Duration of the Preclinical Phase of Chronic Myelogenous Leukemia: A Case Report

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The molecular events that allow for clonal expansion of the malignant population in chronic myelogenous leukemia (CML) are poorly understood. Recent experiments in transgenic mice suggest a close temporal relationship between expression of the aberrant protein and manifestation of a hematologic neoplasm that resembles CML; tracing the same phenomenon in humans has not been possible. We studied a patient who underwent autologous bone marrow harvest after completion of chemotherapy and radiation therapy for advanced stage Hodgkin's disease. At the time of harvest his peripheral blood counts and bone marrow were morphologically normal. Sixteen months later he developed the clinical manifestations of CML. Detailed molecular evaluation of the harvested marrow showed that a small number of cells contained the Philadelphia chromosome. The time interval required for expansion of the malignant clone, as suggested by this particular patient, was at least 16 months although it is recognized that this figure may be variable.

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The blast count was 1.5%. Cytogenetics showed 46, XXY, t(9;22) (q34;q11) in the metaphases positive for the Ph chromosome; no additional abnormalities were observed. A marrow obtained 3 weeks after the transplant showed 20 normal metaphases without the Ph chromosome; no additional abnormalities were observed. A marrow obtained 6 weeks after the transplant showed all 20 metaphases with rearranged BCR.

Table 1. Serial Peripheral Blood, Bone Marrow, Cytogenetic and Molecular Analysis of Patient Who Developed CML After Therapy for Hodgkin's Disease

<table>
<thead>
<tr>
<th>Status</th>
<th>Date</th>
<th>WBC Count (g/dL)</th>
<th>Hemoglobin (g/dL)</th>
<th>Platelets (μL)</th>
<th>BM Status</th>
</tr>
</thead>
<tbody>
<tr>
<td>At time of HD diagnosis (pathologically staged</td>
<td>2/87</td>
<td>9.600 (84%, 6M, 11L)*</td>
<td>13.5</td>
<td>332,000</td>
<td>Normocellular</td>
</tr>
<tr>
<td>After completion of radiation therapy (mantle, para-aortic)</td>
<td>6/87</td>
<td>9,700 (74%, 20M, 5L)</td>
<td>15.1</td>
<td>227,000</td>
<td></td>
</tr>
<tr>
<td>New inguinal adenopathy and B symptoms; lymphocytic lesion left hip</td>
<td>10/87</td>
<td>12,600</td>
<td>11.6</td>
<td>298,000</td>
<td>Hypercellular atypical cells present consistent with HD</td>
</tr>
<tr>
<td>After completion of 9 cycles of MOPP/ABV/CAV (see text) for details and just before autologous marrow harvest</td>
<td>12/88</td>
<td>6,600 (58%, 10M, 32L)</td>
<td>14.8</td>
<td>386,000</td>
<td>Somewhat hypocellular; normal hematopoietic elements seen; no evidence of HD</td>
</tr>
<tr>
<td>Follow-up visit</td>
<td>2/89</td>
<td>6,100</td>
<td>13.8</td>
<td>280,000</td>
<td></td>
</tr>
<tr>
<td>Follow-up visit</td>
<td>4/89</td>
<td>6,900</td>
<td>14.5</td>
<td>316,000</td>
<td></td>
</tr>
<tr>
<td>Follow-up visit</td>
<td>6/89</td>
<td>6,000</td>
<td>14.0</td>
<td>321,000</td>
<td></td>
</tr>
<tr>
<td>Follow-up visit</td>
<td>9/89</td>
<td>7,600</td>
<td>15.2</td>
<td>275,000</td>
<td></td>
</tr>
<tr>
<td>Follow-up visit</td>
<td>1/90</td>
<td>9,600</td>
<td>14.5</td>
<td>316,000</td>
<td></td>
</tr>
<tr>
<td>Follow-up visit</td>
<td>9/90</td>
<td>22,900†</td>
<td>13.1</td>
<td>293,000</td>
<td>Hypercellular; no evidence of HD</td>
</tr>
<tr>
<td>Follow-up visit</td>
<td>10/90</td>
<td>27,400</td>
<td>14.9</td>
<td>373,000</td>
<td></td>
</tr>
</tbody>
</table>

**Results**

Serial blood counts and bone marrows and their relationship to disease status are outlined in Table 1. At the time of the patient's HD diagnosis (February 1987) his CBC, differential, and bone marrow appeared normal. He underwent splenectomy with staging laparotomy followed by radiation therapy to the mantle and para-aortic fields. He developed transient leukocytosis and thrombocytosis with a mild left-shift when HD presented again as new inguinal adenopathy and a lytic lesion in the left hip (October 1987). After completion of chemotherapy, his blood count and

**Preparation of frozen marrow for analysis.** A sample of the marrow that had been harvested and frozen in 1988 was defrosted. The cells were incubated on ice for 30 minutes with DNase (60 U/mL) (Worthington Biochemical, Freehold, NJ) followed by Ficoll-Hypaque (Pharmacia, Piscataway, NJ) separation to remove nonviable cells. A sample of marrow cells derived from the interphase was stimulated overnight with Mo T-cell line conditioned medium (MoCM) kindly provided by Dr David Golde (Memorial Sloan Kettering Cancer Center) before cytogenetic analysis. In addition, the marrow cells were cloned in methyl cellulose as previously described to obtain colony-forming unit granulocyte macrophage (CFU-GM)-derived colonies for detecting the bcr-abl transcript by polymerase chain reaction (PCR) analysis.

**Cytogenetic analysis.** Chromosome preparations from the bone marrow aspirate were obtained following methods described earlier. Air-dried metaphase spreads were G-banded and the karyotypes were described according to the International System for Human Cytogenetic Nomenclature.

**Breakpoint cluster region analysis.** BCR analysis was performed on fresh marrow cells obtained from the patient in May 1990 for Southern blotting following methods previously described. The 5.8-kb Phi-3/bcr probe (Oncogene Science, Inc, Manhasset, NY) was labeled to high specific activity with 32P following the method described by Feinberg and Vogelstein.

**PCR analysis.** This method has been previously described in detail elsewhere. Briefly, individual 14-day CFU-GM-derived colonies were removed from the methyl cellulose cultures with a finely drawn Pasteur pipette and total RNA from each colony was isolated according to the method of Chomczynski and Sacchi. First-strand complementary DNA (cDNA) corresponding to all mRNAs in the sample was obtained by using random hexamers in a reverse-transcription reaction. cDNA then served as the substrate in the PCR analysis. To insure the integrity of the RNA extracted from each colony, β-actin and bcr-abl cDNA sequences were amplified in the same reaction vessel. Positive controls included RNA isolated from K562 colonies and CFU-GM derived from a patient with Ph-positive blast crisis. Negative controls included RNA isolated from normal CFU-GM-derived colonies.
were normal for the next 16 months (April 1990) when exposure. Based on these data, it was calculated that the cells seen in the differential. No evidence of HD was found leukocytosis was again noted, this time with early myeloid clinical manifestations of the disease (Table 1).

A total of seven metaphases were available for cytogenetic analysis from the frozen marrow harvested in December 1988 (Table 1). Only one cell was Ph-positive. Although no clonal rearrangement of the BCR gene could be detected because of an inadequate amount of DNA obtained, PCR analysis of day 14 colonies grown from the defrosted sample showed bcr-abl rearrangement in 1 of 40 colonies examined.

**DISCUSSION**

This patient with HD had the Ph chromosome detected in some hematopoietic precursor cells 18 months after completion of radiation therapy and 1 month after completion of chemotherapy for relapsed disease. However, another 16 months elapsed before the clinical manifestations of the CML appeared. Given the treatment regimens that this patient received, one can question whether these may have played a causative role in the development of CML. While not as commonly reported as secondary myelodysplastic syndromes or acute myelogenous leukemia, CML has been reported after primary treatment for other malignancies with the time interval between initial therapy and the development of CML ranging from 36 to 81 months. Few cases of CML have been reported after treatment for HD. Swaim et al described a patient with HD who developed a CML-like syndrome 7 years after having received a total of 443.2 Gy to various body sites although no cytogenetic data were presented. Verhoef et al reported a patient with stage III-B nodular sclerosing HD who received combination chemotherapy with MOPP for a total of 8 months. Pretreatment bone marrow biopsy and karyotype were normal. This patient subsequently developed Ph-positive CML 7 years after completion of chemotherapy.

Our patient had a 38-month interval between the diagnosis of HD and the laboratory evidence of CML. Uniquely, cytogenetic and PCR documentation of rare Ph-positive cells was made 16 months before the development of the clinical manifestations of the disease (Table 1).

Little information is available on the duration of the preclinical phase of CML. Kamada and Uchino constructed a model of disease evolution after studying 16 atomic bomb survivors who had received close hematologic follow-up for 5 to 10 years before the development of CML and 102 patients with CML with or without atomic bomb exposure. Based on these data, it was calculated that the elapsed time from occurrence of a single cell containing the Ph chromosome to a leukemic cell burden of 100,000 cells/µL was 6.3 years. This formulation appeared reasonable when compared with the peak incidence of CML in atomic bomb survivors that occurred about 6 to 8 years after exposure, with younger individuals (<15 years) having a shorter latency period than older individuals (>30 years). The earliest cases of CML were diagnosed 4 to 5 years after the explosion.

Such estimates are crude, but are nonetheless consistent with previous observations which suggest that there may be a period of at least several years between the original cytogenetic transformation and the development of the disease. Long-term cytogenetic follow-up of patients who have undergone allogeneic bone marrow transplantation (BMT) for CML also suggests that there may be a relatively long period between reappearance of Ph-positive cells in the marrow and hematologic relapse. Ofit et al studied serial cytogenetics in 64 patients with CML who had undergone T-cell-depleted allogeneic BMT. Sixteen patients had a cytogenetic relapse; 12 of these patients relapsed clinically a median of 6 months (range 0 to 12 months) after reappearance of Ph-positive cells. Three patients with evidence of cytogenetic relapse remained free of clinical disease 6, 12, and 22 months from time of cytogenetic relapse. Similarly, Arthur et al reported that 11 of 48 patients who underwent allogeneic BMT in chronic phase CML had recurrence of the Ph chromosome without hematologic relapse.

In other instances it is apparent that the development of the Ph chromosome and the disease manifestations are more closely linked. CML has been reported in a 3-month-old infant, which suggests the time from cytogenetic transformation to frank disease was, in this case, relatively rapid; however, the mass of leukemia cells is of course significantly smaller in infants.

Chronological study of our patient is of interest because it has defined at least a 16-month interval between the appearance of Ph-positive cells and clinical signs of the disease. Few other similar case studies have been reported. Canellos and Whang-Peng reported a patient who had a normal blood count but had metamyelocytes and myelocytes present in the peripheral smear; the bone marrow had the Ph chromosome present in 22% of metaphases but no leukocytosis developed for 5 years.

There are obviously few opportunities to study the very early phase of CML in humans as most patients present simultaneously with the clinical manifestations of the disease and the Ph chromosome present in the majority of cells. It is important to note that in the current study the earliest specimen available for analysis was the frozen sample obtained 16 months before the full manifestations of the disease and that the PCR analysis was performed on the cryopreserved buffy coat marrow cells that were subsequently thawed and grown in methyl cellulose. If fresh buffy coat marrow cells had been available, it is possible that the fraction of Ph-positive cells would have been higher because the major expansion of the CML population has been shown to occur in the later maturation compartment and
the freezing process preferentially destroys more mature progenitor cells. Thus, the ratio of CML: normal progenitors determined from the cryopreserved specimen may not have been an accurate assessment of the size of the CML progenitor population 16 months before the clinical manifestation of the disease.

REFERENCES

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