RAPID COMMUNICATION

A Possible Correlation Between the Type of bcr-abl Hybrid Messenger RNA and Platelet Count in Philadelphia-Positive Chronic Myelogenous Leukemia

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The Philadelphia (Ph1) chromosome, in which the hybrid bcr-abl gene is formed, is thought to be the initial event in chronic myelogenous leukemia (CML). The position of the breakpoint within the breakpoint cluster region (bcr) on Ph1 chromosome and the splicing pattern determine the species of the fused bcr-abl messenger RNA (mRNA). We tried to detect the two types of fused mRNAs in 57 chronic-phase cases of Ph1-positive CML using the polymerase chain reaction procedure (RT-PCR). The bcr exon 2/afl exon 2 fused mRNA (b2-a2) was detected in 17 patients, the bcr exon 3/afl exon 2 fused mRNA (b3-a2) was detected in 34 patients, and both types of mRNA were detected in six patients. The platelet counts of patients who expressed b3-a2 mRNA or both types were significantly higher than those of patients who expressed only b2-a2 mRNA (841.5 ± 375.5 x 10^9/L; P < .015), although there was no significant difference in the white blood cell counts or hemoglobin. This finding suggests a possibility that the type of bcr-abl mRNA may affect the thrombopoietic activity in CML.

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A SHORTENED chromosome 22, designated as the Philadelphia (Ph1) chromosome, is observed in the leukemic cells of more than 90% of chronic myelogenous leukemia (CML) patients. The Ph1 chromosome, which can be considered to be the first karyotypic marker consistently present in a human neoplasm, is the result of a reciprocal translocation between chromosomes 9 and 22, which in turn may affect the clinical features of CML. This translocation moves the c-abl proto-oncogene from chromosome 9 to chromosome 22. The breakpoint of chromosome 22 has been shown to be clustered within a limited region of about 5.8 kb, referred to as the breakpoint cluster region (bcr). Almost all of the patients have genomic breakpoints between exons b2 and b3 or between exons b3 and b4 within bcr. The two chimeric genes may be distinguished by Southern blot analysis. The first indication that the precise location of the breakpoint on chromosome 22 might have some clinical significance came from a study by Schaefer-Rego et al. Next, a study by Eisenberg et al. showed that the mean duration of the chronic phase for patients who had progressed to blast crisis was significantly shorter for patients with a 3'-breakpoint site than for those with a 5'-breakpoint site within bcr. Many studies have reported on this controversial point. Even a small difference in the location of the breakpoint within the bcr gene may cause a change in the amino acid sequence of the fused protein, which in turn may affect the clinical features of CML patients. Recently, we reported that CML patients with a 3' breakpoint within the bcr gene have higher thrombopoietic activity than those with a 5' breakpoint.

Here, we tried to ascertain the relationship between thrombopoiesis and the two potential types of fused bcr-abl messenger RNAs (mRNAs) using the polymerase chain reaction (RT-PCR) in 57 CML patients. As expected, we found that patients with fused b3-a2 mRNA had higher platelet counts than those with fused b2-a2 mRNA.

MATERIALS AND METHODS

Patient population. Blood and bone marrow samples were obtained from 57 Ph1-positive CML patients in the chronic phase of the disease. Most of the patients had not received therapy before RNA analysis. The clinical data of each patient are that at diagnosis.

RT-PCR for detection of bcr-abl fusion mRNA. The total RNA of mononuclear cells was extracted by the CoCl method. RT-PCR was performed using the methods described by Roth et al. and by Kawasaki et al. with a slight modification. Approximately 2 μg of total RNA was used as the template with 10 U of avian myeloblastosis virus reverse-transcriptase (Boehringer-Mannheim, Indianapolis, IN) for 1 hour at 37°C in 50 mmol/L Tris-HCl pH 8.3, 50 mmol/L KCl, 8 mmol/L MgCl₂, 10 mmol/L dithiothreitol, dNTPs at 500 μmol/L each in a total volume of 50 μL with 0.05 OD₅₅₀ units of oligo-primer (abl-RT: 5'-AAGCGAAAGGTGGGGTC-3', antisense strand). Ten microliters of the reverse transcriptase reaction mixture was adjusted to PCR conditions (10 mmol/L Tris-HCl pH 8.3, 50 mmol/L KCl, 15 mmol/L MgCl₂, 2 mmol/L dithiothreitol, 200 μmol/L dNTPs) with 0.0125 OD₅₅₀ units of one of two sets of primers (the first set, A: 5'-AACGAAAAGGTGGGGTC-3', coding strand, and B: 5'-TCACGATCCACCCGACCA-3', coding strand, and B: 5'-TCACGATCCACCCGACCA-3', antisense strand); the second set: C: 5'-GGAGCTGCAGATGCTGACCAAC-3', antisense strand, and D: 5'-TCGACGGTGATCCATACAC-3', antisense strand) and 2 U of Taq polymerase (Thermus aquaticus DNA polymerase; Perkin Elmer Cetus, Norwalk, CT) in a 50 μL reaction volume (Fig. 1). PCR of 40 cycles was performed, consisting of 30 seconds at 94°C (denaturation), 30 seconds at 55°C (annealing), and 1 minute at 75°C (extension). Finally, the PCR products (20 μL) were phenol-extracted, ethanol-precipitated, and electrophoresed through a 2% agarose gel. The PCR products were visualized directly in ethidium bromide-stained gels, photographed, and transferred onto Gene Screen Plus membranes (New England Nuclear, Boston, MA). Southern hybridization was performed using a 0.6HB probe corresponding to the bcr exon 2 (provided by Dr S. Hiroswa, Tokyo Medical and Dental University), or two kinds of oligonucleotides (E: 5'-GCTGAAGGGCTT-
**RESULTS**

RNA samples from 57 CML patients were analyzed for specific *bcr-abl* mRNA. The *bcr-abl* mRNA junctions were amplified by the RT-PCR method using two pairs of primers. The two junctions, *bcr2-abl2* and *bcr3-abl2*, were identified by their electrophoretic mobility and hybridization to *bcr exon2* (0.6HB) probe or junction-specific oligoprobes. An example of the RT-PCR analysis in which a pair of primers (primers A and B) was used is shown in Fig 2. The RT-PCR products of RNA samples from K562 cells and five CML patients were electrophoresed and subsequently visualized by ethidium bromide staining and hybridization to the 0.6HB probe. The 319-bp RT-PCR product is the band specific for *b3-a2* mRNA, while the 244-bp RT-PCR product is specific for *b2-a2* mRNA. The RT-PCR analysis of 57 patients showed the presence of *b3-a2* mRNA in 34 cases and *b2-a2* mRNA in 17 cases, and coexpression of both junctions in six cases. The relationship between the type of *bcr-abl* mRNA and platelet count is shown in Fig 3. The platelet counts of patients expressing *b3-a2* mRNA were significantly higher than those of patients expressing only *b2-a2* mRNA (841.5 vs 373.5 × 10⁹/L; *P* < .015). We also examined the relationship with the white blood cell count and hemoglobin, but no significant correlations were found.

**DISCUSSION**

Ph1-positive CML is thought to be a clonal myeloproliferative disorder resulting from oncogenic transformation of a bone marrow stem cell. In the chronic phase, the disease phenotype is characterized by pronounced granulocytosis and thrombocytosis in peripheral blood and increased myeloid and megakaryocyte compartments in the hypercellular bone marrow.

Recently, our understanding of the pathogenesis of CML has been greatly advanced by the molecular studies. Ph1-positive CML is characterized by the presence of a *bcr* rearrangement. Attempts have been made to elucidate the relationship between the breakpoint site and the duration of survival or the other clinical features by Southern analysis at the DNA level. Shtalrid et al, Jaubert et al, and Morris et al reported that there was a significant correla-
tion between the site of the bcr breakpoint and the duration of survival. CML patients have one of two bcr-abl mRNA types or both. Application of the RT-PCR method to determine the type of bcr-abl mRNA in CML patients has made it easier to identify the site of the bcr rearrangement. The studies using the RT-PCR method are now prevailing in this research area. Recently, we found that CML patients with a 3' breakpoint site within the bcr gene have a tendency to have higher thrombopoietic activity than those with a 5' breakpoint. Therefore, to confirm this preliminary observation, we extensively studied the relationship between the type of bcr-abl mRNA and the patient's platelet count in 57 Ph1-positive CML cases using the PCR method. As expected, the platelet counts were higher in the patients expressing b3-a2 mRNA.

A recent study reported similar finding in Ph1-positive essential thrombocythemia. The b3-a2 type mRNA was observed in five patients and the b2-a2 type mRNA was observed in only one patient. In our present study, 16 patients who had platelet counts of more than 900 x 10^9/L expressed only b3-a2 type mRNA, and almost all of the patients with b2-a2 type mRNA had a platelet count of less than 600 x 10^9/L. There were no apparent differences in hematologic findings between the patients with b3-a2 type mRNA and the CML patients with b2-a2 type mRNA, except for the platelet count. Thus, we speculate that the type of bcr-abl mRNA may affect the thrombopoietic activity in CML, although we are currently unable to explain why the platelet count correlates with the type of bcr-abl mRNA.

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REFERENCES


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