Regional Effects of an Antivascular Endothelial Growth Factor Receptor Monoclonal Antibody on Receptor Phosphorylation and Apoptosis in Human 253J B-V Bladder Cancer Xenografts

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ABSTRACT

Vascular endothelial growth factor (VEGF) is a key angiogenic factor in a variety of solid tumors, making it one of the most attractive therapeutic targets. VEGF promotes the proliferation, survival, and differentiation of vascular endothelial cells by stimulating autophosphorylation and activation of VEGF receptor-2 (VEGFR-2, fetal liver kinase-1, and kinase insert domain-containing receptor). We developed fluorescence-based, quantitative methods to measure total VEGFR-2, VEGFR-2 phosphorylation, apoptosis, and microvessel density and size within whole tumor cross-sections using a laser scanning cytometer. Using these methods, we characterized the effects of DC101, a blocking antibody specific for murine VEGFR-2, on orthotopic human 253J-BV bladder tumors growing in nude mice. Basal levels of receptor phosphorylation were heterogeneous, with approximately 50% of endothelial cells positive for phosphorylated VEGFR-2 at baseline. DC101 therapy resulted in a 50% decrease in overall VEGFR-2 phosphorylation and a 15-fold and 8-fold increase in endothelial cell (CD31-positive) and tumor cell apoptosis, respectively. DC101 also decreased overall tumor microvessel density, but it modestly affected smaller CD105-negative microvessels located in the periphery of the tumor. Intriguingly, anti-VEGFR-2 therapy resulted in increased mean vessel size and an increase in overall VEGFR-2 levels. Increases in total VEGFR-2 levels were localized to the tumor core and were associated with increased expression of the oxygen-sensitive transcription factor, hypoxia inducible factor-1α. These data suggest that VEGFR inhibitors preferentially target discrete populations of tumor endothelial cells associated with the smaller peripheral blood vessels. Thus, agents that target a single receptor (e.g., VEGFR-2) may not be sufficient to completely inhibit tumor angiogenesis.

INTRODUCTION

The growth of solid tumors beyond the diffusion limit of oxygen (1–2 mm) is dependent on the formation of a new vascular network within the tumor (1–4). Tumors appear to initiate angiogenesis by disrupting normal homeostatic control of the pro- and antiangiogenic factors that regulate blood vessel density in normal tissues (5, 6). Prominent among these factors is vascular endothelial growth factor (VEGF; Refs. 7 and 8), a cytokine that plays an obligate role in the formation of new blood vessels during embryogenesis (9). In a variety of different solid tumors, high expression of VEGF is associated with increased microvessel density, disease progression, and metastasis (8, 10). VEGF regulates endothelial cell proliferation, differentiation, and survival via interactions with VEGF receptor-2 (VEGFR-2), also known as kinase insert domain-containing receptor and fetal liver kinase-1. These observations have prompted great interest in developing agents that selectively target VEGF or VEGFR-2 for use in cancer therapy (11–13).

Recent studies have demonstrated that tumor microvessels are qualitatively different from those present in normal tissues, displaying higher proliferative fractions and levels of disorganization (14, 15). These factors probably contribute to the “therapeutic window” observed in preclinical studies using antiangiogenic agents, in which significant antitumoral activity without toxicity has been observed (16, 17). However, other studies indicate that intratumoral vascular heterogeneity can also be significant. For example, determination of tumor microvessel density (MVD) using pan endothelial markers (CD31/CD34) provides prognostic information in some tumors but not in others, and in some cases, using a more selective marker for angiogenic vessels (i.e., endoglin/CD105) has proven to be more informative (18–22). The significance of these observations remains unclear, but variable marker expression may be related to differences in differentiation and/or functional status. Regardless, these observations raise questions about whether an agent intended for a single receptor (i.e., anti-VEGFR-2) can target all of the tumor vasculature.

We investigated these questions in human transitional cell carcinoma of the bladder, which is among the growing list of solid tumors that display increased VEGF expression with progression (23, 24). Preclinical studies have demonstrated that variants of the human 253J transitional cell carcinoma line selected for enhanced local growth (253J B-V) or metastasis to the lung (253J L-4) display increased VEGF expression (25). Conversely, stable transfection of the poorly tumorigenic parental 253J cells with VEGF under the control of an autologous (cytomegalovirus) promoter rendered the cells highly tumorigenic and angiogenic. Using standard immunohistochemical techniques, we recently evaluated the effects of a blocking antibody specific for murine VEGFR-2 (DC101) in orthotopic 253J B-V tumors (17). The results confirmed that the compound significantly inhibited tumor growth and angiogenesis. However, it was not possible to evaluate the intratumoral effects of the drug on VEGFR-2 phosphorylation and downstream biological consequences of the drug-target interaction.

In this study, we used antibodies specific for a number of angiogenesis-related markers and laser scanning cytometry (LSC) to quantitatively assess the effects of VEGFR-2 target inhibition in orthotopic 253J B-V tumors. We initially focused on using the LSC to determine the extent of target expression (activated VEGFR-2) at baseline and after anti-VEGFR-2 therapy. Innovative use of the LSC allowed us to capture information for whole-tumor sections, as opposed to the analyses of “hot spots” or high-power fields conventionally evaluated.
in studies dealing with solid tumors growing in vivo. We also adapted the contouring feature of the LSC to allow for quantification of microvessel densities and relative vessel sizes, as well as endothelial cell death, a downstream consequence of VEGFR-2 inhibition. The quantitative results demonstrate that inhibition of VEGFR-2 phosphorylation increases endothelial cell apoptosis and reduces MVD but also increases VEGFR-2 expression. More important, the results also reveal that VEGF inhibitors preferentially target small, CD105-negative vessels in the tumor periphery but do not significantly affect larger, established vessels within the tumor core.

MATERIALS AND METHODS

Orthotopic Model of Human transitional cell carcinoma and DC101 Therapy. We obtained male athymic BALB/c nude mice from the Animal Production Area of the National Cancer Institute, Frederick Cancer Research Facility (Frederick, MD). The mice were maintained in a laminar air flow cabinet under specific pathogen-free conditions and used at 8–12 weeks of age. All facilities were approved by the American Association for Accreditation of Laboratory Animal Care in accordance with the current regulations and standards of the United States Department of Agriculture, the Department of Health and Human Services, and the NIH. The highly metastatic human bladder carcinoma cell line 253BJ-BV (60–70% confluent) was prepared for injection as described previously (25). Mice were anesthetized with methoxyflurane, and viable tumor cells in HBSS (10^3/mL) were orthotopically implanted into the bladder wall. Formation of a bulla indicated a satisfactory injection.

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LSC-MEDiated Analysis of Angiogenesis Inhibition

For detection of total VEGFR-2 or HIF-1α, tissues were incubated with a 1:400 dilution of rabbit anti-fetal liver kinase-1 antibody (C-20; Santa Cruz Biotechnology, Santa Cruz, CA) or HIF-1α (clone H1a67, Novus Biologicals, Littleton, CO) overnight at 4°C. Tissues were washed with PBS containing 0.1% Brij for 3 min twice and once with PBS for 3 min. Tissues were incubated with a 1:400 dilution of secondary goat antirabbit IgG conjugated to Cy5 for 4 h at room temperature. Tissues were washed with PBS twice for 3 min and counterstained with 1 µg/ml propidium iodide for LSC analysis or a 1:2000 dilution of Hoechst (300 µg/ml) at room temperature for 5 min for visualization on an epifluorescence microscope.

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**LSC Quantification of Apoptosis in Endothelial Cells and Tumor Cells.** Percentages of apoptotic endothelial cells and tumor cells were determined by LSC as described previously (26, 27). All xenografts were stained with H&E and then by pathologically confirm the presence and location of tumor cells (Fig. 4C). Desired tumor areas were visually located using the epifluorescence microscope of the LSC to detect cell nuclei counterstained with propidium iodide, and the scan area was set using WinCyte software (CompCyte Corp., Boston, MA). Lasers were selected to detect red (cell nuclei), green (TUNEL), and red-long (CD31 or CD105) fluorescence and detector gain voltages were set so that a maximum of 50% saturation was achieved for the maximum pixel event scanned. Slides were scanned using an ×200 objective, and the minimum-area threshold was set to optimize single cell contours. Analytical gates (Fig. 6C) were set on the fluorescent properties of the negative staining controls. The gates defined four quadrants that determined the total number of cells within each population (quadrand 2, CD31+/TUNEL−; quadrant 1, CD31−/TUNEL−; and so forth). The relocation feature was used to identify and confirm TUNEL-positive and CD31-positive cells.

**LSC Analysis of Microvessels, Phosphorylated VEGFR-2, and Total VEGFR-2.** MVD is usually quantified by counting CD31-positive structures in several high-powered microscopic fields (×200), focusing on the areas displaying the greatest staining intensity (“hot spots”; Refs. 22–24). Data obtained in this fashion may not, however, be representative of more global effects of the drug within the tumor.

We used the LSC, therefore, to quantify changes in MVD, including vessel size, and changes in other biomarkers in whole-tumor cross-sections to more directly measure locoregional effects of drug treatment. Using the scan area feature of the LSC, we performed a second scan by contouring red-long fluorescence (CD31 or CD105) to count microvessels within whole tumor sections. Slides were scanned using an ×200 objective, and microvessels were contoured using the red-long fluorescence detector with the perimeter option selected (to determine vessel size). The minimum-area threshold was set to optimize contours of individual vessels. Thus, the total number of positive-events counted was equal to the total number of microvessels within the scanned region. Percent MVD was determined by (vessels/total cells × 100). The formula (control-treated/control × 100) was used to calculate changes in MVD. To measure the size of each vessel, the data file was replayed with the area/perimeter ratio selected on the X axis of the histogram window. The histograms represent the mean vessel size within each tumor section.

To determine the levels of phosphorylated VEGFR-2 within each endothelial cell, we selected lasers to detect red (cell nuclei), long-red (CD31), and green (p-VEGFR-2) fluorescence. Slides were scanned using an objective (×200) and detector gain voltages were set so that a maximum of 50% saturation was achieved for the brightest maximum pixel event scanned. The minimum area threshold was set to optimize single cell nuclei contour events. Analytical gates were set based on the fluorescent properties of the negative staining controls. The gates were used to define the quadrants that determined which cells were positive for CD31−/p-VEGFR-2−, and others. The relocation feature was used to visually confirm positive-stained cells. The formula (control-treated/control × 100) was used to calculate changes in endothelial cell expression of phosphorylated-VEGFR-2.
To measure total VEGFR-2 levels, we selected lasers that detect red (cell nuclei) and long-red fluorescence (VEGFR-2). Slides were scanned using a 200 objective, and cell nuclei were contoured by setting the minimum area threshold. Total VEGFR-2 levels were quantified by taking the integral of the long-red fluorescence. Cells were scored as either positive or negative for VEGFR-2 based on the fluorescent properties of the negative control sample with appropriate gating. Relocation was used to visually confirm positive marker expression.

Analysis of Intratumoral Biomarker Expression. After acquisition of the data for each biomarker as described above, we determined the differential expression of biomarkers in the periphery versus the core of each tumor (Table 2). First, an X and Y coordinate position map was generated using the analytical software of the LSC. Each acquired data file containing total cell nuclei detection (using propidium iodide) was replayed to generate a 2-dimensional tumor cross-section tissue map for each tumor as shown in Fig. 6B. Each black pixel represents a single cell within the tumor cross-section. Next, an elliptical draw tool was used to create a boundary that defined the tumor core from the periphery as shown in Fig. 4B. The size and placement of the elliptical boundary was based on morphological evaluation of each specimen (Fig. 4C). Each acquired biomarker data file (e.g., microvessels) was then replayed to determine the number of events within each tumor region as shown in Table 2. For example, Fig. 4B illustrates the distribution of microvessels (represented by each pixel) within each tumor compartment (red = core; black = periphery). Importantly, replay of the data file included only positive events that were based on gating of negative staining controls for each biomarker. For example, in Fig. 4C quadrants 3 and 4 were excluded from the differential analysis. Thus, each quadrant or cell population can be manually selected to determine quantitative distribution within each compartment displayed on the X and Y coordinate position map (Fig. 4B). These steps were repeated to determine differential expression for each biomarker in each tumor (Table 2).

Statistics. All statistical analyses were performed with SPSS software (SPSS, Chicago, IL). Experiments subjected to statistical analysis included an independent sample t test. Differences between values were considered significant for \( P < 0.05 \). The results included three-four animals in each group.

RESULTS

DC101 Inhibits Phosphorylation of VEGFR-2 and Increases Total VEGFR-2 Expression In Vivo. Tumor angiogenesis is dependent on VEGFR-2, but the effects on VEGFR-2 expression after
We next compared total VEGFR-2 levels in control with DC101-treated tumors by immunofluorescence staining (Fig. 2A). LSC analysis of whole-tumor cross-sections revealed that DC101 induced a significant increase in expression of total VEGFR-2 (Fig. 2B, note peak shift to the right), demonstrating that the observed decreases in phosphorylated VEGFR-2 were not attributable to reductions in total receptor levels.

Previous studies have suggested that tumor angiogenesis is more active at the tumor periphery than the tumor core (28–30). LSC-generated tumor tissue maps revealed that baseline levels of phosphorylated VEGFR-2 were highest in the tumor periphery and that DC101 produced the most dramatic inhibition of VEGFR-2 phosphorylation within these regions (Fig. 3; Table 2). In contrast, total VEGFR-2 was localized throughout the tumor at baseline, and the DC101-induced increase in VEGF receptor expression occurred primarily within the tumor core (Fig. 3; Table 2).

Effects of DC101 on the Tumor Vasculature. The patterns of baseline VEGFR-2 phosphorylation observed in the 253J-BV tumors suggested to us that DC101 might preferentially target tumor microvessels located in the tumor periphery. To directly test this possi-

![Fig. 2. Effects of DC101 on total VEGFR-2 levels. Tumor sections were stained for total VEGFR-2 (red), and cell nuclei were counterstained with Sytox (green) as described in “Materials and Methods.” A, representative images demonstrating increased VEGFR-2 staining after DC101 therapy compared with the controls. VEGFR-2, vascular endothelial growth factor receptor-2. B, quantitative analysis of VEGFR-2 expression at the single cell level (Y axis) by laser scanning cytometry. Note the 2-fold increase (shift to the right) in total VEGFR-2 fluorescence intensity (X axis) in DC101-treated tumors (red) compared with the controls (black).](image-url)
Fig. 3. Effects of DC101 on locoregional expression of phosphorylated and total VEGFR-2. Tissues stained in Figs. 1 and 2 were subsequently scanned by LSC to generate an X and Y coordinate position of endothelial cells positive for either phosphorylated VEGFR-2 (top row) or total VEGFR-2 (bottom row) within whole tumor cross-sections. Note that constitutive expression of phosphorylated VEGFR-2 appears most intense at the periphery of untreated tumors. The number of cells positive for phosphorylated-VEGFR-2 decreases after DC101 therapy compared with untreated tumors, indicated by the decrease in the density of pixels. In contrast, DC101-induced increase expression of total VEGFR-2 occurred within the tumor core. Laser scanning cytometry-generated tissue maps are representative of observations made with three independent tumors. VEGFR-2, vascular endothelial growth factor receptor-2.

Locoregional Effects of DC101 on Angiogenesis Inhibition. To obtain more precise information about the effects of anti-VEGFR-2-targeted therapy on endothelial cell apoptosis, we stained tumor sections with antibodies to either CD31 or CD105 and fluorescent TUNEL to measure the effects of DC101 therapy on endothelial cell apoptosis, as described in "Materials and Methods." Representative contour boundaries of peripheral and central regions of tumors are illustrated in Fig. 4B. Results are expressed as percentages of positive cells located within each region. Note that in the case of p-VEGFR-2, relative localization of cells did not change substantially following therapy with DC101, although expression of the marker on a per cell basis dropped by 55% (Fig. 4B). We then used the MVD contour map to compare the changes in vessel density with tumor morphology (detected by H&E staining; Fig. 4C, I and II correspond with the panels in Fig. 4B). We therefore stained tumor sections with an antibody specific for CD105 to measure the effects of DC101 therapy on these vessels. Contour map analyses revealed that CD105-positive vessels were concentrated around the tumor periphery in control tumors (Fig. 5; Table 2). Strikingly, however, the CD105-positive vessels largely persisted in the extreme periphery of tumors harvested from DC101-treated mice, and a new concentration of CD105-positive vessels accumulated within the tumor core (Fig. 5; Table 2). Thus, DC101 therapy did not result in a significant overall decrease in MVD within the CD105-positive subset when microvessel densities were normalized for reductions in total cells (Table 1).

Table 2 Loco-regional effects of DC101 on angiogenesis-related marker expression

<table>
<thead>
<tr>
<th>Treatment group/region</th>
<th>Hypoxia-inducible factor-1α (HIF-1α)</th>
<th>VEGFR-2</th>
<th>p-VEGFR-2</th>
<th>CD105</th>
<th>CD105</th>
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</thead>
<tbody>
<tr>
<td>Control</td>
<td></td>
<td></td>
<td></td>
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</tr>
<tr>
<td>Periphery</td>
<td>92.95% ± 0.63</td>
<td>92.58% ± 1.0</td>
<td>89.92% ± 0.8</td>
<td>82.19% ± 0.6</td>
<td>87.03% ± 0.1</td>
</tr>
<tr>
<td>Core</td>
<td>7.4% ± 0.44</td>
<td>7.42% ± 0.7</td>
<td>10.08% ± 0.5</td>
<td>17.81% ± 0.4</td>
<td>12.97% ± 0.1</td>
</tr>
<tr>
<td>DC101</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Periphery</td>
<td>79.89% ± 1.0</td>
<td>79.22% ± 6.0</td>
<td>73.94% ± 0.2</td>
<td>66.69% ± 2.0</td>
<td>79.55% ± 6.5</td>
</tr>
<tr>
<td>Core</td>
<td>20.11% ± 1.0</td>
<td>20.78% ± 4.0</td>
<td>26.06% ± 2.4</td>
<td>33.31% ± 2.0</td>
<td>23.36% ± 1.7</td>
</tr>
</tbody>
</table>

a VEGFR-2, vascular endothelial growth factor receptor-2; HIF-1α, hypoxia-inducible factor-1α.

b P < 0.001 vs. control.

c P < 0.05 vs. control.
Fig. 4. Effects of DC101 on tumor vasculature. Tissues were stained with anti-CD31 or anti-CD105 antibody, and microvessels were identified by contouring secondary antigen fluorescence by LSC. A, representative LSC-generated scanned images of control (left) and DC101-treated (right) whole tumor cross-sections (×200). The LSC-guided contour appears as a red perimeter surrounding each microvessel. B, whole tumor cross-section contour maps of microvessel locoregional distribution within representative control and DC101-treated tumors. Each microvessel detected by LSC was plotted on an x and y coordinate position map as a single pixel. The red gate within the center of each tumor separates the tumor core from the periphery. Note the overall significant decrease in microvessel density (39%), notably in the periphery, of DC101-treated tumors compared with controls. Roman numerals correspond to regions visualized by H&E staining in Fig. 4C. C, representative histological and morphological characteristics of control and DC101-treated tumors as assessed by H&E staining. Note the decreased cellular density in the periphery of DC101-treated tumors. D, Effects of DC101 on individual tumor microvessel size. The mean area/perimeter ratios (x axis) of all vessels (y axis) were calculated by LSC as a measure of vessel size. Note rightward shift in DC101-treated tumors (red) compared with controls (black), indicating increased mean microvessel size after therapy. LSC, laser scanning cytometry.
identify the subpopulations of endothelial cells that were targeted by DC101 therapy (Fig. 6A). LSC-generated contour maps localized the apoptotic endothelial cells (CD31+ and tumor cells (CD31 -) within whole-tumor sections (Fig. 6B). Average levels of apoptosis in endothelial (CD31+/TUNEL+) and tumor (CD31+/TUNEL+) cells at baseline were 0.25% and 1.0%, respectively (Fig. 6C; Table 1). DC101 treatment resulted in a 15-fold increase in endothelial cell death associated with a 8-fold increase in tumor cell death, both of which were highly significant (P < 0.001; Fig. 6B; Table 1). Consistent with the changes in VEGFR-2 phosphorylation and MVD, the DC101-induced increases in endothelial cell death were most prominent in the tumor periphery (Fig. 6B). Furthermore, dying tumor cells tended to occur in close proximity to dying endothelial cells (note clusters of blue and yellow pixels in Fig. 6B, overlays).

Quantitative analysis of TUNEL staining within the CD105-positive subset of endothelial cells revealed much higher baseline levels of cell death in the CD105-positive vessels (13.55%) than in the CD31-positive vessels (0.25%, see Table 1). Surprisingly, levels of apoptosis did not increase in the CD105-positive subset after therapy with DC101 (Fig. 6A; Table 1).

Effects of DC101 on Expression of HIF-1α. The transcription factor HIF-1α is an oxygen-sensitive protein that is stabilized and accumulates when cells are exposed to hypoxia (31, 32). We, therefore, measured locoregional changes in HIF-1α expression using LSC analysis to obtain a surrogate measure of relative hypoxia in the 253J-BV tumor sections. At baseline, expression of HIF-1α was low and confined to patches in the tumor core and a thin rim around the tumor periphery (Fig. 7A). After DC101 therapy, HIF-1α levels increased dramatically throughout the tumors but especially within the tumor cores (Fig. 7B; Table 2). Closer inspection of HIF-1α staining suggested that protein localization was heterogeneous with some cells displaying prominent nuclear localization and others displaying primarily cytoplasmic localization (Fig. 7C). LSC-based quantitative analyses revealed that DC101 induced a 3-fold increase in HIF-1α protein levels (Fig. 7D).

**DISCUSSION**

The VEGF/VEGFR-2 pathway is required for angiogenesis and neovascularization in many solid tumors (8, 10) including bladder cancer (24). These observations have prompted strong interest in developing blocking antibodies and small molecules specific for the VEGF/VEGFR-2 pathway as candidate anticancer therapeutic agents. Recent studies have shown that these inhibitors attenuate the growth and metastasis of human tumors in mice (16, 17, 33, 34). However, these studies did not characterize the effects of anti-VEGFR-2 agents on the dynamics of VEGFR-2 activation, VEGF receptor modulation, tumor cell growth, and angiogenesis within the entire tumor.

In this study, we used an innovative approach to characterize the locoregional effects of VEGF-2 blockade on VEGF-2 phosphorylation, MVD and vessel size, apoptosis, and the expression of the hypoxia-associated transcription factor HIF-1α. The results demonstrated that constitutive phosphorylated-VEGFR-2 levels in endothelial cells were highest around the tumor periphery and that anti-VEGFR-2 therapy preferentially reduced the number of smaller CD31-positive blood vessels located within the same region. These effects were associated with increased expression of HIF-1α and VEGFR-2, both of which were concentrated within the tumor core. Increases in apoptosis within tumor-associated endothelial cells occurred throughout the tumors but appeared to largely correlate with inhibition in VEGF-2 phosphorylation. Together, our results strongly suggest that the primary effects of VEGFR-2 inhibition are localized to the tumor periphery but that they cause secondary changes, including hypoxia, increased VEGFR-2 expression, and tumor cell death, most notably within the tumor core. Our data are consistent with recent studies demonstrating increases in blood volume in tumors treated with these agents (35) and a larger body of work suggesting that angiogenesis is most active in the leading edge (i.e., periphery) of tumors (28–30).

Although we expected that DC101 would reduce levels of phosphorylated VEGF-2 in the 253J-BV tumors, the observation that total VEGF-2 levels increased after therapy was unanticipated. A trivial explanation for the effect could be that the antibody we used to detect total VEGF-2 reacts more strongly with the unphosphorylated receptor than it does with the phosphorylated receptor, perhaps because one of the phosphorylation sites interferes with the epitope of the antibody. However, we observed the strongest increases in VEGF-2 within the tumor core, whereas levels of baseline phosphorylated-VEGFR-2 were highest in the periphery, arguing against this explanation. Alternatively, the increases in VEGF-2 could represent an adaptive response to the central hypoxia stimulated by DC101 therapy. Growth regulatory pathways are often controlled by feedback loops that reduce the expression of pathway components when signal transduction is active and increase levels when signaling is inactive. The DC101-induced increases in VEGF-2 expression were associated with strong up-regulation of HIF-1α, indicating that induction of VEGF-2 occurred preferentially within regions of relative hypoxia (i.e., in the tumor core). Previous work has demonstrated that VEGF plays a role in the paracrine stimulation of angiogenesis (36, 37) but may also act via an autoregulatory pathway activated when VEGF signal transduction is interrupted (38). In the orthotopic 253J-BV tumor model, up-regulation of VEGF-2 could serve to rapidly reestablish the vascular network once therapy is terminated.

The recognition that tumor microvessels display marked structural and functional heterogeneity has stimulated a search for proteins that might serve to identify and target specific subsets of tumor-associated endothelial cells. Endoglin (CD105) is a 180-kDa hypoxia-induced, proliferation-associated cell surface glycoprotein, expressed exclusively by vascular endothelial cells, that has recently been advanced as one such marker (19). The protein binds to and regulates the signaling activity of transforming growth factor-β (39), a cytokine that has been broadly implicated in angiogenesis (40). Endoglin-deficient mice die during embryonic development because of defects in angiogenesis (41, 42), confirming the central role of the molecule in the process. Other recent studies suggest that CD105 is a more informative marker for tumor angiogenesis than are pan endothelial markers such as CD31 or CD34 (18, 22, 43).
Analysis of CD105 expression in control 253J-BV tumors confirmed that high-level expression was concentrated in the tumor periphery, a region that also contained the highest concentration of phosphorylated-VEGFR-2 and smaller blood vessels, presumably because of active angiogenesis at the leading edge of the tumor. Therefore, we expected that DC101 therapy would produce stronger effects in the CD105-positive vessels than in CD105-negative/CD31-positive vessels. Surprisingly, we found the opposite to be true, in that MVD as measured by CD105-positive staining did not decrease, and CD105-positive cells did not display increases in apoptosis. Further-

Fig. 6. Effects of DC101 on apoptosis. A, representative images of immunofluorescence anti-CD31 or anti-CD105 (red) and TUNEL (green) staining in DC101-treated tumors. Note that more CD31-positive endothelial cells are apoptotic compared with the CD105-positive subset (CD31 or CD105 red + TUNEL green = yellow). TUNEL, terminal deoxynucleotidyl transferase-mediated nick end labeling. B, tissues were scanned by LSC to generate contour maps of the intratumoral distribution of apoptotic endothelial cells (CD31+/TUNEL+, blue pixels) and apoptotic tumor cells (CD31+/TUNEL+, yellow pixels) within whole tumor cross-sections (black pixels represent total cell nuclei). Superimposing CD31+/TUNEL+ cells and CD31+/TUNEL+ cells reveals that DC101-induced apoptosis is heterogeneous, with clusters of dead CD31-positive cells in the tumor periphery. Note the increase in blue and yellow pixels in the DC101-treated tumors (bottom panel) compared with the controls (top panel). Tissue maps are representative of observations in three independent tumors. LSC, laser scanning cytometry. C, LSC-mediated quantification of apoptotic cells in whole tumor sections. Tissues stained for anti-CD31 or anti-CD105 and TUNEL were subsequently scanned by LSC to generate scattergrams. Each cell nucleus was analyzed by LSC and plotted on a scattergram relative to the fluorescent intensity of each antigen (CD31 or CD105/red or TUNEL/green). Gates were set based on the intensity of negative staining controls. Note the increase in apoptotic tumor cells (quadrant 1, yellow) and endothelial cells (quadrant 2, blue) after DC101 therapy compared with controls. Scattergrams are representative of observations in three independent tumors.
more, CD105-positive vessels appeared to accumulate within tumor cores after therapy in parallel with increased VEGFR-2 expression. The most straightforward explanation for these observations is that both events were driven by increased hypoxia produced by therapy. That CD105-positive vessels are relatively refractory to VEGFR-2-directed therapy suggests that they may arise and persist via a VEGF-insensitive mechanism. Additional effort is required to functionally characterize these and other vessel subsets in tumors treated with antivascular agents.

Recent studies have used two-color immunofluorescence detection of CD31 staining and DNA fragmentation (by TUNEL) to identify dying endothelial cells in tumors treated with antiangiogenic agents (16, 17, 44–46). Accurate manual quantification of these events may be impossible in a practical sense. Baseline levels of endothelial and tumor cell apoptosis in the 253J B-V tumors were 0.3 and 1.1%, respectively (Table 1), and these cells were scattered heterogeneously throughout the tumor (Fig. 6B). Therefore, even a large (5–10-fold) increase in cell death would be difficult to detect using conventional strategies. Not only is the LSC able to detect smaller increases in fluorescence, it is also capable of rapidly analyzing many events, allowing for the detection of even modest changes in target levels (47, 48). Our ongoing efforts are aimed at determining whether the assays described here provide useful information about biological responses in biopsies obtained before and after anticancer therapy (27, 47–49).

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