



## Acute myeloid leukemia with a cryptic *NUP98/PRRX2* rearrangement developing after low-dose methotrexate therapy for rheumatoid arthritis

Kazuhisa Chonabayashi<sup>1,2</sup> · Yoshinori Yoshida<sup>2</sup> · Toshio Kitawaki<sup>1</sup> · Yasuhito Nannya<sup>3</sup> · Momoko Nakamura<sup>1</sup> · Shinichiro Oshima<sup>1</sup> · Masakatsu Hishizawa<sup>1</sup> · Kouhei Yamashita<sup>1</sup> · Seishi Ogawa<sup>3</sup> · Akifumi Takaori-Kondo<sup>1</sup>

Received: 25 September 2019 / Accepted: 28 October 2019 / Published online: 14 November 2019  
© Springer-Verlag GmbH Germany, part of Springer Nature 2019

Dear Editor,

*NUP98* is known to be fused to at least 31 different partner genes in both de novo and therapy-related leukemia [1]. Chromosomal translocations juxtaposing the class II homeobox gene *PRRX2* with *NUP98* loci have been reported in therapy-related acute myeloid leukemia (AML), but their clinical significance is unclear [2, 3]. Here, we report a case of AML harboring a cryptic *NUP98/PRRX2* translocation following low-dose methotrexate (MTX) therapy for rheumatoid arthritis.

A 72-year-old Japanese woman presented with anemia, thrombocytopenia, elevated WBC counts, and the appearance of blasts in the peripheral blood. The patient had been diagnosed with rheumatoid arthritis and was subsequently treated with low-dose MTX. The duration of the MTX therapy was 221 months and the accumulated dose was approximately 5000 mg. Bone marrow examination disclosed 55.6% blasts, most of which were positive for myeloperoxidase and specific esterase; the immunophenotype was CD13<sup>+</sup>, CD33<sup>+</sup>, MPO<sup>+</sup>, and partially positive for CD4, CD16, CD34, CD64, and HLA-DR. Bilineage dysplastic changes (dysgranulopoiesis and dyserythropoiesis) were observed in the bone marrow

specimens. Based on these findings, acute myeloid leukemia with myelodysplasia-related changes was diagnosed. The patient showed *FLT3-ITD*, *RUNX1*, and *WT1* mutations (Table 1). A *FLT3* internal tandem duplication mutation was detected by PCR. Although both G-banding and multicolor fluorescence in situ hybridization (FISH) analyses of the bone marrow cells showed a normal karyotype, a *NUP98* disruption was detected in 95.1% of the cells by break-apart FISH analysis (Fig. 1a–c). FISH analysis using the *NUP98* break-apart probes, the subtelomere probes of chromosome 9, and the centromere probes of chromosome 9 and 11 revealed a hidden reciprocal translocation involving 9q and 11p15 (*NUP98*) (Fig. 1d, e). Reverse transcription-PCR and subsequent sequencing analyses allowed for detection of the *NUP98/PRRX2* fusion transcript with the same breakpoint as the previously reported case (Fig. 1f, g) [2]. Although the patient achieved hematological remission following standard induction and consolidation chemotherapy, her AML relapsed 2 months later. At the time of submission of this report, the patient was alive and receiving gilteritinib following anthracycline chemotherapy.

*NUP98/PRRX2*-positive hematological malignancies are rare and there have been only two other reported cases (Table 1). Both patients developed therapy-related AML after chemotherapy with topoisomerase II inhibitors or alkylating agents against antecedent malignancies. Our patient had no history of malignancy and chemotherapy. There have been some reports of AML development in rheumatoid arthritis patients treated with MTX, although it remains unclear whether low-dose MTX therapy may serve a role in pathogenesis of AML [4, 5]. In the present case, long-term MTX therapy for rheumatoid arthritis could be causally associated with the development of AML. *NUP98* fusions have been reported to be associated

✉ Kazuhisa Chonabayashi  
kchona@kuhp.kyoto-u.ac.jp

<sup>1</sup> Department of Hematology and Oncology, Graduate School of Medicine, Kyoto University, 54 Shogoin-Kawahara-cho, Sakyo-ku, Kyoto 606-8507, Japan

<sup>2</sup> Department of Cell Growth and Differentiation, Center for iPS Cell Research and Application, Kyoto University, Kyoto, Japan

<sup>3</sup> Department of Pathology and Tumor Biology, Graduate School of Medicine, Kyoto University, Kyoto, Japan

**Table 1** Summary of published cases of *NUP98/PRRX2*-related neoplasm

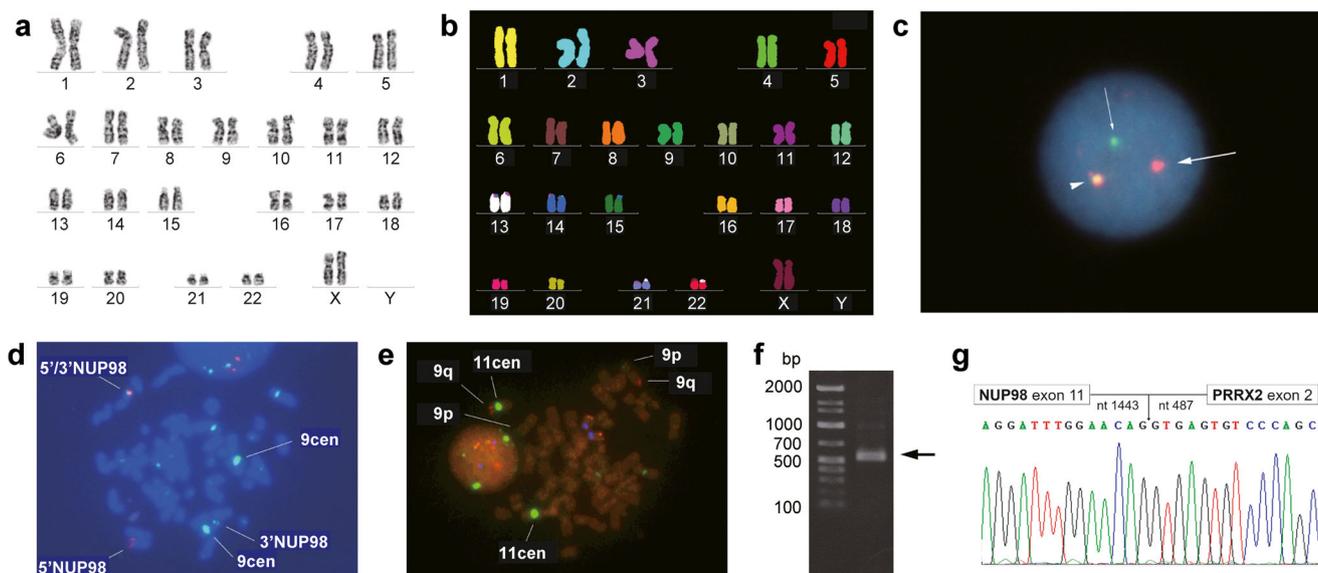
Case number	Age/sex	ATCD	Treatment	Diagnosis	Karyotype	FISH ( <i>PRRX2</i> )	RT-PCR	Molecular mutation	Clinical course
1	65/F	DLBCL	TOPOII, ALK	Therapy-related AML	46,XX,der(9)(q34),der(11)(p15) [8]/46,XX [15]	NA	<i>NUP98</i> exon 11- <i>PRRX2</i> exon 2	NA	NA
2	45/M	PV	ALK	Therapy-related AML	47,XY,der(5)t(5;11)(q35;q13),add(11)(p15),+mar1 [5]/48,idem,+mar2 [10]	Positive	NA	NA	NA
3	72/F	RA	Low-dose MTX	AML-MRC	46,XX [20]	NA	<i>NUP98</i> exon 11- <i>PRRX2</i> exon 2	<i>FLT3-ITD</i> (AR:0.8), <i>RUNX1</i> _S141L, <i>WT1</i> _S364fs	Complete response after intensive chemotherapy but relapse within 2 months

Case 1: Gervais et al. [2]; Case 2: Romana et al. [3]; Case 3: this study

ATCD, antecedent; DLBCL, diffuse large B cell lymphoma; PV, polycythemia vera; RA, rheumatoid arthritis; TOPOII, topoisomerase II inhibitor; ALK, alkylating agent; MTX, methotrexate; AML-MRC, acute myeloid leukemia with myelodysplasia-related changes; NA, not available; AR, allelic ratio

with an unfavorable clinical outcome [1, 6, 7]. However, some *NUP98* chromosomal rearrangements are not detected in the karyotype due to subtelomeric localization of the breakpoints [6, 8, 9]. The present study shows that the

*NUP98* and *PRRX2* translocation may also result from a cryptic chromosomal rearrangement and should be considered even in AML cases with an apparently normal karyotype. Although more cases are needed, adverse clinical



**Fig. 1** Identification of *NUP98/PRRX2* fusion transcripts. **a**, **b** G-banding (**a**) and multicolor FISH (**b**) analyses of the bone marrow cells showed a normal 46, XX karyotype. **c** *NUP98* break-apart FISH analysis showed split red (*NUP98* 5' region) and green (*NUP98* 3' region) signals in 95.1% of the bone marrow cells. **d** FISH analysis using the *NUP98* break-apart probes and the centromere probe of chromosome 9 (green) revealed split a *NUP98* 3' region (green) signal on 9q. **e** FISH analysis using the subtelomere probes of chromosome 9 and the centromere probe of

chromosome 11 (green) revealed 9q probe (red) signal on 11p. **f** 542-bp *NUP98/PRRX2* fusion transcript product (arrow) was obtained at the expected size from the bone marrow sample by reverse transcription-PCR analysis using *NUP98* sense and *PRRX2* antisense primers. **g** Sequencing analysis confirmed that the band was an in-frame fusion between exon 11 of *NUP98* (including up to nt 1443 of GenBank Accession NM\_016320) and exon 2 of *PRRX2* (beginning at nt 487 of GenBank Accession NM\_016307).

outcome in this patient might indicate a potentially poor prognostic role of *NUP98/PRRX2* in AML.

**Funding information** This work was supported by grants from the Project for Cancer Research and Therapeutic Evolution (P-CREATE) (19cm0106235h0002) and the Acceleration Program for Intractable Diseases Research utilizing Disease-specific iPS cells (19bm0804004h0003) of the Japan Agency for Medical Research and Development.

### Compliance with ethical standards

**Conflict of interest** The authors declare that they have no conflict of interest.

**Ethical approval** This article does not contain any studies with human participants or animals performed by any of the authors.

**Informed consent** Informed consent was obtained from the patient included in the study.

### References

1. Struski S, Lagarde S, Bories P, Puisieux C, Prade N, Cuccuini W, Pages MP, Bidet A, Gervais C, Lafage-Pochitaloff M, Roche-Lestienne C, Barin C, Penther D, Nadal N, Radford-Weiss I, Collonge-Rame MA, Gaillard B, Mugneret F, Lefebvre C, Bart-Delabesse E, Petit A, Leverger G, Broccardo C, Luquet I, Pasquet M, Delabesse E (2017) NUP98 is rearranged in 3.8% of pediatric AML forming a clinical and molecular homogenous group with a poor prognosis. *Leukemia* 31(3):565–572. <https://doi.org/10.1038/leu.2016.267>
2. Gervais C, Mauvieux L, Perrusson N, Helias C, Struski S, Leymarie V, Lioure B, Lessard M (2005) 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* 19(1):145–148. <https://doi.org/10.1038/sj.leu.2403565>
3. Romana SP, Radford-Weiss I, Ben Abdelali R, Schluth C, Petit A, Dastugue N, Talmant P, Bilhou-Nabera C, Mugneret F, Lafage-Pochitaloff M, Mozziconacci MJ, Andrieu J, Lai JL, Terre C, Rack K, Cornillet-Lefebvre P, Luquet I, Nadal N, Nguyen-Khac F, Perot C, Van den Akker J, Fert-Ferrer S, Cabrol C, Charrin C, Tigaud I, Poirel H, Vekemans M, Bernard OA, Berger R, Groupe Francophone de Cytogenetique H (2006) NUP98 rearrangements in hematopoietic malignancies: a study of the Groupe Francophone de Cytogenetique Hematologique. *Leukemia* 20(4):696–706. <https://doi.org/10.1038/sj.leu.2404130>
4. Pointud P, Prudat M, Peron JM (1993) Acute leukemia after low dose methotrexate therapy in a patient with rheumatoid arthritis. *J Rheumatol* 20(7):1215–1216
5. Tanaka K, Oshikawa G, Akiyama H, Ishida S, Nagao T, Yamamoto M, Miura O (2017) Acute myeloid leukemia with t(3;21)(q26.2;q22) developing following low-dose methotrexate therapy for rheumatoid arthritis and expressing two AML1/MDS1/EVI1 fusion proteins: A case report. *Oncol Lett* 14(1):97–102. <https://doi.org/10.3892/ol.2017.6151>
6. Hollink IH, van den Heuvel-Eibrink MM, Arentsen-Peters ST, Pratorcorona M, Abbas S, Kuipers JE, van Galen JF, Beverloo HB, Sonneveld E, Kaspers GJ, Trka J, Baruchel A, Zimmermann M, Creutzig U, Reinhardt D, Pieters R, Valk PJ, Zwaan CM (2011) NUP98/NSD1 characterizes a novel poor prognostic group in acute myeloid leukemia with a distinct HOX gene expression pattern. *Blood* 118(13):3645–3656. <https://doi.org/10.1182/blood-2011-04-346643>
7. Ostronoff F, Othus M, Gerbing RB, Loken MR, Raimondi SC, Hirsch BA, Lange BJ, Petersdorf S, Radich J, Appelbaum FR, Gamis AS, Alonzo TA, Meshinchi S (2014) NUP98/NSD1 and FLT3/ITD coexpression is more prevalent in younger AML patients and leads to induction failure: a COG and SWOG report. *Blood* 124(15):2400–2407. <https://doi.org/10.1182/blood-2014-04-570929>
8. Reader JC, Meekins JS, Gojo I, Ning Y (2007) A novel NUP98-PHF23 fusion resulting from a cryptic translocation t(11;17)(p15;p13) in acute myeloid leukemia. *Leukemia* 21(4):842–844. <https://doi.org/10.1038/sj.leu.2404579>
9. de Rooij JD, Hollink IH, Arentsen-Peters ST, van Galen JF, Berna Beverloo H, Baruchel A, Trka J, Reinhardt D, Sonneveld E, Zimmermann M, Alonzo TA, Pieters R, Meshinchi S, van den Heuvel-Eibrink MM, Zwaan CM (2013) NUP98/JARID1A is a novel recurrent abnormality in pediatric acute megakaryoblastic leukemia with a distinct HOX gene expression pattern. *Leukemia* 27(12):2280–2288. <https://doi.org/10.1038/leu.2013.87>

**Publisher's note** Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.