



Chronic myelogenous leukemia

## In Ph<sup>+</sup>BCR-ABL1<sup>P210+</sup> acute lymphoblastic leukemia the e13a2 (b2a2) transcript is prevalent

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### To the Editor:

Philadelphia-chromosome positive (Ph<sup>+</sup>), BCR-ABL1<sup>+</sup> acute lymphoblastic leukemia (ALL) is a distinct entity that is characterized by specific genomic alterations, low sensitivity to chemotherapy, unstable responsiveness to tyrosine kinase inhibitors (TKIs), and a poor prognosis [1–3]. The frequency of Ph<sup>+</sup> ALL varies with age, ranging from <10% in children to about 50% in the elderly [3, 4]. Ph<sup>+</sup> ALL is driven by a reciprocal translocation between chromosome 9 and chromosome 22, leading to the formation of hybrid fusion genes, that are all leukemogenic but can vary depending on the site of the breakpoints [5, 6]. The most common gene, that accounts for about 70–80% of all cases, results from the fusion of BCR exon 1 on chromosome 22 with ABL1 exon 2 on chromosome 9, much more rarely with ABL1 exon 3. The resulting e1a2 (or e1a3) fusion gene codes for a leukemogenic protein of 185–190 kd (P190). In 20–30% of cases, the breakpoint on chromosome 22 is downstream to BCR exon 1, resulting from the fusion of ABL1 exon 2 on chromosome 9 with either BCR exon 13 or BCR exon 14 on chromosome 22. The resulting fusion transcripts are named e13a2 (also known as b2a2), and e14a2 (also known as B3A2), respectively. The fusion e13a2 can give rise to only one transcript (e13a2) and one leukemogenic protein of 210 kd (P210). The fusion e14a2 usually give rise to one transcript (e14a2) that is longer, and

codes for a leukemogenic protein that is also called P210, but has 25 additional amino acids and different secondary structure elements [5, 6]. Sometimes the e14a2 fusion gene, that retains BCR exon 13, can also generate a minor amount of e13a2 transcript, because of alternative splicing mechanisms. Therefore, the BCR-ABL1<sup>P210+</sup> leukemias have two different molecular signatures: e13a2, and e14a2 (+\_e13a2). The frequency of the two signatures has never been systematically investigated. In a paper from the MD Anderson Cancer Center it was reported that of 17 patients with Ph<sup>+</sup>, BCR-ABL1<sup>P210+</sup> 76% expressed e13a2 [7].

In a previous international study of the frequency of the two transcripts in 45,503 patients with newly diagnosed BCR-ABL1<sup>P210+</sup> chronic myeloid leukemia (CML), it was found that 17,216 patients (37.9%) expressed only e13a2, with a proportion that varied with age, from 39.6% in children and adolescents down to 31.6% in the elderly, and with sex, from 36.5% in females up to 39.2% in males [8]. To assess the frequency of e13a2 in BCR-ABL1<sup>P210+</sup> ALL, we collected the molecular data from 849 patients with Ph<sup>+</sup>, BCR-ABL1<sup>P210+</sup> ALL, from 39 Institutions, as a first quick step of a project that was designed to evaluate the clinical and biological characteristics and the outcomes of BCR-ABL1<sup>+</sup> ALL according to the different transcripts. Completing the project will take more time and more resources, and we report here the first data set: 497 patients (58.5%) expressed only e13a2, a proportion that was significantly higher than the proportion of e13a2 that was found in newly diagnosed chronic phase CML (37.9%) (Fisher's exact test, two-sided, *p* value < 0.0001). This difference cannot be explained by age; indeed the frequency of Ph<sup>+</sup> ALL increases with age and is highest

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in the elderly, where the frequency of e13a2 in CML is the lowest [3, 4, 8]. The finding that the distribution of the different breakpoints in BCR-ABL1 fusion gene is not by chance, being significantly different between CML and Ph+ ALL is of interest. While we are collecting data to compare the characteristics, the response to therapy and the outcomes according to transcript, other important questions, are unanswered. First, why is the distribution different, is the cause related to the cell where the translocation occurs (a multipotent stem cell versus a committed lymphoid progenitor)? Is it due to a different chromatin structure that may influence the position of the breakpoint and the formation of the hybrid gene [9], or to an aberrant activity of the machinery for V(D)J or class switch recombination, or to different DNA-repair mechanisms, or to a microenvironment with a different oxygen tension? Second, what are the biological and clinical consequences of the difference in transcript types, the e13a2 gene being possibly associated with a minor sensitivity to TKIs in CML [8], and at the same time being prevalent in an aggressive leukemia like ALL, that is only temporarily sensitive to TKIs [10–12]? Third, is the transcription efficacy of the two fusion genes identical, or is the turnover of the two mRNAs different, resulting in different amounts of transcript? Fourth, have the two proteins the same leukemogenic potency, have they the same turnover, is the cellular level identical? Fifth, is the sensitivity of the two chimeric proteins to TKIs different? Sixth, is the immunogenicity of the two chimeric transcripts and of the two resulting proteins identical? Of course all these questions need to be addressed also for the more common form of Ph+, BCR-ABL1<sup>P190+</sup> ALL (e1a2 or e1a3) [13–15], not forgetting that P190 can also cause CML, although rarely [8]. The answer to these questions may help to optimize the management of Ph+ ALL patients, and also to improve our knowledge on the relationships of genes and gene/protein expression with leukemia.

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### Compliance with ethical standards

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

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