Prognostic significance of cellular vascular endothelial growth factor expression in chronic phase chronic myeloid leukemia

Srdan Verstovsek, Hagop Kantarjian, Taghi Manshouri, Jorge Cortes, Francis J. Giles, Anna Rogers, and Maher Albitar

The impact of elevated vascular endothelial growth factor (VEGF) expression on the course of chronic myeloid leukemia (CML) is unknown. By radioimmunoassay, we measured pretreatment cellular VEGF protein in bone marrow samples from 184 (148 chronic and 36 accelerated/blast phases) CML patients and found the levels to be 1.6-fold higher than in 31 normal control bone marrow samples ($P = .0001$). No significant differences were found in VEGF levels by different phases of CML ($P = .1$). VEGF levels correlated with older age ($P = .01$) and higher platelet count ($P = .0003$), but also with smaller spleen size ($P = .004$), lower white blood cell count ($P = .0006$), and lower percentage of peripheral blasts ($P = .04$). With the use of Cox proportional hazard model and VEGF levels as a continuous variable, high VEGF levels correlated with shorter survival of patients in chronic CML ($P = .008$). Multivariate analysis showed that VEGF was not independent of the synthesis stage ($P = .09$). These data suggest that VEGF plays a role in the biology of CML and that VEGF inhibitors should be investigated in CML. (Blood. 2002;99:2265-2267)

Introduction

Increased microvessel density has been documented in the bone marrow of patients with several hematologic cancers, including chronic myeloid leukemia (CML). Vascular endothelial growth factor (VEGF) plasma levels have also been shown to be significantly higher in CML patients compared with normal controls.1 Lundberg et al2 reported the number of VEGF+ bone marrow cells to be significantly higher in samples from CML patients than in normal controls and to correlate with bone marrow vascularity. Ratajczak et al3 reported that VEGF was produced by granulocyte-macrophage colony-stimulating factor/interleukin 3–supported cell colonies derived from CML patients and that VEGF costimulated colony formation of cells obtained from approximately 15% of CML patients studied. Furthermore, VEGF receptor–1 messenger RNA was detected in all 15 chronic phase CML samples examined.3 The clinical relevance of VEGF expression on CML outcome is unknown. Several therapeutic approaches targeting the VEGF/VEGF-receptor (VEGF-R) system have recently been developed.4 Thus, it is important to understand the significance of VEGF in CML to better define the potential role of these approaches in CML therapy. In this study, we examined cellular VEGF protein expression in the bone marrow of patients in different phases of CML and assessed its prognostic significance.

Study design

Patients and controls

Pretreatment cellular VEGF protein concentrations were measured in bone marrow samples collected from 184 patients with CML at presentation to the University of Texas M D Anderson Cancer Center, and in 31 “normal” control bone marrow samples obtained as a part of staging from patients with suspected lymphoma but without evidence of lymphoma in the bone marrow. Although the control samples are actually not normal, they show cell populations similar to those seen in normal bone marrows and are the closest to normal available to us. All samples were obtained under protocols approved by the Internal Review Board and with the patient’s written informed consent. The characteristics of patients are shown in Table 1.

Protein extraction and Western blot analysis

Protein extraction was performed as previously reported in detail.5 VEGF protein was analyzed by means of the Western blot technique as described previously.5 All controls for equal loading of protein were performed as previously described.5

Solid-phase radioimmunoassay

Solid-phase radioimmunoassay (RIA) was used to measure VEGF protein, as described previously.5

Statistical considerations

Associations among variables were assessed by means of the Spearman rank correlation analysis. The Kruskal-Wallis test was used to compare various groups of data. The log-rank test was used to study correlation with patient survival when a cutoff point was used for a given variable. The Cox proportional hazard model was used to study correlation with patient survival when a variable was used as a continuum. The sample size of the chronic phase patient group was chosen on the basis of our goal of analyzing survival. The chronic phase group had 68 events, adequate for fitting a multiple regression model with the 6 covariates (based on the role of approximately 10 events per covariate to protect against overfitting of the data). This covers most of the known important covariates in CML. The
Predictors of shorter survival of patients with chronic phase CML

Characteristics of patients with chronic phase CML, %

<table>
<thead>
<tr>
<th>Disease phase</th>
<th>No.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chronic (early/late)</td>
<td>148</td>
</tr>
<tr>
<td>Accelerated</td>
<td>25</td>
</tr>
<tr>
<td>Blastic</td>
<td>11</td>
</tr>
</tbody>
</table>

Table 1. Study patients

Table 2. Patients with chronic phase CML

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Results and discussion

Western blot analysis showed detectable VEGF protein in samples with significantly increased VEGF protein (Figure 1). RIA, a more specific assay, showed VEGF protein in all bone marrow samples. VEGF levels in 184 CML samples were normalized to the median VEGF value in 31 normal control bone marrow samples, which was assigned a value of 1. The median VEGF value in CML samples was 1.6-fold (range, 0.8–11.3-fold) higher than in normal control samples. The normal control group was comparable to the CML group in age. There were no significant differences of VEGF levels among 118 patients in early chronic, 30 patients in late chronic, 25 patients in accelerated, and 11 patients in blastic phase. The use of Cox proportional hazard model and VEGF levels as a continuous variable, increasing VEGF levels in samples from patients with leukemias. The prognostic significance of VEGF expression has been analyzed in chronic lymphocytic leukemia and in acute myeloid leukemia (AML). In AML, high levels of cellular VEGF were independent predictors of shorter survival and lower complete remission rates. In this study, we showed cellular VEGF protein levels to be highly expressed in all phases of CML and to have significant influence on survival in patients with chronic phase CML. The mechanism behind this observation is not clear. Previous studies have suggested the presence of both autocrine and paracrine VEGF/VEGF-R systems in leukemia. The CML progenitor cell has been recently suggested to arise from a hemangioblastic progenitor cell, the progeny of which are malignant blood cells and genotypically clonal endothelial cells. If this is correct, then malignant endothelial cells might play a role in the increased marrow vascularity in CML, and VEGF might be pathophysiologically linked to CML development. Thus, the examination of endothelial cell mitogens as well as surface markers in the bone marrow of CML patients may contribute to our understanding of its pathophysiology and offer targets for new type of treatments. Role of vascular endothelial growth factor (VEGF) and placenta-derived growth factor (PiGF) in regulating human haemopoietic cell growth. Br J Haematol. 1998;103:969-979.

References

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