

# Angiogenesis in Gliomas: Biology and Molecular Pathophysiology

Ingeborg Fischer<sup>1,2,3</sup>; Jean-Pierre Gagner<sup>1,2,3</sup>; Meng Law<sup>4,5,6</sup>; Elizabeth W. Newcomb<sup>2,6</sup>; David Zagzag<sup>1,2,3,5,6</sup>

<sup>1</sup>Microvascular and Molecular Neuro-oncology Laboratory, <sup>2</sup>Department of Pathology, <sup>3</sup>Division of Neuropathology, <sup>4</sup>Department of Radiology, <sup>5</sup>Department of Neurosurgery, <sup>6</sup>New York University Cancer Institute, New York University School of Medicine.

Corresponding author:

David Zagzag, MD, PhD, Department of Pathology, Division of Neuropathology, New York University Medical Center, 550 First Avenue, New York, NY 10016 (E-mail: dz4@nyu.edu)

**Glioblastoma multiforme (GBM) is characterized by exuberant angiogenesis, a key event in tumor growth and progression. The pathologic mechanisms driving this change and the biological behavior of gliomas remain unclear. One mechanism may involve cooption of native blood vessels by glioma cells inducing expression of angiopoietin-2 by endothelial cells. Subsequently, vascular apoptosis and involution leads to necrosis and hypoxia. This in turn induces angiogenesis that is associated with expression of hypoxia-inducible factor (HIF)-1 $\alpha$  and vascular endothelial growth factor (VEGF) in perinecrotic pseudopalisading glioma cells. Here we review the molecular and cellular mechanisms implicated in HIF-1-dependent and HIF-1-independent glioma-associated angiogenesis. In GBMs, both tumor hypoxia and genetic alterations commonly occur and act together to induce the expression of HIF-1. The angiogenic response of the tumor to HIF-1 is mediated by HIF-1-regulated target genes leading to the upregulation of several proangiogenic factors such as VEGF and other adaptive response molecules. Understanding the roles of these regulatory processes in tumor neovascularization, tumor growth and progression, and resistance to therapy will ultimately lead to the development of improved antiangiogenic therapies for GBMs.**

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## INTRODUCTION

Angiogenesis is recognized as a key event in the natural progression of gliomas (15, 40, 197). Of all solid tumors, those of the brain show the highest degree of vascular proliferation (28). Newly formed brain tumor blood vessels possess a defective blood-brain barrier that contributes to the pathogenesis of tumor-associated edema (47, 182, 203, 207). They are associated with increased risk of intratumoral hemorrhage (41, 105) and are responsible for contrast enhancement (39, 45, 53, 179, 203). Unlike tumors in other locations, intracranial tumors rarely metastasize to distant organs and their malignant behavior and prognosis are determined by their histological grade. The WHO classification distinguishes low grade from high grade diffuse astrocytomas by the presence of microvascular proliferation as a diagnostic criterion and an independent prognostic parameter (1, 32, 45, 94, 169). Neovascularization in brain tumors correlates directly with their biological aggressiveness, degree of malignancy and clinical recurrence and inversely with the post-operative survival of patients with

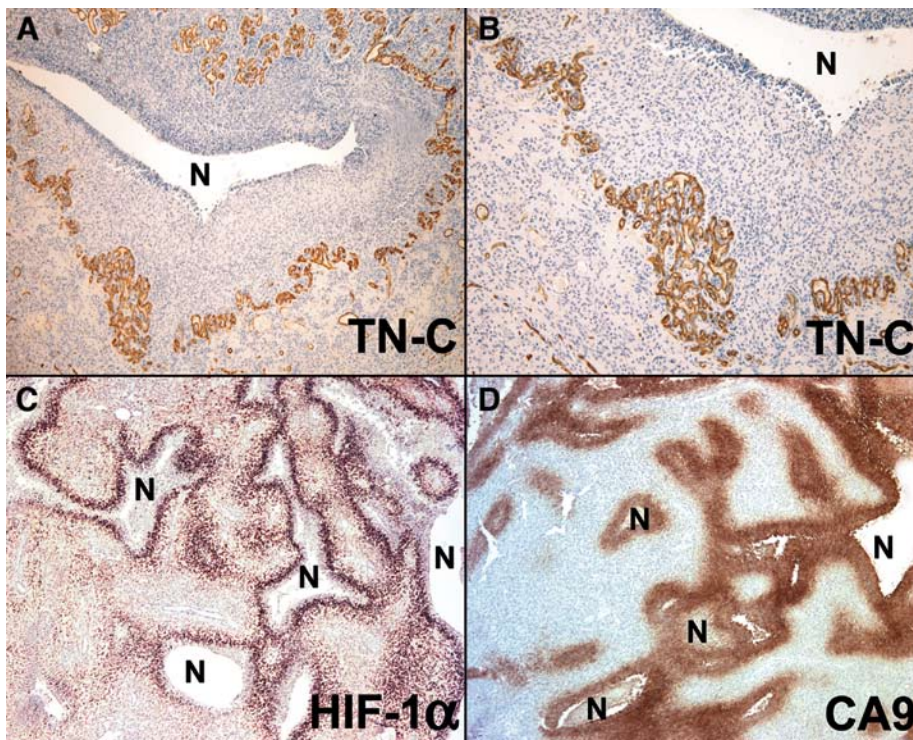
gliomas (32, 45, 94). Diffuse astrocytomas tend to progress from grade II to grade III tumors with a time interval of several years, whereas, progression of grade III to grade IV is more rapid, typically 2 years. The time intervals for tumor progression are variable and the pathologic mechanisms driving the change in biologic behavior between different grades remain unclear. GBMs that arise from a low-grade glioma lesion are called "secondary glioblastoma" (94). However, in most cases, GBMs appear "de novo" and are thus termed "primary glioblastoma" (95). Regardless of their mode of progression, primary and secondary GBMs are morphologically indistinguishable and show their histologic hallmarks, ie, "glomeruloid" microvascular tufts and necrosis (Figure 1A, B).

The characteristic vascular morphology in the GBMs has led to the hypothesis that the formation of new blood vessels or angiogenesis is crucial to their growth. GBMs were first recognized to be angiogenic, eg, capable of inducing vascular sprouting, when implanted in the rabbit cornea, a well-characterized angiogenesis assay

(27). In addition, glioma cells were found to have angiogenic activities, eg, capillary morphogenesis and endothelial mitogenic activities in vitro (2, 170). Subsequently, vascular endothelial growth factor (VEGF), characterized as an endothelial-cell mitogen (60) and a permeability factor (52, 148), was found to be present in pseudopalisading tumor cells adjacent to necrotic zones and hyperplastic vessels, implicating its role in glioma angiogenesis (140, 163). The discovery of hypoxia inducible factor-1 (HIF-1) (161) and the observation that hypoxia-induced HIF-1 $\alpha$  expression in pseudopalisading cells (Figure 1C) (209) was concomitant with the expression of one of its target genes, VEGF (140, 163), established a biological link between hypoxia and angiogenesis (161). Since then, the field of angiogenesis research in gliomas has evolved rapidly (15, 22, 46, 121).

The formation of new blood vessels occurs physiologically during embryogenesis (34, 194). In adult life it is observed in the female reproductive system and during wound healing (175) and in a wide range of pathologic settings, such as ischemic diseases, chronic inflammatory reactions, and neoplasia (35, 65). During embryonic development, blood vessels are newly formed from endothelial precursors and hematopoietic stem cells, a process known as vasculogenesis (194). In contrast, angiogenesis, the sprouting of new blood vessels from pre-existing ones (65, 74, 194) results from an altered balance of proangiogenic factors (Table 1) and antiangiogenic factors (Table 2). The role of endothelial cell progenitors in angiogenesis is unclear and will be discussed below.

For the most part, cells need access to the vascular system to provide a source of nutrients and oxygen as well as to eliminate metabolic waste products. To a limited



**Figure 1.** Immunohistochemistry for tenascin-C (TN-C), HIF-1 $\alpha$  and carbonic anhydrase (CA9) expression in a GBM. **A, B.** TN-C immunoreactivity decorates the hyperplastic vessels seen adjacent to a necrotic zone (N); **C, D.** HIF-1 $\alpha$  and CA9: Pseudopalisading cells around areas of necrosis (N) show intense immunoreactivity for HIF-1 $\alpha$  (**C**) and CA9 (**D**); (immunoperoxidase, **A**  $\times 100$ ; **B**  $\times 200$ ; **C, D**  $\times 50$ ).

extent, this can be accomplished by diffusion if the cells are situated within  $\sim 100$   $\mu\text{m}$  of the nearest blood vessel (64, 147). In several experimental tumor systems, the balance between proliferation and apoptotic rates is characteristic of the dormant state (64, 74). It is now well accepted that a change in this balance is associated with malignant transformation and that the recruitment of a new blood supply is critical for tumor growth (74). Angiogenesis results in exponential growth of the tumor beyond the limit of a few millimeters seen in the absence of angiogenesis (64). The sequence of events leading to the formation of new blood vessels is well characterized and involves an initial VEGF-mediated increase of vascular permeability leading to extravasation of plasma proteins associated with dilatation of native vessels and reduction in their pericyte coverage. Subsequently, endothelial cells migrate and proliferate. For this cascade to occur, deposition of a proangiogenic matrix for the newly sprouting vessel is essential. This involves breakdown of the vascular basement membrane and extracellular matrix (ECM) through the action of cathepsin B, matrix metalloproteases (MMPs) and other enzymes as well as the expression of matrix proteins such as

fibronectin, laminin, tenascin-C and vitronectin (68, 106, 122, 200, 201). Several of these ECM molecules enhance phosphorylation of focal adhesion kinase, a critical step in glioma angiogenesis (75, 202, 208). Finally, the angiogenic process culminates in the assembly of endothelial cells to form a vascular lumen followed by the elaboration of a new basement membrane and the recruitment of pericytes (52, 65, 74). The important roles that ECM and proteases play in mediating angiogenesis in gliomas is reviewed in the accompanying articles (see Wang et al and Lakka et al; this issue).

As described above, early models of tumor growth presumed that tumors showed angiogenic activity only when they had grown to a size beyond that which the tumor cells could no longer be nourished by mere diffusion (64). However, recent *in vivo* experiments performed with experimental gliomas provided evidence contrary to this notion (80, 198). In contrast to the accepted dogma that tumor development occurs in 2 phases (avascular and vascular), we observed that tumor growth in the brain follows 2 vascular phases. In the first vascular phase, the vessels are native cerebral vessels, which are coopted by tumor cells, while in the second phase, there is true neo-

vascularization arising from existing vessels. During the transition period between these two phases, hypoxia driven HIF-1 expression occurs which results in VEGF secretion and the induction of neovascularization. As illustrated in Figure 2, glioma cells first accumulate around existing vasculature (Stage I). This is associated with a mechanical disruption of the normal contact between endothelial cells and the basement membrane by the insinuating glioma cells lifting off the astrocytic foot processes (198). In response, the endothelial cells of the coopted blood vessels express angiopoietin-2 (Ang-2) (80, 198, 204). This leads to the destabilization of the blood vessel wall associated with decreased pericyte coverage (80, 198, 204). In Stage II, perivascular proliferation takes place. In Stage III, these blood vessels become apoptotic and undergo involution (80, 198). This vascular collapse results in the loss of neighbouring tumor cells. In Stage IV, angiogenesis adjacent to the necrotic area is triggered in response to increased expression of HIF-1 $\alpha$  and VEGF, a process that rescues the remaining tumor cells (80, 198). Thus, our experimental evidence suggests four sequential steps in glioma progression (Figure 2): *i*) perivascular organization, *ii*) proliferation, *iii*) vascular regression followed by necrosis, and *iv*) angiogenesis (198).

In addition to the vascular collapse described above, it has been suggested that a procoagulative state combined with the inherent genetic instability of the tumor could elicit the necrosis typically observed in GBMs (142). Necrosis has been consistently used as a grading criterion in gliomas (32, 94, 127) and reported to predict poor patient outcome (14, 98). For example, tissue factor, the catalyst of the extrinsic pathway of hemostasis, is overexpressed under hypoxic conditions and could be involved in vascular thrombosis (26, 150). Thus, vascular regression and necrosis constitute necessary events for the subsequent development of angiogenesis. As mentioned earlier, this angiogenic response results from an altered balance of a large number of proangiogenic (Table 1) and antiangiogenic factors (Table 2). Among the proangiogenic factors described in gliomas, the best characterized and the most important in glioma progression include VEGF and the angiopoietins.

Factors	Descriptions	Ligand Chromosomal Locations*	Cognate Receptors	Receptor Chromosomal Locations*	References
<b>Tyrosine Kinase Receptor Ligands</b>					
Angiopoietin-1, -4	Tie2 agonists	8q22, 20p13	Tie2	9q21	121
EGF	Epidermal Growth Factor	4q25	EGFR/HER1	<b>7p12.3-p12.1</b>	51
aFGF	acidic Fibroblast Growth Factor, FGF-1	5q31	FGFR-1/-2	8p11.2-p11.1, <b>10q26</b>	51
bFGF	basic Fibroblast Growth Factor, FGF-2	4q25-q27	FGFR-1/-2	8p11.2-p11.1, <b>10q26</b>	51, 121
HGF/SF	Hepatocyte Growth Factor/Scatter Factor	7q21.1	c-Met	7q31	46
PDGFAA	Platelet-Derived Growth Factor, A homodimer	7p22	PDGFR $\alpha$	4q12	51, 121
PDGFBB	Platelet-Derived Growth Factor, B homodimer	<b>22q12.3-q13.1</b>	PDGFR $\alpha/\beta$	4q12, <b>5q31-q32</b>	51, 121
PLGF-2	Placental Growth Factor-2	14q24-q31	VEGFR-1, NRP-1	13q12, <b>10p12</b>	6, 78
TGF $\alpha$	Transforming Growth Factor, Alpha	2p13	EGFR/HER1	<b>7p12.3-p12.1</b>	51
TGF $\beta$	Transforming Growth Factor, Beta	<b>19q13.1</b>	TGFBR-1/-2	9q33-q34, 3p22	51, 121
VEGF-A, -B	Vascular Endothelial Growth Factor	6p12, 11q13	VEGFR-1/-2, NRP-1	13q12, 4q12, <b>10p12</b>	30, 70, 78, 121
<b>Other Receptor Type Ligands</b>					
Adrenomedullin	calcitonin-like peptide	11p15.4	CRLR/RAMP2/3	17q12-q21.1, 7p13-p12	46
Endothelin-1	survival/antiapoptotic peptide	6p24-p23	EDRNA/B	4q31.2, 13q22	54
IGF-1, -2	Insulin-like Growth Factor-1, -2	12q22-q24.1, 11p15.5	IGF1R	15q25-q26	79, 108
IGFBP-2, -3	IGF Binding Protein-2, -3	2q33-q34, 7p14-p12			69, 103
Interleukin-6	cytokine	7p21	IL6R	1q21.3	107
Interleukin-8	CXCL8 chemokine	4q12-q13	IL8RA/B	2q35, 2q35	25
Pleiotrophin	angiogenic/mitogenic heparin-binding protein	7q33	RPTPzeta	7q31.3	121
SDF-1	Stromal cell-Derived Factor-1, CXCL12	<b>10q11.1</b>	CXCR4	2p21	144, 155
PGE2	prostaglandin E2	n.a.	EPs	many	31, 128, 178

**Table 1.** Endogenous proangiogenic factors in gliomas. Abbreviations: CRLR/RAMP2/3, calcitonin receptor-like receptor/receptor activity-modifying protein-2/-3; CXCL, CXC chemokine ligand; CXCR, CXC chemokine receptor; EDRNA/B, endothelin receptor type A or B; EP, prostaglandin E2 receptor; HER1, human epidermal growth factor receptor 1; n.a., not applicable; NRP-1, neuropilin-1; RPTPzeta, receptor protein tyrosine phosphatase zeta; Tie2, Tyrosine kinase with Immunoglobulin and Epidermal growth factor homology domain 2. \*Chromosomal locations with known gene overexpression, mutation or loss of heterozygosity are indicated in bold (See accompanying article by Gagner et al; this issue). Chromosomal location information was obtained from the Online Mendelian Inheritance in Man website.

## THE VEGF FAMILY

The VEGF family includes 6 secreted glycoproteins referred to as VEGF-A, VEGF-B, VEGF-C, VEGF-D, VEGF-E, and placental growth factor (PLGF) (11, 12, 60, 78). VEGF-A, the prototype of the VEGF family, is simply referred to as VEGF in this review. VEGF mRNA undergoes alternative splicing to yield several mature isoforms, with VEGF<sub>165</sub> being the predominant isoform expressed in a variety of human solid tumors (60, 78). VEGF is required for normal development of blood vessels, and loss of a single allele during embryonic development is lethal (34). In postnatal life, VEGF expression levels are minimal, except at sites of physiologically active angiogenesis, such as the uterus or during wound healing (175). In tumors, overexpression of VEGF leads to increased vascularity and vascular permeability. In fact, VEGF was first described as “vascular permeability factor,” since it was observed

to render both existing and newly formed tumor blood vessels leaky (52, 148).

The migration and proliferation of endothelial cells occur along the proangiogenic ECM (201, 208) following chemotactic signals mediated by growth factors, such as VEGF (212). Using a murine glioma model, overexpression of VEGF was shown to produce formation of hyperplastic microvascular proliferations known as “glomeruloid bodies” which share structural similarities with the glomeruloid proliferation seen in GBMs (171). The microvascular glomeruloid proliferations in GBMs are composed of hyperplastic endothelial cells surrounded by a basement membrane of irregular thickness and a discontinuous layer of smooth-muscle actin positive pericytes and vascular smooth muscle cells. Astrocytic foot processes are typically absent (189). These microvascular proliferations regress upon VEGF withdrawal (171).

The VEGF isoforms exert their function through three cognate VEGF receptor ty-

rosine kinases: VEGFR-1/Flt-1, VEGFR-2 Flk-1/KDR, and VEGFR-3 and 2 neuropilins receptors, NRP-1 and NRP-2 (48, 49, 61, 123, 183). NRP-1 and NRP-2 are VEGFR co-receptors. The VEGF receptors are primarily expressed on tumor endothelium, but are absent in normal surrounding tissue (139). VEGFR signaling triggers increased vascular permeability and proliferation, differentiation, survival and migration of endothelial cells (97, 183, 211). The effect of VEGF signaling depends on the receptor subtype (61, 77, 211). For example, VEGFR-2 is primarily responsible for proliferation (77, 78).

VEGF mRNA is highly expressed in pseudopalisading cells around necrotic zones (17, 140, 163). The expression of VEGF and VEGFR-1 and VEGFR-2 correlates with the grade in diffuse astrocytomas, is crucial for glioma growth, and displays a temporal and spatial correlation with the angiogenesis seen in human gliomas (1, 17, 40, 100, 139, 140, 156, 165, 177, 199).

Factors	Descriptions	Chromosomal Location <sup>†</sup> of Parent Molecules	Cognate Receptors or Target Mechanisms	Protein or Receptor Chromosomal Locations <sup>†</sup>	References
<b>Matrix and Plasma-Derived Proteins</b>					
Angiostatin	internal fragment of plasminogen	6q26	αvβ3 integrin, others	many	132, 143
Endostatin	C-terminal fragment of collagen type XVIII	21q22.3	α5β1 integrin, HSPG, others	many	132, 143
PEX	C-terminal fragment of MMP-2	16q13	αvβ3 integrin, MMP-2	many	132, 143
TFPI-2	Tissue Factor Pathway Inhibitor-2	7q22	TF - FVIIa - FXa	many	193
TIMP-1	Tissue Inhibitor of Metalloprotease-1	Xp11.3-p11.2	MMPs, VEGF, others	many	132, 143
TIMP-3, -4	Tissue Inhibitor of Metalloprotease-3, -4	<b>22q12.1-q13.2</b> , 3p25	MMPs, VEGF, others	many	126, 132, 143
TSP-1, -2, -3	Thrombospondin-1, -2, -3	15q15, 6q27, 1q21	CD36, MMPs, others	7q11.2, many	132, 143
<b>Factors and Receptors</b>					
Angiopoietin-2*	antagonist to angiopoietin-1	8p23	Tie2	9q21	121
BAI-1, -2, -3	Brain-specific Angiogenesis Inhibitor-1, -2, -3	<b>8q24, 1p35</b> , 6q12	n.d.	n.d.	92
Vasculostatin	proteolytic extracellular domain of BAI-1	8q24	n.d.	n.d.	89
ING4	Inhibitor of Growth 4	12p13.3	n.d.	n.d.	66
Interferon-α, -β	cytokine	9p22, 9p21	IFNAR-1	21q22.1	132
Interleukin-4	cytokine	5q31.1	IL4RA	16p12.1-p11.2	132, 152
PEDF	Pigment Endothelial-Derived Factor, SERPINF1	17p13.3	TSP-1, VEGF, others	many	132, 143
Platelet factor-4	CXCL4 chemokine	4q12-q13	CXCR3, HSPG, others	8p12-p11.2, many	121, 143
16KDa PRL	16 KDa fragment of prolactin	6p22.2-p21.3	16KDa PRL receptor	n.d.	42, 44
PRP	Proliferin-Related Peptide	n.d.	n.d.	n.d.	16, 44
Somatostatin	peptide hormone	3q28	somatostatin receptor-2, -3	17q24, <b>22q13.1</b>	38, 120
VEGI	Vascular Endothelial Growth Inhibitor, TNFSF15	9q33	n.d.	n.d.	191
sVEGFR-1/Flt-1	soluble VEGFR-1/Flt-1	13q12	acts as decoy receptor	13q12	100, 132

**Table 2.** Endogenous antiangiogenic factors in gliomas. Abbreviations: CXCL, CXC chemokine ligand; CXCR3, CXC chemokine receptor 3; HSPG, heparan sulfate proteoglycan; IFNAR-1, interferon alpha, beta, and omega receptor 1; MMP, matrix metalloprotease; n.d., not determined; SERPINF1, serine protease inhibitor F1; TF - FVIIa - FXa, tissue factor-factor VIIa-factor Xa complex; Tie2, Tyrosine kinase with Immunoglobulin and Epidermal growth factor homology domain 2; TNFSF15, tumor necrosis factor ligand superfamily 15. \*Isolated expression of Angiopoietin-2 not followed by VEGF signaling leads to endothelial cell apoptosis (80).

† Chromosomal locations with known gene overexpression, mutation or loss of heterozygosity are indicated in bold (See accompanying article by Gagner et

Similarly, PLGF and NRP-1 are upregulated in GBMs and their expression correlate with tumor grade (30, 49, 130, 135).

PLGF deficient mice showed normal vascular development, but impaired tumor vascularization (36). PLGF acts synergistically with VEGF in increasing tumor vascularization (6, 11, 12, 36, 110) and recruits hematopoietic stem cells to the tumor vasculature (76). However, such contribution of endothelial progenitor cells and hematopoietic stem cells to tumor vasculature has not been entirely elucidated. Specifically, the capacity to recruit these precursors to the vascular bed may depend on the tumor type and production by the tumor of mobilization signals for endothelial precursor cells (71, 86, 111, 112, 114).

**Regulation of VEGF expression.** The transcriptional activation of VEGF is enhanced largely through the transcription factor HIF-1 (161). Other transcription factors capable of inducing VEGF tran-

scription, include ETS-1 proto-oncogene and STAT-3 (107, 181). Through binding to specific ETS response element DNA sequences, ETS proteins activate genes such as VEGFR-1 and VEGFR-2, integrin β<sub>3</sub>, some MMPs and urokinase plasminogen activator (uPA) (151). VEGF itself, induces ETS-1 in adjacent endothelial cells, therefore enhancing VEGFR signaling (181). Accordingly, ETS-1 expression is increased in GBMs compared to low grade astrocytomas. Its distribution correlates with vascular proliferation, with the most prominent expression observed in the glomeruloid tufts of GBMs (181). Inactivation of ETS-1 reduced rat C6 glioma cell proliferation (151). In addition to transcription factors, cytokines and growth factors, including TGF-β, EGF, PDGF-B, basic FGF, up-regulate VEGF (43, 62, 73, 107, 138, 176, 185). Genetic alterations seen in gliomas, such as EGFR activation and PTEN mutation (13, 50, 102, 109, 133, 134, 141, 167, 187), lead to enhanced VEGF expression

thereby promoting angiogenic activity as described in more detail below.

### THE ANGIOPOIETIN FAMILY

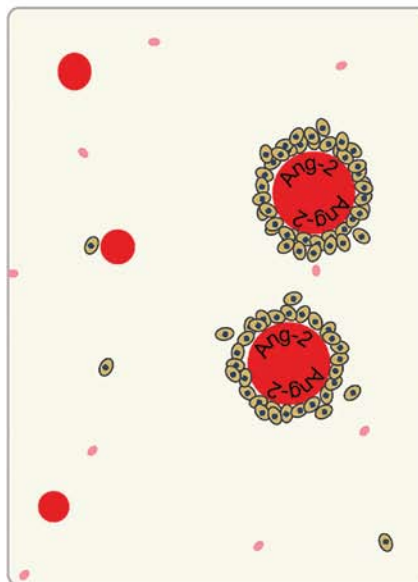
The angiopoietins are important endothelial growth factors which signal via the Tie2 receptor tyrosine kinase expressed on endothelial cells. In particular, Ang-1 and -2, have been implicated in glioma angiogenesis (80, 168, 196, 198, 202, 204). Ang-1 mediated activation of Tie2 is required for stabilization, remodelling and maturation of blood vessels (115). Overexpression of Ang-1 in a rat glioma model promotes angiogenesis and tumor growth and is associated with an increased number of highly branched vessels covered by pericytes (113). While VEGF and Ang-1 may act in concert (proliferation and maturation), Ang-2 has been implicated in further remodeling of the initial microvasculature (80, 168, 198, 204). Increased expression of Ang-2 on GBM microvasculature appears early during glioma angiogenesis (168, 198, 204). However, binding of Ang-

2 to the Tie2 receptor on endothelial cells antagonizes this receptor's phosphorylation, thereby disrupting contacts between endothelial and periendothelial support cells and disengaging pericytes from the tumor vessels during initiation of vessel sprouting or regression (80, 115, 204). Examination of the expression patterns of angiopoietins and their receptors suggest a role in GBM vasculature and malignant transformation (168, 177, 196, 198, 204). For example, increased Tie2 expression has been observed with increasing grade of human astrocytoma (196). Ang-2 and Tie2 expression are absent in the normal brain vasculature but are induced in tumor endothelium of coopted tumor vessels prior to their regression (168, 198, 204). Of particular importance, treatment of glioma cell derived mouse xenografts with a dominant negative form of Tie2 results in a significant decrease in tumor growth (196). The role of angiopoietins in glioma angiogenesis is reviewed in an accompanying article (see Reiss et al; this issue).

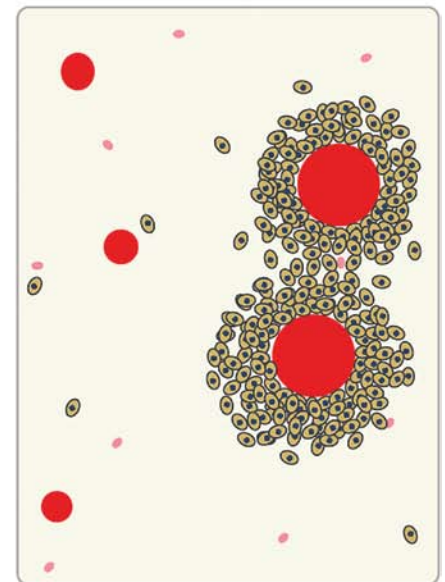
#### OTHER ANGIOGENIC FACTORS

A number of other factors modulate the neovascularization seen in GBMs (197) as shown in Table 1. These include fibroblast growth factor (FGF), platelet derived growth factor (PDGF), hepatocyte growth factor (HGF) and tumor necrosis factor (TNF)- $\alpha$ , (29, 51, 121, 197). The FGF family includes several proteins that share structural properties. Both acidic FGF (FGF1) and basic FGF (FGF2) are upregulated in GBMs (158, 206) and are responsible for resistance of endothelial cells to apoptosis (7). The presence of basic FGF in cerebrospinal fluids from children and adults with brain tumors has been correlated with tumor microvessel formation (101). Furthermore, *in vivo* tumor growth of C6 glioma cells is inhibited when the cells are transfected with dominant negative FGF receptor (FGFR1 or FGFR2), an effect associated in part with inhibition of angiogenesis (10). PDGF-B and PDGFR- $\beta$  mRNA are upregulated in GBMs (162, 164). PDGF's effects on angiogenesis are mediated, at least in part, by VEGF (73, 185). In gliomas, the expression of HGF, also known as Scatter Factor (HGF/SF), correlates with microvessel density (124, 158). In addition, c-met, the HGF receptor is upregulated by hypoxia (137). The exact

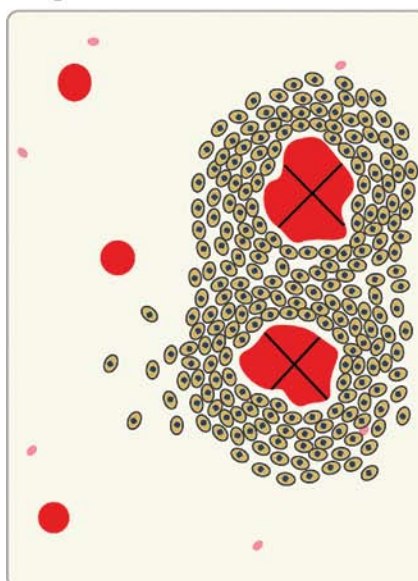
**Stage I - Perivascular Organization**



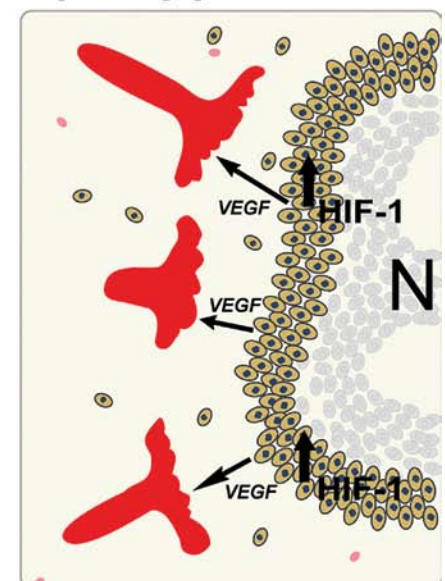
**Stage II - Proliferation**



**Stage III - Vascular Involution/Necrosis**



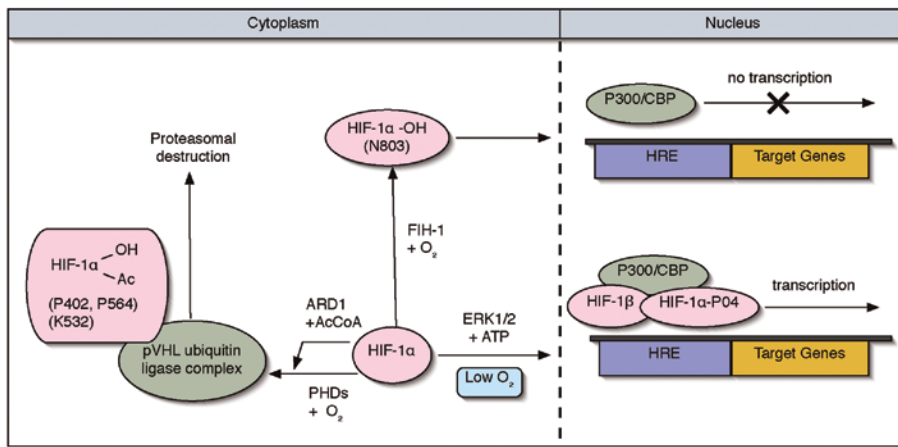
**Stage IV - Angiogenesis**



**Figure 2.** Schematic representation of distinct stages of glioma growth. **Stage I:** Perivascular organization in which tumor cells are concentrated around some native vessels. Endothelial cells express Ang-2. **Stage II:** Proliferation phase when tumor cells actively proliferate around existing viable blood vessels. **Stage III:** Vascular involution of the host vascular cells resulting in degeneration of blood vessels. This leads to necrosis and hypoxia, which in turn promotes tumor-derived VEGF expression and angiogenesis. **Stage IV:** Angiogenesis occurs as blood vessels grow towards and vascularize the now necrotic tumor (N). The overexpression of HIF-1 $\alpha$  and VEGF mRNA in pseudopalisading cells leads to the release of VEGF and induction of angiogenesis in neighboring blood vessels.

role of TNF- $\alpha$  in glioma's angiogenesis remains unclear. Although enhanced VEGF expression has been reported in TNF- $\alpha$ -treated glioma cells (125), treatment of brain microvascular endothelial cells with TNF- $\alpha$  inhibits their proliferation (129). Among the other factors that have been linked to angiogenesis in GBMs are interleukins (IL)-6 and -8, adrenomedullin, insulin-like growth factor binding proteins

(IGFBPs), and stromal cell derived factor (SDF-1) (Table 1). Many of these factors are overexpressed with increasing tumor grade in gliomas (9, 23, 25, 55, 79, 144, 149, 154, 155) and predict adverse clinical outcome (9, 149).



**Figure 3.** Oxygen-dependent and -independent posttranslational regulation of HIF-1 $\alpha$ . In tissues, O<sub>2</sub> is a limiting substrate and the enzymes Factor Inhibiting HIF (FIH-1) and Prolyl Hydroxylase Domain proteins (PHDs) serve as oxygen sensors because of their utilization of O<sub>2</sub>. Under normoxic conditions, hydroxylation of HIF-1 $\alpha$  at asparagine 803 catalyzed by FIH-1 prevents the recruitment of coactivator p300/CBP (cAMP-response element binding protein (CREB)-Binding Protein) and inhibits the transcriptional response. Also, hydroxylation of HIF-1 $\alpha$  at prolines 402 and 564 by PHD isozymes targets the HIF-1 $\alpha$  subunit to the von Hippel-Lindau (pVHL) ubiquitin ligase complex that mediates its proteasomal degradation. However, under hypoxic conditions, these hydroxylases are inactive, resulting in accumulation of the constitutively expressed HIF-1 $\alpha$  protein. This subunit is phosphorylated by Extracellular signal-Related protein Kinase (ERK)-1/2 and translocated to the nucleus, where it dimerizes with the HIF-1 $\beta$  subunit, recruits p300/CBP, binds to hypoxia response elements (HRE) upstream of HIF-1-regulated target genes and initiates their transcription. Other oxygen-independent posttranslational modifications of HIF-1 $\alpha$  include acetylation of lysine 532 by ARrest Defective-1 (ARD1) acetyltransferase and acetyl-coenzyme A (AcCoA), which promotes HIF-1 $\alpha$  binding to the pVHL ubiquitin ligase complex. The interdependence among these different modifications (eg, ARD1 and PHDs) has been simplified for illustration purposes and is still being investigated (24).

### NATURALLY-OCCURRING ANGIOGENESIS INHIBITORS

A number of endogenous inhibitors of angiogenesis have been identified in gliomas as shown in Table 2. They exert their effects through multiple protein-protein or protein-proteoglycan interactions (eg, angiostatin, endostatin) or through specific receptor binding (eg, interferons). In many but not all studies, the expression level of some of these inhibitors was actually increased in GBM tumor biopsies compared to low grade gliomas, which suggests the existence of a host antiangiogenic response that partially antagonizes the tumor-driven angiogenesis (143). For example, the levels of angiostatin, endostatin, thrombospondin (TSP)-1 and -2, and tissue inhibitor of metalloprotease (TIMP)-1 were predominantly expressed in the hyperplastic vessels of GBMs. On the other hand, the expression of other endogenous inhibitors correlated inversely with glioma histologic grade in some studies (90, 143; Wang et al; this issue). Some examples are pigment endothelial-derived factor (PEDF) and TIMP-4. These factors mediate some of their antiangiogenic effects through inhibition or downregulation of VEGF or other proan-

giogenic molecules (132, 143). Therefore, in addition to a potential host antiangiogenic response, stimulation of angiogenesis as a result of reduced expression of endogenous inhibitors also occurs during glioma progression.

### HYPOXIA, HIF-1 AND GLIOMA PROGRESSION

Eukaryotic cells require oxygen for their metabolism and survival. The condition of low oxygen or hypoxia results in growth arrest or apoptosis. Cells can respond acutely to hypoxia, at the cellular level, by a variety of molecular mechanisms. For example, upregulation of glucose transporters on the cell membrane and switching from aerobic to anaerobic metabolism, ensure continued ATP supply. This adaptation is mediated by the upregulation of a wide variety of hypoxia-inducible genes induced by several transcription factors including HIF-1, NF $\kappa$ B, and Activator Protein-1 (AP-1) (96, 99, 159, 161, 195). Of these, HIF-1 is of special interest, since it is regulated by a unique oxygen-sensing mechanism (160). HIF-1 overexpression has been consistently linked with malignant progression and un-

favourable outcome in various tumor types (173, 214).

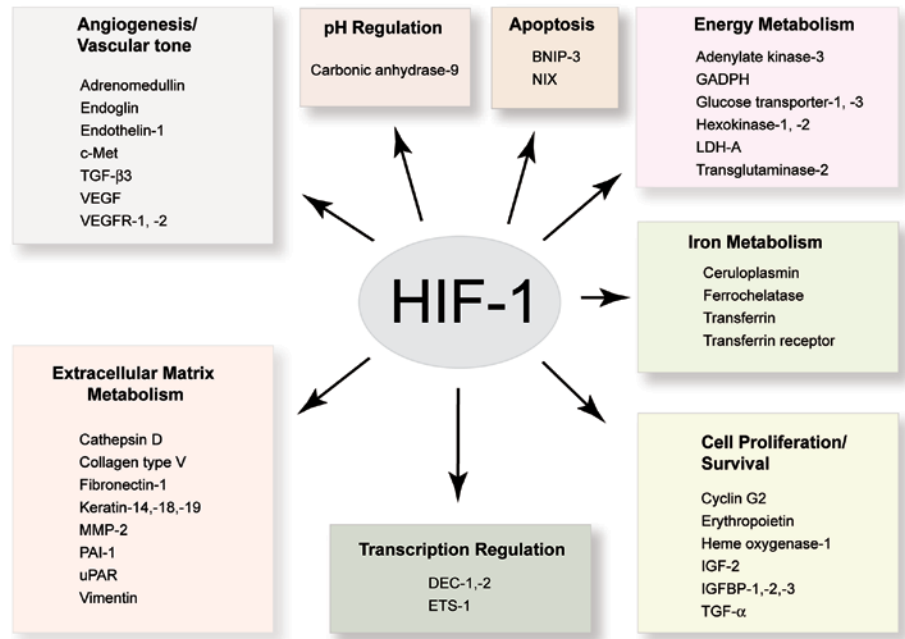
**Hypoxia-inducible factor-1.** The transcription factor HIF-1 and its target genes play a critical role in glioma-induced angiogenesis. The HIF-1 transcriptional complex is a heterodimer composed of two bHLH (basic helix loop helix)-PAS subunits, HIF-1 $\alpha$  and HIF-1 $\beta$  (also termed aryl hydrocarbon nuclear translocator (ARNT) (160, 161). To date, three HIF- $\alpha$  isoforms have been described, with the best characterized being HIF-1 $\alpha$  and HIF-2 $\alpha$ . HIF-2 $\alpha$  was first designated HRF/EPAS-1/HLF (HIF-related factor/endothelial PAS protein-1/HIF-like factor) (57, 63, 188). In GBMs, HIF-1 $\alpha$  is overexpressed in pseudopalisading cells around necrotic foci (Figure 1C; 209), a pattern similar to that of VEGF mRNA. Moreover, the expression of HIF-2 $\alpha$  is upregulated in GBMs both at the mRNA and at the protein level (4, 91).

**HIF-1 regulation.** Whereas the  $\beta$ -subunit of HIF-1 is constitutively expressed, the  $\alpha$ -subunit is subject to complex regulatory mechanisms at the transcriptional and posttranslational levels. The stability of the HIF-1 $\alpha$  protein is tightly regulated by an oxygen-sensing as well as other mechanisms as shown in Figure 3. Under normoxic conditions, HIF-1 activity is inhibited following hydroxylation of prolyl residues by prolyl hydroxylase (PHD) enzymes leading to rapid degradation of the HIF-1 $\alpha$  subunit (160). The oxygen-, 2-oxoglutarate-, iron-, and ascorbate dependent prolyl hydroxylase PHD1-4 isozymes mediate the hydroxylation of the HIF-1 $\alpha$  subunit at proline residues 402 and 564. This hydroxylation allows for binding of the von-Hippel-Lindau protein (pVHL), which mediates ubiquitination of HIF-1 $\alpha$  and subsequent proteasomal degradation (81, 84, 104, 116-118). The prolyl hydroxylases themselves are also subject to proteasomal degradation. Physiologically, the VHL E3 ubiquitin ligase plays a similar role in the regulation of both HIF-1 $\alpha$  and HIF-2 $\alpha$ . Since the prolyl hydroxylation requires oxygen for catalysis, HIF-1 $\alpha$  protein accumulates only under hypoxic conditions. Subsequently, HIF-1 $\alpha$  translocates to the nucleus where it dimerizes with the  $\beta$ -subunit and binds to the hypoxia-responsive element (HRE) of a wide array of hypoxia inducible target genes, activating

their transcription (Figure 4). The coactivator proteins p300/CBP, Ref-1, SRC-1, and thioredoxin activate the transcriptional complex (37, 56). In addition, HIF-1 is hydroxylated at asparagine residue 803 by factor inhibiting HIF-1 (FIH-1), which prevents the binding of the coactivator p300/CBP thereby interfering with HIF-1 mediated target gene transcription. Additional posttranslational modifications of HIF-1 $\alpha$  also occur, including acetylation, phosphorylation, and SUMOylation (24). Finally, the recently characterized 35-kDa protein CITED2/p35srj is upregulated by hypoxia and by HIF-1 and competes with HIF-1 for the coactivator p300/CBP, thus representing a negative feedback mechanism (18).

HIF-1 is further regulated at the transcriptional level through intracellular signaling pathways induced by growth factors. These growth factors include EGF, TGF- $\alpha$ , PDGF-A, IGF-1 and -2, insulin, angiotensin, and thrombin (5, 82, 146, 210), many of which have proangiogenic properties (Table 1) and also upregulate VEGF (62, 73, 176, 185, 192). Growth factor induced transcription of HIF-1 is part of several positive feedback-loops. For example, binding of TGF- $\alpha$  to EGFR activates the intracellular PI3K pathway and induces HIF-1 $\alpha$  transcription. HIF-1 itself activates TGF- $\alpha$  transcription through binding to an HRE in the promoter region of the TGF- $\alpha$  gene (161). In a similar fashion, activation of IGFR-1 induces HIF-1, which activates the transcription of HRE-regulated genes encoding the ligand for the IGFR-1 receptor and for the IGFs (59, 161). GBMs often express high levels of IGFs, IGF receptors and IGFs compared with normal brain tissue (55, 213).

**Effects of HIF-1 transcriptional activity.** HIF-1 activity in gliomas induces a wide variety of genes as shown in Figure 4 (99, 159, 161, 195). The protein products of these genes play crucial roles in angiogenesis and vascular tone, pH regulation, apoptosis, iron metabolism, cell proliferation and survival, transcriptional regulation, and extracellular matrix metabolism and invasion, which confers increased resistance of the tumor cells to the hostile tumor microenvironment. Hypoxia through HIF-1 is one of the most potent stimulators of VEGF expression in vitro and in vivo (161). HIF-1



**Figure 4.** Examples of genes transcriptionally activated by HIF-1.

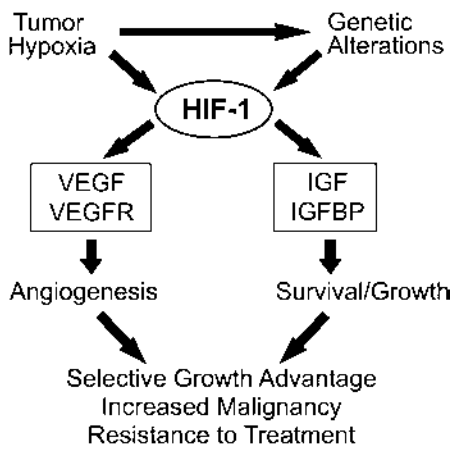
binds to the HRE in the VEGF promoter region leading to increased VEGF transcription (161). To control energy metabolism glucose transporters, such as GLUT-1 and GLUT-3, and enzymes of the glycolytic pathways are induced to ensure an adequate supply of ATP for the cells under hypoxic conditions. Lactate, one of the endproducts of the glycolytic pathways, contributes to the typically acidic microenvironment of gliomas and the transcriptional activation of the carbonic anhydrase CA9 by HIF-1, which enables glioma cells to regulate their intracellular pH (85, 161, 190). CA9 expression is increased in pseudopalisading cells of GBMs showing colocalization with HIF-1 $\alpha$  (Figure 1D). HIF-1 target genes include growth factors such as adrenomedullin that sustains glioma growth (93). In addition, HIF-1-induced genes include uPAR and plasminogen activator inhibitor-1 (PAI-1) (161) known to be upregulated in gliomas (8). These genes act in synergy with the MMPs to aid in the breakdown of the ECM, facilitating endothelial cell migration during the angiogenic process (8).

More recently, HIF-1 activity, in relation to apoptosis, has been investigated (33, 83). Upregulation of HIF-1 has been associated with both proapoptotic (20, 33, 136) and antiapoptotic (83) effects. For example, HIF-1 $\alpha$  activates the proapoptotic proteins BNIP3 and NIX (20, 166). Similarly, overexpression of HIF-2 $\alpha$  in rat gliomas enhances angiogenesis but reduces growth of

these tumors, in part by increasing tumor cell apoptosis (4).

#### GENETIC ALTERATIONS AND HYPOXIA IN GLIOMA PROGRESSION

During progression from low grade to high grade, gliomas accumulate genetic alterations in tumor suppressor genes and oncogenes (109, 184). These include loss of function of p53, amplification of EGFR and chromosome 10 alterations, including inactivation of PTEN through mutations and loss of heterozygosity (13, 50, 102, 133, 134, 167). Also, loss of heterozygosity of chromosomes 1, 10, 19, and/or 22 would be associated with loss of gene loci encoding proangiogenic (Table 1) and/or antiangiogenic (Table 2) factors or their receptors in patients with gliomas harboring these chromosomal abnormalities (reviewed in Gagner et al; this issue). These genetic alterations combine with hypoxia to drive chromosome instability (145, 186) promoting continual selective growth advantage for the tumor cells (Figure 5). In support of this concept that the hypoxic microenvironment of GBMs drives genomic instability, comparative genome hybridization (CGH) analysis of GBM xenograft specimens showed increased number of genetic alterations in poorly vascularized and hypoxic xenografts compared with well-vascularized and less-hypoxic ones (67). Some of these genetic alterations also affect HIF-1 activity and thus angiogenesis.



**Figure 5.** Molecular mechanisms by which tumor hypoxia and genetic alterations promote angiogenesis and tumor growth or survival. Tumor cells respond to decreased  $O_2$  concentration by increasing HIF-1 transcriptional activity that induces adaptive changes in gene expression patterns (eg, increased VEGF, VEGFR, IGF and IGFBP) that result in enhanced tumor angiogenesis, growth and survival. Alternatively, genetic alterations, such as gain-of-function mutations in oncogenes (eg, EGFR), loss-of-function mutations in tumor-suppressor genes (eg, PTEN, p53) and chromosomal alterations, accumulate in tumor cells that lead to  $O_2$ -independent increase in HIF-1 activity associated with similar changes in gene expression patterns. In addition, severe hypoxia itself can induce genetic instability that can result in genetic and chromosomal alterations (for review, see 145, 186). These adaptive responses have been associated with tumor growth advantage, increased malignancy as well as treatment resistance and failure (161).

Several studies looking at gene expression profiling of gliomas have demonstrated clusters of genes highly linked to the angiogenic phenotype, eg, VEGF, VEGFR-1, IGFBP2, pleiotrophin, AP-1 (69, 103, 119, 131, 153). These results support the crucial role of genetic changes, hypoxia and angiogenesis in glioma growth and progression.

**Tumor suppressor genes.** In addition to growth factors, tumor suppressor genes and oncogenes modulate HIF-1 activity and angiogenesis in gliomas. For example, wild type PTEN downregulates HIF-1 mediated gene expression (215). In addition, induced expression of PTEN in glioma cells has been shown to decrease accumulation of HIF-1 $\alpha$  in vitro and induce TSP-1 expression and reduce angiogenesis in vivo (3, 187, 215). The tumor suppressor gene p53 competes with HIF-1 for its coactivator p300 under hypoxic conditions (157). Cells with mutant p53 upregulate basic FGF expression

(172) that could be suppressed when the mutant cells are transfected with wild-type p53 (180). VHL mutations are rare in gliomas (88). As described above, VHL protein is essential for proteasomal degradation of the HIF-1 $\alpha$  subunit. Therefore, loss of function of pVHL leads to a constitutive activation of HIF-1 and consequently to the upregulation of HIF-1 target genes such as VEGF, erythropoietin, CXCR4 and CA9 (161, 205).

**Oncogenes.** Both Ras and v-src have been shown to modulate angiogenesis in gliomas (72, 174). Genetic alterations in EGFR, EGFRvIII and PDGFR in GBMs activate the Ras signaling pathways (72, 82, 133). Chronically active Ras and PI3K pathway signaling enhanced angiogenesis in GBMs whereas Ras inhibition in vitro, achieved by trans-farnesylthiosalicylic acid, down-regulates HIF-1 $\alpha$  and its target genes (21). V-src expression in gliomas has been shown to modulate angiogenesis (174) and v-src induces HIF-1 expression and its transcriptional activity (87).

Thus, independently of hypoxia-induced HIF-1 expression, genetic alterations can affect HIF-1 expression at the transcriptional or at the proteasomal degradation level leading to the upregulation of proangiogenic factors to promote angiogenesis (Table 1). This “pseudohypoxic” HIF-1 activation, ie, the involvement of an oncogenic stimulus rather than a physiologic stimulus as a source for HIF-1 $\alpha$  expression is highly relevant for GBM progression (19, 209).

## CONCLUSION

GBMs are amongst the most angiogenic tumors. Both proangiogenic and antiangiogenic mechanisms control tumor neovascularization. The observation that angiogenic inhibitors decrease tumor growth in vivo suggests that angiogenesis is not merely an epiphenomenon of malignancy. For example, the VEGFR-1, PDGF-B, and basic FGF tyrosine kinase inhibitor SU6668 decreased tumor growth in a rat glioma model, which is associated with decreased vascularization and peritumoral edema (58). Because diffusely infiltrating gliomas are mostly refractory to current surgical and adjuvant treatments, the topic of angiogenesis and its relation to tumor growth, progression, and resistance to therapy is of

special interest. A variety of antiangiogenic approaches are currently undergoing pre-clinical or clinical trials (22). In the future, these experimental strategies may develop and find wide clinical applications equivalent to “traditional” radiotherapy and chemotherapy. Progress made in imaging angiogenesis and hypoxia in gliomas and in developing antiangiogenic therapeutics are reviewed in an accompanying article (see Gagner et al; this issue).

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