Expression of Endocrine Gland-derived Vascular Endothelial Growth Factor in Ovarian Carcinoma

Lin Zhang, Nuo Yang, Jose-Ramon Conejo-Garcia, Dionyssios Katsaros, Alisha Mohamed-Hadley, Stefano Fracchioli, Katia Schlienger, Alanna Toll, Bruce Levine, Stephen C. Rubin, and George Coukos


ABSTRACT

The first tissue-specific angiogenic molecule, endocrine gland-derived vascular endothelial growth factor (EG-VEGF), was identified recently in human ovary, raising hopes of developing tumor type-specific angiogenesis inhibitors. In the present study, we analyzed the expression of EG-VEGF mRNA in normal human tissues and ovarian neoplasms by quantitative real-time reverse transcription-PCR. EG-VEGF mRNA was expressed in all ovarian neoplasms examined. No significant difference was identified among benign, low malignant potential neoplasms or stage I carcinos and may play a marginal role in promoting angiogenesis in advanced ovarian carcinoma. We postulate that EG-VEGF-targeted antiangiogenic therapy may prove useful in early stage but not in advanced stage ovarian carcinoma.

INTRODUCTION

Angiogenesis is one of the most critical steps in embryonic development, reproductive function, and tumorigenesis (1–3). The mechanisms underlying angiogenesis and vascular remodeling are revealed to be increasingly complex thanks to the recent identification of important regulatory molecules (4). VEGF is believed to be the most important proangiogenic factor (5, 6) and exhibits distinct isoforms in different tissues (7, 8) and developmental stages (7). VEGF may act as the earliest signal molecule to switch the angiogenic cascade (5), whereas angiotropins and their receptor Tie-2 as well as ephrins and their receptors appear to act at a later stage of angiogenesis (1, 9). Importantly, the above angiogenic factors appear to be universal in their distribution and function, for they provide general signals promoting angiogenesis in most tissues (10, 11). Several experiments have suggested the existence of additional tissue-specific angiogenic factors, which locally regulate vascularization in different organs (10, 12–14).

EG-VEGF, the first tissue-specific angiogenic molecule, was identified recently in steroidogenic endocrine organs, including the ovary, testis, adrenal, and placenta (11, 15). Although EG-VEGF does not show any homology to the VEGF family (11), it possibly induces activation of mitogen-activated protein kinase p44/42 and phosphatidylinositol-3 kinase pathways and leads to proliferation, migration, and survival of endothelial cells (15), a role reminiscent of VEGF. EG-VEGF selectively induces proliferation, migration, and fenestration (the formation of membrane discontinuities) in capillary endothelial cells specifically derived from endocrine glands, suggesting the existence of tissue-restricted specific receptors (11). Importantly, EG-VEGF contributes to the endocrine function of these organs, as endothelial cell fenestration may accelerate the entry of hormones in the bloodstream (10, 11). Because angiogenic factors play a critical role in tumorigenesis, the discovery of tissue-specific angiogenic mechanisms raises hopes of developing tumor type-specific angiogenesis inhibitors (10, 11).
Angiogenesis mechanisms play a critical role in ovarian carcinogenesis. VEGF is overexpressed in ovarian carcinoma (16–19), where it exerts important biological functions, such as promoting tumor growth and the formation of ovarian cysts and ascites (20–23). Importantly, increased serum and/or tumor levels of VEGF have been associated with poor clinical outcome (24–28). To date, it is unknown whether EG-VEGF is expressed in ovarian carcinoma and whether it plays a role in supporting angiogenesis and tumor growth. In the present study, we analyzed the expression of EG-VEGF and VEGF mRNA in human ovarian neoplasms. We report for the first time that EG-VEGF is expressed in human ovarian carcinoma but most likely derives from nonneoplastic components of the tumor, including stroma cells and tumor-infiltrating leukocytes.

MATERIALS AND METHODS

Patients and Specimens. Specimens from 50 ovarian neoplasms were collected between October 1991 and July 1999 at the University of Turin, Italy, following informed consent, from patients undergoing exploratory surgery for the presence of abnormal adnexal masses. Normal ovaries were collected from premenopausal patients undergoing elective pelvic surgery for nonovarian indications. Specimens were immediately snap frozen and stored at −80°C. Four tumors were benign, four were of low malignant potential, and 42 were malignant, including 9 stage I and 33 stage III carcinomas. Tumors were surgically staged and graded according to the International Federation of Gynecology and Obstetrics. All ovarian carcinoma specimens were collected from patients untreated previously during primary debulking surgery. Twenty-eight stage III tumors, which were collected from patients achieving complete response to chemotherapy, were used for outcome analysis. DFI was defined as the time between completion of chemotherapy and first recurrence. Six ovarian cancer specimens were collected fresh at the University of Pennsylvania Medical Center after obtaining appropriate informed consent under Institutional Review Board-approved protocols. Twelve normal human tissues were provided by the Cooperative Human Tissue Network.

Cell Lines and Cell Culture. A total of 17 human ovarian cancer cell lines (A2780, A2780/C30, A2780/CP70, A2008, A1847, SKOV-3, PE01, PE04, OVCAR2, OVCAR3, OVCAR4, OVCAR5, OVCAR7, OVCAR8, OVCAR10, UPN251, and OAW42) was generously provided by Drs. Steven Johnson and Kang-Sheng Yao, Department of Cancer Pharmacology, University of Pennsylvania. All cell lines were cultured in 5% CO2 atmosphere, at 37°C, and in DMEM medium supplemented with 10% fetal bovine serum and 100 units/ml penicillin. HOSE cells were isolated from nonepithelial components of the tumor, including stroma cells, and tumor-infiltrating leukocytes.

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PBLs were isolated by elutriation from the apheresis product of normal healthy donors and cultured at 1 × 106 cells/ml in RPMI 1640 containing 10% human AB sera (BioWhittaker, Walkersville, MD) at 37°C and 5% CO2. Cells stimulated by anti-CD3/anti-CD28-coated beads (29) were cultured at a 3:1 bead:cell ratio at a final concentration of 1 × 105/ml for 48 h. Cells were then harvested, beads were removed by magnetic separation, and cells were subjected to RNA isolation.

Flow Cytometry. Single-cell suspension from fresh tumor nodules were generated as described previously (30). Briefly, fresh tumor specimens were mechanically dissected and enzymatically digested overnight at room temperature with type IV collagenase (0.1%; Sigma Chemical Co., St. Louis, MO), type IV DNase (30 units/ml; Sigma), and type V hyaluronidase (0.01%; Sigma). The tumor suspension was then filtered through a wire grid to yield a single-cell suspension. Cells were separated on a percoll (Pharmacia Biotech AB, Uppsala, Sweden) density gradient for 30 min at 1,500 × g at room temperature and subjected to four-color flow cytometry on a FACS-Calibur flow cytometer using CellQuest 3.2.1f software (Becton Dickinson, San Jose, CA), using monoclonal antibodies against CD45 (HI30), CD3 (UCHT-1), CD4 (RPA-T4), CD8 (RPA-T8), CD19 (HIB19), CD57 (NK-1), IgG1, and IgG2a (BD PharMingen, San Diego, CA). Data representing 10,000–30,000 events were recorded and analyzed with CellQuest software (Becton Dickinson).

Isolation of Tumor-infiltrating Lymphocytes. Tumor-infiltrating lymphocytes were isolated as described previously (30). Briefly, single-cell suspensions obtained from dispersed tumor specimens, as described above, were separated on a percoll density gradient. The dense layer, enriched for lymphocytes, was collected. Tumor-infiltrating T lymphocytes were selected by fluorescence-activated cell sorting using monoclonal antibodies against CD4 and CD8 (BD PharMingen) and a MoFlo cell sorter (Cytomation, Fort Collins, CO) equipped with an argon laser beam.

Immunohistochemistry and Immunofluorescent Staining. Immunohistochemical staining was performed using the avidin-biotin-peroxidase method. Sections were fixed in cold acetone for 10 min, pretreated with 3% H2O2 for 20 min to block endogenous peroxidase activity, and incubated in normal serum (Vector, Burlingame, CA) for 30 min. After incubation with the primary antibody (Table 1) in a humid chamber for 1 h, the VECTASTAIN avidin-biotin complex method kit was applied as described by the manufacturer (Vector). Briefly, sections were incubated in biotin-labeled secondary antibody for 30 min, followed by incubation in biotin-peroxidase/avidin complex for 30 min. The immunoreactive sites were visualized with freshly prepared 3,3′-diaminobenzidine (Vector) containing H2O2. All staining steps were performed at room temperature. Sections were counterstained lightly with Gill’s hematoxylin (Vector). Images were acquired through Cool SNAP Pro color digital camera (Media Cybernetics, Carlsbad, CA). For immunofluorescent staining, sections were sequentially incubated in 5% normal serum, antihuman cytokeratin antibody (DAKO, Carpinteria, CA) diluted at 1:500 for 1 h, and FITC-labeled antirabbit IgG (Vector) for 2 h.

LCM. Stage III ovarian cancer specimens were screened for LCM by immunohistochemical staining using a polyclonal antibody against cytokeratin to select the ones allowing for clear identification of tumor islets and stroma (Fig. 2A). LCM was performed as described by others (31, 32), implementing minor
 modifications as suggested by the manufacturer of the LCM used. Briefly, cryosections (6 μm) from selected tumors were mounted on a polyethylene foil slide (SL Microtest, Jena, Germany) according to the manufacturer’s instructions. After rapid H&E staining, sections were subjected to LCM using the Laser-MicroBeam System (SL Microtest), which uses a fine UV ablation, the material to be extracted is never directly exposed to cold areas following precisely a drawn incision path. By this cold extraction, the material to be extracted is never directly exposed to the laser. This LCM system also enables the contact-free isolation of single cells or groups of cells (Fig. 2b). Microdissected cells were catapulted into the lid of a 0.5-ml reaction tube containing RNA isolation buffer. RNA was isolated by Micro RNA isolation kit (Ref. 32; Stratagene, La Jolla, CA).

**Design of Primers.** Specific oligonucleotide primers for human EG-VEGF and VEGF (Table 2) were designed based on published sequences (11, 33). To avoid false positive results caused by amplification of contaminated genomic DNA in the cDNA preparation, all primers were designed to reside on exons 1–5 of EG-VEGF outer F

<table>
<thead>
<tr>
<th>Primer</th>
<th>Sequence</th>
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<tr>
<td>EG-VEGF F&lt;sup&gt;a&lt;/sup&gt;</td>
<td>ATC AGC CTT CTT CCA G</td>
</tr>
<tr>
<td>EG-VEGF R&lt;sup&gt;a&lt;/sup&gt;</td>
<td>AAG GAC AGG TGT GGT GCT TG</td>
</tr>
<tr>
<td>VEGF F</td>
<td>AAC CAT GAA CTT TCT GCT GTG TTG</td>
</tr>
<tr>
<td>VEGF R</td>
<td>TTC ACC ACT TCG TGA TGA TTC TG</td>
</tr>
<tr>
<td>GAPDH R</td>
<td>CAT GAG TCC TTC CAC GAT ACC A</td>
</tr>
<tr>
<td>GAPDH F</td>
<td>CCT GCA CCA CCA ACT GCT TA</td>
</tr>
<tr>
<td>EG-VEGF outer F&lt;sup&gt;a&lt;/sup&gt;</td>
<td>AAC TGT GTC TGA CTG TGC TG TGT GA</td>
</tr>
<tr>
<td>EG-VEGF outer R&lt;sup&gt;a&lt;/sup&gt;</td>
<td>CAA GCA AGG ACA GGT GTG GT</td>
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<sup>a</sup> F, forward; R, reverse.  
<sup>b</sup> Used in nested PCR.

**RNA Isolation and RT-PCR.** Total RNA was isolated from 100–500 mg of frozen tumor tissues or 1 × 10<sup>6</sup> cultured cells by TRIzol reagent (Invitrogen). After RNase-free DNase (Invitrogen) treatment for 15 min at room temperature, RNA was further purified with RNasy RNA isolation kit (Qiagen, Valencia, CA). Total RNA (1 μg) was reverse transcribed in a 20-μl reaction system using superscript first-strand synthesis kit for RT-PCR (Invitrogen) under conditions described by the supplier. Reverse transcribed cDNA (2 μl) was amplified in a 25-μl PCR reaction system containing 200 μM each deoxynucleotide triphosphate and 300 nM each primer, and the standard buffer was supplemented with 0.25 unit of Taq polymerase (Roche, Mannheim, Germany) and 1.5 mM MgCl₂. After an initial denaturation step at 94°C for 4 min, 42 cycles of PCR were performed with denaturation at 94°C for 30 s, annealing at 60°C for 30 s, and extension at 72°C for 45 s. The last extension was at 72°C for 7 min.

**Real-time RT-PCR.** The mRNA expression of EG-VEGF and VEGF was quantified by real-time RT-PCR on the ABI Prism 7700 Sequence Detection System (Applied Biosystems, Foster City, CA). PCR was performed using SYBR Green PCR Core Reagents (Applied Biosystems) according to the manufacturer’s instructions. PCR cycles consisted of an initial denaturation step at 95°C for 10 min, followed by 40 cycles at 95°C for 15 s and at 60°C for 60 s. A standard curve was constructed with PCR products containing the same fragments amplified by the Taqman system. The relative expression in each sample was calculated with respect to the standard calibration curve, as described previously (34, 35). Normalization of cDNA load was performed against housekeeping GAPDH. Each sample was analyzed twice, and each PCR experiment included two nontemplate control wells. PCR products were confirmed as single bands using gel electrophoresis and by DNA sequencing.

**Nested PCR.** To detect the expression of EG-VEGF mRNA in ovarian cancer cell lines, a two-step nested PCR was used. Briefly, after a first round of PCR performed with the outer primers (Table 2), a second round of PCR was carried out using 0.5 or 3 μl of the first round PCR product and inner primers (real-time PCR primers). Conditions for both the first and second round of PCR reactions were the same as with standard RT-PCR mentioned above, PCR products were run on a 2.5% agarose gel.

**Statistical Analysis.** Data statistical analysis was performed using the SPSS statistics software package (SPSS, Chicago, IL). All results were expressed as mean ± SE, and <i>P</i> < 0.05 was used for significance. Survival distributions were depicted with Kaplan-Meier curves, and Log-rank statistics were used to compare curves.

**RESULTS**

EG-VEGF mRNA Expression in Normal Human Tissues. Expression of EG-VEGF at the mRNA level was analyzed by real-time quantitative RT-PCR in 12 different normal human tissues. EG-VEGF mRNA expression levels were ≥20-fold higher in normal human testis and premenopausal ovary than in other organs. EG-VEGF mRNA could be detected at low levels in brain, colon, skeletal muscle, small intestine, spleen, thymus, uterus, and liver, whereas it was undetectable in non-
lactating breast and skin (Fig. 1A). In contrast, VEGF mRNA was detected in nonlactating breast and skin. EG-VEGF mRNA was detected by RT-PCR in PBLs from two normal healthy donors. Both resting PBLs (group 1) and PBLs activated 

Expression of EG-VEGF mRNA in normal human tissues and ovarian cancer. A, EG-VEGF mRNA levels in normal human tissues quantified by real-time RT-PCR. In normal ovary and testis, mRNA levels of EG-VEGF are dramatically higher than in other normal tissues. No EG-VEGF is detected in nonlactating breast and skin. B, EG-VEGF mRNA detection by RT-PCR in PBLs from two normal healthy donors. Both resting PBLs (group 1) and PBLs activated 

EG-VEGF Expression in Ovarian Neoplasms. EG-VEGF mRNA was expressed in benign and low malignant potential neoplasms, as well as early stage (stage I) ovarian cancer by real-time RT-PCR. No significant difference was identified among these tumor types (P = 0.994), whereas 2-fold lower levels were observed in these tumors compared with normal premenopausal ovaries. EG-VEGF mRNA levels were significantly decreased in late stage (stage III) ovarian cancer compared with stage I carcinomas, low malignant potential, or benign tumors (P < 0.05; Fig. 1C). In contrast to EG-VEGF, malignant ovarian tumors significantly overexpressed VEGF mRNA compared with benign and low malignant potential neoplasms (P < 0.05; Fig. 1D). No significant difference was identified between stage I and III carcinomas (P = 0.866). Because EG-VEGF can be up-regulated by hypoxia via the same mechanism as VEGF (11), we analyzed the correlation between the EG-VEGF and VEGF mRNA in stage III tumors. No correlation was found between the mRNA levels of these two angiogenic molecules (P = 0.462; Fig. 1E).

EG-VEGF Expression in Stroma and Tumor Islets. EG-VEGF mRNA was quantified comparatively in tumor islets and peritumoral stroma. First, stage III tumor specimens were screened by immunohistochemistry using cytokeratin, an epithelial tumor marker, to identify tumors with clear architectural distinction between tumor islets and stroma. Only specimens with such distinction (Fig. 2A) were selected to perform LCM (Fig. 2B). By immunohistochemistry, we determined that as many as 70–80% of cells within tumor islets were cytokeratin-positive tumor cells, whereas no cytokeratin-positive cells could be seen in peritumoral stroma areas. EG-VEGF mRNA was detected in both stroma and tumor islets. Remarkably, mRNA levels were consistently higher in peritumoral stroma compared with tumor islets, with a ratio of stroma:islets ranging between 2 and 7 (Fig. 2C shows two representative cases).

EG-VEGF Expression in Established Ovarian Cancer Cell Lines. We investigated the constitutive expression of EG-VEGF by ovarian carcinoma cells in vitro. A total of 17 epithelial ovarian cancer cell lines was analyzed by RT-PCR. EG-VEGF was undetectable in all cell lines (Fig. 3A). The
quality of cDNA was tested by analysis of housekeeping gene GAPDH, which was detected in all cell lines (data not shown). For comparison, VEGF mRNA expression was also tested in the same specimens. High levels of VEGF mRNA were found in all 17 ovarian cancer cell lines (Fig. 3). To enhance the sensitivity of RT-PCR, we used nested RT-PCR. In 15 of 17 cell lines, a detectable band was observed at the expected molecular weight, the intensity of which depended on the amount of the first-round PCR product (Fig. 3B). Finally, no EG-VEGF could be detected by RT-PCR in cultured HOSE cells (data not shown). The above data indicate that EG-VEGF mRNA is present at extremely low levels in ovarian cancer cell lines in vitro.

EG-VEGF Expression in Tumor-infiltrating Lymphocytes. We sought to assess whether immune cells could contribute to EG-VEGF expression in ovarian carcinoma. First, we examined ovarian carcinomas for the presence of tumor-infiltrating immune cells. By immunohistochemistry, we found that ovarian carcinomas were heavily infiltrated by CD3+ T lymphocytes (Fig. 4A), including CD4+ and CD8+ subsets (data not shown) in >50% of patients. By contrast, other types of lymphocytes, such as CD19+ B cells (Fig. 4B) and CD57+ NK cells (Fig. 4C), were scarcely represented. By flow cytometry, we confirmed that CD45+ leukocytes represent ≤20–35% of cells isolated from mechanically dispersed and enzymatically di-
gested ovarian carcinomas, whereas T cells were the main
immune cell population encountered in ovarian carcinoma (Fig. 4D), representing 35.1 ± 3.3% of tumor-infiltrating
leukocytes (Table 3). EG-VEGF expression was assessed in tumor-infiltrating T cells by RT-PCR. In all cases, EG-VEGF mRNA was expressed in tumor-infiltrating T lymphocytes (Fig. 4E).

**EG-VEGF Expression and Patient Outcome.** VEGF overexpression has been associated with poor clinical outcome in ovarian carcinoma (24–28). To assess whether the expression of EG-VEGF also predicts clinical outcome, 28 specimens from stage III patients with complete clinical response to platinum-based chemotherapy and documented relapse were analyzed. Patients were stratified based on relative expression of EG-VEGF or VEGF mRNA below or above the median. VEGF overexpression (above median) was associated with significantly shorter DFI (P = 0.0027; Fig. 5B), but no difference in outcome was observed between patients with relatively high and low levels of EG-VEGF (P = 0.491; Fig. 5A).

**DISCUSSION**

EG-VEGF is the first tissue-specific angiogenic factor identified, reportedly being expressed only in steroidogenic endocrine tissues, including the ovaries (11). As such, EG-VEGF provides the first potential target for tissue-specific, and potentially tumor type-specific, antiangiogenic therapy. This study focused on characterizing the expression of EG-VEGF in ovarian carcinoma and assessing whether indeed this angiogenic factor should be considered as a potential therapeutic molecular target in this disease.

The normal ovary is formed by cells belonging to three distinct lineages: (a) the germ cell lineage, which comprises all eggs; (b) the sex cord-stroma lineage, which comprises the cortical stroma, the cumulus oophorus surrounding the eggs, the granulosa, and theca layers of follicles and interstitial stroma; and (c) the epithelial lineage, which comprises the surface epithelium (36–38). In the normal ovary, EG-VEGF mRNA is highly expressed in elements of the sex cord-stroma lineage, including the cortical stroma, the cumulus oophorus, as well as the granulosa and theca layers of developing follicles (11). Epithelial ovarian carcinomas, which represent >90% of ovarian cancers, likely derive from the epithelial lineage of the ovary (39–41). EG-VEGF was found to be expressed at the mRNA level in all human epithelial ovarian neoplasms, including benign cystadenomas, tumors of low malignant potential, and invasive carcinomas. However, the present data indicate that tumor cells are not an important source of EG-VEGF in ovarian cancer. In fact, EG-VEGF expression was lower in cystadenomas, tumors of low malignant potential, and early stage carcinomas to normal premenopausal ovary. In addition, through LCM and RT-PCR, we showed that EG-VEGF levels were consistently higher in tumor stroma compared with tumor islets. Finally, EG-VEGF mRNA was not detected in primary ovarian
EG-VEGF levels, suggesting different mechanisms of regulation. Furthermore, no correlation could be found between VEGF and EG-VEGF in the biology of ovarian cancer, we sought to establish associations of EG-VEGF with stage, tumor outcome, or VEGF levels. Although an association of VEGF overexpression could be readily established with advanced stage or poor outcome in stage III ovarian carcinoma, such association was not evident for EG-VEGF. In fact, EG-VEGF expression declined in late stage ovarian cancer compared with stage I tumors. Furthermore, no correlation could be found between VEGF and EG-VEGF levels, suggesting different mechanisms of regulation. Taken together, these data suggest that EG-VEGF likely plays a marginal role in promoting angiogenesis in advanced stage disease. Ovarian carcinomas may exhibit an abundant rich stroma component, which may be highly cellular. It has been postulated that stroma-epithelial cell interactions may inhibit the growth of tumorigenic surface epithelium in early stages of ovarian oncogenesis (44, 45). In a xenograft model, it was shown that normal ovarian stromal cells, when admixed with tumor cells, had the ability to inhibit the growth of ovarian carcinoma transplants but were gradually substituted by host (murine) stromal cells, which were recruited to the tumor and supported its growth (46). These experimental data are supported by histopathologic data; only 13% of ovarian cancer specimens examined in one series displayed evidence of stromal luteinization (47), whereas in another series, steroid cells were identified in <3% of advanced ovarian cancers, most of which were of the relatively uncommon mucinous histotype (48). It is possible that the overall influence of ovarian steroidogenic stroma on tumor development might be inhibitory, resulting in its progressive loss during malignant progression, which might provide an explanation for the decline of EG-VEGF expression.

In the present study, we found that EG-VEGF mRNA is dramatically overexpressed in two steroidogenic organs, ovary and testis, but is also expressed in other normal tissues at markedly lower levels. The difference in our results is likely attributable to the use of RT-PCR, which is more sensitive than Northern blot, and the tissue RNA array used in LeCoutur’s study (11). Additional studies need to be performed to assess whether EG-VEGF expression in nonsteroidogenic tissues has any physiological function. The most interesting finding in our present study was that EG-VEGF mRNA is also expressed in resting as well as activated PBLs, which is consistent with the detection of EG-VEGF mRNA in lymphoid tissues, such as spleen and thymus. Tumor-infiltrating T cells were also found to express EG-VEGF. This is the first evidence that peripheral and tumor-infiltrating T cells secrete EG-VEGF. T cells are known to secrete VEGF (49). Furthermore, tumor-infiltrating T cells may secrete VEGF and promote angiogenesis (50). The potential roles of EG-VEGF in tumor-infiltrating T cells remain to be elucidated.

In summary, in this study, we provide evidence indicating that EG-VEGF, a purported tissue-specific angiogenic factor, is expressed in ovarian carcinoma but is most likely derived from nontumor cells of the sex cord-stromal lineage, as well as tumor-infiltrating T lymphocytes. Furthermore, in contrast to VEGF, the expression of EG-VEGF in advanced stage tumors significantly declines compared with early stage cancers, low malignant potential tumors, or benign tumors and does not correlate with outcome in advanced stage disease. On the basis of these findings, we postulate that EG-VEGF-targeted antiangiogenesis therapy may prove useful in early stage but not in advanced stage ovarian carcinoma.

ACKNOWLEDGMENTS

We thank Drs. Steven Johnson and Kang-Sheng Yao for providing us with the ovarian cancer cell lines.

**Fig. 5** EG-VEGF mRNA level does not correlate with patient outcome in stage III ovarian cancer. A total of 28 stage III ovarian cancer specimens with complete clinical response to platinum-based chemotherapy and detailed follow-up information were used for outcome analysis. Patients were stratified based on relative expression of EG-VEGF or VEGF mRNA below or above the median. In A, no difference in outcome is observed between patients with relatively high and low levels of EG-VEGF (P = 0.491). In B, VEGF overexpression is associated with significantly shorter DFI (P = 0.003).
REFERENCES


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