Tumor Endothelial Markers Define Novel Subsets of Cancer-Specific Circulating Endothelial Cells Associated with Antitumor Efficacy

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Abstract

Circulating endothelial cells (CEC) are derived from multiple sources, including bone marrow (circulating endothelial progenitors; CEP), and established vasculature (mature CEC). Although CECs have shown promise as a biomarker for patients with cancer, their utility has been limited, in part, by the lack of specificity for tumor vasculature and the different nonmalignant causes that can impact CEC. Tumor endothelial markers (TEM) are antigens enriched in tumor versus nonmalignant endothelia. We hypothesized that TEMs may be detectable on CEC and that these circulating TEM+ endothelial cells (CTEC) may be a more specific marker for cancer and tumor response than standard CEC. We found that tumor-bearing mice had a relative increase in numbers of circulating CTEC, specifically with increased levels of TEM7 and TEM8 expression. Following treatment with various vascular-targeting agents, we observed a decrease in CTEC that correlated with the reductions in tumor growth. We extended these findings to human clinical samples and observed that CTECs were present in patients with esophageal cancer and non–small cell lung cancer (N = 40), and their levels decreased after surgical resection. These results demonstrate that CTECs are detectable in preclinical cancer models and patients with cancer. Furthermore, they suggest that CTECs offer a novel cancer-associated marker that may be useful as a blood-based surrogate for assessing the presence of tumor vasculature and antiangiogenic drug activity.

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Introduction

Angiogenesis is a key step in tumor progression, including the spread and growth of metastases. Therefore, considerable effort has been directed at targeting the vascular component of malignant disease. Antiangiogenic agents targeting the VEGF pathway, such as the monoclonal antibody bevacizumab and the tyrosine kinase inhibitor AZD2171, have demonstrated clinical activity in multiple malignancies, including non–small cell lung cancer (NSCLC), renal cell cancer, and colorectal cancer (1–5). Currently, clinical studies evaluating the efficacy of such agents are hindered by the lack of validated surrogate markers of drug activity. Availability of blood-based biomarkers would be paramount because they could predict which patients are most likely to benefit from treatment before clinical progression (6, 7).

In recent years, we and other investigators have studied a number of circulating biomarkers for VEGF pathway inhibition in peripheral blood that are derived from circulating endothelial cells (CEC) and myeloid lineage cells, circulating proangiogenic factors and receptors, and soluble markers of hypoxia and endothelial damage (7–11). Elevated levels of CECs (CD45−CD31+CD146+ cells) are detected in patients with renal cell carcinoma as compared with the levels found in normal control subjects and are associated with advanced disease (12). It has become evident that among CECs in blood, some express a progenitor-like phenotype defined as circulating endothelial progenitors (CEP), whereas others show the characteristics of mature, terminally differentiated cells (mature CECs). Although mature CECs are thought to shed from existing vessels, CEPs are derived from the bone marrow and can home to sites of angiogenesis and participate in the generation of new vessels in adults (13, 14).

Both CECs and CEPs have been investigated as biomarkers for antiangiogenic therapy in preclinical models and clinical studies (8–10, 15–18). Levels of mature CECs typically change...
in patients treated with antiangiogenic or vasculature-targeting agents (8, 15–17). We have also observed that among patients with gastrointestinal stromal tumors, changes in CECs were a marker of clinical benefit for patients treated with the multitargeted kinase inhibitor sunitinib (8).

Not specific to cancer, CECs occur during pathologic conditions such as vasculitis (19), infection (20), and myocardial infarction (21). There is an unmet need to identify CEC populations that more precisely reflect the presence of, or changes in, tumor vasculature. Global analysis of altered gene expression patterns in endothelial cells from human colorectal cancer tissues revealed a series of genes termed tumor endothelial markers (TEM; ref. 22). Since being first described, TEMs have received considerable attention as potential markers or targets of tumor vasculature. Further studies have indicated that some TEM expression may not be limited to the tumor vasculature. In addition to TEMs, published reports have indicated that CD276 (B7-H3), a leukocyte costimulatory molecule, may be overexpressed by endothelial cells during pathologic but not physiologic angiogenesis (23).

We hypothesized that a subset of CECs may originate from tumor endothelium sloughed into peripheral circulation, and that such CECs could be distinguished from CECs derived from other sources by the presence of TEMs. Here, we evaluated CECs in both murine models of human NSCLC and patients with esophageal carcinoma. Our data suggest that specific subpopulations of CECs bear TEMs, and circulating TEM+ endothelial cells (CTEC) may be useful as blood-based markers for detecting the presence of cancer or monitoring response to therapies that affect the tumor vasculature.

Materials and Methods

Cell lines

The adenocarcinoma cell line H1975 was provided by Drs. John Minna and Adi Gazdar (The University of Texas Southwestern Medical School, Dallas, TX). MS-1 and Lewis lung cancer cells were obtained from American Type Culture Collection. All cell lines were maintained in RPMI-1640 medium with 10% FBS, penicillin-streptomycin, and t-glutamine.

Mice

Athymic nude mice (Ncr-nu) were purchased from Charles River Laboratories. All animals were housed under pathogen-free conditions in facilities approved by the Association for Assessment and Accreditation of Laboratory Animal Care and in accordance with current regulations and standards of the United States Department of Agriculture and NIH. At the time of the studies, the nude mice were 8 to 10 weeks old and the C57BL/6 mice were 6 to 8 weeks old.

Flow cytometric analysis of circulating endothelial cells in mice

For both humans and mice, CECs in peripheral blood were evaluated by flow cytometry as previously described (24, 25). Red cell lysis was performed using FACSLyse solution (BD Biosciences) as per the manufacturer’s directions, and 100 μL of blood was analyzed for each mouse. The following directly conjugated antibodies were used for detection of CECs and CEPs in peripheral blood in mice: anti-mouse CD45-PerCP, Flk-1-Alexa 700 (mouse VEGFR-2), CD31-APC (platelet/endothelial cell adhesion molecule-1), and CD117-PE-Cy7 (c-kit receptor; all from BD Biosciences). Syto 16 (Molecular Probes) was used as a nuclear stain to identify nucleated cells and exclude debris, platelets, and macroparticles. It was not used to distinguish between apoptotic and nonapoptotic cells (24). As previously described, in mice CECs were characterized as CD31+CD45+VEGFR-2+CD117–, and CEPs as CD31+CD45+VEGFR-2+CD117+. For detection of CD276, cells were stained with phycoerythrin (PE)-conjugated streptavidin. Flow cytometry was done using a FACS Canto flow cytometer (BD Biosciences), and acquired data were analyzed with FlowJo software (Tree Star) with analysis gates designed to remove residual platelets and cellular debris. For each mouse, a minimum of 100,000 events were typically counted. MS-1 cells, a transformed murine endothelial cell line isolated from pancreatic islets of C57BL/6 mice, were used as a positive control for endothelial cells. The gating strategy from a representative mouse blood specimen is shown in Supplementary Fig. S1.

Flow cytometric analysis of circulating endothelial cells in human specimens

For human specimens, CTEC and CEC/CEP populations were evaluated by eight-color flow cytometry. The following antibodies were used: CD276-PE (R&D Systems), CD146-PerCP-Cy5 (Beckman Coulter), CD31-PECy7 (BD Biosciences), CD133-APC (Miltenyi Biotec), and CD45-APC-Cy7(eBiosciences), Syto16 (Molecular Probes) was used as a nuclear stain to identify nucleated cells and exclude debris, platelets, and macroparticles. It was not used to distinguish between apoptotic and nonapoptotic cells. Cells were gated on the basis of side scatter (SSC) and forward scatter (FSC) to display major blood components of the Syto16+ peripheral blood mononuclear cells (PBMC). Antibodies directed against CD45 were used to exclude hematopoietic cells. CD133 antibodies were used to identify progenitor cells. Endothelial cells were identified with antibodies against CD146 and CD31. CECs were identified as CD45−CD133+/CD146+/CD31+. CEPs were identified as CD45−CD133+/CD146−/CD31+. CTECs were identified as CD45−CD133−/CD146−/CD31−/CD276−. To establish absolute CEC counts, the volume of blood analyzed was determined by using the lymphocyte or mononocyte counts obtained from the patients’ differential white cell counts. The gating strategy from a representative human blood specimen is shown in Supplementary Fig. S2.

Xenograft model and antiangiogenic treatment

A total of 1.0 × 106 murine Lewis lung carcinoma (LLC) tumor cells and 1.0 × 106 H1975 human NSCLC cells were injected subcutaneously into the flanks of C57BL/6 mice and nude mice, respectively. When tumors reached a volume
of 300 mm³, mice were stratified into treatment groups of 5 animals per group. Animals received vehicle (91% polysorbate 80) by oral gavage or the VEGF receptor (VEGFR)-2 inhibitor AZD2171 (6 mg/kg; gavage) daily for 14 days. For VEGF treatment, mice were injected intraperitoneally with 10 μg of recombinant human VEGF (National Cancer Institute, Biological Resources Branch, Bethesda, MD) daily for 5 days.贝伐单抗 was administered intraperitoneally at a dose of 5 mg/kg twice weekly.

Animals were weighed weekly and tumor volume was measured twice weekly. After treatment, mice were given isoflurane anesthesia, and blood was collected by retro-orbital puncture and anticoagulated using 0.5 mol/L EDTA. After mice were euthanized, tumors were harvested and frozen in OCT embedding medium (Sakura Finetek).

**Immunohistochemistry**

Frozen tumor sections were fixed in acetone for 10 minutes and washed three times with PBS. Sections were blocked for 1 hour with 5% normal horse serum and 1% normal goat serum in PBS and incubated with primary antibodies TEM7 (1:1000; Imgenex), TEM8 (1:500; Abcam), and CD276 (1:1000; eBioscience) overnight at 4°C. Slides were washed with PBS and incubated with secondary antibody Alexa 488 (1:600, Molecular Probes) for 1 hour at room temperature.

For double staining, each slide was washed with PBS and incubated with antibodies directed against CD31 (1:500, BD Biosciences) or smooth muscle actin (Dako) at 4°C overnight. After being washed with PBS, slides were incubated with secondary antibody Alexa 488 (1:600, Molecular Probes) for 1 hour at room temperature. Cell nuclei were stained using 4,6-diamidino-2-phenylindole (Vector Laboratories).

**Isolation of endothelial cells**

Endothelial cells were isolated from tumor xenografts by using a Magnetic Cell Sorting (MACS) system (Miltenyi Biotec). Tumors were excised when they reached approximately 1 cm in diameter. Normal endothelial cells were obtained from excised skin, lung, liver, and epididymal fat pads of the same mice. Excised tissue was minced and digested with collagenase II (Worthington). Blood cells were removed by single sucrose step-gradient centrifugation with Histopaque 1077 (Sigma-Aldrich), (Worthington). Blood cells were removed by single sucrose step-gradient centrifugation with Histopaque 1077 (Sigma-Aldrich) according to the manufacturer's instructions. Then, the cells were resuspended in cell-freezing medium (20% dimethyl sulfoxide, 80% RPMI-1640) and stored in liquid nitrogen until the day of analysis. Baseline and follow-up samples for each patient were analyzed together to minimize inter assay variability.

**Statistical analysis**

For animal studies, Mann–Whitney test was used to compare differences in CTECs, CECs, and CEPs between treatment groups. Mann–Whitney test was used to compare differences in CTECs/ECs among patients with cancer and healthy volunteers. Wilcoxon signed rank test was used to look at changes in those values in terms of absolute differences between the samples collected before and after surgery. Correlation between CTECs cell counts and tumor size was determined by Spearman rho correlation test. Survival was analyzed using the Kaplan–Meier method.

**Results**

**Expression of tumor endothelial markers**

As a first step toward assessing whether TEMs could be detected on tumor-derived CECs, we evaluated the effect of expression of various TEMs and CD276 on the vasculature of normal tissue and LLC tumor tissue in the C57BL/6 mouse model by immunohistochemistry (Fig. 1). The immunoreactivity of TEMs was detectable in all tumor tissues and was absent or minimally detectable in normal lung tissue with the exception of TEM5, which was expressed on endothelium from both tumor and normal tissues in our analysis. TEM expression was also absent in normal skin from mice (data not shown). TEM7, TEM8, and CD276 colocalized with CD31, suggesting that their expression is primarily limited to the tumor endothelium (Fig. 1), although some staining of perivascular cells was noted for TEM7. TEM1 and TEM4 exhibited considerable expression in tumor pericytes, which was confirmed by double staining with the smooth muscle marker actin (data not shown). Our observation that TEM1 and TEM5 are expressed on perivascular cells and normal endothelium, respectively, is consistent with previous reports (23, 26). These results indicated that the expression of most TEMs was relatively tumor specific and that for some TEMs expression was not limited to tumor endothelial cells. TEM7, TEM8, and CD276 seemed to be the most promising markers based on these immunohistochemical results.

**Expression of TEMs on endothelial cells isolated from normal and tumor tissues assessed using flow cytometry**

Using flow cytometry, we next investigated whether TEMs could be detected on endothelial cells isolated from tumor
tissue or normal tissue. In preliminary studies, we identified antibodies against TEM7 and CD276, but not TEM8, which were suitable for use in flow cytometry. Murine endothelial cells were purified from both the normal and tumor-derived tissues of H1975 xenografts using CD31-immunomagnetic beads. The purity of endothelial cells was confirmed using the FITC-conjugated cell surface protein BSI-B4.

CTECs were defined on the basis of the presence of CEC markers (CD31+CD45−VEGFR-2−CD117+; ref. 7) as well as CD276 or TEM7 immunoreactivity. CD276 or TEM7 immunoreactivity was detected in 6% to 10% of total endothelial cells from normal skin or lung tissue, and in 30% and 22%, respectively, of tumor endothelial cells (Fig. 2). Because CD276 expression on liver endothelium has previously been described (27), liver endothelial cells were included in our analysis. Consistent with earlier reports, CD276 could be detected on tumor endothelial cells by flow cytometry, and the expression of CD276 could also be detected on endothelial cells from liver tissue in nontumor-bearing mice.

**Circulating TEM+ endothelial cells are elevated in tumor-bearing animals**

We used blood from mice bearing H1975 human NSCLC xenografts to test our hypothesis that the number of CTECs would be higher in tumor-bearing than nontumor-bearing mice. As previously described, CECs and CEPs were characterized as CD31+CD45−VEGFR-2−CD117− and CD31+CD45−VEGFR-2−CD117−, respectively (7, 9, 17, 28, 29). We refer to the CECs coexpressing TEM7 and CD276 as TEM7 CTECs and CD276 CTECs, respectively. We found that levels of CECs and CEPs were higher in tumor-bearing than nontumor-bearing mice, although the differences were not significant (P = 0.41 and 0.26, respectively). In contrast, the numbers of CD276 CTECs and TEM7 CTECs were significantly increased in the blood of tumor-bearing mice compared with the controls (P = 0.041 and 0.032, respectively; Fig. 2B), demonstrating relative specificity of CTECs for the presence of tumor.

<table>
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<tr>
<th>Characteristic</th>
<th>N (%)</th>
<th>Before Median (range) cells/μL</th>
<th>One month after Median (range) cells/μL</th>
<th>P</th>
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<tr>
<td>Overall</td>
<td>40 (100)</td>
<td>0.38 (0.00–2.40)</td>
<td>0.11 (0.00–0.66)</td>
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<tr>
<td>Female</td>
<td>13 (32.5)</td>
<td>0.49 (0.16–1.39)</td>
<td>0.11 (0.01–0.66)</td>
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<td>Male</td>
<td>27 (67.5)</td>
<td>0.33 (0.00–2.40)</td>
<td>0.10 (0.00–0.37)</td>
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<tr>
<td>Caucasians</td>
<td>34 (85)</td>
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<td>0.10 (0.00–0.66)</td>
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<tr>
<td>Others</td>
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<td>0.54 (0.05–0.97)</td>
<td>0.13 (0.00–0.56)</td>
<td>0.116</td>
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<tr>
<td>Never</td>
<td>9 (22.5)</td>
<td>0.24 (0.05–0.91)</td>
<td>0.06 (0.00–0.30)</td>
<td>0.028</td>
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<tr>
<td>Ever</td>
<td>31 (77.5)</td>
<td>0.41 (0.00–2.40)</td>
<td>0.11 (0.00–0.66)</td>
<td>&lt;0.001</td>
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<td>0.14 (0.01–0.66)</td>
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<tr>
<td>Yes</td>
<td>27 (67.5)</td>
<td>0.35 (0.00–2.40)</td>
<td>0.10 (0.00–0.56)</td>
<td>&lt;0.001</td>
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<td>Complete pathologic response</td>
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<td>21 (52.5)</td>
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<td>0.13 (0.00–0.66)</td>
<td>&lt;0.001</td>
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<td>Yes</td>
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<td>0.00 (0.00–0.21)</td>
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<td>Lung</td>
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<td>0.47 (0.16–1.49)</td>
<td>0.14 (0.00–0.66)</td>
<td>0.002</td>
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<tr>
<td>Esophagus</td>
<td>22 (55)</td>
<td>0.23 (0.00–2.40)</td>
<td>0.06 (0.00–0.37)</td>
<td>&lt;0.001</td>
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<td>Adenocarcinoma</td>
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<td>0.11 (0.00–0.66)</td>
<td>&lt;0.001</td>
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<td>Squamous cell carcinoma</td>
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<td>0.10 (0.00–0.14)</td>
<td>0.109</td>
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<td>Other</td>
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<td>0.11 (0.01–0.23)</td>
<td>0.680</td>
</tr>
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</tr>
<tr>
<td>I</td>
<td>10 (25)</td>
<td>0.33 (0.16–1.39)</td>
<td>0.11 (0.00–0.66)</td>
<td>0.009</td>
</tr>
<tr>
<td>II</td>
<td>13 (32.5)</td>
<td>0.37 (0.02–2.40)</td>
<td>0.11 (0.00–0.36)</td>
<td>0.005</td>
</tr>
<tr>
<td>III</td>
<td>17 (45.5)</td>
<td>0.44 (0.00–1.43)</td>
<td>0.10 (0.00–0.37)</td>
<td>0.005</td>
</tr>
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<tr>
<td>No</td>
<td>22 (55)</td>
<td>0.31 (0.00–1.43)</td>
<td>0.12 (0.00–0.66)</td>
<td>0.001</td>
</tr>
<tr>
<td>Yes</td>
<td>18 (45)</td>
<td>0.47 (0.00–2.40)</td>
<td>0.10 (0.10–0.56)</td>
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experiment, 77% of CD276\(^+\) CTECs were also TEM7\(^+\), and 57% of TEM7\(^+\) cells also expressed CD276. Because CTECs are a subset of CECs, we evaluated the population of CTECs as a fraction of CECs (Supplementary Fig. S3). In tumor-bearing mice, the mean percentage of CD276\(^+\) or TEM7\(^+\) CECs was 31% and 55%, respectively. However, in normal mice, the mean percentage of CD276\(^+\) or TEM7\(^+\) CECs was 16% and 15.8%, respectively.

One potential shortcoming of CECs and CEPs as cancer-specific biomarkers is that their levels increase in response

Figure 1. Expression of TEM representative images showing CD31 (red) and TEM (green) markers of histologic sections of LLC (56) and normal lung tissues. TEM8, TEM7, and CD276 colocalized with CD31, suggesting that its expression is localized to the tumor endothelium. TEM1 and TEM exhibited perivascular expression patterns.

Figure 2. Expression of TEM7 and CD276 in endothelial cells. A, endothelial cells from both normal and tumor-derived tissues in H1975 xenografts were immunopurified using CD31-immunomagnetic beads. TEM7 and CD276 expression was evaluated using flow cytometry for established markers for mouse endothelium (CD31\(^+\) CD45\(^-\) VEGFR-2\(^+\) CD117\(^-\)). Values are mean ± SEM. \(\ast\), \(P < 0.05\). B, CECs and CEPs in peripheral blood were evaluated using four-color flow cytometry. CTECs were first identified on the basis of the staining pattern of CECs and further characterized using CD276 and TEM7 antibodies. CD276 CTECs and TEM7 CTECs were expressed at significantly higher levels in tumor-bearing mice than in normal controls (\(P = 0.041\) and 0.032, respectively). Values are mean ± SEM.
to stimuli other than cancer, including ischemia, infection, and organ regeneration, and in response to proangiogenic factors such as VEGF and SDF-1α (13, 24, 28, 30–39). Using H1975 xenografts, we examined the impact of VEGF injection or the presence of tumors on different endothelial cell populations. The number of TEM7 CTECs in tumor-bearing mice was significantly higher than that in nontumor-bearing mice that had (VEGF treated) or had not (control) received a VEGF injection (P = 0.018 and 0.020, respectively; Fig. 3A). The level of CD276 CTECs was also significantly higher in tumor-bearing than nontumor-bearing control mice (P = 0.015). In contrast, levels of CECs and CEPs were not significantly higher in tumor-bearing mice than in control or VEGF-treated mice, suggesting that CTECs had greater specificity for the presence of tumor than CECs or CEPs did.

**CTECs as surrogate markers for antiangiogenic activity**

We next examined whether CTECs may serve as markers of angiogenesis inhibitor activity, as has been previously reported for CECs and CEPs (7, 8, 16, 17, 24, 29, 40). We injected mice with H1975 tumor cells subcutaneously, and once tumors reached a volume of 300 mm³, the animals were treated with vehicle only or with the VEGFR tyrosine kinase inhibitor AZD2171 (cediranib) or sunitinib, or the human VEGF monoclonal antibody bevacizumab. After 2 weeks of treatment, tumor growth was inhibited by 77% to 83% in VEGF monoclonal antibody bevacizumab. After 2 weeks of inhibitor AZD2171 (cediranib) or sunitinib, or the human treated with vehicle only or with the VEGFR tyrosine kinase control) were significantly increased. The number of these cell types, although the degree of reduction varied. Reduced levels of CD276 CTECs (relative to control) were significantly correlated with the reductions in tumor growth (R² = 0.96, P < 0.05).

**Detection of CTECs in clinical specimens**

To investigate whether CECs and CTECs could be detected in patients with cancer and were associated with the presence of cancer, we investigated CTECs in patients before and after resection of their tumor. The cancer patient group was composed of 22 (55%) patients with esophageal cancer and 18 (44%) with lung cancer with a mean age of 60 ± 10.45 and 64 ± 9.28, respectively. Twenty-seven patients received induction chemotherapy, 19 patients with esophageal carcinoma and 8 with lung carcinoma. The tumor was successfully resected in all patients. There was no postoperative mortality. Eighteen patients had recurrence in the course of their follow-up (Table 1). The control group of normal healthy volunteers consists of 9 patients, 6 men and 3 women, ages from 22 to 58 years (median 52 years). Although the primary goal of this analysis was to assess changes in CEC and CTECs after resection, we first explored the levels of CECs and CTEC in patients with esophageal and lung cancer compared with normal volunteers. CTECs (CD45+/CD31+/TEM7+) were present at significantly higher levels in patients with cancer (P < 0.001; Fig. 4A). This was true for both patients with lung and those with esophageal cancer (Fig. 4A). Consistent with earlier studies, mature CECs (CD45+/CD133+/CD31+) were present at a higher level in patients than in healthy volunteers, although this difference was not significant (P = 0.13). CTECs were elevated in patients with cancer compared with healthy volunteers regardless of whether they received induction chemotherapy (Fig. 4B). Given the limited size of the normal control group, however, this analysis was merely exploratory.

To investigate whether CTEC counts decreased following surgery, we analyzed blood samples collected before and one month following surgery in the same group of patients. We observed a significant decrease in patient CTEC levels following surgical removal of the tumor (P < 0.001; Fig. 5A). The effect...
was similar whether the patients had lung or esophageal cancer but more pronounced with lung cancer (Fig. 5E). This postsurgical decrease in CTECs was observed regardless of whether patients received induction chemotherapy (Fig. 5B). This pattern was preserved if the patients had a recurrence (Fig. 5D). Patients who had induction therapy responded in a similar fashion after surgery, indicating that despite the clinical response, surgery decreased the counts even further (Fig. 5C).

Discussion

CECs (41) are known to consist of at least two distinct populations: bone marrow-derived CEPs (42), which may contribute to pathologic neovascularization, and mature CECs derived from existing mature vasculature. CECs have emerged as a potentially useful biomarker for highly vascular and angiogenic tumors (7, 9, 16, 17). Increased levels of CECs have been observed in patients with cancer relative to normal subjects and have been associated with disease progression (43, 44). In murine models, VEGF pathway inhibitors can have differential effects on mature CECs and CEPs in that inhibition of tumor angiogenesis is associated with an initial increase in mature CECs (7), followed by a subsequent reduction. Preclinical studies have demonstrated that CECs can be used as a surrogate marker for therapeutic activity of antiangiogenic agents (9, 29, 45). In a previous study of patients with breast cancer receiving metronomic chemotherapy, an increase in apoptotic CECs, presumably being shed from the tumor vasculature, was shown to correlate with clinical benefit (16). Despite these discoveries, the clinical application of CECs as a cancer-specific biomarker is limited, at least in part, because CECs and CEPs have been shown to increase in response to stimuli other than cancer, including pathologic conditions (e.g., infection, ischemia, and sickle cell anemia) and physiologic conditions (e.g., pregnancy and menstrual cycles), or in response to pro-angiogenic factors (e.g., VEGF and SDF-1α) (13, 24, 28, 30–39).

In an effort to identify more specific markers reflecting tumor vasculature, we investigated subpopulations of CECs bearing tumor endothelial cell-specific markers, which we term CTECs. In an earlier study by St. Croix and colleagues (22), 46 TEMs were identified by isolating the endothelial cells in human colorectal tumors by serial analysis of gene expression (SAGE), and further studies on a subset of TEMs (TEM1–TEM9) revealed their highly elevated levels specifically in the angiogenic state (22). Subsequent studies demonstrated counterparts of many of these TEMs in mice (23, 46, 47). Consistent with these earlier studies, we observed tumor endothelial staining for TEM8 and CD276 in our murine cancer models (23, 46). Prior studies of TEM7 have shown more varied results. Expression in human tumor endothelium has been observed in a number of studies (22, 23, 48, 49). In mouse studies, however, TEM7 expression was demonstrated by real-time PCR in one study of human melanoma and liposarcoma xenografts (47) but not observed in syngeneic melanoma tumors or human colon cancer xenografts by in situ hybridization or by SAGE analysis (23, 46). These differences may be, in part, due to the different methodologies used (e.g., SAGE, which identifies differentially expressed gene transcripts vs. immunohistochemistry, and flow cytometry, which evaluates protein levels of TEM7). Furthermore, given that vascular beds from different sites are morphologically and functionally distinct (50), our preclinical findings may be influenced by the fact that the tumors were grown subcutaneously. In addition, because tumor cells can influence tumor-associated endothelial cells though paracrine signaling, differences between the preclinical studies may also be due to differences in the tumor models used (23).

TEM8, a cell-surface glycoprotein identified as an anthrax toxin receptor, is also upregulated on tumor vessels in mouse and human cancers (46, 51). In TEM8 knockout mice, developmental angiogenesis and wound healing occur normally, whereas tumor growth is impaired, indicating that TEM8 may be required for tumor angiogenesis but not for physiologic vascular processes (52, 53). In preclinical cancer models, targeting of TEM8 inhibited tumor angiogenesis and tumor growth (53).
Expression of CD276, a leukocyte costimulatory molecule, on endothelial cells has been evaluated previously. Using mouse models and comprehensive SAGE analysis, CD276 was identified as being expressed during pathologic but not physiologic angiogenesis (23). CD276 levels are elevated in colon and lung tumors compared with normal tissue, and although the tumor cells themselves expressed low levels of CD276, tumor-associated endothelial cells expressed high levels of CD276 (23).

Consistent with prior reports, in our initial immunohistochemical analysis of Lewis lung cancer xenograft tissue, we found that with the exception of TEM5, TEMs were present at higher levels in these tumors than in normal tissues (skin and lung). In some cases, localization was not exclusively limited to tumor endothelial cells, for example, immunoreactivity for TEM1, TEM4, TEM7, and CD276 was also detected in perivascular cells in tumors. Consistent with earlier reports, CD276 was also expressed in normal liver endothelium (27).

To further investigate whether TEMs could be detected on endothelial cells isolated from tumor or normal tissue, we used four-color flow cytometry with a panel of established antibodies (24, 54). As expected, endothelial cells isolated from tumors expressed significantly higher levels than endothelial cells detected from normal skin and lung tissues but not normal liver tissue, the endothelial cells of which expressed high levels of CD276.

We next examined whether we could detect CTECs in the blood of mice. We found that CTECs, but not CECs or CEPs, were present at significantly higher levels in tumor-bearing mice than in nontumor-bearing mice or, for TEM7 CTECs, mice treated with VEGF. This finding suggested that CTECs are relatively more specific for tumors than CECs or CEPs and are relatively less responsive to a proangiogenic stimulus (i.e., VEGF) in the absence of tumor. As a subpopulation of CECs, CTECs may provide information distinct from that of CEPs or CECs. This difference may be due to CTECs being derived in part from the shedding of fragile, mature endothelium from tumor vasculature into the circulation, whereas CEPs are mobilized from the bone marrow in response to a variety of proangiogenic stimuli, such as VEGF, and subsequently

![Figure 5. Evaluation CTECs in patients with esophageal and lung cancer. A, levels of CTECs decreased in patients following surgical removal of the tumor \( (P < 0.001) \). B, this postsurgical decrease in CTECs was observed with or without induction chemotherapy. C, this pattern was preserved if the patients had a recurrence (D) or if they had a clinical response. E, levels of CTEC in patients who had esophagectomy \( (N = 22) \) and those who had resection for lung cancer \( (N = 18) \).]
differentiate into mature CECs. It is worth noting, however, that a low level of CTECs was detected in nontumor-bearing mice. The source of these cells is not clear but, given that TEMs are relatively but not perfectly specific for tumor endothelial cells, this may reflect a true population of rare TEM \(^+\) endothelial cells in nontumor-bearing mice or alternatively a small degree of antibody cross-reactivity.

To address whether the increase in CTECs occurred after treatment with agents thought to selectively reduce tumor angiogenesis, we tested the effect of the VEGF pathway inhibitors AZD7121 (cediranib), sunitinib, and bevacizumab in our H1971 xenograft mouse model. Each of these agents decreased the number of CTECs as well as CECs and CEPs. The reduction of all three types correlated with decreased tumor volume. An antiangiogenic agent may affect these cell populations differently; for instance, an angiogenic inhibitor could reduce VEGF-induced CEP mobilization but increase mature CEC and CTEC shedding. Additional studies are needed to determine whether these changes could serve as markers of biologic activity.

Finally, we observed that in both NSCLC and esophageal cancer patients, CTEC levels decreased significantly after resection. A postresection decrease was observed both in patients who had previously received induction chemotherapy and those who did not, suggesting that CTEC changes were not merely changes induced by chemotherapy, as previously observed for CECs (55). We also observed that CTECs are present in patients with both NSCLC and esophageal cancer at levels higher than normal, healthy control subjects but given the small size of this control group (\(N = 9\)), this finding is hypothesis generating and larger studies would be needed to more thoroughly evaluate the potential use of CTECs for the detection of cancer.

On the basis of the findings presented here, CTECs may be an appealing marker for several reasons. CTECs are more specific for cancer than CECs and CEPs and less influenced by nonmalignant stimuli. Circulating tumor cells (CTC) are also specific for cancer but, unlike CTCs, it seems that a limited number of TEMs are present on the majority of tumor endothelium although the number of different tumor types whose TEMs have been characterized is limited. In theory, therefore, CTECs may be more cancer specific than CECs and a limited number of TEM markers on CECs could cover the vast majority of tumor types. More studies are needed to determine the clinical utility of CTECs.

The current study indicated that TEMs and CD276 are potentially useful diagnostic and prognostic markers for lung and esophageal cancer. CTECs are detectable and are found in increased numbers in tumor-bearing mice than in nontumor-bearing mice. We propose that CTECs derive from endothelial cells shed from the tumor and that they are a novel cancer-specific subset of CECs and, given the number of nonmalignant conditions that can influence CEC levels, may be more useful than CECs for detecting tumors. However, many questions pertaining to TEMs remain and will need to be addressed in future mechanistic and prospective clinical studies.

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