

Growth factors in glioma angiogenesis: FGFs, PDGF, EGF, and TGFs

Ian F. Dunn^{1,2,3}, Oliver Heese^{1,2,3} and Peter McL. Black^{1,2,3}

¹Brain Tumor Research Center, ²Brigham and Women's Hospital, ³Department of Surgery, Harvard Medical School, Boston, MA, USA

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Summary

It has become well accepted that solid tumors must create a vascular system for nutrient delivery and waste removal in order to grow appreciably. This process, angiogenesis, is critical to the progression of gliomas, with vascular changes accompanying the advancement of these tumors. The cascade of events in this process of blood vessel formation involves a complex interplay between tumor cells, endothelial cells, and their surrounding basement membranes in which enzymatic degradation of surrounding ground substance and subsequent endothelial cell migration, proliferation, and tube formation occurs. It is likely that a host of growth factors is responsible for mediating these key events. To date, a role for Vascular Endothelial Growth Factor (VEGF) in glioma angiogenesis has been convincingly demonstrated. This review explores the contribution of other growth factors—Fibroblast Growth Factors (FGFs), Platelet-Derived Growth Factor (PDGF), Epidermal Growth Factor (EGF), and Transforming Growth Factors (TGFs)—to glioma angiogenesis. These growth factors may influence glioma angiogenesis by directly stimulating endothelial cell proliferation, by mediating the expression of key proteases on endothelial cells necessary for angiogenesis, or by regulating the expression of VEGF and of each other.

Introduction

Angiogenesis, the formation of new blood vessels from pre-existing ones, is a central component in the development, progression, and metastasis of a number of human tumors including gliomas [1,2]. Gliomas appear to obey the central tenet of angiogenesis: that to grow rapidly beyond 1–2 mm³, they must create a system of blood vessels for nutrient delivery and waste removal [3]. Consistent with this observation, vascular changes accompany the malignant progression of gliomas and are included in the criteria used for glioma grading [4–8]. Noted vascular alterations include endothelial cell proliferation and loss of vessel structural integrity [9,10]. Moreover, neovascularization is correlated with biological aggressiveness, degree of malignancy, and clinical recurrence of gliomas and is inversely correlated with postoperative survival of patients [7,11].

Angiogenesis in gliomas is both similar and distinct from neovascularization in extracranial solid tumors.

Gliomas require neovascularization for growth and continued progression, as do extracranial solid tumors. However, additional consequences of the recruitment of structurally compromised vessels to the glioma tumor bed – namely, ischemic steal from hyperemia, peritumoral edema, and increased likelihood of spontaneous hemorrhage – are of great concern in an organ of exquisite oxygen-dependence and sensitivity to increased intracranial pressure [12–14]. Hence the particular context of oxygen and pressure sensitivity in which glioma angiogenesis takes place compounds the morbidity of the tumor growth and invasion fueled by new blood vessel growth. A thorough understanding of angiogenesis in gliomas is thus necessary for therapeutic targeting of this process.

During angiogenesis, new blood vessels grow by sprouting from established blood vessels; this process is characterized by a cascade of events including enzymatic degradation of basement membrane and endothelial cell migration, proliferation, and tube formation [15]. Vascular endothelial growth factor

(VEGF) appears to be the most potent of the myriad angiogenic growth factors described to date. (It is discussed in a separate chapter.) Identical to vascular permeability factor (VPF), tumor- or endothelial-derived VEGF exerts its effects in an autocrine or paracrine manner in gliomas through binding to high affinity tyrosine kinase receptors KDR/Flk-1 and Flt-1 on endothelial cells [16,17]. A precise role for the neuropilins, the most recent addition to the VEGF receptor family [18], has yet to be described in glioma angiogenesis. In addition to stimulating normal and tumor angiogenesis and vasculogenesis, VEGF also induces blood vessel permeability and protein extravasation; hence it is responsible for both new blood vessel formation and for the accompanying vasogenic edema observed in tumor angiogenesis [19–21].

The role of VEGF in glioma angiogenesis has been convincingly demonstrated [22], and while it may be the principal angiogenic factor in this process, a number of other growth factors like Fibroblast Growth Factor (FGF), Platelet-Derived Growth Factor (PDGF), Epidermal Growth Factor (EGF), and the Transforming Growth Factors- α and - β (TGF- α and - β) and their corresponding receptors may also play roles in regulating and modifying tumor angiogenesis in malignant gliomas. These tumor-secreted growth factors have both direct and indirect effects on glioma angiogenesis: they can directly stimulate endothelial cell proliferation, mediate the expression of key proteases on endothelial cells necessary for angiogenesis, and regulate the expression of VEGF and of each other. They can act in a paracrine fashion, in which ligand is produced by cells distinct from the cells expressing receptor, or they may act in an autocrine manner in which the same cell type expresses ligand and receptor. In this review, we will discuss FGFs, PDGF, EGF, and TGF- α and - β in turn, highlighting the basic properties of these growth factors and their cognate receptors, their expression in gliomas, and their roles in angiogenesis in these tumors.

FGF

Ligand and receptor

The FGF growth factor family now comprises 19 polypeptides: FGF-1 (acidic FGF) [23], FGF-2 (basic FGF) [24,25], FGF-3 (int-2) [26], FGF-4 (hst-1/kaposi-FGF) [27,28], FGF-5 [29], FGF-6 (hst-2) [30], FGF-7

(keratinocyte growth factor) [31], FGF-8 (androgen induced growth factor) [32], FGF-9 (glia-activating factor) [32] and FGFs 10 and 12-19 [34–42] which as new members still have incompletely characterized biological functions. The FGFs are involved in a wide range of biological activities and have been shown to be involved in mitogenesis, differentiation, chemotaxis, and angiogenesis; as such they have been implicated in the development of skeletal, nervous, and vascular systems, tissue integrity and repair, and wound healing, as well as a host of pathophysiologic processes [43,44]. Here, we will focus on those FGFs that have been reported to have roles in glioma angiogenesis: FGF-1 and FGF-2. Additionally, a potential role for FGF-4 in this process will also be discussed.

Of the 19 proteins in the FGF family, FGF-1 and FGF-2 have been studied in greatest depth. Both have been shown to be potent inducers of endothelial cell migration, proliferation, and tube formation *in vitro* and are highly angiogenic in a number of tissues *in vivo* [43,45]. FGF-1, or acidic FGF (aFGF), is encoded on chromosome 5q [23] and is a 154-amino acid protein (with N-terminal truncation forms of 140 and 134 amino acids) with a molecular mass of 18 kDa [43,46] (Table 1). FGF-2, encoded on chromosome 4q [47,48], is expressed in 4 forms of varying molecular masses: 18, 22, 22.5, and 24 kDa [48,49]. The 18 kDa form has 55% sequence homology to aFGF [46]. An intriguing structural feature of FGF-1 and FGF-2 is the absence of a classical hydrophobic signal sequence for secretion despite their extracellular activities. That these proteins may be secreted during inhibition of classical secretory routes suggests that secretion occurs through an unconventional non-ER/Golgi pathway [51,52]. The molecular weights and chromosomal locations of all growth factors and receptors discussed in this review are listed in Table 1.

While the targets of these factors are many, each exerts its effects through one or more members of four well-characterized FGF receptor families: FGF receptor-1 (flg) [53], FGF receptor-2 (bek) [54], FGF receptor-3 (FGFR-3) [55], and FGF receptor-4 (FGFR-4) [56–58]; these are located on chromosomes 8p, 10q, 4p, and 5q, respectively [59–62]. Once secreted, acidic and basic FGF exert their effects by binding to FGFRs 1–4. These proteins are receptor tyrosine kinases. FGF molecules – perhaps bound as dimers [63] – bind to FGFRs to induce receptor dimerization, which is required to initiate the protein tyrosine kinase activity and subsequent

Table 1. Angiogenic growth factors and receptors: size and genetic location

Factor	Molecular weight (kDa)	Chromosome
FGF-1	18 ²⁴	5q ²⁴
FGF-2	18, 22, 22.5, 24 ^{50,51}	4q ^{46,47}
FGF-4	18 ²⁷	11q ²⁸
FGFR-1	150 ⁵³	8p ⁵⁹
FGFR-2	135 ⁵⁴	10q ⁶⁰
FGFR-3	125 ⁵⁵	4p ⁶¹
FGFR-4	95, 110 ⁵⁶	5q ⁶²
PDGF-A	15 ⁹⁷	7p ^{98,99,100}
PDGF-B	15 ⁹⁷	22q ^{9,103}
PDGFR- α	170 ¹⁰⁹	4q ¹⁰⁹
PDGFR- β	180 ^{107,108,109}	5q ^{107,108,109}
TGF- α	5–20 ¹³⁷	2p ¹⁴³
EGFR	170–180 ¹³²	7p ¹⁴⁸
TGF- β 1	12–15 ^{184,190}	19q ¹⁸⁷
TGF- β 2	12–15 ^{182,188}	1q ¹⁸⁸
TGF- β 3	12–15 ^{182,188}	14q ¹⁸⁹
T β R-I	55 ¹⁹¹	9q ¹⁹⁵
T β R-II	75 ¹⁹¹	3p ¹⁹⁵
T β R-III	250–350 ¹⁹³	1p ¹⁹⁷
Endoglin	68 ¹⁹⁴	9q ¹⁹⁸

trans-autophosphorylation events and activation (Figure 1).

It has been shown that heparan sulfate proteoglycans (HSPGs) such as heparin may increase the binding affinity of FGFs to their receptors [64]. Proteins such as phospholipase-C γ (PLC- γ) and Ras GTPase Activating Protein (GAP), for instance, then bind the phosphorylated regions, engaging the receptor tyrosine kinase signaling cassette en route to mediating gene transcription events.

Expression in gliomas and roles in angiogenesis

FGF-1 and FGF-2, two of the first angiogenic factors isolated [65], have been implicated in glioma angiogenesis. Early *in vitro* studies demonstrated high levels of expression of FGF-2 mRNA and protein in U87MG glioma cell lines [66]. Robust expression of FGF-1 in glioma as compared to normal brain has also been shown; an early study showing FGF-1 overexpression in gliomas by Northern blot analysis and *in situ* hybridization reported that 93% of tumors studied showed elevated FGF-1 mRNA expression as compared to nonmalignant control brain tissue [67]. FGF-2 overexpression has been linked to increased endothelial activity, as well. Strong expression of FGF-2 has been reported in the perivascular space of

more malignant tumors as compared to normal brain [67]. Peritumoral endothelial cell FGF-2 immunoreactivity has also been shown to correlate with tumor grade; capillaries in glioblastoma and anaplastic astrocytoma are immunoreactive for FGF-2, in contrast to those of low-grade astrocytomas [68]. Higher levels of FGF receptors have also been demonstrated in gliomas; indeed, it has been suggested that glioma grade is marked by the differential expression of FGFR molecules, with the malignant progression from glial cell to glioblastoma accompanied by diminishing levels of FGFR-2 and increasing levels of FGFR-1 [69,70]. These results suggest that alterations in FGFR signal transduction pathways may play a critical role in the malignant progression of astrocytic tumors. While these changes have been reported in glioma cells, there is conflicting evidence regarding the status of FGFR expression on intratumoral endothelial cells [69–71].

It is thought that FGF-1 and FGF-2 may participate in angiogenesis in two primary ways: by modulating endothelial cell activity and by regulating VEGF expression in tumor cells. Both factors are well-established mitogens and chemoattractants for endothelial cells [65,72,73]. In order to invade extracellular matrix to vascularize new tissues, endothelial cells must enhance their expression of molecules that activate key proteases such as plasmin [74–76]. One of such molecules, urokinase-type plasminogen activator (uPA), acts to convert the inactive zymogen plasminogen to the active proteolytic enzyme plasmin [77]. Plasmin, in turn, is able to degrade multiple extracellular matrix (ECM) components including fibronectin and laminin, permitting endothelial cell migration into new tissue space [78]. FGF-2 has been shown to upregulate uPA and collagenase expression on endothelial cells [79] and has also been shown to induce expression of the receptor for uPA [80], thus modulating endothelial cell migration in a feed-forward fashion. Hence one way in which FGF-2 may participate in angiogenesis is by mediating the proteolytic digestion of ECM by invading endothelial cells. Furthermore, FGF-2 is chemotactic for endothelial cells [81] and has been shown to induce capillary endothelial cells to migrate into three-dimensional collagen matrices to form capillary-like tubes [82].

A second way in which FGF-2 may participate in angiogenesis is by inducing expression of VEGF, an endothelial cell mitogen [83–86] which has been shown to be a potent angiogenesis factor in human gliomas *in vivo* [86]. FGF-2 has been shown to stimulate VEGF

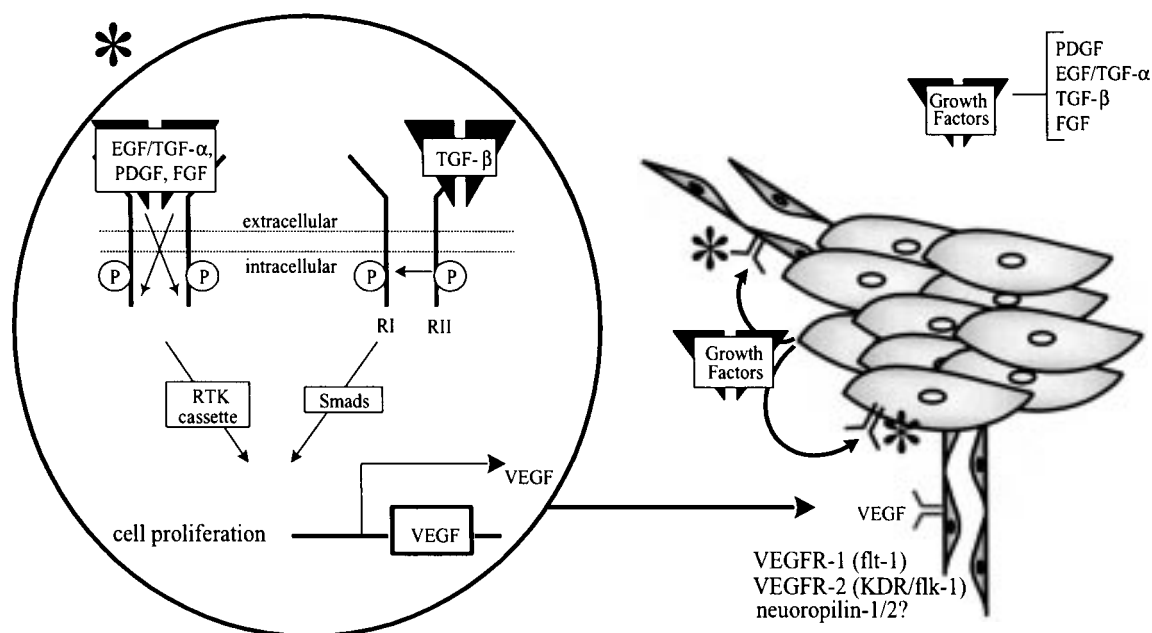


Figure 1. Growth factor-mediated angiogenesis in gliomas. In this scheme, tumor cells secrete indicated growth factors represented by dimerized triangles which bind their respective receptors either on the same or adjacent tumor cells or on surrounding tumor endothelial cells. Growth factor receptors are marked by asterisks and are shown in greater detail in the inset. Growth factor binding may lead to cell proliferation, upregulation of key proteases, and/or initiation of signaling leading to VEGF transcription in tumor cells or endothelial cells. VEGF secreted from tumor cells and/or endothelial cells after growth factor-mediated signaling may then bind to one of its receptors, flt-1 or KDR/flk-1. Neuropilins 1 and 2 were recently shown to be the newest members of the VEGF receptor family and may be involved in glioma angiogenesis. *Inset:* Details of signaling by growth factor receptors (marked by asterisks in figure). Proposed growth factor-mediated signaling pathways leading to VEGF transcription in tumor cells or endothelial cells. EGF, TGF- α , the FGFs, and PDGF signal through receptor tyrosine kinases (RTKs); the ligands, which are dimerized, bind to tyrosine transreceptor subunits and induce dimerization. This in turn leads to *trans*-autophosphorylation by the intracellular receptor tyrosine domains, and subsequent signaling through molecules such as Raf/Ras and others, represented by 'RTK cassette' above. The details of TGF- β signaling differ. First, TGF- β – again binding as a dimer – binds to only the RII subunit, and binding induces recruitment of the RI subunit and *trans*-phosphorylation of RI by the constitutively phosphorylated RII. Downstream signaling is initiated by activated RI and is mediated by Smad proteins.

secretion in a dose-dependent fashion using U-105MG and D-54MG glioma cell lines [87]. Thus FGF-2 secreted by tumor cells may induce angiogenesis in a paracrine fashion, acting on endothelial cells directly as well as stimulating tumor cells in an autocrine and paracrine fashion to synthesize VEGF.

Studies such as these have established that FGF-1 and FGF-2 may modulate endothelial cell activity directly and indirectly. While high levels of these growth factors have been detected in gliomas, functional roles for these proteins in glioma angiogenesis have also been investigated directly. Direct evidence for the role of FGF-2 in glioma angiogenesis is given by *in vivo* studies in which intracranially implanted U87MG tumors showed a significantly lower degree of neovascularization after treatment with an anti-FGF-2 antibody as compared to untreated tumors [88]. Addi-

tionally, endothelial tube formation stimulated by the presence of glioma cells in a three-dimensional collagen was markedly inhibited after incubation with an anti-FGF-2 antibody [89].

In addition to reports establishing both the presence and functional involvement of FGFs in glioma angiogenesis, studies have also correlated FGF expression with clinical tumor progression and patient prognosis. Increased neovascularization accompanies the mitotic and pleomorphic cellular changes in the malignant progression of gliomas. Immunohistochemical studies on primary glioma specimens showing that FGF-2 is expressed in human gliomas also showed that FGF-2 levels are increased in high grade as compared to low-grade gliomas [68]. Additional studies have also reported increasing FGF-2 levels with glioma grade, noting that FGF-2 expression correlates with glioma

vascularity [90]. Moreover, Li *et al.* detected FGF-2 in the CSF of 62% of patients with brain tumors (16/26), while no FGF-2 was detected in controls [91]. Endothelial cells from CSF that contained FGF-2 were more proliferative when compared with controls; the degree of endothelial cell stimulation correlated with FGF-2 levels; and the level of FGF-2 correlated with microvessel density. Most strikingly, patients with CSF containing FGF-2 recurred earlier, with earlier tumor recurrence correlating with increased microvessel density. Interestingly, while a number of different types of brain tumors were included in this study, the highest level of FGF-2 was detected in a pilocytic astrocytoma. Studies from our laboratory have supported the importance of microvessel density as a prognostic indicator of postoperative survival of patients with astroglial brain tumors [92].

Research to date has focused on the involvement of FGF-1 and FGF-2. A recent study provided evidence that FGF-4 may also participate in glioma angiogenesis [93]. In 18 glioblastomas, 17 anaplastic astrocytomas, and 19 low-grade gliomas, Western blot and immunohistochemical analysis demonstrated the presence of FGF-4 and its related receptors, FGFRs-1, 2, and 4, in tumor and tumor-associated endothelial cells. The expression of these proteins was undetectable in control non-neoplastic tissue. Moreover, the expression of FGF-4 and its receptors correlated with histological grade, tumor type, microvessel count, and cell density. These observations were corroborated by *in vitro* studies in which U87MG, U373MG, and U118MG glioma cell lines were shown to secrete FGF-4. Additional studies showed that FGF-4 could regulate VEGF expression and the formation of new blood vessels. These data suggest that other FGF family members such as FGF-4, in addition to FGF-1/2, may be important in blood vessel growth in gliomas.

PDGF

Ligand and receptor

Platelet-derived growth factor (PDGF) has also been implicated in glioma angiogenesis. PDGF was initially discovered as a mitogen for fibroblasts contained in human serum and localized in the alpha granules of platelets [94,95]. While initially described as a platelet alpha-granule release product, subsequent studies have shown that PDGF is produced by a variety of cell types and that among its many targets of action are

capillary endothelial cells, vascular smooth muscle cells, osteoblasts, glia, and neurons [96–98]. PDGF has pleiotropic effects and has roles in embryonic development, CNS development, the vascular system, tissue homeostasis, and wound healing. An angiogenic role has also been demonstrated, albeit weaker than the angiogenic effects of VEGF and the FGFs [98].

PDGF is a 30 kDa protein consisting of disulfide-bonded dimers of A and/or B chains. The A and B subunits are approximately 100 amino acids in length and share a 60% sequence homology; the isoforms are functionally active when dimerized as either PDGF-AA, PDGF-AB, or PDGF-BB [97,99]. PDGF-A is encoded by a gene on chromosome 7p [100–102]; PDGF-B, the cellular homolog of the retroviral oncogene *v-sis* carried by the Simian Sarcoma Virus (SSV) [103,104], is encoded by the *c-sis*/PDGF-2 gene on chromosome 22q [101,105].

The PDGF receptors are members of the protein tyrosine kinase family of receptors [106] and as such are activated by ligand-induced dimerization of receptor subunits. Two receptor subunits have been described: PDGF receptor- α (PDGFR- α) and PDGF receptor- β (PDGFR- β). PDGFR- α , a 170 kDa protein, is encoded on chromosome 4q, while PDGFR- β , a 180 kDa protein, is encoded on chromosome 5q [107–109]. Ligand binding and subsequent dimerization leads to juxtaposition of the two tyrosine kinase domains and *trans*-autophosphorylation, and to the activation of signal transduction pathways and downstream gene transcription events (Figure 1).

PDGF dimer combinations bind to dimeric combinations of PDGF receptor subunits. PDGF-A binds only to PDGFR- α , whereas PDGF-B binds to the β receptor with higher affinity but can bind both subtypes. Consequently, PDGF-AA can only activate the $\alpha\alpha$ receptor complex; PDGF-AB can activate $\alpha\alpha$ or $\alpha\beta$; and PDGF-BB can activate $\alpha\alpha$, $\alpha\beta$ and $\beta\beta$ [110–112]. PDGF-BB is able to activate all three receptor complexes and has been shown to be the most mitogenic of the PDGF dimer combinations [113–117].

Expression in gliomas and roles in angiogenesis

Human astrocytomas express high levels of both the PDGF ligand and corresponding receptor subtypes. *In situ* hybridization and immunocytochemistry studies have demonstrated that PDGF-A is expressed in low-grade and anaplastic astrocytomas as well as in glioblastomas. and that expression increases with

tumor grade [118]. PDGFR- α was also expressed at higher levels in gliomas as compared to control gliosis cases. PDGF-B, while still expressed, was found at lower levels than PDGF-A in cell-rich areas; PDGFR- β was not detected in glioma cells. Later studies have corroborated these results, and studies in oligodendrogliomas have demonstrated similar ligand and receptor expression [123,125]. The overexpression of PDGFR- α in all tumor grades and the increasing expression of PDGF-A and PDGF-B with tumor grade are consistent with the concept that the establishment of a functional autocrine/paracrine loop may be important in glioma pathogenesis [118,120–124]. Interestingly, robust expression of both PDGF-B and PDGFR- β was reported in hyperplastic tumor endothelial cells in glioblastoma [119]. Further *in situ* hybridization and immunocytochemistry studies in normal brain, low-grade astrocytoma, anaplastic oligo-astrocytoma, and glioblastoma have demonstrated that PDGFR- β mRNA is expressed in the vasculature of glioma tissue, most notably in areas of endothelial cell proliferation in glioblastoma tissue [126]. No mRNA message was detected in normal brain and expression in tumors appeared to be confined to tumor endothelial cells. The detection of increased levels of PDGF-B and PDGFR- β on high-grade astrocytoma endothelial cells suggests a role for PDGF in glioma angiogenesis. Subsequent *in vitro* studies have taken steps towards addressing the biological significance of these observations. PDGF was shown to be a chemotactic factor in rat brain capillary endothelial cells, with PDGF-BB having a more potent effect than PDGF-AA [127]. Earlier studies by Westermarck and co-investigators provide a possible molecular basis for this effect by showing that PDGFR- β is able to mediate the actin reorganization necessary for a chemotactic motility response [128].

Most recently, the observed overexpression of PDGFR- β on tumor endothelial cells was studied by transfecting aortic endothelial cells with wild-type PDGFR- β . Incubation with PDGF-B led to increased transcription and secretion of VEGF by endothelial cells expressing the β receptor. Furthermore, it was shown that VEGF regulation by PDGF was mediated by phosphoinositol-3 kinase (PI-3 kinase) as PI-3 kinase-specific inhibitors abrogated the PDGF-induced VEGF expression [129]. Interestingly, Tsai *et al.* demonstrated that physiological concentrations of PDGF-BB and not PDGF-AA can also induce VEGF secretion in a variety of human glioma cell lines [87]. Moreover, it was demonstrated that activation of con-

vergent signaling pathways of EGF, PDGF-BB, and FGF-2 led to increased VEGF secretion.

The emerging picture is that inappropriate expression of PDGF by astrocytes and the upregulation of the PDGF receptor on the surrounding endothelial cells may represent an important step in the development, proliferation and maintenance of malignant astrocytomas [126,130,131]. An increase in PDGF activity *in vivo* may stimulate VEGF expression in endothelial cells and in tumor cells, establishing both paracrine and autocrine loops for endothelial cell activation and proliferation. PDGF-induced VEGF expression may contribute not only to expansion of an established tumor but also to the regulation of the angiogenic switch for initial tumor development as induction of PDGFR- β on endothelial cells may occur in early stages of glioma formation.

EGF/TGF- α /EGFR

Ligand and receptor

EGF, TGF- α , and their receptor, epidermal growth factor receptor (EGFR), are thought to be important in the mediation of proliferative and transforming response in a variety of cancers via autocrine or paracrine mechanisms [132–134]. A considerable body of work has demonstrated its importance in glioma transformation. In these tumors, overexpression of EGFR is a late event, and may be one of the last molecular event to occur in the pathogenesis of gliomas [135]. Ligands which bind EGFR include EGF, TGF- α , heparin-binding epidermal growth factor-like growth factor (HB-EGF), amphiregulin, and epiregulin [136–140]. Of these, EGF and TGF- α have been implicated in glioma angiogenesis. EGF – one of the earliest peptide growth factors purified – is a 53-amino acid protein of molecular weight 6 kDa whose gene has been mapped to chromosome 4q [132,141,142]; it is involved in the regulation of cell proliferation and differentiation in a number of physiological systems. TGF- α , which in active form is 50 amino acids long and is 5–20 kDa depending on extent of glycosylation, maps to chromosome 2p [137,143]. First found in the medium of retrovirally transformed fibroblasts [133,144], TGF- α shares 42% homology with EGF [145] and is widely expressed in developing embryos and in a number of normal adult tissues. It is thought to have roles in wound healing and homeostasis in number of tissues, and to serve as

a broad regulator of normal growth and development [146]. It is structurally unrelated to TGF- β and binds to an entirely different set of receptors.

EGF and TGF- α both exert their effects through EGFR, the cellular homolog of the viral oncogene *erbB* from the avian erythroblastosis virus [147]. EGFR (ErbB1), encoded on chromosome 7p [148], is a receptor tyrosine kinase with a molecular weight of 170–180 kDa [132,137,145]. A classic receptor tyrosine kinase, two molecules of EGFR are cross-linked and brought together by dimerized ligand binding, which can occur among two EGFR molecules or among other members of the EGF receptor protein tyrosine kinase family, such as ErbB2, ErbB3, ErbB4 [149–151]. It has recently been demonstrated that EGF most likely expedites receptor subunit dimerization by itself binding as a dimer, and the same may be true for TGF- α [152]. Receptor dimerization induces *trans*-autophosphorylation and recruitment and activation of various signal transduction pathways (Figure 1); the Ras pathway has been implicated in EGFR-activated glioma pathogenesis [153].

A number of altered forms of EGFR – the result of gene rearrangements, alternative splicing, deletions, and/or translational alterations – have been detected in human glioma tissue and cell lines. The most common mutant form, termed p140^{EGFR}, EGFRvIII, or Δ EGFR, lacks a significant portion of the extracellular binding site of the wild-type protein and is constitutively phosphorylated and hence activated [154,155]. This truncated mutant has been shown to confer a considerable growth advantage when stably expressed *in vivo* when stably expressed in U87MG astrocytoma cells in nude mice [156]. Other mutant EGFR molecules that have been detected in gliomas lack cytoplasmic regions necessary for receptor downregulation [157,158].

Expression in gliomas and roles in angiogenesis

EGFR is rarely present in normal glial cells but is expressed in human gliomas, certain neurons, and in reactive astrocytes [159]. Studies have demonstrated the expression of EGFR in gliomas in the cell membrane, cytoplasm, and nucleus of positive cells by EGF binding and by immunohistochemistry [160,161].

Increased levels of EGFR in glioma are due to amplification of the *erbB-1* gene, the first major molecular genetic alteration identified in human gliomas [162]. Amplification has been detected in 3% of low-grade

astrocytomas, 7% of anaplastics, 40%–50% glioblastomas [160, 162–164], and in a number of glioma cell lines. Moreover, in a large number of glioblastomas with EGFR gene amplification, the EGFR gene undergoes rearrangements and/or deletions; 50% of glioblastomas in which EGFR amplification occurred expressed EGFR in its preponderant mutant form, EGFRvIII [154,158]. In addition to amplification of mutant EGFR, wild-type EGFR, as well as EGF and TGF- α mRNA, appear to be upregulated in gliomas. Hence not only is the mutant receptor able to induce mitogenesis and activation, but the wild-type ligand and receptor system is also induced [165]. The overexpression of EGFR has been inversely correlated with the length of survival for patients with malignant glioma [166], but others have not shown a significant correlation [167,183]. Interestingly, Bello has shown that urinary EGF levels correlated with tumor anaplasia, and that immunohistochemistry on tumor specimen correlated with urinary EGF levels [168]. Additionally, recent studies have reported expression of other members of the EGF receptor family members such as *erbB-2* in gliomas [145,169].

TGF- α is secreted by a number solid tumors [170], including gliomas; its expression has been reported to correlate not only with tumor grade but also with EGFR and Ki-67 expression [171–173]. Like EGFR, it has been suggested that increased TGF- α levels are due to gene amplification [174], but this has not been supported by subsequent studies [175]. TGF- α is a potent mitogen and its functional effects on glioma cell proliferation were demonstrated by growth inhibition of U251 cells by antisense TGF- α [176]. Direct consequences of increased expression in tumor cells of a TGF- α /EGFR autocrine or paracrine loop include increased cell proliferation and survival. Increased EGFR activity, whether through mutation or by TGF- α binding, increases cell proliferation and survival and has been shown to confer a growth advantage on cells *in vitro* [177].

The TGF- α /EGFR pathway is also purported to play a role in glioma angiogenesis. Tumor endothelial cells are immunoreactive for TGF- α and EGFR, and both TGF- α and EGF are potent mitogens *in vitro* for endothelial cells. Both molecules have been shown to be angiogenic *in vivo*, with TGF- α having a more profound effect [178]. In addition to its mitogenic effects on endothelial cells, EGFR in glioma may mediate its angiogenic effects by regulating VEGF expression. Engagement of the EGFR by EGF and

TGF- α has been shown to stimulate VEGF expression by glioma cells *in vitro* [87,180,181]; this secretion was blocked by incubation with anti-EGFR [182]. Moreover, Feldkamp and investigators recently showed that the EGFRvIII – the truncated and constitutively activated EGFR – is able to increase VEGF expression in glioma cells [183]. Hence as in the other growth factor systems discussed, the TGF- α /EGFR system may mediate glioma angiogenesis through both direct and indirect effects on endothelial cells.

TGF- β

Ligand and receptor

The TGF- β proteins are members of a large group of closely related growth factors including Bone Morphogenic Proteins (BMPs), Mullerian Inhibiting Substance (MIS), inhibin, and the activins [184,185]. The TGF- β proteins affect cell fate by regulating proliferation, differentiation, motility, adhesion, and apoptosis [186], but are most notable for inhibiting proliferation in a variety of systems.

At least three genes encode TGF- β precursors in humans: TGF- β 1, on chromosome 19q; TGF- β 2, on 1q; and TGF- β 3, on 14q [187,188,189]. The corresponding TGF proteins share 64%–82% sequence homology and interestingly have nearly identical effects in some biological systems and opposite effects in others [190]. Like the other growth factors discussed in this review, TGF- β proteins act functionally as disulfide-linked dimers, each subunit of which is about 112 amino acids in length and 12–15 kDa in molecular weight [184,190]. The proteins are initially inactive and are activated by enzymatic cleavage of the latent form.

The TGF- β proteins bind with high affinity to a set of receptors distinct from others discussed in this review. TGF- β receptors I and II (T β R-I/II) are transmembrane serine/threonine receptor kinases of 55 and 75 kDa [190,191], respectively, which together mediate the intracellular signals induced by TGF- β binding. The current view is that these subunits work in tandem, with the TGF- β dimer first binding to the constitutively phosphorylated RII subunit. The RI subunit is then recruited and *trans*-phosphorylated by RII, subsequently transmitting the signal to the cell by phosphorylation of Smad proteins which may operate independently or in conjunction with other signaling pathways to produce their responses

(Figure 1) [186,192]. TGF- β is known to bind other cell surface proteins such as betaglycan (T β R-III), which is expressed on a variety of cell types including microvascular endothelial cells [185,193], and endoglin (CD105), which is expressed primarily on endothelial cells [194]. These have no apparent role in directly transducing cellular signals but may present TGF- β proteins to T β R-II [192]. T β R-I has been mapped to chromosome 9q [195]; T β R-II, to 3p [196]; betaglycan, to 1p [197]; and endoglin, to 9q [198].

Expression in gliomas and roles in angiogenesis

To date, immunohistochemical studies have revealed that the TGF- β proteins, as well as their functional signaling receptors T β R-I/II, are expressed in glioblastoma and anaplastic astrocytoma, but are barely detectable, if at all, in low-grade gliomas, gliosis, and normal brain [199–202]. In these studies, levels of TGF- β 1 and of T β R-I/II were high in higher grade glioma tissue, while low-grade astrocytomas and gliosis cases had moderate expression of T β R-I and weak immunopositivity for TGF- β proteins and T β R-II [199,201]. TGF- β II/III were also upregulated, but not significantly. Interestingly, immunohistochemical studies of TGF- β and T β R have demonstrated that areas of neovascularization in gliomas are strongly immunoreactive [201,203]. In normal endothelial cells, TGF- β is expressed primarily as an inactive precursor; T β R-I/II, betaglycan, and endoglin are also expressed, though T β R-I/II have been most easily detected *in vitro* [193,204,205]. Moreover, increasing levels of TGF- β expression has been correlated inversely with survival among malignant glioma patients [206].

The functional significance of increased TGF- β activity in glioma has also been investigated. Despite its central physiologic role as a growth inhibitor, TGF- β has been shown to be mitogenic for a number of glioma cell lines [201,206,207]. The switch from TGF- β 's inhibitory to proliferative effects may be explained by a selective resistance to TGF- β binding to T β R through mutation of the receptor, or to a downregulation of the receptors [202]. However, while T β R-I/II are considerably downregulated in other extracranial neoplasms such as colorectal cancer [208], studies to date indicate that receptor expression is upregulated in glioma, suggesting that TGF- β 's switch from a growth inhibitor to a mitogen may be due to other growth factor mediators such as PDGF which are upregulated by TGF- β , or to a

dysregulation in the TGF- β signaling pathway. Indeed, TGF- β proteins have been shown to induce expression of the proto-oncogene *c-sis* (PDGF-B), PDGFR- β , and PDGF-A in glioma cells [209,210], suggesting that TGF- β 's conversion from inhibitor to mitogen may be due in part to modulation of expression of other growth factor systems.

TGF- β 's pleiotropic effects include roles in angiogenesis, but the exact nature of its participation in this process is unclear. TGF- β has been described as angiogenic or anti-angiogenic, depending on the nature of the assay. *In vivo* disc angiogenesis studies suggest a role in angiogenesis [211], but *in vitro* studies on endothelial cells have demonstrated an inhibitory effect on endothelial cell proliferation [212–214], as well as decreased expression of molecules necessary for endothelial cell migration such as plasminogen activators and a correspondent increase in Plasminogen Activator Inhibitors (PAIs) [215,216]. TGF- β has also been shown to increase synthesis and secretion of specific ECM proteins including fibronectin and collagen. These effects, coupled with its induction of endothelial cell quiescence, have led some to speculate that TGF- β takes part in the resolution phase of angiogenesis in which endothelial cells cease proliferating and functional basement membranes and ECM complexes are laid down [215,216].

TGF- β may also participate in angiogenesis in glioma by influencing the activity and/or expression of proteins in other growth factor systems. When added at low concentrations to endothelial cells in a three-dimensional collagen gel model, TGF- β 1 potentiates angiogenic effects of VEGF and bFGF [217] such as cord formation *in vitro*. TGF- β 1 has also been shown to induce PDGF-A and -B chain synthesis in endothelial cells [218,219] and to increase PDGFR- β expression in vascular smooth muscle cells [220]. In addition to possible regulation of the FGF and PDGF systems, TGF- β has also been shown to induce EGFR [221]. Interestingly, Koochekpour and co-investigators have demonstrated that TGF- β isoforms differentially stimulate VEGF production in glioma cells [222]. TGF- β 1 has also been observed to upregulate expression of VEGF in bone angiogenesis and breast cancer cells [223,224], further suggesting that TGF- β may act as an indirect angiogenic factor.

Other evidence suggesting a role for the TGF- β system in glioma angiogenesis includes the high immunopositivity for endoglin in childhood gliomas [225]. Endoglin, a TGF- β binding protein, is expressed

primarily on endothelial cells and appears to be essential for angiogenesis, recently demonstrated by the defective vascular development in mice lacking the gene [226]. Consistent with a possible role in angiogenesis, endoglin binds the TGF- β proteins TGF- β 1 and TGF- β 3 that have been shown to be most angiogenic in other studies [227].

Thus, studies to date suggest that TGF- β proteins may participate in glioma angiogenesis in three main ways. First, TGF- β may mediate its effects through the regulation of expression and activity of other growth factors and/or growth factor receptors such as FGF-2, PDGF, PDGFR, and EGFR. Secondly, like other growth factors discussed in this review, it may stimulate secretion of VEGF from the same or surrounding tumor cells in an autocrine or paracrine fashion. Third, it may interact directly with endothelial cells in two ways: by acting as a mitogen in advanced glioma malignancy despite its physiologic role as an inhibitor of proliferation [200f] or by participating in the resolution phase of angiogenesis in gliomas by inducing endothelial cell quiescence and by increasing levels of secretion of basement membrane proteins.

Conclusion

We have reviewed the potential involvement of FGFs, PDGF, EGF, and TGF- α/β in glioma angiogenesis. The immunohistochemical studies, mRNA expression, and *in vitro* and *in vivo* studies discussed herein suggest a pattern of involvement of these growth factors in the progression of malignant gliomas in which increased levels of these tumor-derived growth factors and/or their cognate receptors mediate their angiogenic effects in three primary ways: by direct endothelial action and tube formation; by indirect endothelial stimulation through increasing VEGF or other growth factor expression from tumor or endothelial cells, or both; and by upregulation of key proteases on endothelial cells to remodel surrounding ECM, permitting endothelial cell migration. Acting as such, glioma-derived angiogenic factors such as FGFs, PDGF, EGF, and TGF- α/β may bridge the interdependent processes of tumor cell and endothelial cell proliferation in gliomas. Taken together, the process of glioma angiogenesis appears to depend on an array of growth factors. While VEGF is perhaps the most critical to the process of neovascularization in these tumors and likely provides the

strongest therapeutic target to limiting this process, an understanding of the roles of supporting growth factors such as FGFs, PDGF, EGF, and TGFs may also prove beneficial.

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Address for offprints: Peter McL. Black, Longwood Medical Research Center, Room 121, 221 Longwood Avenue, Boston, MA 02115, USA; Fax: 417 7342628; E-mail: rhoudou@1.thc.harvard.edu