

RESEARCH

Open Access



Two rare cases of acute myeloid leukemia with t(8;16)(p11.2;p13.3) and 1q duplication: case presentation and literature review

Meng Liu^{1,2}, Yuan Ren^{1,2}, Xianfu Wang², Xianglan Lu², Ming Li^{2,3}, Young Mi Kim², Shibo Li² and Lijun Zhang^{1*} 

Abstract

Background: Acute myeloid leukemia (AML) is a complex hematological disease characterized by genetic and clinical heterogeneity. The identification and understanding of chromosomal abnormalities are important for the diagnosis and management of AML patients. Compared with recurrent chromosomal translocations in AML, t(8;16)(p11.2;p13.3) can be found in any age group but is very rare and typically associated with poor prognosis.

Methods: Conventional cytogenetic studies were performed among 1,824 AML patients recorded in our oncology database over the last 20 years. Fluorescence in situ hybridization (FISH) was carried out to detect the translocation fusion. Array comparative genome hybridization (aCGH) was carried out to further characterize the duplication of chromosomes.

Results: We identified three AML patients with t(8;16)(p11.2;p13.3) by chromosome analysis. Two of the three patients, who harbored an additional 1q duplication, were detected by FISH and aCGH. aCGH characterized a 46.7 Mb and 49.9 Mb gain in chromosome 1 at band q32.1q44 separately in these two patients. One patient achieved complete remission (CR) but relapsed 3 months later. The other patient never experienced CR and died 2 years after diagnosis.

Conclusion: A 1q duplication was detected in two of three AML patients with t(8;16)(p11.2;p13.3), suggesting that 1q duplication can be a recurrent event in AML patients with t(8;16). In concert with the findings of previous studies on similar patients, our work suggests that 1q duplication may also be an unfavorable prognostic factor of the disease.

Keywords: 1q duplication, Acute myeloid leukemia, t(8;16)(p11.2;p13.3), Prognostic factor

Background

Acute myeloid leukemia (AML) is a common disease characterized by immature myeloid cell proliferation and bone marrow failure, which can be subdivided into 9–11 pathogenetically different subtypes [1]. Over the past two decades, the incidence has increased by 30% [2, 3]. Furthermore, AML has poor long-term survival with a

high relapse rate [4]. Therefore, AML represents a substantial health problem that requires strict monitoring and innovative treatment strategies. The development of newer, effective treatment strategies is necessary for AML patients.

To date, the detection of cytogenetic abnormalities has been regarded as a critical prognostic tool for AML treatment [5]. Hence, it is urgently necessary to identify chromosomal rearrangements in AML patients and provide the whole spectrum of cytogenetic abnormalities for AML [6]. According to the World Health Organization classification system updated in 2008, AML with recurrent genetic abnormalities including t(8;21)(q22;q22),

*Correspondence: lzhang202003@163.com

¹ Department of Hematology, The First Hospital of China Medical University, 155 Nanjing North Street, Shenyang 110000, Liaoning, People's Republic of China

Full list of author information is available at the end of the article



© The Author(s). 2020 **Open Access** This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <http://creativecommons.org/licenses/by/4.0/>. The Creative Commons Public Domain Dedication waiver (<http://creativecommons.org/publicdomain/zero/1.0/>) applies to the data made available in this article, unless otherwise stated in a credit line to the data.

t(11q23)/*MLL*, t(15;17)(q24;q21), inv(16)(p13.1q22), and t(16;16)(p13.1;q22) has been identified [7, 8]. Non-random chromosomal abnormalities, such as deletions and translocations, have been detected in approximately 52% of all adult AML patients. Moreover, chromosomal abnormalities have been recognized as genetic events that can cause and promote this disease [9]. Certain cytogenetic abnormalities, including t(8;21)(q22;q22), t(15;17)(q24;q21) and inv(16)(p13.1;q22), are associated with longer remission and survival, while alterations of chromosomes 5, 7, 11q23 and complex karyotypes are associated with poor response to therapy and shorter overall survival [10]. Chromosomal translocations such as t(15;17)/*PML-RARA*, t(8;21)/*RUNX1-RUNX1T1*, inv(16)/*CBFB-MYH11* and t(11q23)/*MLL* are usually found in AML patients [11, 12]. However, AML with t(8;16)(p11.2;p13.3)/*KAT6A-CREBBP* is a very rare AML subtype and can be found in any age group, from infancy to the eighth decade of life, with a female predominance [13–17]. A majority of adult patients with t(8;16)(p11.2;p13.3) are therapy related [14–17], and pediatric patients tend to be de novo [13]. There are approximately 160 cases reported in the literature [13–17], and the first t(8;16)(p11.2;p13.3) in an infant was described in 1983 [18]. Some AML patients with t(8;16)(p11.2;p13.3) have a bleeding tendency and disseminated intravascular coagulopathy, which are overlapping clinical features that mimic acute promyelocytic leukemia (APL) [17]. Unlike APL, AML with t(8;16)(p11.2;p13.3) has an unfavorable treatment response and outcome [14, 19]. As a sole chromosomal anomaly, t(8;16)(p11.2;p13.3) is found in more than 50% of reported cases, and one or more additional chromosomal anomalies can be seen in the remaining cases [20]. The most common secondary chromosomal anomalies are total or partial trisomy 8 and monosomy 7 or deletion of the long or short arm of chromosome 7 [13–16, 19]. Comparatively, the gain of 1q in variable sizes has also been frequently noticed in patients with t(8;16)(p11.2;p13.3) in these large studies [13–15, 19].

Recurrent cytogenetic abnormality t(8;16)(p11.2;p13.3) is seldom associated with AML, and the 1q duplication in AML patients with t(8;16)(p11.2;p13.3) has never been discussed. In the present study, a total of 1,824 de novo or treatment-related AML patients were collected from our laboratory oncology database. Among them, three patients were detected with t(8;16)(p11.2;p13.3)/*KAT6A-CREBBP*, and two of these three showed an additional copy of partial chromosome 1q.

Methods

Patients

This study was approved by the Institutional Review Board (IRB) of Oklahoma University (IRB Number:

2250). A total of 1,824 AML patient samples were studied cytogenetically from 2000 to 2019 at the Genetics Laboratory of Oklahoma University Health Sciences Center. Bone marrow samples were obtained from three of the 1,824 patients who had t(8;16)(p11.2;p13.3).

Conventional cytogenetic analysis

Short-term cultures of unstimulated bone marrow samples were established and harvested according to standard laboratory protocols. Karyotype analysis was performed using Giemsa and trypsin techniques for G-banding. The cytogenetic abnormalities were described according to the International System for Human Cytogenetic Nomenclature (ISCN 2016).

Fluorescence in situ hybridization analysis

Fluorescence in situ hybridization (FISH) assays were performed according to the manufacturer's instructions in combination with our established laboratory protocols. A *PML/RARA* dual-color, dual-fusion translocation probe (Abbott Molecular Inc., Des Plaines, IL, USA), subtelomere-specific probes for chromosome 3 p-arm and q-arm, and whole chromosome painting (WCP) probes for chromosomes 1, 3 and 14 were purchased from Cytocell Ltd, NY, USA. A spectrum green-labeled probe mapping to the 8p11.21 region and a spectrum orange-labeled probe mapping to the 16p13.3 region were created in house with the following BAC/PAC clones: RP11-642I24[chr8: 41,676,336-41,856,494(hg19)] and RP11-589C21[chr8: 41,873,702-42,036,222(hg19)], RP11-619A23[chr16: 3,720,076-3,914,571(hg19)] and RP11-95J11[chr16: 3,860,374-4,025,510(hg19)] (Children's Hospital Oakland Research Institute, Oakland, CA, USA). The *KAT6A* gene located on 8p11.21 and the *CREBBP* gene located on 16p13.3 were covered by the green-labeled and red-labeled home-brewed probes, respectively. All probes were validated before use. Chromosome spreads were counterstained with 4,6-diamidino-2-phenylindole (DAPI4) in antifade medium (Vector Laboratories Inc., CA, USA). Digital images carrying specific hybridization signals were captured and processed on CytoVision version 7.0 (Applied Spectral Imaging, Carlsbad, CA, USA).

aCGH analysis

Genomic DNA was extracted from each of the three patients' bone marrow pellets according to the standard operating procedure using the phenol and chloroform method with a commercially available DNA extraction kit (Puregene blood kit, Qiagen, Valencia, CA) or Nucleic Acid Isolation System (QuickGene-610L, FUJIFILM Corporation, Tokyo, Japan). Two aCGH platforms, NimbleGen and Agilent, were used in this study. For the

NimbleGen aCGH platform, human reference genomic DNA was purchased from Promega Corporation (Promega Corporation, Madison, WI, USA). The patient's DNA and the reference DNA were labeled with either Cyanine 3 (Cy-3) or Cyanine 5 (Cy-5) by random priming, and then equal quantities of both labeled products were mixed and loaded onto a 720 K oligonucleotide chip (Roche NimbleGen Inc., Madison, WI, USA) to hybridize at 42 °C for 40 h in a MAUI hybridization system (BioMicro Systems, Salt Lake City, UT) according to the manufacturer's protocols with minor modifications. The slides were washed with washing buffers (Roche NimbleGen Inc.) after hybridization and scanned using a Roche Scanner MS 200 Microarray Scanner (Roche NimbleGen Inc.). Images were analyzed using NimbleScan software version 2.6 and SignalMap software version 1.9 (Roche NimbleGen Inc.). The genomic positions were determined using GRCh36/hg18, UCSC Genome Browser. For the Agilent aCGH platform, human reference genomic DNA was purchased from Agilent Corporation (Agilent Corporation, Santa Clara, CA, USA). The patient's DNA and the purchased reference DNA were labeled with either Cyanine 3 (Cy-3) or Cyanine 5 (Cy-5) by random priming (Agilent Corporation). Patient DNA (labeled with Cy-3) was combined with a normal control DNA sample (labeled with Cy-5) of the same sex and hybridized to an Agilent 2 × 400 K oligo microarray chip (Agilent Technologies) by incubating in an Agilent Microarray Hybridization Oven (Agilent Technologies). After 40 h of hybridization at 67 °C, the slides were washed and scanned using the NimbleGen MS 200 Microarray Scanner (Roche NimbleGen Inc.). Agilent's CytoGenomics 2.7 software (Agilent Technologies.) was applied for data analysis. The genomic positions were determined using GRCh37/hg19, UCSC Genome Browser.

Case presentation

Case 1 An 82-year-old male presented with anemia was referred to us for AML evaluation. His subsequent lab results and hospital records were not available in our clinical database.

Case 2 A 28-year-old female presented with disseminated intravascular coagulopathy was referred to rule out APL. Her complete blood examination and bone marrow aspirate smears were not available. Flow cytometry revealed 57% monocytic cells positive for CD4, CD11b (partial), CD13 (bright), CD14 (partial), CD15, CD33 (bright) and HLA-DR (partial) but negative for CD3, CD7, CD34, CD117, MPO and TdT, consistent with a diagnosis of AML with monocytic differentiation (subtype M5). The patient achieved hematological CR on day

15 and cytogenetic CR on day 33 after induction chemotherapy and then relapsed 3 months later.

Case 3 A 69-year-old female with a medical history of breast cancer after lumpectomy, chemotherapy, and radiation presenting with generalized weakness, pancytopenia, and fever was referred to us for disease progression evaluation. A complete blood examination showed a white blood cell count of $216 \times 10^9/L$ with 53% blasts, a hemoglobin count of 66 g/L and a platelet count of $31 \times 10^9/L$. Her bone marrow aspirate smear demonstrated over 90% myeloblasts. Flow cytometry revealed that 69% of the blast cells expressed CD45 (moderate), CD34 (dim), CD38, HLA-DR, CD13, CD15, and CD33 and were negative for CD117, consistent with a diagnosis of AML with monocytic differentiation (subtype M5). The patient started consolidation chemotherapy but had spontaneous regression and died 2 years after AML diagnosis.

Results

In case 1, routine chromosome analysis detected an abnormal karyotype with a translocation between the short arms of chromosomes 8 and 16 (Fig. 1a) in 17 of 20 cells, consistent with a diagnosis of AML with t(8;16)(p11.2;p13.3). The nomenclature of the cytogenetic findings in patient 1 was t(8;16)(p11.2;p13.3)[17]/46,XY[3]. No other consistent karyotypic aberrations were detected. Thus, this male patient was excluded from subsequent FISH and aCGH analyses.

In case 2, chromosome analysis demonstrated the same chromosome rearrangement between 8 and 16 in all 20 cells. Besides, 11 of these cells showed an extra chromosome segment attached to chromosome 14 (Fig. 1b). The karyotypes in patient 2 were described as 46,XX,t(8;16)(p11.2;p13.3), add(14)(p11.2)[11]/46,XY[9]. Negative FISH results for t(15;17)(q24;q21)/PML-RARA further ruled out a diagnosis of APL (data not shown). Metaphase FISH analysis confirmed the t(8;16)(p11.2;p13.3)/KAT6A-CREBBP fusion and demonstrated a part of chromosome 1 on chromosome 14 (Fig. 2a and b). In addition to characterizing the extrachromosomal 1 material, aCGH was carried out. aCGH confirmed the FISH findings and detected a 46.7 Mb gain from chromosome 1 at bands q32.1q44 (201,304,064-248,102,389 bp, GRCh36/hg18, UCSC Genome Browser) (Fig. 3a).

In case 3, t(8;16)(p11.2;p13.3) with a gain of a similar chromosome segment on the long arm of chromosome 3 was detected in 18 of 20 cells by karyotyping analysis (Fig. 1c). FISH confirmed the KAT6A-CREBBP fusion and revealed additional chromosome 1 material (Fig. 2c and d). Loss of the end portion of the chromosome 3 long arm was not found by FISH (Fig. 3e). aCGH further detected a gain from chromosome 1 at bands 1q32.1q44



a Patient 1



b Patient 2

Fig. 1 Representative abnormal karyotypes of three patients with t(8;16)(p11.2;p13.3). **a** Karyotype of patient 1 showing 46,XY,t(8;16)(p11.2;p13.3) as the sole abnormality; **b** and **c** Karyotypes of patients 2 and 3 showing 46,XX,t(8;16)(p11.2;p13.3) and an additional chromosome segment attached to the short arm of chromosome 14 and the long arm of chromosome 3, respectively. Translocated derivatives 8 and 16 are indicated by black arrows, and derivatives 14 and 3 are indicated by red arrows



(201,408,592-251,323,872 bp, GRCh37/hg19, UCSC Genome Browser) (Fig. 3b). The molecular size was 49.9 Mb.

Discussion

AML is one of the most common diseases characterized by the proliferation of blast cells in bone marrow or peripheral blood, which accounts for approximately 30% of adult leukemia cases. As reported previously, common chromosomal translocations such as $t(8;21)/RUNX1-RUNX1T1$, $t(15;17)/PML-RARA$, and $inv(16)/CBFB-MYH11$ are frequently observed, and numerous uncommon chromosomal aberrations also exist in AML [12]. The detection of these fusion transcripts is important for the diagnosis and progression monitoring of AML patients [21].

In previous large studies, approximately 160 AML cases with $t(8;16)(p11.2;p13.3)$ have been reported [13–20]. Among them, 9 cases showed a gain by 1q of variable sizes [13–15, 19]. As an uncommon entity, $t(8;16)$ accounts for 0.2–0.4% of all cases of AML [13–20]. In our study, three patients with $t(8;16)(p11.2;p13.3)$ were identified: one man and two women. The two women were

both diagnosed with AML (subtype M5) and showed an extra copy of 1q at the same bands (q32.1q44), which were different from the nine reported cases above. The clinical features and cytogenetic data of the 11 cases of AML with $t(8;16)(p11.2;p13.3)$ and 1q duplications are summarized in Table 1. To the best of our knowledge, this is the first study of the delineation of 1q duplication by aCGH in AML patients with $t(8;16)(p11.2;p13.3)$.

AML patients with this abnormality often show unique clinical and biological characteristics [22]. Compared with the current categories $t(15;17)$, $t(8;21)$, $inv(16)$, and $t(11q23)$ in AML, $t(8;16)$ is clustered closer to $t(11q23)$ and shares commonly expressed genes [15]. Xie et al. reported 15 adult AML cases with $t(8;16)(p11.2;p13.3)$, indicating that $t(8;16)(p11.2;p13.3)$ commonly exhibits monoblastic or myelomonocytic differentiation and arises in patients with a history of cytotoxic-treated cancer. Patients with de novo AML with $t(8;16)$ or treatment-related AML with $t(8;16)$ without adverse prognostic factors have a good outcome [14]. Identifying adverse prognostic factors is of importance to the choice of therapy and evaluation of survival in AML patients with $t(8;16)$.

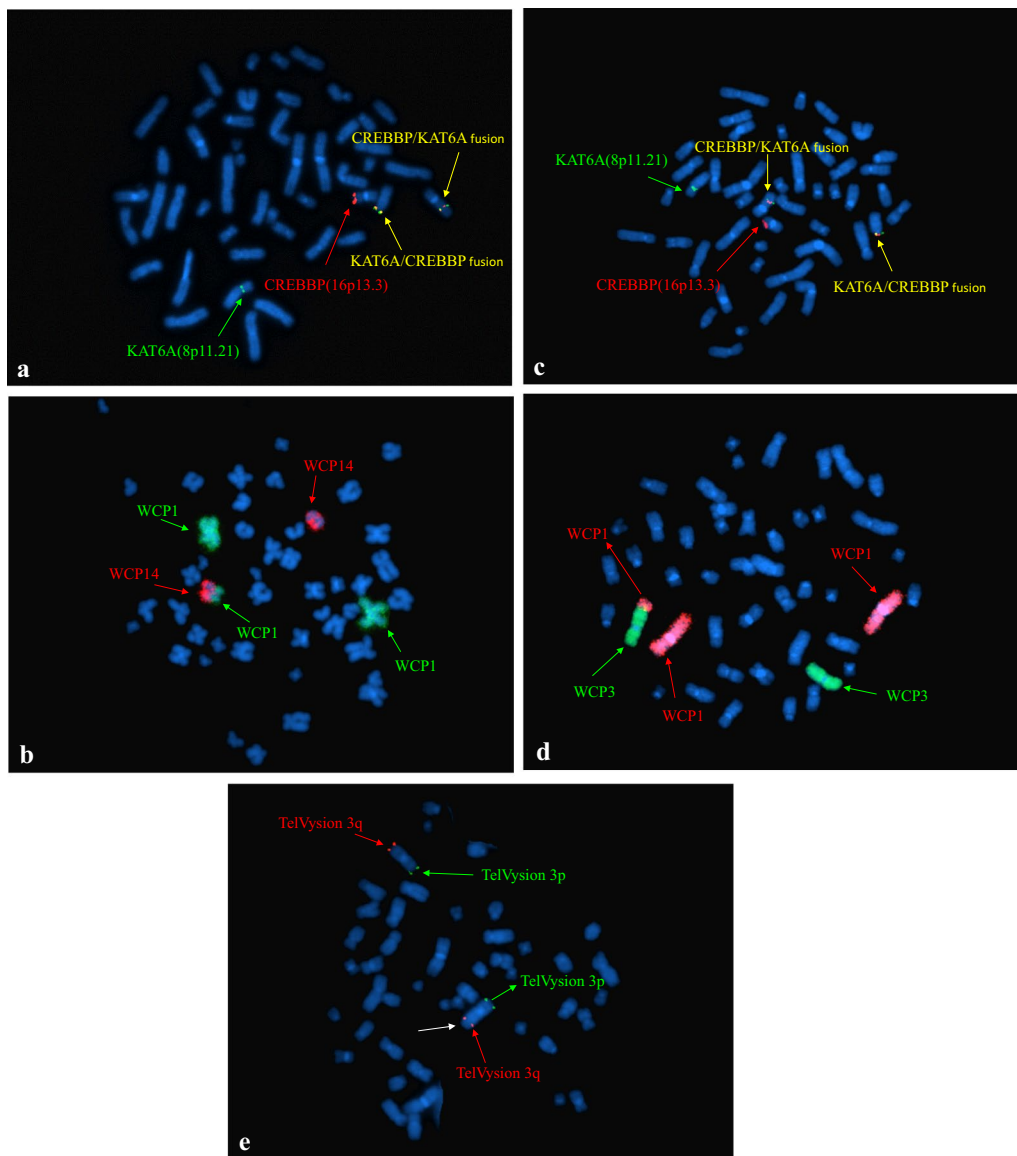
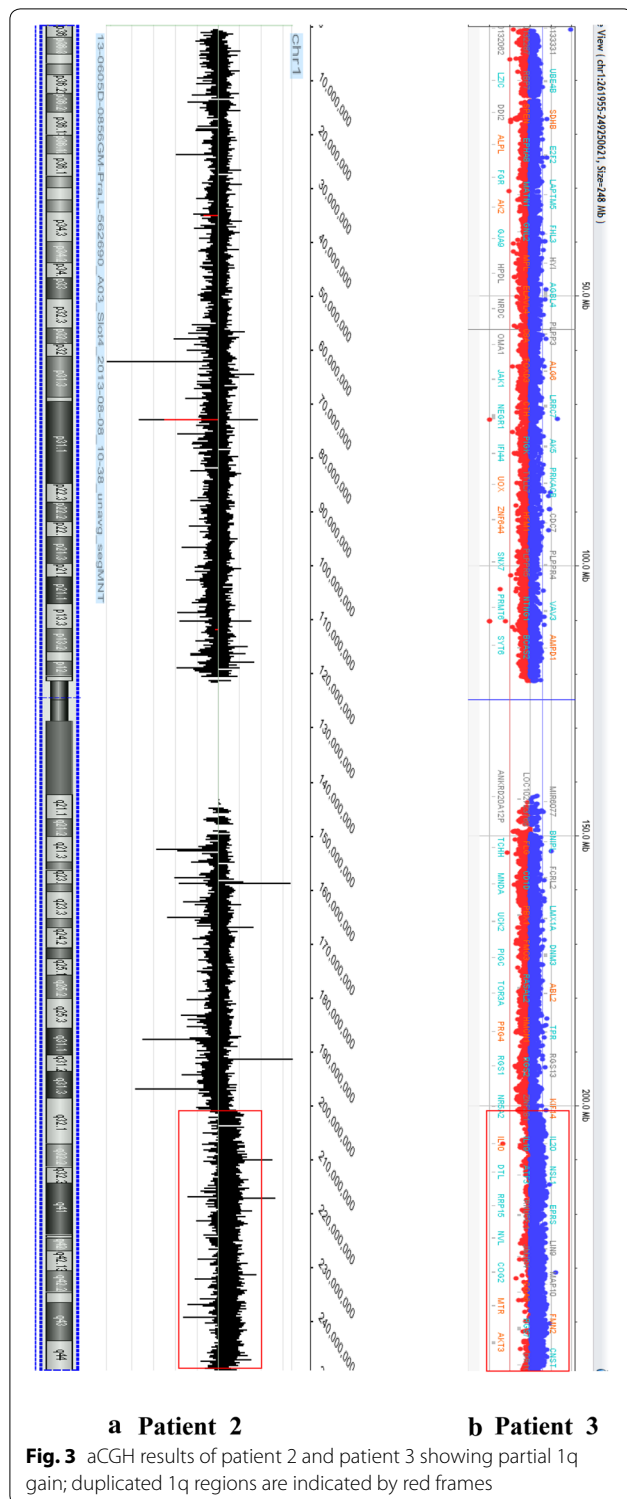


Fig. 2 Metaphase FISH of patient 2 (**a**) and 3 (**c**) showing *KAT6A/CREBBP* fusion signals. WCP FISH indicating the extra chromosomal materials on chromosome 14 and chromosome 3 were both from chromosome 1 (**b** and **d**). No loss of the end portion of the chromosome 3 long arm was indicated (**e**)

Over the past 15 years, cytogenetic and molecular technologies have largely promoted the efficiency of the identification and characterization of this disease [5]. Compared with conventional cytogenetic analysis and FISH methods, aCGH is an attractive method for the investigation of cancer genomes [23]. aCGH has higher resolution, simplicity, high reproducibility, shorter turnaround time and precise mapping of

aberrations. Most importantly, it avoids the need for cell culture and dividing cells [24–26]. Furthermore, aCGH chromosomal analysis facilitates rapid detection and duplication of cytogenetic abnormalities previously undetectable by conventional cytogenetics [27]. In our investigation, we applied aCGH to characterize the additional chromosome 1 materials in patients 2 and 3 and interestingly found that the two patients



revealed the same extra copy of 1q at bands q32.1q44. Patients with 1q duplication have also demonstrated a wide range of multiple malformations, such as intellectual disability, macrocephaly, large fontanels, prominent foreheads, broad flat nasal bridges, high-arched palates, retrognathia, low-set ears, and cardiac defects [28, 29]. More recent studies have shown that a 1q gain is also related to a portion of solid tumors. For instance, the gain of 1q is well known as a poor prognostic biomarker of Wilms tumor [30], and it plays an important role in predicting poor clinical outcome in patients with thyroid carcinoma as well [31]. In addition, patients with a 1q duplication showed worse survival and high risk in acute leukemia, Burkitt lymphoma, and myeloproliferative neoplasms [32–36]. The outcomes of 1q duplication in the nine reported AML patients with t(8;16)(p11.2;p13.3) are summarized in Table 1. Seven patients' data were available. These seven patients (two adult and five pediatric) all received induction chemotherapy, and six achieved CR. At the time of last follow-up, two adult patients and three of five pediatric patients had died. Only two pediatric patients were alive. We reported two adult patients here: patient 2 achieved CR but relapsed 3 months later, and patient 3 had spontaneous regression and died 2 years after diagnosis. Taken together, the findings suggest that 1q duplication might be associated with adverse outcomes in AML patients with t(8;16)(p11.2;p13.3). However, the significance of the 1q duplication in AML with t(8;16) needs to be further investigated. Since such changes have been seldom reported, the pathogenic effects of 1q duplication in AML patients with t(8;16)(p11.2;p13.3) require more studies to be delineated.

Conclusion

Three patients were detected with t(8;16)(p11.2;p13.3) from an 1,824 AML patient database. Two female patients were identified with a 1q duplication by FISH and aCGH analyses. Combining our investigation with the findings of published studies, we conclude that 1q duplication is a recurrent finding in AML patients with t(8;16). Our data also suggest that 1q duplication might be associated with unfavorable prognosis in these cases. The understanding of cytogenetic data would contribute to the diagnosis and treatment evaluation of AML.

Table 1 The previously reported AML cases with t(8;16)(p11.2;p13.3) and 1q duplication

	Sex	Age (years)	FAB type	Karyotype	1q Bands	Outcome (years)	Last state
Case 2	F	28	M5	46,XX,t(8;16)(p11.2;p13.3), add(14)(p11.2)[11]/46,XX[9]	1q32.1q44	CR after induction Relapsed 3 months later	Alive
Case 3	F	69	M5	46,XX,t(8;16)(p11.2;p13.3)[2]/46,idem,add(3)(q27)[18]	1q32.1q44	spontaneous regression	Died
Haferlach et al.	F	39	M5a	45,XX,t(8;16)(p11;p13),der(10;13)(q10;q10)[10]/46,XX,der(7)t(1;7)(q21;q35),t(8;16)(p11;p13)[2]/46,XX[1]	1q21	NA	NA
Diab et al.	M	14.5	M4	46,XY,+1,del(1)(p22),t(8;16)(p11;p13),-10,der(14)t(10;14)(q11.2;p11.2)[8]/47,XY,del(1)(q11),+der(1)t(1;8)(p11;q11.2)x2,+i(5)(p10),-8,-10,der(14)t(10;14)(q11.2;p11.2),der(16)t(8;16)	Partial 1q gain	CR for 10.5	Dead
Diab et al.	F	14.2	M4/5	5,XX,t(8;16)(p11;p13),-18,der(21)t(1;21)(q12;p13)[4]/46,XX[16]	1q12	CR for 5	Alive
Diab et al.	F	1.2	M4	46,XX,t(8;16)(p11;p13)[3]/46,idem,der(10)t(1;10)(q11;p11)[5]/46,idem,add(7)(p21),der(10)t(1;10)(q11;p11)[2]/46,idem,add(7)(p21)[2]/46,XX[2]	1q11	CR for 0.6	Died
Diab et al.	F	14.1	M4	46,XY,t(8;16)(p11;p13),der(14)t(1;14)(q31;p11)[20]*	1q31	CR for 11.5	Alive
Diab et al.	F	7.3	M5	46,X,der(X)t(X;1)(q26;q23),t(8;16)(p11;p13),der(11)t(11;11)(p11;q13)	1q23	NA	NA
Xie et al.	M	28	M4	46,XY,der(3)t(3;8)(q27;q13),del(6)(p22),t(8;16)(p11.2;p13.3),del(10)(q21;q25),add(13)(p11.2),del(16)(p12),del(20)(p11.2),del(20)(q11.2;q13.3)[4]/46,idem,del(1)(p35p36.3),del(15)(q23),add(19)(p13.1)[2]/46,XY,t(8;16)(q27;q13),del(12)(q21q24.1),del(13)(q21q31),-16,der(19)t(1;19)(q32;p13.3),+mar[3]/46,XY,del(6)(p22),t(8;16)(p11.2;p13.3)[cp2]/46,XY[9]	1q32	CR for 7 months	Dead
Brown et al.	M	71	M4	47,X,der(Y)t(Y;1)(q12;q21),+6,t(8;16)(p11;p13)[6]/47,idem,del(13)(q3q3)[checked with CAD data]	1q21	No CR	Died 1 month after treatment
Brown et al.	F	1.2	M4	46,XX,t(8;16)(p11;p13)[3]/46,idem,der(10)t(1;10)(q11;p11)[5]/46,idem,add(7)(p21),der(10)t(1;10)(q11;p11)[2]/46,idem,add(7)(p21)[2]/46,XX[2]	1q11	Early remission after course 1. Relapsed at 5 months and 7 months after diagnosis	Died

AML acute myeloid leukemia, FAB French–American–British, M male, F female, NA not available, CR complete remission

Abbreviations

AML: Acute myeloid leukemia; aCGH: Array comparative genomic hybridization; FISH: Fluorescence in situ hybridization; APL: Acute promyelocytic leukemia; WCP: Whole chromosome painting; CR: Complete remission.

Acknowledgements

Not applicable.

Authors' contributions

M Liu and YR gathered clinical information and drafted the manuscript. YR, YK and M Liu performed routine cytogenetic analysis and participated in the interpretation of the results. M Li performed FISH analysis and participated in the interpretation of the results. XL supervised the FISH analysis and helped draft the manuscript. XW performed CGH array analysis and helped draft the manuscript. LZ and SL conceived the study, participated in its design, and

extensively reviewed and revised the manuscript. All authors have read and approved the final manuscript.

Funding

This study has received no funding support.

Availability of data and materials

All data generated or analyzed during this study are included in this published article.

Ethics approval and consent to participate

This study was approved by University of Oklahoma Institutional Review Board for the Protection of Human Subjects.

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

Author details

¹ Department of Hematology, The First Hospital of China Medical University, 155 Nanjing North Street, Shenyang 110000, Liaoning, People's Republic of China. ² Department of Pediatrics, University of Oklahoma Health Sciences Center, Oklahoma City, OK, USA. ³ Department of Neurology, The Second Hospital of Jilin University, Jilin, People's Republic of China.

Received: 22 April 2020 Accepted: 12 August 2020

Published online: 25 August 2020

References

- Braess J. Acute myeloid leukemia. *Dtsch Med Wochenschr.* 2016;141:1748–51.
- Luppi M, Fabbiano F, Visani G, Martinelli G, Venditti A. Novel agents for acute myeloid leukemia. *Cancers (Basel).* 2018;10:429.
- Cancer Research UK. Acute myeloid leukaemia (AML) incidence statistics. 2018. <https://www.cancerresearchuk.org/health-professional/cancer-statistics/statistics-by-cancer-type/leukaemia-aml/incidence>. Accessed 31 Aug 2018.
- Jung J, Cho BS, Kim HJ, Han E, Jang W, Han K, Lee JW, Chung NG, Cho B, Kim M, Kim Y. Reclassification of acute myeloid leukemia according to the 2016 WHO classification. *Ann Lab Med.* 2019;39:311–6.
- Murphy T, Yee KWL. Cytarabine and daunorubicin for the treatment of acute myeloid leukemia. *Expert Opin Pharmacother.* 2017;18:1765–80.
- Byrd JC, Mrózek K, Dodge RK, et al. Pretreatment cytogenetic abnormalities are predictive of induction success, cumulative incidence of relapse, and overall survival in adult patients with de novo acute myeloid leukemia: results from Cancer and Leukemia Group B (CALGB 8461). *Blood.* 2002;100:4325–36.
- Lindsley RC, Mar BG, Mazzola E, et al. Acute myeloid leukemia ontogeny is defined by distinct somatic mutations. *Blood.* 2015;125:1367–76.
- Vardiman JW, Thiele J, Arber DA, et al. The 2008 revision of the World Health Organization (WHO) classification of myeloid neoplasms and acute leukemia: rationale and important changes. *Blood.* 2009;114:937–51.
- Saultz JN, Garzon R. Acute myeloid leukemia: a concise review. *J Clin Med.* 2016;5:33.
- Döhner H, Weisdorf DJ, Bloomfield CD. Acute myeloid leukemia. *N Engl J Med.* 2015;373:1136–52.
- Strickland SA, Shaver AC, Byrne M, et al. Genotypic and clinical heterogeneity within NCCN favorable-risk acute myeloid leukemia. *Leuk Res.* 2018;65:67–73.
- Yang JJ, Park TS, Wan TSK. Recurrent cytogenetic abnormalities in acute myeloid leukemia. *Methods Mol Biol.* 2017;1541:223–45.
- Coenen EA, Zwaan CM, Reinhardt D, et al. Pediatric acute myeloid leukemia with t(8;16)(p11;p13), a distinct clinical and biological entity: a collaborative study by the International-Berlin-Frankfurt-Munster AML-study group. *Blood.* 2013;122:2704–13.
- Xie W, Hu S, Xu J, Chen Z, Medeiros LJ, Tang G. Acute myeloid leukemia with t(8;16)(p11.2;p13.3)/KAT6A-CREBBP in adults. *Ann Hematol.* 2019;98:1149–57.
- Haferlach T, Kohlmann A, Klein HU, et al. AML with translocation t(8;16)(p11;p13) demonstrates unique cytomorphological, cytogenetic, molecular and prognostic features. *Leukemia.* 2009;23:934–43.
- Gervais C, Murati A, Helias C, et al. Acute myeloid leukaemia with 8p11 (MYST3) rearrangement: An integrated cytologic, cytogenetic and molecular study by the groupe francophone de cytogénétique hématologique. *Leukemia.* 2008;22:1567–75.
- Diab A, Zickl L, Abdel-Wahab O, et al. Acute myeloid leukemia with translocation t(8;16) presents with features which mimic acute promyelocytic leukemia and is associated with poor prognosis. *Leuk Res.* 2013;37:32–6.
- Schouten TJ, Hustinx TW, Scheres JM, Holland R, de Vaan GA. Malignant histiocytosis. Clinical and cytogenetic studies in a newborn and a child. *Cancer.* 1983;52:1229–36.
- Brown T, Swansbury J, Taj MM. Prognosis of patients with t(8;16)(p11;p13) acute myeloid leukemia. *Leuk Lymphoma.* 2012;53:338–41.
- Barrett R, Morash B, Roback D, et al. FISH identifies a KAT6A/CREBBP fusion caused by a cryptic insertional t(8;16) in a case of spontaneously remitting congenital acute myeloid leukemia with a normal karyotype. *Pediatr Blood Cancer.* 2017;64:10.
- Schumacher J, Szankasi P, Kelley TW. Detection and quantification of acute myeloid leukemia-associated fusion transcripts. *Methods Mol Biol.* 2017;1633:151–61.
- Díaz-Beyá M, Navarro A, Ferrer G, et al. Acute myeloid leukemia with translocation (8;16)(p11;p13) and MYST3-CREBBP rearrangement harbors a distinctive microRNA signature targeting RET proto-oncogene. *Leukemia.* 2013;27:595–603.
- Veigaard C, Nørgaard JM, Kjeldsen E. Genomic profiling in high hyperdiploid acute myeloid leukemia: a retrospective study of 19 cases. *Cancer Genet.* 2011;204:516–21.
- Yasar D, Karadogan I, Alanoglu G, et al. Array comparative genomic hybridization analysis of adult acute leukemia patients. *Cancer Genet Cytogenet.* 2010;197:122–9.
- van der Veken LT, Buijs A. Array CGH in human leukemia: from somatics to genetics. *Cytogenet Genome Res.* 2011;135:260–70.
- Laskowska J, Szczepanek J, Styczyński J, Tretyn A. Array comparative genomic hybridization in pediatric acute leukemias. *Pediatr Hematol Oncol.* 2013;30:677–87.
- Mehrotra M, Luthra R, Ravandi F, et al. Identification of clinically important chromosomal aberrations in acute myeloid leukemia by array-based comparative genomic hybridization. *Leuk Lymphoma.* 2014;55:2538–48.
- Kulikowski LD, Bellucco FTS, Nogueira SI, et al. Pure duplication 1q41-qter: further delineation of trisomy 1q syndromes. *Am J Med Genet A.* 2008;146A:2663–7.
- Nowaczyk MJM, Bayani J, Freeman V, Watts J, Squire J, Xu J. De novo 1q32q44 duplication and distal 1q trisomy syndrome. *Am J Med Genet A.* 2003;120A:229–33.
- Cone EB, Dalton SS, Van Noord M, Tracy ET, Rice HE, Routh JC. Biomarkers for Wilms tumor: a systematic review. *J Urol.* 2016;196:1530–5.
- Xu B, Ghossein R. Genomic landscape of poorly differentiated and anaplastic thyroid carcinoma. *Endocr Pathol.* 2016;27:205–12.
- Fournier A, Florin A, Lefebvre C, Solly F, Leroux D, Callanan MB. Genetics and epigenetics of 1q rearrangements in hematological malignancies. *Cytogenet Genome Res.* 2007;118:320–7.
- Lancman G, Tremblay D, Barley K, et al. The effect of novel therapies in high-molecular-risk multiple myeloma. *Clin Adv Hematol Oncol.* 2017;15:870–9.
- Bacher U, Schnittger S, Grüneisen A, Haferlach T, Kern W, Haferlach C. Inverted duplication dup(1)(q32q21) as sole aberration in lymphoid and myeloid malignancies. *Cancer Genet Cytogenet.* 2009;188:108–11.
- Marcellino BK, Hoffman R, Tripodi J, et al. Advanced forms of MPNs are accompanied by chromosomal abnormalities that lead to dysregulation of TP53. *Blood Adv.* 2018;2:3581–9.
- Beach DF, Barnoski BL, Aviv H, et al. Duplication of chromosome 1 [dup(1)(q21q32)] as the sole cytogenetic abnormality in a patient previously treated for AML. *Cancer Genet.* 2012;205:665–8.

Publisher's Note

Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.