sato Kazuya

Journal
International Journal of Hematology 121 , 265 - 271

Published
2024-12-04

URL (The Version of Record)
https://doi.org/10.1007/s12185-024-03881-2

International Journal of Hematology
https://doi.org/10.1007/s12185-024-03881-2

CASE REPORT

Acute myeloid leukemia with *NUP98::RARG* rearrangement: a case report and review of the relevant literature

Junki Inamura[1] · Takeshi Taketani[2] · Miho Mochida[3] · Tsukimi Goto[4] · Ritsuro Suzuki[5] · Sho Igarashi[1] · Nodoka Tsukada[1] · Masayo Yamamoto[6] · Motohiro Shindo[6] · Kazuya Sato[1]

Received: 16 May 2024 / Revised: 9 November 2024 / Accepted: 14 November 2024

Abstract

We herein report a rare case of acute myeloid leukemia (AML) with t(11;12)(p15;q13) and *NUP98::RARG*, which seems to be involved in the development of AML. The morphological features were similar to those of classic acute promyelocytic leukemia (APL), but unlike classic APL, this leukemia was resistant to treatment with all-trans retinoic acid (ATRA). We decided to use standard chemotherapy for AML with monitoring of minimal residual disease (MRD) by qualitative reverse transcriptase–polymerase chain reaction (RT-PCR) analysis for *NUP98::RARG* mRNA. Although MRD disappeared after induction chemotherapy, it later reappeared, and hematological relapse occurred during subsequent chemotherapies. The patient received haploidentical hematopoietic stem cell transplantation while not in remission and achieved a second molecular remission. However, relapse occurred 4 months after transplantation. The specific mechanism of ATRA resistance in this unique case of AML remains unclear, and no standard treatment has been determined. This is the first case report of AML with *NUP98::RARG* rearrangement in Japan. Qualitative RT-PCR analysis for *NUP98::RARG* mRNA was helpful for the accurate diagnosis and evaluation of MRD to choose an adequate treatment for this type of AML.

Keywords Acute promyelocytic leukemia · NUP98 · RARG · Haploidentical transplantation

Introduction

The Nucleoporin 98 (*NUP98*) gene on chromosome 11p15 encodes part of the nuclear pore complex, which is responsible for protein and RNA transport through the nuclear membrane [1, 2]. *NUP98*-fused oncogenes can be observed in various hematological malignancies, especially in pediatric acute myeloid leukemia (AML). To date, more than 30 partner genes have been identified [1]. There are few acute promyelocytic leukemia (APL) phenotypes in the French American British (FAB) classification. Among the NUP98-fused proteins, the N-terminus of NUP98 alters the transcriptional activity of the partner protein at the C-terminus, which is thought to play a key role in leukemogenesis [3, 4]. The cases of AML with an *NUP98*-fused gene are categorized as a subset of high-risk leukemia [1].

In contrast, most cases of APL show rearrangement of retinoic acid receptor alpha (RARA), which belongs to the retinoic acid receptor subfamily [5]. Recently, AMLs with retinoic acid receptor gamma (RARG) rearrangement have been reported, the morphology of which resembles that of classic APL with *PML::RARA* rearrangement [6]. Similar to RARA, RARG is a retinoic acid-inducible transcriptional factor whose *RARG* gene is located on chromosome 12q13 [5].

In this report, we present a rare case of AML with t(11;12)(p15;q13) having *NUP98::RARG* fusion. We also review unique cases of AML that have been reported in the

✉ Junki Inamura
j_inamura@hotmail.com

1 Department of Hematology/Oncology, Asahikawa Kosei Hospital, Asahikawa, Japan

2 Department of Pediatrics, Faculty of Medicine, Shimane University, Izumo, Japan

3 Regenerative Medicine Center, Shimane University Hospital, Izumo, Japan

4 Clinical Laboratory Division, Shimane University Hospital, Izumo, Japan

5 Department of Hematology, Shimane University Hospital, Izumo, Japan

6 Division of Hematology, Department of Internal Medicine, Asahikawa Medical University, Asahikawa, Japan

Published online: 04 December 2024

relevant literature, highlighting characteristics such as morphological features, treatment, and the prognosis.

Case presentation

A 44-year-old woman with leukopenia and thrombocytopenia was referred to our hospital. A blood examination showed cytopenia and fibrinolytic abnormalities: white blood cell count, 600/μL (neutrophils 62%, lymphocytes 35%, monocytes 2%, basophils 1%, and no blasts); hemoglobin concentration, 12.0 g/dL; platelet count, 34×10^3/μL; fibrin degradation products, 41.2 μg/mL (reference value: 0.0–5.0 μg/mL); D-dimer, 17.7 μg/mL (reference value: 0.0–1.0 μg/mL). Neither the prothrombin time nor the activated partial thromboplastin time was prolonged.

Bone marrow (BM) aspiration revealed that 75.4% of the nucleated cells were abnormal tumor cells with invaginated or roughly lobed nuclei and rich azurophilic granules or Auer rods in the cytosol (Fig. 1A), which were strongly positive on peroxidase staining. A fluorescence-activated single cell sorting analysis (threshold: 20%) showed that surface markers on leukemic cells were positive for MPO, CD4, CD7, CD13, CD14, CD33, CD117, and HLA-DR, whereas negative for CD1a, CD2, CD3, CD5, CD8, CD10, CD19, CD20, CD22, CD30, CD34, CD38, CD41, CD56, CD138, GP-A, and TdT.

As classic APL was strongly suspected, prompt treatment with all-trans retinoic acid (ATRA) was initiated after admission (day 1). However, her peripheral blood count was unaffected, and her fibrinolytic abnormalities worsened. In addition, re-examination of the patient's BM on day 4 showed no significant morphological changes in the tumor cells (Fig. 1B), with increased leukemic cells (Table 1).

Since her leukemia cells were resistant to ATRA, standard induction chemotherapy for AML with idarubicin and cytarabine was initiated on day 9, and ATRA was discontinued on day 15.

Molecular and cytogenetic analyses of the patient's BM revealed that abnormal karyotypes containing t(11;12)(p15;q13) were present in 10 of 20 cells (Fig. 1C), and the *PML::RARA* fusion gene was not detected by reverse

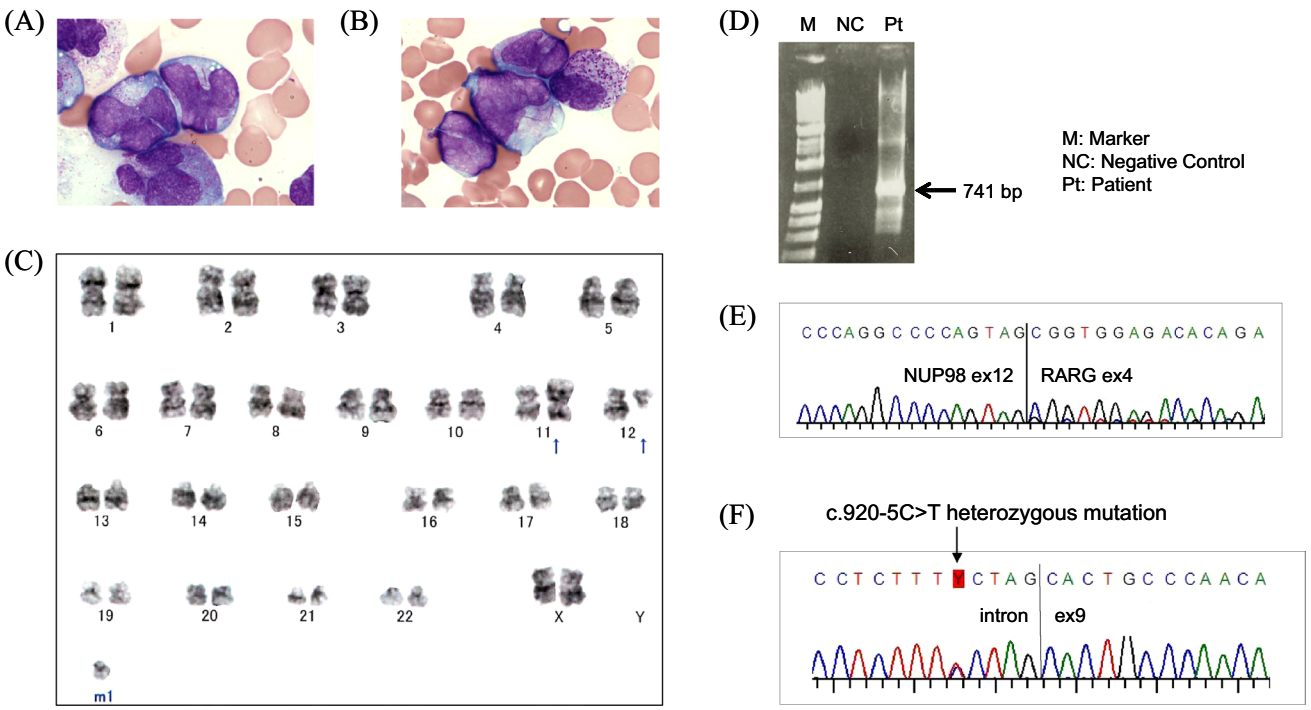

Fig. 1 A bone marrow analysis at the diagnosis. **A** May–Giemsa staining of bone marrow at the diagnosis before the administration of ATRA (×400). The nucleus has invaginations or rough locations, and the cytosol is rich in Azur granules or Auer rods. These morphological features closely resemble those of classic APL cells.**B** Bone marrow after a 3-day use of ATRA (×400). The cells showed almost no change in comparison to picture (**A**), and no apoptotic cells were observed.**C** Three karyotypes were detected: 46, XX, t(11;12)(p15;q13) [10]/47, idem, mar1 [3]/46, XX [7]. This figure represents the second type. The marker chromosome was derived from chromosome 21 according to a SKY-FISH analysis (data not shown). **D E** An RT-PCR analysis of bone marrow cells revealed the presence of the *NUP98::RARG* fusion gene. **D** Gel electrophoresis detected 741-bp *NUP98::RARG* transcripts. **E** A chromatogram and base call of the direct sequence analysis, which revealed that NUP98 exon 12 was fused in-frame with *RARG* exon 4. **F** To confirm the second-hit mutation, we performed direct sequence analyses for *TP53*, *WT1*, *IDH2*, *NRAS*, *KRAS*, *FLT*-ITD, *FLT*-TKD, *HRAS*, *PTPN11*, *KIT*, *NPM1*. Heterogeneous mutations were detected in the introns of *TP53*. The mutation was described as c.920-5C > T

Table 1 Change of the residual disease in bone marrow

Timing	At diagnosis		AfterI + A (day 39)	After M + A (day 98)	After D + A (day 157)	After A + A (day 207)	After A + triple V (day 245)
	Before ATRA	ATRA day 4					
Microscopic leukemic cells (%)	75.6	92.4	< 5	< 5	< 5	< 5	< 5
t(11;12)(p15;q13) by G-Band (/20)	13	6	0	0	0	1	0
NUP98 FISH (%)	94	(ND)	0	0	0	0	0
WT1 mRNA (copies/μgRNA)	(ND)	6.8×10^4	6.6×10^2	(ND)	3.8×10^2	4.0×10^3	3.6×10^3
NUP98::RARG mRNA	+	(ND)	–	–	+	(ND)	+

I + *A*: idarubicin + cytarabine as induction chemotherapy, *M* + *A*: mitoxantrone + cytarabine, *D* + *A*: daunorubicin + cytarabine, *A* + *A*: aclarubicin + cytarabine, *A* + *triple V*: cytarabine + etoposide + vincristine + vindesine, *ATRA*: all-trans retinoic acid, *FISH*: florescence *in-situ* hybridization, *ND*: no data

transcriptase–polymerase chain reaction (RT-PCR). However, *NUP98* split signals were positive in 94.0% of interphase fluorescence in-situ hybridization (FISH) analyses.

AML with *NUP98::RARG* rearrangement was suspected because her clinical features and karyotype were similar to those of a previous case [7]. To identify the specific fusion gene by RT-PCR, we prepared the following primers: *NUP98* forward, 5'-TTGGCACAAATACCAGTGGG-3' and *RARG* reverse, 5'-CCCAGCAAAGGCAAAGACAA-3.' As a result, *NUP98::RARG* fusion was detected (Fig. 1D), and the patient was diagnosed with AML with *NUP98::RARG* rearrangement.

Direct sequence analyses were also performed to identify the breaking points of both *NUP98* and *RARG* genes and to confirm the accompanying second-hit mutations. As a result, *NUP98* exon 12 was fused in-frame to *RARG* exon 4 (Fig. 1E), as previously reported [7–13]. In addition, a heterozygous mutation in the intron of *TP53* (c.920-5C > T) was detected (Fig. 1F). There were no mutations in *WT1*, *IDH1*, *IDH2*, *NRAS*, *KRAS*, *HRAS*, *FLT3*-tyrosine kinase domain (TK), *FLT3*-internal tandem duplication (ITD), *PTPN11*, *KIT*, or *NPM1* (data not shown).

A BM examination (day 39) revealed molecular complete remission (CR) because the patient was negative for minimal residual disease (MRD), as assessed by RT-PCR for *NUP98::RARG* mRNA. However, the *TP53* mutation remained in the same BM sample (Fig. 2), thus indicating that there was a single nucleotide polymorphism (SNP) (https://www.ncbi.nlm.nih.gov/snp/rs34361146).

Since no appropriate stem cell donors were available from her siblings, the domestic BM or cord-blood banks, 4 courses of consolidation chemotherapy were planned in accordance with the JALSG AML201 protocol [14]. Although a molecular CR was maintained (day 98) after the first course of consolidation therapy, marrow MRD of *NUP98::RARG* fusion mRNA (day 157) was detected after the second consolidation therapy. After the third consolidation therapy, one cell with an obviously abnormal karyotype of 46 XX, t(3;17)(q21;q21.2), t(11;12)(p15;q13),

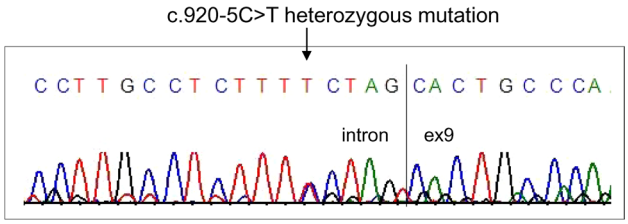

Fig. 2 To confirm whether the *TP53* mutation found at the time of diagnosis is a somatic mutation or a germline polymorphism, we performed a direct sequence analysis again using extracted DNA from a bone marrow sample taken on day 39 when molecular complete remission had been achieved. A heterogeneous mutation of c.920-5C > T in *TP53* was detected which was identical to the mutation which had been found at the time of diagnosis (Fig. 1F), thus indicating that it was derived from a germline

was detected in 20 analyzed cells in BM, which indicated cytogenetic relapse (day 207). The additional breakpoint of 17q21.2 was not associated with the *RARA* gene by FISH analysis. The patient remained positive for MRD until day 245, although the karyotype returned to normal after the fourth consolidation therapy. The patient was transferred to an advanced treatment hospital for haploidentical hematopoietic stem cell transplantation (HSCT).

The patient then received one course of combination chemotherapy with azacitidine and venetoclax as bridging therapy because dental management was needed before HSCT. However, hematological relapse occurred in the BM; 71.8% of the promyelocytes were abnormal (day 301). Although she then received 5 days of high-dose cytarabine as re-induction chemotherapy, her BM blasts remained (71.0%, day 338). She received haploidentical HSCT on the non-remission status (day 361), which was based on the JSCT Haplo14 MAC protocol, and received conditioning therapy with fludarabine (150 mg/m^2), busulfan (12.8 mg/kg), and total body irradiation (4 Gy), and graft-versus-host disease (GVHD) prophylaxis with 2 days of cyclophosphamide (50 mg/kg/day), tacrolimus, and mycophenolate mofetil [15]. RT-PCR for *NUP98::RARG* mRNA became

Table 2 Reported cases of acute myeloid leukemia with *NUP98::RARG* rearrangement

Case no	Age/sex	Description of karyotype at diagnosis	Descriptions of cell morphology at diagnosis	Second hit gene mutations at diagnosis	High DD or low Fib (yes/no)	Sensitivity to		Induction chemotherapies		HSCT donor/status on transplant	MCR after HSCT (yes/no)	Outcome (period)	Ref
						ATRA	ATO	1st regimen/result	Number of ICs until CR				
1	10/M	47, XY, del(7)(q23q34), +8, del(11)(p13p15), add(12)(p11.2) [15]/46, XY [5]	PMs, hypergranular, invaginated nuclei	*WT1*	Yes	R	R	IA/failure	2	Twin/CR	Yes	Alive (8 Mo)	8
2	18/M	Normal karyotype	PMs, hypergranular, invaginated nuclei	*RUNX1*	(NA)	R	R	Dox-A/failure	2	(NA)	(NA)	Dead (> 6 Mo)	9
3	22/M	Normal karyotype	PMs	*WT1*	(NA)	R	R	HAA/failure	3	(Planned)	(NA)	Alive (no data)	10
4	32/M	46, XY, add(1)(p22), ?del(9)(p22), t(11;12)(p15;q13), inc [cp18]/46, XY [2]	PMs, Auer rods	*WT1*	Yes	R	R	IA/failure	4	Uncertain donor/CR	< 0.1%	Alive (> 24 Mo)	11
5	35/M	t(11;12)(p15;q13) [16/20]	Atypical PMs, hypergranular, Auer rods, invaginated nuclei	(NA)	Yes	(U)	(NA)	IA/CR	1	Cord blood/CR	(NA)	Dead (> 2 Y)	7, 17
6	39/F	46, XX, t(11;12)(p15;q13), t(15;21)(q11.1;q21) [20]	Abnormal PMs	(NA)	Yes	(NA)	(NA)	HCAG/CR	1	rHID/CR	Yes	Alive (> 20 Mo)	12
7	45/F	t(11;12)(p15;q13) [6]/46, XX [4]	PMs, hypergranular, invaginated nuclei, Auer rods	*WT1*	yes	R	R	AA/death	-	(NA)	(NA)	Dead (35D)	13

Table 2 (continued)

Case no	Age/sex	Description of karyotype at diagnosis	Descriptions of cell morphology at diagnosis	Second hit gene mutations at diagnosis	High DD or low Fib (yes/no)	Sensitivity to		Induction chemotherapies		HSCT donor/status on transplant	MCR after HSCT (yes/no)	Outcome (period)	Ref
						ATRA	ATO	1st regimen/result	Number of ICs until CR				
8	47/F	45, X,-X,del(9)(q13q22), t(11;12)(p15;q13)[20/20]	Abnormal PMs, hypergranular, Auer rods, invaginated nuclei	*IDH2*, *TET2*, *ASXL1*, *TP53*, *WT1*	yes	R	R	IA/failure	2	(NA)	(NA)	Alive (24 Mo)	18
9	53/M	46, XX, t(11;12)(p15,q13) [5]	PMs, hypergranular, no Auer rods, round/quasi-circular/irregular nuclei	*WT1*, *SPEN*, *ARID1B*	yes	R	R	(NA)		(NA)	(NA)	Dead (21 D)	19
10	64/F	46, XX, t(11;12)(p15;q13) [19]/46, XX [2]	Abnormal PMs, Auer rods	*WT1*, *NRAS*	yes	R	R	IA/death	–	(NA)	(NA)	Dead (IC day 2)	11
our case	44/F	46, XX, t(11;12)(p15;q13) [10]/47,idem, mar1 [3]/46, XX [7]	PMs, hypergranular, Auer rods, invaginated or roughly lobated nuclei	*TP53* (SNP)	yes	R	(NA)	IA/CR	1	rHID/non-CR	Yes	Dead (18 Mo)	

M male, *F* female, *PMs* promyelocytes, *NA* not administered, *SNP*: single nucleotide polymorphism, *DD* D-dimer, *Fib* fibrinogen, *ATRA* all-trans retinoic acid, *ATO* arsenic trioxide, *R* resistance, *U* unevaluable, *IC* induction chemotherapy, IA Idarubicin + Cytarabine, *Dox-A* Doxorubicin + Cytarabine, *HAA* Homoharringtonine + Aclarubicin + Cytarabine, *HCAG* Homoharringtonine + Cytarabine + Aclarubicin + granulocyte colony-stimulating factor, *AA* Aclarubicin + Cytarabine, *HSCT* Hematopoietic stem cell transplant, *CR* complete remission, *MCR* molecular CR, *rHID* related haploidentical donor, *Mo* months, *Y* years, *D* days, *Ref.* reference

negative for MRD again (day 399). Unfortunately, second relapse occurred in 34.8% of the marrow blasts (day 483). Although the tumor cells in her peripheral blood disappeared after two cycles of gemtuzumab ozogamicin followed by donor lymphocyte infusion, she eventually died from GVHD and veno-occlusive disease on day 565.

From the initial diagnosis to day 245, we evaluated the presence of residual disease in the BM after each round of chemotherapy using different modalities: the microscopic leukemic cell count, a chromosomal analysis by the G-band method, FISH analysis targeting the *NUP98* split signal, and RT-PCR for *WT1* mRNA and *NUP98::RARG* mRNA (Table 1). Molecular relapse with *NUP98::RARG* mRNA was confirmed at an earlier time than the elevation of *WT1* mRNA and cytogenetic relapse by the G-band analysis. The FISH analysis did not detect any residual disease at any point.

Discussion

To the best of our knowledge, this is the first reported case of AML with *NUP98::RARG* rearrangement in Japan. In addition, the present case enables RT-PCR of *NUP98::RARG* mRNA as a contractual clinical test for the first time in Japan.

Eleven cases of AML with *NUP98::RARG* gene rearrangement, including ours, are summarized in Table 2. Karyotype is not necessarily a simple t(11;12)(p15;q13); some have additional chromosomal abnormalities, and others exhibit a normal karyotype. Their cell morphology was almost the same as that of M3 in the FAB classification. Analyses to detect second-hit mutations were performed in nine patients at the time of their diagnosis, and all had one or more mutations. *WT1* mutations were the most common (6 cases). Fibrinogen and D-dimer aberrations were observed at a high rate. Neither ATRA nor arsenic trioxide (ATO) was effective in all administered patients. Induction chemotherapy was performed in all but one of the patients (Case 9). Only three patients, including our patient, achieved a CR after the 1st induction chemotherapy. Eight patients eventually achieved a CR. HSCT was selected in five cases, including ours. To the best of our knowledge, our case is the first to achieve molecular remission after haploidentical HSCT in non-remission state. Five patients died during follow-up. This outcome may be poorer than that of classic APL.

In our case, although the classic combination chemotherapy resulted in a molecular CR, subclinical relapse occurred during consolidation chemotherapy. A detailed check of the residual disease revealed that the qualitative RT-PCR analysis for *NUP98::RARG* mRNA would be more sensitive than other modalities for the evaluation of molecular relapse. We can then choose an appropriate treatment strategy for AML with *NUP98::RARG* rearrangement, which is not specific to APL, and should monitor MRD using RT-PCR analysis of *NUP98::RARG* mRNA.

Zhu et al. [6] summarized a study cohort of 34 AMLs with *RARG*-fused gene. The reported partner genes of *RARG* were *CPSF6* ($n=14$), *NUP98* ($n=11$), *HNRNPc* ($n=6$), *HNRNPm* ($n=1$), *PML* ($n=1$), and *NPM1* ($n=1$). Although their morphologies resemble classic APL, their sensitivities to ATRA are completely different. Sixteen patients received treatment with doublet ATRA + ATO for ≥ 14 days, and none of them exhibited effectiveness. Therefore, the consensus that AMLs with *RARG* rearrangements are resistant to ATRA and ATO is currently acceptable at the present time.

According to several studies on hematological malignancy with *NUP98*-fusion genes, patients tend to have some second-hit mutations at the diagnosis, and mutations in *FLT3*-ITD and *WT1* genes are seen at high rates [1, 16]. A recent study of AMLs with any type of *RARG* rearrangement revealed that *WT1* mutations were the most frequent (14 of 24 genetically analyzed patients), but no *FLT3*-ITD mutations were detected at the diagnosis [6]. As for AMLs with *NUP98::RARG* rearrangement (Table 2), *WT1* mutations were frequent, but *FLT3*-ITD mutations were not observed.

Our patient had no detectable somatic second-hit mutations, but she did have a heterozygous SNP in *TP53* (c.920-5C > T). According to the gnomAD database v4.1.0, it is almost exclusively seen in East Asians with an allele frequency of (0.0005351 https://gnomad.broadinstitute.org/variant/17-7673613-G-A?dataset=gnomad_r4). Its clinical significance has been described as benign, likely benign, or uncertain in the ClinVar archive (https://www.ncbi.nlm.nih.gov/clinvar/variation/185487/).

However, no functional analyses of the SNP have been performed to date. Moreover, 9 of the 11 cases shown in Table 2 are from East Asia (China: cases 1–4, 7–10, Japan: our case). It is possible that the SNP is one of the geographic and genetic backgrounds for developing AML with *NUP98::RARG* rearrangement. The accumulation of more cases, including additional information about SNPs, is, therefore, desired.

In conclusion, we strongly suggest that hematologists should recognize the existence of non *RARA*-associated AMLs that closely mimic classic APL, especially in cases of ATRA resistance. In such cases, RT-PCR to detect *NUP98::RARG* mRNA should be considered to make a diagnosis and determine the treatment strategy. The accumulation of AML cases with *NUP98::RARG* rearrangement, which shows a poor prognosis, is desired to establish an optimal treatment strategy.

Funding This study was approved by the Institutional Review Boards of Asahikawa Kosei Hospital and Asahikawa Medical University Hospital.

Declarations

Conflict of interest The authors declare no conflicts of interest in association with the present study.

References

1. Michmerhuizen NL, Klco JM, Mullighan CG. Mechanistic insights and potential therapeutic approaches for NUP98-rearranged hematologic malignancies. Blood. 2020;136(20):2275–89.
2. Mohanty S. NUP98 Rearrangements in AML: molecular mechanisms and clinical implications. Onco. 2023;3:147–64.
3. Qiu JJ, Zeisig BB, Li S, Liu W, Chu H, Song Y, et al. Critical role of retinoid/rexinoid signaling in mediating transformation and therapeutic response of NUP98-RARG leukemia. Leukemia. 2015;29:1153–62.
4. Kasper LH, Brindle PK, Schnabel CA, Pritchard CE, Cleary ML, van Deursen JM. CREB binding protein interacts with nucleoporin-specific FG repeats that activate transcription and mediate NUP98-HOXA9 oncogenicity. Mol Cell Biol. 1999;19(1):764–76.
5. di Masi A, Leboffe L, De Marinis E, Pagano F, Cicconi L, Rochette-Egly C, et al. Retinoic acid receptors: from molecular mechanisms to cancer therapy. Mol Aspects Med. 2015;41:1–115.
6. Zhu H-H, Qin Y-Z, Zhang Z-L, Liu Y-J, Li-Jun Wen M, You J, et al. A global study for acute myeloid leukemia with RARG rearrangement. Blood Adv. 2023. https://doi.org/10.1182/bloodadvances.2022008364.
7. Such E, Cervera J, Valencia A, Barragán E, Ibañez M, Luna I, et al. A novel NUP98/RARG gene fusion in acute myeloid leukemia resembling acute promyelocytic leukemia. Blood. 2011;117(1):242–5.
8. Zhang J, Shen H, Song H, Shen D, Liao C, Fang M, et al. A Novel NUP98/RARG gene fusion in pediatric acute myeloid leukemia resembling acute promyelocytic leukemia. J Pediatr Hematol Oncol. 2022;44(3):e665–71.
9. Wei W, Liu Q, Song F, Cao He, Liu M, Jiang Y, et al. Alkaloid-based regimen is beneficial for acute myeloid leukemia resembling acute promyelocytic leukemia with NUP98/RARG fusion and RUNX1 mutation: a case report. Medicine. 2020;99(40): e22488.
10. Zhang X, Li F, Wang J, Suo S, Ling Q, Wenjuan Yu, et al. RARg-rearrangements resemble acute promyelocytic leukemia and benefit from 3 + 7 regimen. Leuk Lymphoma. 2019;60(7):1831–4.
11. Wang M, Lin H, Chu X, Wang Z, Yang X, Cen J, et al. Identification of a recurrent fusion NUP98-RARG in acute myeloid leukaemia resembling acute promyelocytic leukaemia. Br J Haematol. 2022;197(6):e73–8.
12. Yuan J, Pei R, Ying Lu. Successful haploidentical hematopoietic stem cell transplantation with azacitidine and venetoclax maintenance therapy for acute myeloid leukemia with NUP98-RARG gene fusion. Turk J Haematol. 2023;40(1):75–6.
13. Luo H, Zhang S, Li Ke, Chen X-H, Li Y-C, Sun Y, et al. A novel entity of acute myeloid leukaemia with recurrent RARG-rearrangement resembling acute promyelocytic leukaemia. Leuk Res. 2019;77:14–6.
14. Ohtake S, Miyawaki S, Fujita H, Kiyoi H, Shinagawa K, Usui N, et al. Randomized study of induction therapy comparing standard-dose idarubicin with high-dose daunorubicin in adult patients with previously untreated acute myeloid leukemia: the JALSG AML201 Study. Blood. 2011;117(8):2358–65.
15. Sugita J, Kagaya Y, Miyamoto T, Shibasaki Y, Nagafuji K, Ota S, et al. Myeloablative and reduced-intensity conditioning in HLA-haploidentical peripheral blood stem cell transplantation using post-transplant cyclophosphamide. Bone Marrow Transplant. 2019;54(3):432–41.
16. Taketani T, Taki T, Nakamura T, Kobayashi Y, Ito E, Fukuda S, et al. High frequencies of simultaneous FLT3-ITD, WT1 and KIT mutations in hematological malignancies with NUP98-fusion genes. Leukemia. 2010;24(11):1975–7.
17. Such E, Cordón L, Sempere A, Villamón E, Ibañez M, Luna I, et al. In vitro all-trans retinoic acid sensitivity of acute myeloid leukemia blasts with NUP98/RARG fusion gene. Ann Hematol. 2014;93(11):1931–3.
18. Tao S, Song L, Deng Y, Chen Y, Shi Y, Gan Y, et al. Acute myeloid leukemia with NUP98-RARG gene fusion similar to acute promyelocytic leukemia: case report and literature review. Onco Targets Ther. 2020;13:10559–66.
19. Danyang Wu, Gao R. Acute myeloid leukemia with NUP98::RARG resembles acute promyelocytic leukemia accompanied by an ARID1B gene mutation. Hematology. 2023;28(1):2227495.