

B-ALL Relapses After Autologous Stem Cell Transplantation Associated With a Shift from e1a2 to e14a2 *BCR-ABL* Transcripts: A Case Report

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Abstract. *Background/Aim:* The Philadelphia chromosome is found in 30% of acute lymphoblastic leukemia (ALL) patients, a distinct ALL subgroup where the *BCR-ABL* fusion gene is associated with poor prognosis. Treatment with tyrosine kinase inhibitors (TKIs) often induces complete remission and these patients subsequently undergo an autologous stem cell transplantation (ASCT). However, 20% of subjects experience a relapse associated with the selection of point-mutations in the *BCR-ABL* kinase domain. We report the clinical evolution of a Philadelphia-positive ALL patient co-expressing the e1a2 and e14a2 *BCR-ABL* transcript at diagnosis. *Materials and Methods:* Multiplex reverse transcriptase (RT)-PCR was used to detect *BCR-ABL* transcripts and their levels were measured by quantitative Real Time PCR. Clonal sequencing and next-generation sequencing (NGS) were used to identify mutations. *Results:* Although the patient underwent ASCT following treatment with multiple TKIs, he relapsed twice. The first time he exhibited the e1a2 transcript and the second time he presented only the e14a2 variant. Mutation analysis, performed by clonal sequencing and NGS, detected two alterations after the first relapse and a single mutation at the time of the second relapse. *Conclusion:* The observed shift

from the e1a2 to the e14a2 variant and the selection of TKI-resistant clones heavily contributed to the fatal evolution of the disease.

The Philadelphia (Ph) chromosome, resulting from the reciprocal translocation of the *ABL* gene at 9q34 with the *BCR* gene at 22q11, is the most frequent cytogenetic abnormality in both chronic myelogenous leukemia (CML) and adult acute lymphoblastic leukemia (ALL) (1-3). At the molecular level, the t(9;22) translocation generates the *BCR-ABL* chimeric oncogene that may encode for a 210-kD or a 190-kD protein both displaying constitutive tyrosine kinase activity and favoring cell-cycle progression (4-7). The fusion gene is found in more than 95% of patients with CML (8), and in 20-30% of adult ALL patients, with the incidence rising to more than 50% in patients aged >50 years where it is associated with an inferior prognosis (9). Several reports have found the e1a2 transcript to coexist with e13a2 or e14a2 isoform in patients with Ph-positive ALL (10, 11).

In the pre-tyrosine kinase inhibitor (TKIs) era, Allogeneic Stem Cell Transplant (allo-SCT) in first complete remission was the only potentially curative option (12) for the disease. Currently, the standard of care for patients with Ph-ALL is a combination of chemotherapy and a TKI followed by allo-SCT. However, 60-70% of Ph-ALL individuals are ineligible for allo-SCT due to their age, lack of an HLA-matched sibling, lack of a matched-unrelated donor or a suitable cord blood unit. These patients can then be considered for autologous stem cell transplantation (ASCT), although this procedure is associated with a higher incidence of relapse (13). Hence, TKIs can be used for the *in vivo* eradication of the malignant clone before ASCT, followed by maintenance therapy after transplantation.

In the present report, we describe a Ph-positive ALL patient who displayed both the e1a2 and e14a2 *BCR-ABL*

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mRNAs at diagnosis developing two relapses each expressing a different single oncogenic transcript.

Case Report

In December 2014, a 53-year-old man presented with a 3-week history of fever, fatigue and abnormal blood cell counts; his hemoglobin (Hgb) was 6.5 g/dl with 18.000 white blood cells (WBC) and 13.000 platelets (PLT). Flow cytometry analysis identified 53% of HLA-DR⁺, CD19⁺, CD20⁺, CD10⁺ and CD34⁺ leukemic blasts while conventional cytogenetics detected the Philadelphia chromosome in all examined metaphases with no additional cytogenetic abnormalities (karyotype 46, XY, t(9;22)(q34;q11)). Multiplex reverse transcriptase (RT)-PCR revealed the presence of the e14a2 BCR-ABL transcript with BCR-ABL/ABL levels of 95.25% measured by Real Time (Q-PCR) (14). However, the patient also displayed the e1a2 BCR-ABL variant with 10.13% BCR-ABL/ABL transcripts that were barely noticeable at the multiplex RT-PCR amplification (Figure 1A).

The patient received chemotherapy according to the HyperCVAD protocol (15), but after a single course of treatment all drugs were temporarily discontinued because of grade IV gastrointestinal and cutaneous toxicities. Upon reinstating the HyperCVAD regimen, he achieved a deep molecular response with BCR-ABL/ABL levels of 0.0029% (e14a2) and no e1a2 transcript detected. He subsequently received Dasatinib 140 mg/day (Figure 1B). Since an HLA-matched donor could not be found, in the presence of a deep molecular response (undetectable e14a2 transcript and 0.0061% e1a2 BCR-ABL/ABL), the patient underwent peripheral blood stem cell mobilization and collection for an ASCT that was performed in July 2015.

In September 2015, he maintained a deep molecular response for both the e14a2 and the e1a2 transcripts. However, three months later e1a2 BCR-ABL/ABL levels began to increase (0.00266%) (Figure 1B). He was, therefore, placed on imatinib 400 mg/day as it was impossible to restart dasatinib because of regulatory constraints of the Italian Agency for Antineoplastic Drugs.

Nevertheless, in April 2016 the patient experienced his first disease relapse. At this time, his leukocyte count rose to 69,000/mm³ with 70% blasts bearing an immunophenotype indicative of B-ALL. The e1a2 BCR-ABL/ABL levels increased to 145.13%, with e14a2 transcripts still compatible with a deep molecular response. Mutational analysis performed both by clonal sequencing (to discriminate between compound and/or polyclonal mutations) and next generation sequencing (NGS, to detect variants below the 1% threshold) identified a T315I mutation in all Ph-positive clones. NGS also detected a 35-nucleotide insertion from ABL intron 8 (at the junction between exons 8 and 9) in 3.8% of the leukemic blasts (Figure 1B). He, therefore, received 4 cycles of

chemotherapy with vincristine (2 mg/week) and doxorubicin (36 mg/m²) once weekly as debulking therapy achieving a complete hematological remission (blast cells <5 % on bone marrow smear and undetectable e1a2 BCR-ABL/ABL) and in May 2016 ponatinib (45 mg/die) was started maintaining the attained response (Figure 1B).

However, in November 2016 a second relapse occurred (40% lymphoid blasts in the bone marrow smear), with conventional cytogenetic analysis detecting novel chromosomal abnormalities: 46, XY, del (20)(q13) (2 metaphases/20); 45, XY, -3, der(7)t(3;7)(q11;p11), t(9;22)(q34;q11)del(9)(p12), del (11)(q15), del (20), q13) (6 /20); 46, XY (12/20). Molecular analysis displayed an increase only in e14a2 BCR-ABL transcripts (56.9%) while the e1a2 variant remained undetectable. Furthermore, mutational analysis performed by NGS showed the E279K substitution in 35% of the Ph-positive clones. This mutation has been associated with moderate sensitivity to ponatinib (16, 17).

In January 2017 the patient received one course of inotuzumab ozogamicin (IO) which was administered according to the schedule 0.8 mg/m² i.v. on day +1 and 0.5 mg/m² iv on days +8 and +15 (the drug was obtained through a compassionate use program) as described by Piroso *et al.* (18) (Figure 1B). A bone marrow biopsy performed after IO showed disease remission (e14a2 BCR-ABL/ABL 0.01071% with undetectable e1a2). In February 2017, the patient also received one course of chemotherapy with cyclophosphamide 1,000 mg/m² day +1 and cytarabine 75 mg/m² i.v. days +2, +3, +4, +5, as a maintenance regimen. Complete remission was sustained until May 2017 (as evidenced by bone marrow morphology, immunophenotyping and PCR with an e14a2 BCR-ABL/ABL level of 0.00785% in the absence of detectable e1a2 transcripts) (Figure 1B).

Central nervous system (CNS) surveillance with periodical rachicenteses performed in March and May 2017 was negative for leukemia relapse. In June 2017, he lamented frequent headaches with emotional disturbance. A lumbar puncture confirmed leukemic spread to the CNS. The clinical picture evolved rapidly to uncontrollable epilepsy shortly thereafter followed by death.

Materials and Methods

Total cellular RNA was extracted from peripheral blood or bone marrow leucocytes, using the RNeasy mini kit (Qiagen, KJ Venlo, The Netherlands), according to the manufacturer's protocol. cDNA synthesis was carried out using random hexamers (Invitrogen, Paisley, UK). Both e1a2 and e14a2 BCR-ABL fusion transcripts were screened by Q-PCR according to the suggested recommendations (19) and molecular analysis was performed as previously reported (14). Cytogenetic analysis was performed using conventional techniques (20). Mutation analysis of the ABL kinase domain by clonal sequencing or NGS was performed as previously described (21, 22).

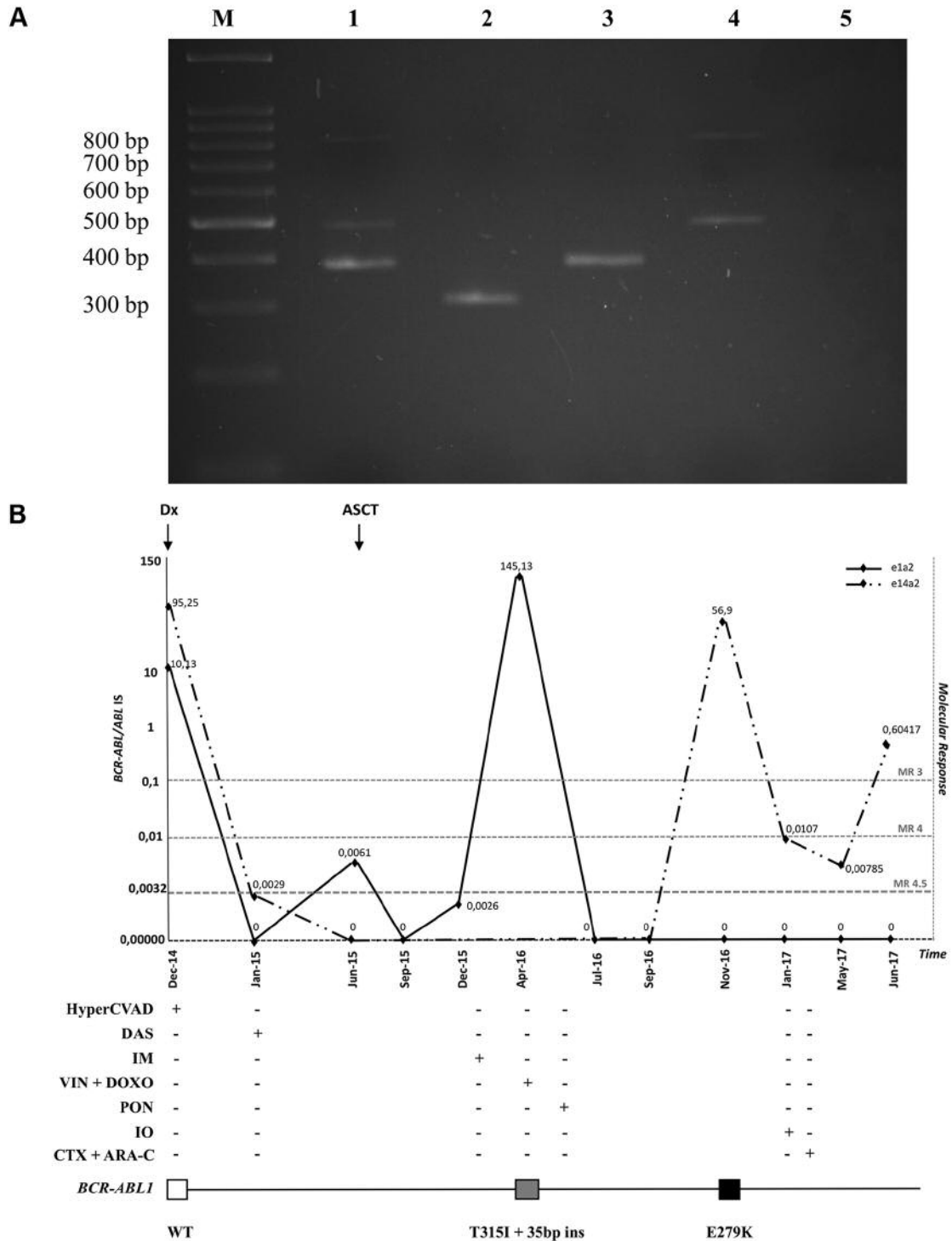


Figure 1. Clinical evolution of the patient. A. Multiplex RT-PCR analysis of different *BCR-ABL* fusion transcripts. Lane M=Molecular size marker (100-bp ladder); lane 1=e1a2 (481 bp) and e14a2 (385 bp) from the patient; lane 2=e13a2 (310 pb) positive control; lane 3=e14a2 positive control; lane 4=e1a2 positive control; lane 5=negative control. B. Molecular response to different TKIs in combination with chemotherapy. Monitoring of the patient's disease evolution indicating variations in the e1a2 and e14a2 transcripts (top panel), drug treatments (middle panel) or *BCR-ABL* mutant clones (bottom panel). Dotted lines represent achievement of a major (MR3) or a deep (MR4; MR4.5) molecular response. A white square indicates wild-type *BCR-ABL*, a gray square denotes the T3151 mutation and the 35-bp insertion and a black square indicates detection of the E279K substitution. ASCT: Autologous stem cell transplant; DAS: dasatinib; IM: imatinib; VIN: vincristine; DOXO: doxorubicin; PON: ponatinib; IO: inotuzumab ozogamicin; CTX: cyclophosphamide; ARA-C: cytarabine.

Informed consent was received from the patient for the publication of the report. The patient gave written consent to participate in the study as specified in the Declaration of Helsinki.

Discussion and Conclusion

Adults diagnosed with Ph-positive ALL display poor overall survival, as expression of the *BCR-ABL* oncoprotein confers an inferior prognosis compared to other ALL subtypes. In this disease, the e1a2 or the e13/e14a2 *BCR-ABL* transcripts are commonly detected in the leukemic clones although less frequent breakpoints on both the *BCR* and *ABL* genes may also occur generating additional atypical transcripts (23, 24). Moreover, different investigators have previously described the coexistence of e1a2 and e13/e14a2 *BCR-ABL* transcripts in the same patients (25, 26).

In this report, we describe the case of a patient with Ph-positive ALL that, at diagnosis, co-expressed both the e1a2 and e14a2 *BCR-ABL* variants. Although the patient underwent ASCT, his disease relapsed twice after this procedure. Interestingly, the first relapse was attributable to a leukemic clone only expressing the e1a2 *BCR-ABL* transcript while the second relapse was due to an e14a2-positive clone in the absence of the previous shorter *BCR-ABL* mRNA. While we did not formally establish if the two different *BCR-ABL* transcripts were expressed by the same clone (*via* alternative splicing mechanisms) or represented two distinct cellular types each characterized by a specific *BCR-ABL* rearrangement (e1a2 or e14a2), the occurrence of two different relapses always involving the emergence of a different single *BCR-ABL* variant strongly supports the second hypothesis. It remains to be seen if co-expression of multiple *BCR-ABL* transcripts in the same or in different leukemic clones modifies the prognosis of Ph-positive ALL patients.

As identification of the T315I mutation in Ph-positive ALL or CML is associated with an inferior prognosis, each time the patient lost a previously acquired response he was subjected to a timely molecular analysis in order to take the appropriate therapeutic decisions (27, 28).

As the patient received dasatinib, imatinib and ponatinib during the course of his disease, the clones causing the two ALL relapses displayed mutations conferring either insensitivity (T315I) or limited sensitivity (E279K) to the different TKIs prescribed. Hence, at least initially, even when acquiring TKI resistance the disease remained dependent on *BCR-ABL* kinase activity.

Unfortunately, CNS relapse is still extremely difficult to treat and is often associated with a dismal outcome as in the case of this patient that had previously benefited from multiple chemotherapeutic regimens associated with different TKIs.

Conflicts of Interest

The Authors declare that they have no competing interests regarding this study.

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