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<td>As Published</td>
<td><a href="http://dx.doi.org/10.1016/j.ccr.2011.11.024">http://dx.doi.org/10.1016/j.ccr.2011.11.024</a></td>
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<td>Publisher</td>
<td>Elsevier B.V.</td>
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<td>Version</td>
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<td>Accessed</td>
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Pericyte Depletion Results in Hypoxia-Associated Epithelial-to-Mesenchymal Transition and Metastasis Mediated by Met Signaling Pathway

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DOI 10.1016/j.ccr.2011.11.024

SUMMARY

The functional role of pericytes in cancer progression remains unknown. Clinical studies suggest that low numbers of vessel-associated pericytes correlated with a drop in overall survival of patients with invasive breast cancer. Using genetic mouse models or pharmacological inhibitors, pericyte depletion suppressed tumor growth but enhanced metastasis. Pericyte depletion was further associated with increased hypoxia, epithelial-to-mesenchymal transition (EMT), and Met receptor activation. Silencing of Twist or use of a Met inhibitor suppressed hypoxia and EMT/Met-driven metastasis. In addition, poor pericyte coverage coupled with high Met expression in cancer cells speculates the worst prognosis for patients with invasive breast cancer. Collectively, our study suggests that pericytes within the primary tumor microenvironment likely serve as important gatekeepers against cancer progression and metastasis.

INTRODUCTION

Metastasis is the leading cause of death in cancer patients. The formation of secondary tumors or metastasis is greatly influenced by multifaceted tumor-stroma interactions, in which stromal components of the tumor microenvironment can influence the behavior of the cancer cells (Coussens et al., 2000; Joyce, 2005; Thiery, 2009). While cancer cell-autonomous changes are undoubtedly critical for cancer progression and metastasis, the functional contribution of stromal cells is still emerging.

Pericytes are an integral component of the tissue vasculature. As perivascular stromal cells, pericytes provide structural support to blood vessels and regulate tissue physiology via its influence on vascular stability (Dore-Duffy and Cleary, 2011; Kim et al., 2006). Due to their essential function in vascular development, pericytes are also speculated to play an important role in tumor angiogenesis. Angiogenesis is required for the growth of tumors, and VEGF-mediated proliferation and migration of endothelial cells is critical for the generation of new capillaries, which is further supported by the recruitment of pericytes (Raza et al., 2010). Some studies have explored strategies that target both endothelial cells and pericytes (Bergers et al., 2003; Lu et al., 2007) or pericytes alone (Lu et al., 2007; Ozerdem, 2006a) to inhibit tumor angiogenesis and tumor growth. However, clinical data correlates low pericyte coverage with poor patient prognosis (O’Keefe et al., 2008; Stefansson et al., 2006; Yonenaga et al., 2005), and disruption of pericytes has also been suggested to enhance metastasis (Xian et al., 2006).

The growth of tumors is often associated with defective tumor vasculature that cannot keep up with the overall oxygen and metabolic needs, ultimately resulting in tumor hypoxia (Harris, 2002; Semenza, 2003). Diminished oxygen levels lead to the

Significance

Pericyte coverage and its relation to metastasis are poorly understood. This study suggests that pericyte coverage on tumor vasculature serves as a key negative regulator of metastasis. Clinical studies suggest that cancer patients with low numbers of vessel-associated pericytes exhibit a high mortality rate. Cancer cell autonomous changes cooperate with stromal changes to determine the rate of cancer progression and metastasis.
activation and stabilization of the transcription factor HIF1α
(Pouysségur et al., 2006), and hypoxia and HIF1α expression are
coordinated with poor prognosis and metastasis in cancer patients
(Birmer et al., 2000; Bos et al., 2003; Brizel et al., 1997;
Vleugel et al., 2005). Hypoxia induces epithelial-to-mesenchymal
transition (EMT) of cells specifically via HIF1α activation of the
master regulator of EMT Twist (Sun et al., 2009; Yang et al.,
2008), which is suggested to play an essential role in
promoting metastasis (Yang et al., 2004).

Met, the receptor for hepatocyte growth factor (HGF), is also
a key promoter of EMT (Birchmeier et al., 2003). Furthermore,
the Met promoter contains HIF1α binding sites and is regulated
by both hypoxia and HIF1α (Hara et al., 2006; Hayashi et al.,
2005; Pennacchiotti et al., 2003). HGF/Met expression is also
upregulated in many cancers (Di Renzo et al., 1991), correlating
with disease progression and metastasis (Di Renzo et al., 1995;

Using genetically engineered mouse models (GEMMs) and
pharmacological targeting of pericytes, we examined whether
pericyte deficiency positively or negatively affects metastasis
and explored possible underlying mechanisms.

RESULTS

Low Pericyte Coverage Is Associated with Invasive
Breast Cancer and Correlates with Decreased
Patient Survival

Pericyte coverage of the tumor vasculature was evaluated in
tissue samples from breast cancer patients with invasive
ductal carcinoma via immunostaining for NG2, a vascular pericytes
marker (Bergers and Song, 2005; Jain, 2003; Ozerdem et al.,
2001a; Xian et al., 2006). To validate the promoter
expression of NG2-YFP, we expressed NG2-YFP under the control
of the NG2 promoter in NG2-tk transgene, in vitro culture of NG2+ cells from NG2-tk
and wild-type (WT) mice were treated with varying GCV concen-
trations (Figure S1D). Dose-dependent ablation of NG2+ cells
was observed, with 75% ablation at 500 μM GCV.

4T1-GFP cancer cells were implanted into the mammary
fat pad of NG2-tk mice and wild-type littermates. Primary
tumor growth was monitored and daily GCV injections were initi-
ated when tumors reached ~500 mm3 and continued until
tumors reached ~2,000 mm3 (Figure 1A). Tumor volumes
decreased upon initiation of GCV treatment in the NG2-tk mice
and remained significantly smaller until the experimental
endpoint (Figure 1B). The number of NG2+ cells, CD31+ cells,
and percent vessel-associated NG2+ cells in the primary tumors
of NG2-tk-GCV mice were significantly reduced when com-
pared to control GCV-treated wild-type littermates (WT+GCV
mice) (Figure 1C). To investigate whether pericyte depletion
was associated with vascular abnormalities, we infused tumor-
bearing mice with FITC-conjugated dextran and observed a
greater amount of extravascular FITC-dextran in pericyte-
depleted tumors (Figure 1D).

While pericyte ablation reduced primary tumor growth, 4T1
tumor-bearing NG2-tk-GCV mice exhibited increased lung
metastasis when compared to WT+GCV mice (Figure 1E).
FACS and quantitative PCR analysis of genomic DNA for the
cancer cell-associated GFP gene revealed that the number
of circulating cancer cells and metastatic cancer cells in the lungs
was greater in NG2-tk-GCV mice than in WT+GCV mice.
Reduced tumor size and increased metastasis were also
observed when pericytes were ablated in the MMTV-PyMT
spontaneous mammary tumor model using GCV-treated
MMTV-PyMT/NG2-tk double transgenic mice (Figures 1F and
1G). However, upon intravenous injection of 4T1 cancer cells
into NG2-tk-GCV and WT+GCV mice, pericyte ablation had no
significant effects on metastasis in the absence of a primary
tumor (Figure S1E).

PDGFRβ has also been used as a marker to identify pericytes
(Dore-Duffy, 2008; Hellström et al., 1999; Liebner et al., 2000;
Ozerdem et al., 2001a; Xian et al., 2006). To validate the prome-
tastatic effects of pericyte depletion observed in NG2-tk-GCV
mice, we generated PDGFRβ-tk mice in which viral thymidine
kinase is expressed under the PDGFRβ promoter and found that
PDGFRβ-RFP expression colocalized with PDGFRβ antibody staining in 4T1 tumors. To determine the efficacy of the
PDGFRβ promoter, we also generated PDGFRβ-RFP mice in which red fluorescent protein (RFP) is ex-
pressed under the same PDGFRβ promoter element (Figures
S2A and S2B) and found that PDGFRβ-RFP expression colocal-
ized with PDGFRβ antibody staining in 4T1 tumors. To determine the efficacy of the PDGFRβ transgene, in vitro culture of PDGFRβ+ cells from PDGFRβ-tk and WT mice were subjected
to increasing concentrations of GCV (Figure S2C). Dose-depen-
dent ablation of PDGFRβ+ cells was observed, with 60% ablation
at 50 μM GCV.

4T1 cancer cells were implanted into the mammary fat pad of
PDGFRβ-tk mice and WT littermates. Tumor volumes decreased
upon initiation of GCV treatment in PDGFRβ-tk mice and
remained significantly smaller until the experimental
endpoint when compared to WT+GCV mice (Figures 2A and 2B).
However, metastasis was greatly enhanced following ablation
of PDGFRβ+ cells (Figure 2C). Immunostaining with PDGFRβ
Cancer Cell 21, 66–81, January 17, 2012 ©2012 Elsevier Inc. 67
Figure 1. Reduced Tumor Growth and Increased Metastasis after Depletion of Vessel-Associated NG2+ Cells

(A) Orthotopic implantation of 4T1 cancer cells in NG2-tk mice and wild-type littermates, with daily ganciclovir (GCV) or saline (PBS) injections beginning when tumors reached \( \approx 500 \) mm\(^3\).

(B) Tumor volumes over the experimental time course.

(C) Representative images of tumor sections from WT+GCV and NG2-tk+GCV mice immunolabeled for NG2 (green)/CD31 (red), and quantification of number of NG2+ cells, CD31+ cells, and percent vessel-associated NG2+ cells in each group. DAPI = nuclei. Scale bar, 50 μm. High-magnification images are located in the upper right corner. Scale bar, 10 μm.
antibody in the tumors of PDGFRβ-tk+GCV mice revealed 80% reduction in vessel-associated PDGFRβ cells (Figure 2D). PDGFRβ shares ~90% colocalization with NG2 on tumor vasculature (Sugimoto et al., 2006), and vessel-associated NG2+ cells were also reduced by 80% in the tumors of PDGFRβ-tk+GCV mice (Figure 2D). The overall pericyte coverage (assessed by vessel-associated NG2+/PDGFRβ+ double-positive cells) and the number of CD31+ cells were reduced in PDGFRβ-tk+GCV mice when compared to WT+GCV mice (Figure 2D).

As an alternative model for inhibiting PDGFRβ+ cells, 4T1 tumor-bearing mice were treated with PDGFRβ-specific antibodies to suppress PDGFRβ activity. PDGFRβ antibody treatment significantly decreased tumor volume and increased metastatic burden (Figures 2E and 2F), in association with a significant reduction in the percent vessel-associated PDGFRβ+ cells (Figure 2G).

Enhanced Hypoxia, HIF1α Expression, and EMT Program in Pericyte-Depleted Tumors

To gain insight into the molecular mechanisms associated with increased metastasis resulting from pericyte depletion, we performed gene expression profiling of tumors from NG2-tk+GCV and WT+GCV mice. We employed gene expression analysis to identify significantly upregulated genes (grouped as pathways [Table S2] and network processes [Table S3]) in NG2-tk+GCV mice when compared to WT+GCV mice. The overlapping processes identified were (1) response to hypoxia, (2) response to stress, and (3) cell motion/migration (Table S3). Reduced pericyte coverage can decrease vessel stability and increase hypoxia (Huang et al., 2010). In concordance, pericyte depletion in the NG2-tk+GCV mice induced a gene expression profile that reflected a hypoxic state. We assessed hypoxia levels by examining pimonidazole adduct formation in the tumors of NG2-tk+GCV and WT+GCV mice and found increased hypoxic levels in the NG2-tk+GCV pericyte-depleted tumors (Figure 3A). In addition, expression of the hypoxia-inducible transcription factor HIF1α was also significantly increased in the tumors of NG2-tk+GCV mice (Figure 3B).

The exact mechanism connecting hypoxia and cancer invasiveness remains unknown; however, several have been proposed (Dachs and Tozer, 2000; Gupta and Massague, 2000; Rofstad, 2000; Yang et al., 2008). Because cell motion/migration was identified as one of the primary processes upregulated by NG2-tk+GCV tumors in the gene expression profiling analysis, we hypothesized that EMT may be a mechanism connecting hypoxia and cancer invasiveness. Further examination of the microarray data revealed that the expression of many EMT-associated genes were upregulated in NG2-tk+GCV tumors when compared to WT+GCV tumors (Table S4). To identify epithelial cells undergoing EMT, tumors from NG2-tk+GCV and WT+GCV mice were immunostained for the epithelial marker Cytokeratin-8 (CK8) and the mesenchymal marker αSMA; the number of CK8+/αSMA+ double-positive cells was significantly increased in NG2-tk+GCV pericyte-depleted tumors (Figure 3C).

Next, we performed quantitative RT-PCR and confirmed that expression of CK8 was significantly downregulated, while transcription factors associated with EMT induction, such as Twist and Snail, were significantly upregulated in NG2-tk+GCV tumors (Figure 3D). Other epithelial genes such as E-cadherin and α-catenin were also downregulated, while genes driving mesenchymal phenotype such as Slug, Lox, and Fibronectin were upregulated.

In agreement with the data from the NG2-tk+GCV mice, tumors from MMTV-PyMT/NG2-tk+GCV mice revealed increased hypoxia along with increased numbers of CK8+/αSMA+ double-positive cells, reduced E-cadherin expression, and increased Twist and Snail expression, when compared to tumors from MMTV-PyMT/WT+GCV mice (Figures 3E–3G). Tumors from PDGFRβ-tk+GCV mice also showed increased hypoxia, increased HIF1α expression, and acquisition of an EMT program shift when compared to control mice (data not shown).

The transcription factor Twist has been termed the master regulator of EMT (Yang et al., 2004). To evaluate whether inhibition of EMT via silencing of Twist abrogates the metastatic phenotype seen in NG2-tk+GCV mice, we orthotopically injected 4T1 cancer cells with stably-silenced Twist (two different clones of 4T1-twist shRNA) into NG2-tk+GCV and WT+GCV mice. Tumor volume in 4T1-twist shRNA tumor-bearing NG2-tk+GCV mice was reduced when compared to 4T1-twist shRNA tumor-bearing WT+GCV mice (Figure 4A). Moreover, metastatic burden was decreased in 4T1-twist shRNA tumor-bearing WT+GCV mice when compared to 4T1 tumor-bearing WT+GCV mice, while metastasis was further suppressed in 4T1-twist shRNA tumor-bearing NG2-tk+GCV mice (Figures 4B–4E).

Met Protooncogene Activation in Pericyte-Depleted Tumors

Quantitative RT-PCR for Met revealed significantly increased Met expression in NG2-tk+GCV tumors when compared to WT+GCV tumors (Figure 5A). Additionally, increased phosphorylation of Met was also observed in tumors from NG2-tk+GCV and MMTV-PyMT/NG2-tk+GCV mice when compared to tumors from control mice (Figures 5B and 5C), as well as in PDGFRβ-tk+GCV mice (data not shown).

Next, we explored whether pharmacological targeting of Met can suppress metastasis in pericyte-ablated mice. Treatment of MMTV-PyMT/NG2-tk mice with both GCV and the Met
inhibitor PF2341066 completely suppressed the enhanced metastasis of MMTV-PyMT/NG2-tk mice treated with GCV alone (Figures 5D–5F). The baseline lung metastasis observed in the control tumors (without pericyte depletion, hypoxia, HIF-1α expression, Met activation, and EMT) did not respond to Met inhibition.

Enhanced Metastasis upon Pericycle Targeting Using Pharmacological Inhibitors Is Suppressed by Concomitant Met Inhibitor Treatment

Many studies have reported that imatinib (which targets pericytes via PDGFRβ) and sunitinib (which targets both endothelial cells and pericytes via VEGFR1, VEGFR2, VEGFR3, and
PDGFR(β)), drugs currently in clinical use, can inhibit tumor progression (Bergers et al., 2003; Ebos et al., 2009; Lu et al., 2007; Mendel et al., 2003; Páez-Ribes et al., 2009; Pietras and Hanahan, 2005); however, there have been limited studies examining their effects on metastasis. Treatment with sunitinib and another receptor tyrosine kinase inhibitor sorafenib have been demonstrated to increase metastasis in animal tumor models (Ebos et al., 2009; Páez-Ribes et al., 2009); however, the molecular mechanism for which remains largely unknown. Therefore, we examined whether imatinib and sunitinib enhance metastasis due to mechanisms similar to shown above.

4T1 tumor-bearing mice were treated with either imatinib or sunitinib. Imatinib treatment reduced pericyte coverage (as determined by vessel-associated NG2+/PDGFR(β) double-positive cells) by more than 60% (Figure S3A). In concordance with previous reports (Lu et al., 2007), decreased pericyte coverage was not accompanied by net reduction of tumor vessels (Figure S3A). Quantitative RT-PCR showed negligible expression levels of c-Kit and Abl1 (additional targets of imatinib) in 4T1 tumors, and their expression remained unchanged upon imatinib treatment (Figure S3A). Sunitinib treatment led to reduced numbers of both NG2+/PDGFR(β) double-positive cells and CD31+ endothelial cells (Figure S3A).

4T1 tumor-bearing mice treated with sunitinib exhibited reduced tumor volume and growth with increased levels of apoptosis, while imatinib-treated tumor-bearing mice revealed similar tumor growth kinetics when compared to mice treated with PBS-vehicle (Figures 6A–6C). Analysis of lungs revealed a significantly higher level of metastatic burden in both the imatinib-treated and sunitinib-treated groups (Figure 6D). Quantification of FITC-dextran revealed increased amount of extravascular dextran in the tumors of imatinib-treated and sunitinib-treated mice (Figure 6E). Furthermore, tumors in imatinib-treated and sunitinib-treated mice showed significant increase in hypoxia as assessed by pimonidazole staining (Figure 6F), as well as increased expression of HIF1α (Figure 6G). Similar to results obtained with the transgenic mice, however, imatinib or sunitinib treatment had no significant effects on metastasis when 4T1 cells were injected intravenously (Figure S3B).

Next, we evaluated whether pharmacological targeting of pericytes also induced an EMT program in the cancer cells. Tumors from imatinib-treated and sunitinib-treated mice exhibited an EMT program in the cancer cells. Tumors from imatinib-treated and sunitinib-treated mice also induced an EMT program in the cancer cells. Tumors from imatinib-treated and sunitinib-treated mice (Figures 7A–7F), despite retaining the imatinib- or sunitinib-induced changes in vessel integrity and tumor hypoxia (Figures 7G–7I). PF2341066 treatment of imatinib-treated and sunitinib-treated mice successfully inhibited both Met and phosphorylated Met levels (Figure S4B). Although PF2341066 is also an inhibitor of ALK (Zou et al., 2007), quantitative RT-PCR (data not shown) and immunostaining revealed that ALK was not expressed in 4T1 tumors with or without PF2341066 treatment (Figure S4C). The baseline tumor weight and lung metastasis observed in the control tumors (without pericyte deficiency, hypoxia, HIF1α expression, Met activation, and EMT) did not respond to Met inhibition alone (Figure S4D).

To further investigate whether targeting pericytes leads to increased metastasis in other tumor types, we subcutaneously implanted B16F10 mouse melanoma cells into C57Bl6 mice (Figure S4E) and orthotopically implanted 786-O human renal cell carcinoma cells under the renal capsule of nude mice (Figure S4F). The mice were then treated with PBS, sunitinib, PF2341066 or a combination of both sunitinib and PF2341066. Sunitinib treatment led to reduced B16F10 tumor volume and weight but led to an increase in metastasis. Sunitinib-treated tumors also showed increase in hypoxia, phosphorylated Met, and induction of EMT. Treatment with PF2341066 did not affect primary tumor volume and weight; however, concomitant treatment with PF2341066 and sunitinib significantly suppressed metastasis, despite hypoxia remaining high in these tumors. Similarly, mice with RCC tumors treated with sunitinib showed increased lung metastasis, increased hypoxia, increased phosphorylated Met, and enhanced EMT program. Concomitant treatment of RCC tumor-bearing mice with sunitinib and PF2341066 suppressed metastasis and EMT despite high levels of hypoxia. Sunitinib-treated mice intravenously injected with RCC (to bypass the primary tumor), however, showed significantly reduced metastasis when compared to PBS-treated mice.

To explore the impact of targeting only endothelial cells on metastasis without targeting pericytes, RCC tumor-bearing mice were treated with anti-human VEGF-A blocking antibody (Bevacizumab) and 4T1 tumor-bearing mice with anti-mouse VEGF-A blocking antibody. Bevacizumab treatment led to decreased tumor volume; however, metastasis was unchanged (Figure S4G). Tumors from bevacizumab-treated mice did not show an increase in hypoxia or Met activation (Figure S4G). 4T1 tumor-bearing mice treated with VEGF-A antibody showed reduced tumor growth and metastasis when compared to control mice (Figure S4H). Similar results were obtained when pancreatic neuroendocrine (PNET) and RCC tumor-bearing mice were treated with endogenous inhibitors of angiogenesis that target endothelial cells, such as tumstatin and endostatin (data not shown; Xie et al., 2011).

**Loss of Pericytes Coupled with High Met Expression Is Associated with Decreased Survival of Breast Cancer Patients**

Our experiments with mice suggested that loss of pericytes leads to enhanced tumor hypoxia and metastasis via increased Met expression in cancer cells. We evaluated breast cancer...
Figure 3. Increase in Hypoxia and EMT in Pericyte-Depleted Tumors

(A) Hypoxia was detected by immunohistochemistry staining of pimonidazole adducts in 4T1 tumor sections from NG2-tk+GCV and WT+GCV mice. Nuclear counterstain: hematoxylin stain. Quantitative analysis of the percent hypoxic area per visual field.

(B) Immunostaining for HIF1α. DAPI = nuclei. Quantification of HIF1α immunostaining and western blot analysis for HIF1α expression; GAPDH is used as an internal control.

(C) EMT as detected by immunofluorescent staining for Cytokeratin 8 (red) and α-SMA (green). DAPI = nuclei. Arrows point to CK8+/αSMA+ double-positive cells. Quantification of EMT is plotted as fold change in the number of CK8+/αSMA+ double-positive cells per visual field.

(D) Quantitative RT-PCR for α-catenin, Cytokeratin 8 (CK8), E-cadherin, Fibronectin, Slug, Snail, Twist, and Lox comparing expression levels in tumor tissues from NG2-tk+GCV mice relative to WT+GCV mice and plotted as log10 relative expression.
samples for pericyte coverage, HIF1α expression and Met expression. Invasive ductal carcinoma (IDC) patients with high levels of HIF1α exhibited poor prognosis with diminished disease-free survival, as has been also suggested by other studies (Baba et al., 2010; Koukourakis et al., 2002; Vleugel et al., 2005). While high Met expression in cancer cells was associated with a drop in disease-free and overall survival, the coupling of poor pericyte coverage together with high Met expression correlated with an additional drop in disease-free and overall survival (Figures 8A and 8B). Furthermore, pericyte coverage coupled with Met expression correlated with breast cancer stage, depth of invasion, and the presence of distant metastasis (Figure 8C).

**DISCUSSION**

Tumors induce angiogenesis to generate new blood vessels (Folkman, 1971, 1974, 1995; Hanahan and Weinberg, 2000), and pericytes are important structural and functional components of blood vessels (Dore-Duffy and Cleary, 2011). In normal

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**Figure 4. Decreased Metastasis in Mice with Pericyte-Depleted Tumors after Inhibition of EMT**

(A) Tumor volumes over the experimental time course in WT+GCV and NG2-αk+GCV mice implanted with 4T1 or 4T1-Twist shRNA cells. (B–D) Representative photomicrographs of H&E-stained lung sections of WT+GCV and NG2-αk+GCV mice implanted with (B) 4T1 cells, (C) 4T1-Twist shRNA cells-clone 5 and (D) 4T1-Twist shRNA cells-clone 7. Arrows point to metastatic nodules. (E) Quantification of metastatic area. Error bars display SEM; asterisks denote significance (*p ≤ 0.05). NS, nonsignificant. Scale bar, 50 μm.
tissue, pericytes play an important role in regulating the physiological function of blood vessels; however, their precise role in the context of tumor vasculature is largely unexplored. Studies related to pericycle coverage on tumor blood vessels suggest that coverage can vary; some tumor types exhibit greater pericyte coverage whereas others exhibit limited and abnormal coverage (Eberhard et al., 2000). Many studies have suggested that targeting pericytes alone or in combination with endothelial cells might be beneficial to control tumor growth (Bergers et al., 2003; Lu et al., 2010; Ozerdem, 2006a, 2006b), while other...
Figure 6. Decreased Pericyte Coverage, Altered Vasculature, Enhanced EMT, and Increased Metastasis in Imatinib- and Sunitinib-Treated Mice

(A) Orthotopic implantation of 4T1 cancer cells into PBS-, imatinib- and sunitinib-treated mice and tumor volumes over the experimental time course.
(B) Tumor weight at the experimental endpoint.
studies have suggested that pericyte deficiency may facilitate cancer metastasis (Xian et al., 2006). Our preliminary clinical studies with tissue samples from patients with invasive ductal carcinoma suggested that low numbers of vessel-associated pericytes significantly correlated with poor prognosis. Therefore, in this study, we explored the function of pericytes in cancer progression and metastasis.

Tumors in mice generally do not exhibit a significant drop in pericyte coverage until they reach a very large size (unpublished data). Therefore, we used multiple transgenic and pharmacological approaches to target pericytes and achieve their loss in tumors of reasonable size. Our data demonstrated that pericyte loss increased metastasis and was further associated with emergence of tumor hypoxia and increased expression of HIF1α. It is possible that such stromal changes can cooperate with cancer cell-autonomous changes to enhance metastasis. Met expression in cancer cells is detected in many advanced stage tumors including invasive breast cancer (Garcia et al., 2007). We propose that such induction of Met expression is a result of increased tumor hypoxia, among other possible mechanisms. In support of this notion, our results show that tumors without significant levels of hypoxia exhibit negligible expression levels of Met and treatment of these tumors with a Met inhibitor has little impact on their progression.

The reason why a drug such as sunitinib that targets both endothelial cells and pericytes leads to enhanced metastasis raises some questions. We speculate that regardless of their ability to target endothelial cells, drugs that can target pericytes in primary tumors, such as sunitinib and sorafenib (Ebos et al., 2009), may increase metastasis. More studies are required to clarify these observations, but our studies suggest that pericytes may serve as negative regulators of metastasis.

It is important to note that increased metastasis is associated with poor pericyte coverage in the primary tumor. However, if pericyte are targeted to mimic adjuvant therapy in the clinic, an increase in metastasis is not observed. In fact, sunitinib treatment of mice after intravenous introduction of RCC results in decreased metastatic colonization, consistent with the clinical experience of treating RCC patients with sunitinib as an adjuvant therapy to control metastasis (Motzer et al., 2007). Collectively, our data support the notion that sunitinib used in the adjuvant setting possibly helps to control metastasis of certain cancers but it might lead to increased metastasis when used in the neo-adjuvant setting.

One of the challenges in studying the effect of pericyte ablation on tumor growth and metastasis is that pericytes are reported to express different markers such as NG2, PDGFRβ, αSMA, desmin, and RGS5 (Bergers and Song, 2005), and their expression may be tissue specific. During vascular morphogenesis, NG2 is exclusively present on pericytes (as determined by their perivascular location) (Ozerdem et al., 2001b), and NG2 and PDGFRβ share greater than 90% colocalization in the tumor microenvironment (Sugimoto et al., 2006). Additionally, NG2 and PDGFRβ have been repeatedly reported as reliable markers for pericytes (Bergers and Song, 2005; Hellström et al., 1999; Ozerdem et al., 2002; Schlingemann et al., 1990; Sennino et al., 2007; Xian et al., 2006). It should be noted that in our study we achieve pericyte ablation using different transgenic mouse models that use NG2 and PDGFRβ promoters. While many studies have demonstrated the utility of NG2 and PDGFRβ to label pericytes in the tumor, it is possible that other cells are also identified by these markers. Therefore, despite using the most useful reagents currently available, one cannot rule out the possibility of nonpericyte cells contributing to the phenotype we observe in this study. Nevertheless, our approach of using multiple distinct strategies offers some confidence that our observations are related to pericyte targeting.

Our studies demonstrated that depletion of pericytes led to diminished primary tumor growth associated with decreased microvessel density (MVD) and hypoxia. Imatinib, which did not lead to reduced MVD, nevertheless, reduced the number of vessel-associated pericytes and also led to increased hypoxia possibly due to altered vascular integrity. The differential effects on MVD in the setting of the transgenic mouse models versus imatinib treatment raises the possibility that imatinib targeting of PDGFRβ is subtly distinct from strategies that eliminate proliferating pericytes. We speculate that imatinib treatment may induce an unknown proangiogenic response to compensate for the loss of pericytes, which may not be present in the transgenic mice. In this regard, we observed more non-vessel-associated NG2+ cells in the imatinib-treated tumors when compared to tumors from NG2-tk+GCV and PDGFRβ-tk+GCV (data not shown). Such cells, while not associated with vasculature, may still potentially offer paracrine support to the defective vessels in imatinib-treated tumors, leading to vessel retention.

VEGF is a hypoxia and HIF1α-responsive gene and the pericyte-ablated tumors revealed defective vasculature associated with hypoxia, suggesting that any possible rebound angiogenic effect due to increased VEGF in these hypoxic tumors do not overcome the overall disruption of the tumor vasculature due to pericyte deletion. Interestingly, when VEGF-A is directly targeted using a mouse VEGF-A antibody in the 4T1 setting or...
bevacizumab in the context of human renal cell carcinoma, tumor volume decreases due to the decrease in angiogenesis. Hypoxia, Met expression, and metastasis, however, are not increased in this setting. These results suggest that targeting endothelial cells alone may leave behind vessels that are normalized (appropriately pruned), while targeting pericytes (alone or in combination with endothelial cells) leads to leaky vasculature, increased hypoxia, increased Met, increased EMT, and enhanced metastasis (Carmeliet and Jain, 2011; Tong et al., 2004).

EMT is considered to be the first step in the metastatic cascade of carcinoma cells using the same response to migrate.
away from the primary tumors as normal epithelial cells employ during the development (Acloque et al., 2009; Thiery et al., 2009). EMT is enhanced by hypoxia and has been implicated in tumor invasiveness (Kalluri, 2009; Kalluri and Weinberg, 2009; Thiery et al., 2009; Trimboli et al., 2008; Yang et al., 2008). Hypoxia is a classic stress-induced factor in the tumor microenvironment, and it promotes both cellular quiescence and induction of survival pathways (Xie and Huang, 2003). Hypoxia can tip a tumor to a more invasive phenotype via mechanisms of increased extracellular proteases such as MMP2 (Muñoz-Nájar et al., 2006), invoking induction of Met activation (Eckerich et al., 2007; Pennacchietti et al., 2003) and EMT (Chen et al., 2010; Erler et al., 2006). Our results suggest that pericyte depletion promotes leaky/hyperpermeable vessels, which may lead to increased interstitial plasma exudates, possibly increasing the concentration of plasma proteins (including albumin) in the intratumoral/interstitial region. Such increase in the intratumoral plasma volume may increase the interstitial pressure and alter fluid dynamics, which leads to compression of remaining tumor vessels and decreases the blood flow (Jain, 1987; Stohrer et al., 2000). Collectively, such changes lead to hypoxia and set in motion a series of events that lead to increased metastasis. Hypoxia-induced EMT can be prevented by Met targeting and thus our work suggests that pericyte targeting could be combined with Met inhibitors to achieve a synergistic benefit in controlling primary tumor growth and metastasis. This notion is in agreement with previously published reports where dual inhibitors of HGF and VEGFR (XL880 and XL184) were used (Qian et al., 2009; You et al., 2011). Patients with invasive ductal carcinoma who exhibit poor pericyte coverage coupled with high Met expression revealed a significant drop in disease-free and overall survival. Collectively, our results suggest that an analysis of pericyte coverage on tumor vessels coupled with Met expression can serve as a useful biomarker to inform patient prognosis. More in-depth clinical studies are required to further evaluate such potential clinical utility.
Experimental Procedures

Cell Lines
4T1 BALB/c mammary tumor epithelial cells, B16F10 C57Bl6 melanoma cells, and 786-O human renal cell carcinoma cells were obtained from ATCC and grown in DMEM media supplemented with 10% fetal calf serum (FCS), 100 U/ml penicillin and 100 U/ml streptomycin. 4T1-tweak shRNA cells (clones 5 and 7, a gift from Dr. Robert Weinberg, MIT) were cultured in DMEM media supplemented with 5% heat inactivated FCS, 5% heat activated FCS, 100 U/ml penicillin, and 100 U/ml streptomycin.

Animal Experiments and Immunohistochemistry
Generation of transgenic mice, tumor models, drug treatments, immunohistochemistry, and additional experimental procedures are described in Supplemental Experimental Procedures. All animal experiments were reviewed and approved by the Beth Israel Deaconess Medical Center Institutional of Animal Care and Use Committee.

Quantitative PCR Analysis
Expression was determined using the Applied Biosystems 7300 Sequence Detector System and SYBR green as the fluorescence reporter. Measurements were standardized to the housekeeping gene acidic ribosomal phosphoprotein PO (ARP3/684). To assess the number of 4T1-GFP+ cells in the lung, quantitative PCR for GFP was performed using genomic DNA as a template. Primer sequences are listed in Supplemental Experimental Procedures.

Clinical Study
Breast cancer patients were recruited for biopsy at the A. C. Carmargo Hospital in Sao Paulo, Brazil after approval by the institutional review board and informed consent. The analysis was performed on 130 biopsies from patients with invasive ductal carcinoma (IDC). The tissue microarrays (TMAs) were constructed from 1.50 mm cores of formalin-fixed paraffin-embedded breast tissue. Immunostaining and scoring of the TMAs for CD31, NG2, HIF1α, and Met are described in Supplemental Experimental Procedures.

Statistical Analysis
For comparison between two groups, a two-tailed unequal variance t test was used. Association between clinical characteristics and NG2 or Met expression levels was verified by a two-tailed Fisher’s exact test. For survival analysis, Kaplan-Meier curves were drawn and differences between the curves were calculated by the log-rank test. Independent prognostic significance of HIF1α, Met and NG2 were computed by the Cox proportional hazards. *p ≤ 0.05 was considered statistically significant. All data analysis was performed using R software version 2.13.0 (http://www.R-project.org).

Accession Numbers
The microarray data have been deposited in the Array Express database under the accession number E-MTAB-525.

Supplemental Information
Supplemental Information includes four figures, four tables, and Supplemental Experimental Procedures and can be found with this article online at doi:10.1016/j.ccr.2011.11.024.

Acknowledgments
This work was primarily supported by funds from NIH Grants CA125550, CA155370, CA151925, DK81576, CA163191, and DK55001. R.K. is funded by the Champalimaud metastasis programme and is a Champalimaud investigator. V.G.C. is funded by NRSA F32 Ruth Kirschstein Post-doctoral Fellowship from NIH/NIDDK (5F32DK082119-02). V.S.L. is funded from the NIH Research Training Grant in Cancer Biology (ST32CA081156-08), a NIH supplemental grant (CA125550) to support diversity, and the United Negro College Fund–Merck Postdoctoral Science Research Fellowship. H.S. is funded by the NIH Training Grant in Cardiovascular Medicine (5T32HL007374-30). J.T.O. is funded by the DoD Breast Cancer Research Predoctoral Traineeship Award (W81XWH-09-1-0008). We wish to thank J. Christensen of Pfizer, Inc. for providing us PF2341066.

Received: October 1, 2010
Revised: September 5, 2011
Accepted: November 29, 2011
Published: January 17, 2012

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