CASE REPORT

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Several different cytogenetic clones arising during treatment of Philadelphia positive chronic myeloid leukemia with tyrosine kinase inhibitors lead to the progression into Philadelphia negative acute myeloid leukemia

Različiti citogenetski klonovi nastali tokom lečenja Filadelfija pozitivne hronične mijelodne leukemije inhibitorima tirozin kinaze sa progresijom u Filadelfija negativnu akutnu mijeloidnu leukemiju

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Abstract

Introduction. Additional karyotype abnormalities in the Philadelphia-positive (Ph+) clone can emerge during the progression of chronic myeloid leukemia (CML) and are often associated with the resistance to treatment with tyrosine kinase inhibitors (TKI). Sometimes, during the TKI treatment, karyotype abnormalities can appear in the Philadelphia-negative (Ph-) cells as well but do not seem to adversely affect the outcome except for chromosome 7 abnormalities. **Case report.** The patient presented was in the chronic phase of Ph+ CML with highly diverse karyotype abnormalities. The abnormalities appeared in three unrelated clones during the TKIs treatment, followed by the evolution of the disease into acute myeloid leukemia (AML). The primary Ph+ clone was revealed during the chronic phase of CML, and therapy with imatinib mesylate was commenced. After a three-year hematologic and cytogenetic remission period, the evolution of the primary clone was noticed. Nilotinib was introduced, leading to a good molecular response and the disappearance/loss of the Ph+ clone with additional abnormalities but with the appearance of the Ph- clone with trisomy 8. Finally, after 5.5 years of nilotinib therapy, the Ph- clone with monosomy 7 occurred during the deep molecular response for BCR-ABL. At that time, the FISH analysis for trisomy 8 was negative, but the rise in blast count was noticed in the bone marrow, and the diagnosis of the secondary AML was established soon after. **Conclusion.** The achievement of the deep molecular response in CML patients does not rule out regular cytogenetic testing of their bone marrow. This is of crucial importance for detecting adverse karyotype abnormalities leading to the development of the myelodysplastic syndrome and AML.

Key words:
leukemia, myelogenous, chronic, bcr-abl positive; leukemia, myeloid, acute; karyotyping; enzyme inhibitors; cytogenetics.

Apstrakt

Uvod. Dodatne kariotipske abnormalnosti u Filadelfija-pozitivnom (Ph+) klonu mogu se javiti tokom progresije hronične mijeloidne leukemije (CML) i često su povezane sa rezistencijom na terapiju tirozin kinaznim inhibitorima (TKI). Ponekad se tokom terapije TKI kariotipske abnormalnosti javljaju i u Filadelfija-negativnim (Ph-) ćelijama, ali ne utiču na progresiju bolesti, izuzev abnormalnosti hromozoma 7. **Prikaz bolesnika.** Kod bolesnice u hroničnoj fazi CML, tokom lečenja TKI uočene su kariotipske abnormalnosti prisutne u tri nezavisna klona sa evolucijom bolesti u akutnu mijeloidnu leukemiju (AML). Primarni Ph+ klon je otkriven tokom hronične faze CML i započeta je terapija imatinib mesilatom. Nakon tri godine hematološke i citogenetske remisije, uočena je evolucija primarnog klona. Započeta je terapija nilotinibom koja je dovela do molekularnog odgovora i povlačenja Ph+ klona sa dodatnim aberacijama, ali i pojavljivanja novog Ph- klona sa trizomijom 8. Nakon 5,5 godina lečenja nilotinibom i postizanja kompletnog molekularnog odgovora, uočen je Ph- klon sa monozomijom 7. Fluorescentna *in situ* hibridizacija (FISH) pokazala je

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odsustvo trizomije 8 i prisustvo monozomije 7. Istovremeno, registrovan je porast broja blasta u koštanoj srži i ubrzo je postavljena dijagnoza sekundarne AML. **Zaključak.** Postizanje kompletnog molekularnog odgovora primenom TKI terapije ne treba da isključi redovno citogenetsko testiranje koštane srži bolesnika sa CML. Otkrivanje kariotipskih abnormalnosti sa lošom prognozom je od velikog značaja zbog mogućnosti razvoja sekundarnih maligniteta – mijelodisplastičnog sindroma i AML.

Ključne reči:
leukemija, mijeloidna, hronična, bcr-abl pozitivna; leukemija, mijelocitna akutna; kariotip, određivanje; enzimi, inhibitori; citogenetika.

Introduction

The BCR-ABL fusion gene, generating the Philadelphia chromosome (Ph), is a sole genetic abnormality in 90% of chronic myeloid leukemia (CML) patients in the chronic phase [1]. With the progression of the disease, additional karyotype changes in the Philadelphia positive (Ph+) clone emerge and are often associated with resistance to imatinib mesylate and/or nilotinib. The resistance can be a consequence of one of the numerous mutations in the tyrosine kinase domain or some other underlying mechanism and is usually overwhelmed with some of the novel tyrosine kinase inhibitor (TKI) drugs. Sometimes, during the TKI treatment, karyotype changes in the Philadelphia negative (Ph-) cells can appear [2]. These aberrations, similar to those frequently seen in the myelodysplastic syndrome (MDS) and acute myeloid leukemia (AML), include trisomy 8 (+8), the deletion or monosomy of chromosome 7 (del(7q)/-7), and nullisomy of Y (-Y). However, chromosome abnormalities in the Ph- clone do not seem to adversely affect the outcome with the exception of the chromosome 7 abnormalities [1]. Monosomy 7 and del (7q) require frequent bone marrow follow-up as several case reports indicate the development of the MDS and subsequent AML [3–7].

A CML patient with highly diverse karyotype abnormalities was presented in this paper. The abnormalities appeared in three unrelated clones during the treatment with imatinib mesylate and nilotinib. The patient mentioned developed AML in the end.

Case report

A 44-year-old female was diagnosed with CML in the chronic phase in April 2002. The cytogenetic analysis revealed the translocation t(9;22) (q34;q11) (Ph chromosome) in 20/20 mitoses (Figure 1A). The prognostic Sokal and Hasford scores implied a low-risk patient at presentation, without comorbidities or any other additional treatment. The antileukemic therapy was commenced with hydroxyurea and interferon with a subsequent increase in interferon dosage. Regardless of achieving hematological remission, no cytogenetic response was obtained after 6 months of the treatment. As the patient had no available stem cell donor, imatinib mesylate in a standard dose (400 mg a day) was started in September 2002. Six months later, the patient achieved partial cytogenetic response (PCgR) with 53% Ph-negative metaphases. After 12 months, a complete cytogenetic response (CCgR) was achieved, although a b2a2 transcript of the BCR-ABL fusion was detected by "nested" RT-PCR. During the next three years, the patient remained in a stable chronic phase with CCgR, on 400 mg of imatinib. However, in August 2005, the follow-up cytogenetics revealed complex translocation t(5;6;12) with t(9;22) (Figure 1B) in all analyzed cells, without any clinical or laboratory sign of disease progression. The tyrosine-kinase domain mutations were negative by direct sequencing.

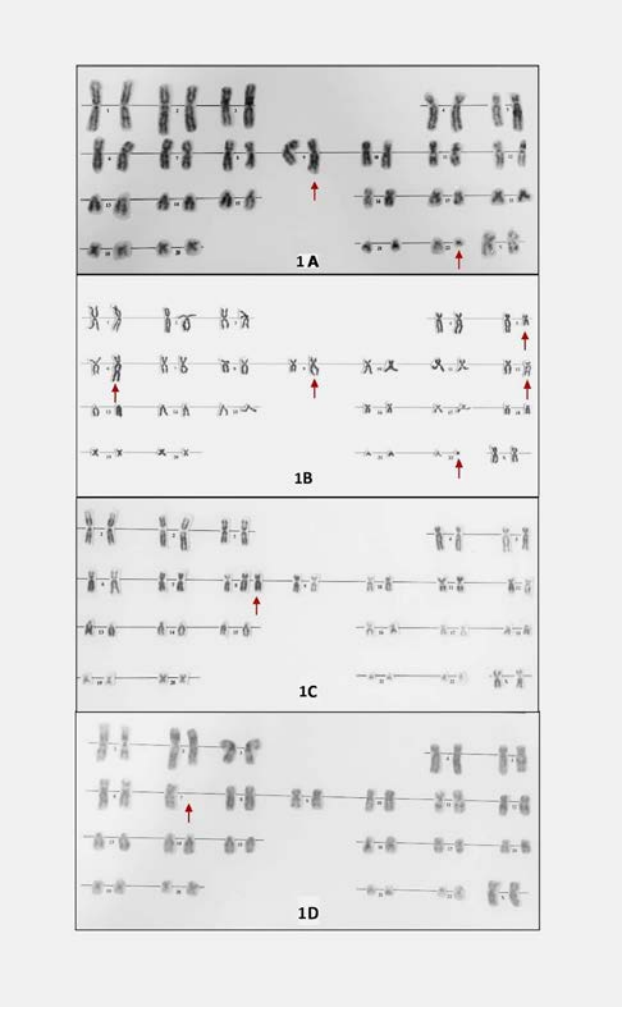

Fig. 1(A–D): A) (46,XX,t(9;22) (q34;q11) at presentation; B) [46,XX,t(5;6;12)(q14?;q21?;q23?),t(9;22)(q34;q11) imatinib (400 mg), TT 36 m]; C) 47,XX,+8 nilotinib (800 mg), TT 6 m; D) 45,XX,-7 nilotinib (800 mg), TT 66 m.

The patient was treated with an escalated dosage of imatinib (800 mg a day) since October 2006 without success. The patient was switched to nilotinib, 800 mg a day, from July 2008 through the "compassionate use program".

However, due to hematologic and hepatic toxicity, after only a month, nilotinib was reduced to 400 mg. After 6 months of 400 mg nilotinib, the patient achieved CCgR again, but at 12 months, the reappearance of Ph+ clone with t(5;6;12) was noticed in 45% of metaphases, suggesting PCgR. Along with the Ph-positive cells, the Ph-negative clone with +8 was seen in 10% of mitoses. After the recovery of blood counts and the hepatic function 6 months later, the patient was escalated to the full dosage of nilotinib (800 mg) again. She achieved a major cytogenetic response [MajCgR, 10% of Ph+ with t(5;6;12) clone] at 24 months of nilotinib treatment, and finally, after 30 months on nilotinib, the patient achieved CCgR. During the next 3 years on 800 mg of nilotinib, her follow-up showed CCgR and a stable molecular response (MR3), though the Ph-negative clone with +8 was constantly present in 10–30% of metaphases (Figure 1C).

However, during the regular follow-up in February 2014 (5.5 years of nilotinib therapy), profound neutropenia without anemia and thrombocytopenia was noticed (hemoglobin 120 g/L, white blood cells 2.5×10^9/L, 76% lymphocytes, 4% blasts, 10% monocytes, platelets 258 × 10^9/L) together with elevated transaminases (alanine aminotransferase − ALT 86 U/L). Immediate bone marrow evaluation revealed dysplastic changes in erythroid and megakaryocyte lineages together with 6% of blasts. The karyotype revealed the poor quality of chromosomes, but the clonal change with a loss of one chromosome from the C group was evident in 60% of mitoses. The fluorescence *in situ* hybridization (FISH) analysis with the BCR-ABL probe was negative both for the Ph chromosome and trisomy 8, but the CEP7 probe revealed the monosomy of chromosome 7 in 80% of interphase nuclei.

The administration of nilotinib was stopped. Two months later, the patient's bone marrow was hypocellular with less dysplasia than at the previous examination but with the rise in blast count (12%). The cytogenetic examination confirmed -7 in all analyzed cells (20/20) and the absence of trisomy 8 (Figure 1D). Real-time qualitative polymerase chain reaction (RQ-PCR) for BCR-ABL revealed a deep molecular response, MR4.

After one month, in April 2014, further evaluation revealed leukemic progression and development of AML (30% of blasts) confirmed by the flow cytometry immunophenotype (HLA-DR^{med}, CD34^{high}, CD117^{med}, CD13^{high}, CD33^{med}, CD7^{+}). The patient was treated with the antileukemic treatment (3 + 7 regimen) without success, followed by the "salvage" protocol FLAG-Ida without achieving any morphological or cytogenetic response. Unfortunately, the patient died of aplasia during the treatment.

Cytogenetic study and response criteria

The cytogenetic study was performed on unstimulated bone marrow cells using a standard technique. The Giemsa-banded metaphases were analyzed, and the result was reported by the International System for Human Cytogenetic Nomenclature standards, 2013. The cytogenetic response was classified according to the standard of the UK Medical Research Council practice as complete (0% Ph+ metaphases), major (1–34% Ph+), partial (35–65% Ph+ metaphases), minor (66–95% Ph+) and no response (95–100% Ph+). The cytogenetic clonal evolution was defined as the presence of any abnormality other than a single Ph chromosome.

Reverse transcription-polymerase chain reaction (RT-PCR) and "nested"

The total RNA was extracted from peripheral blood cells according to the guanidine thiocyanate-phenol-chloroform extraction method [8]. Reverse transcription was performed on 1 μg of total RNA after heating at 65 ºC for 15 minutes. Reverse transcription was performed with the 1st Strand cDNA Synthesis Kit for RT-PCR (AMV) (Roche Diagnostics Corporation, Indianapolis, IN, USA) according to the manufacturer's manual. The amplification was done with slight modifications as described by Moravcová et al. [9].

The FISH analysis for centromere regions of chromosomes 7 and 8 (CEP7 and CEP8) was performed on interphase nuclei and metaphase cells according to the manufacturer's instructions (Vysis/Abbott Laboratories, Des Plaines, IL).

Discussion

Our case demonstrates highly diverse karyotype changes appearing one after another in three unrelated clones during the treatment with tyrosine kinase inhibitors. Complex aberrations in the Ph-positive clone emerged during the management with imatinib, while +8 and -7 appeared separately in the Ph-negative clones during the nilotinib treatment.

Karyotype changes in the Ph+ clone emerged 40 months after the imatinib therapy was started as the only sign of disease relapse. This distinctive karyotype included complex translocation and the rare event of centromere fission, which were previously published [10, 11]. A negative search for mutations by Sanger sequencing in the kinase domain further contributed to the complexity of the case.

Only after the introduction of a more potent TKI treatment, nilotinib, the Ph+ clone slowly decreased, but trisomy 8 in the Ph-negative cells appeared. The CCgR was achieved after 30 months on nilotinib, while +8 remained and existed in up to 30% of analyzed cells during the next 2.5 years of follow-up.

Nota bene, the Ph-negative clones are less frequent in patients treated with second-generation TKIs and after the failure of imatinib due to higher pressure on leukemic and residual normal hematopoiesis [12]. However, when present, their type and frequency are very similar to those seen in patients on imatinib, as well as their incidence and effect in evolution to MDS/AML [12].

Our patient developed secondary AML after 66 months of the nilotinib treatment. The cytogenetic and FISH analysis revealed -7 in 60% of metaphases and 80% of interphase

nuclei, respectively, along with the absence of BCR-ABL and +8. The clone with -7 quickly progressed to 100% of the analyzed cells in two months, while RQ-PCR still showed a stable MR4. Despite introducing a high-dose therapy for AML, the patient died 6 months after the diagnosis of the secondary AML had been established.

The Ph-negative clones with -7 were described in the CML cases with a high propensity to evolve into MDS/AML [13]. However, there have been rare cases with -7 without disease evolution [4, 5, 14].

In several studies, factors contributing to the appearance of chromosomal aberrations in the Ph-negative clone have been discussed. The previous cytotoxic treatment [13], the negative effect of TKIs on DNA repair mechanisms [15–17], or the innate genetic instability in the CML marrow [18] are described as potential causes of the Ph-negative clone appearance. However, among all the abnormalities, only those involving chromosome 7 [del(7q) and/or -7] bear a higher risk of secondary malignancies [5, 19]. We can conclude that while the patient was in a stable chronic phase of CML, complex chromosomal aberrations in the Ph-positive cells might reflect a highly unstable genome, which could contribute to a further lower sensitivity to a subsequent alternative treatment and thus, negatively affect overall survival.

Other parameters that could lead to the development of MDS/AML are pretreatment with interferon or hydroxyurea, a persistent aberration in the Ph-negative clone, and clone size > 50% [19]. Unfortunately, our patient had all the negative features mentioned above in developing secondary malignant disease.

During the treatment with TKIs, it is highly important to reveal the biological diversity of the Ph-negative clones, which in some patients can lead to disease transformation (clone with -7), while in others, it does not have the propensity towards secondary hematological malignancy (clone with +8). Minimal investigations should include blood test results (cytopenia), bone marrow morphology (dysplastic changes and blast count), and cytogenetic (evidence of the Ph-negative clones and -7). In cases with the additional Ph-negative clones, further evaluation of changes with the FISH and real-time PCR analyses are highly recommended.

Conclusion

The evolution of karyotype and the occurrence of diverse clones arising from the stem cell level in our patients, warrants the need for thorough follow-up and evaluation of all related hematological and biological findings during the treatment with tyrosine kinase inhibitors, including the standard karyotype, although, some study groups tend to omit any bone marrow evaluation in the current monitoring schedule.

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