THE ROLE OF TRANSFORMING GROWTH FACTOR-BETA IN PRIMARY BRAIN TUMORS

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1. ABSTRACT

Dramatic therapeutic benefits of targeting specific signal transduction pathways in some cancers have pushed rational molecular targeting to the forefront of cutting-edge cancer therapy. The identification and targeting of pathways critical to the phenotype of cancers offers new hope in the treatment of many patients. Transforming growth factor beta (TGF-beta) is a multifunctional cytokine that is frequently expressed in multiple types of malignant brain tumors. TGF-beta exerts a complex set of effects in cancers with an early tumor suppressive effect through growth inhibition but later effects in cancer development that are tumorigenic including increased tumor cell motility and invasion, induction of angiogenesis, and immune suppression. Early preclinical and clinical studies have shown promise of anti-TGF-beta strategies in the treatment of malignant gliomas suggesting TGF-beta may be a potential new therapeutic target in neuro-oncology.

2. INTRODUCTION

Primary brain tumors, like all cancers, share a relatively restricted set of characteristics critical to the tumor phenotype – proliferation in the absence of external growth stimuli, avoidance of apoptosis and on limits of replication, escape from external growth suppressive forces and the immune response, new blood vessel formation, and ability to spread into normal tissues (reviewed in 1). The molecular determinants of these behaviors are becoming increasingly well understood, and this understanding is providing novel "targeted" therapies. Prominent amongst the signal transduction pathways that play a critical role in a broad range of tumors is the transforming growth factor-(TGF-beta) pathway. Malignant gliomas, meningiomas, medulloblastomas, and ependymomas

express high levels of TGF-beta ligand (2-7). In glioma cultures, TGF-beta regulates several aspects of the malignant phenotype, including immune escape, angiogenesis, and tumor invasion. The importance of TGF-beta in gliomas is illustrated by the fact that modulation of the TGF-beta function in gliomas has already been proven to be of value in preclinical trials, and early clinical trials to suppress TGF-beta function have been initiated. Several key points are important to understand the role of TGF-beta in malignant brain tumors: 1) The TGF-beta signal transduction pathways are complicated and interact significantly with many other signal transduction pathways, 2) The functional outcome of TGF-beta signal transduction is strongly dependent on cell type and cell state, 3) TGF-beta has an impact on a large number of cellular processes including proliferation, apoptosis, cell-extracellular matrix and cell-cell interactions, immune function and angiogenesis, 4) TGF-beta can act as a tumor suppressor at early stages of cancer development by suppressing growth and a tumor promoter at later stages, and 5) Malignant brain tumors generally have lost growth suppressive effects of TGFbeta but retain TGF-beta mediated effects on angiogenesis, invasion, and immunosuppression. These points will be developed during the course of this review.

3. TRANSFORMING GROWTH FACTOR BETA SIGNAL TRANSDUCTION

3.1. Normal TGF-beta Signal Transduction

Dramatic advances in our understanding of the TGF-beta mediated signal transduction pathway have occurred in the past decade. The TGF-beta pathway is regulated by numerous mechanisms at multiple levels to permit the integration of the activities of a wide spectrum of other signal transduction pathways. Thus, the cellular context critically determines TGF-beta activation and target gene regulation.

TGF-beta represents the prototype of a large set of structurally related polypeptide growth factors that are involved in nearly every cellular activity: TGF-beta superfamily members regulate growth differentiation (11-13), angiogenesis (14-16), extracellular interactions (17-22), invasion (23), and immune system function (24-32). TGF-beta family members are grouped into subsets of more closely related factors including the transforming growth factors beta, activins, growth differentiation factors, Mullerian inhibitory substance, and the bone morphogenetic proteins (BMPs) (reviewed in 33). In the central nervous system, both TGF-beta and BMP family members play complex roles in brain development and response to injury, including cell lineage determination and regulation of survival (reviewed in 34-36).

Roberts and Sporn originally described TGF-beta as a factor capable of inducing fibroblast growth in soft agar (reviewed in 37). There are three known isoforms of TGF-beta (TGF-beta 1-3) in mammals. The isoforms have 64-82% similarity at the amino acid level (38-40). TGFbeta ligands elicit similar effects in vitro, but the divergent amino acid sequences outside the highly conserved invariant cysteines may contribute to differential biological activities. For example, TGF-beta₁ and TGF-beta₃ potently inhibit the growth of some cells on which TGF-beta, has no effect (41-43). Sequence differences at the C-terminus likely mediate the specificity in isoform effects (44). The high affinity binding of TGF-beta₁ is eliminated when six amino acids in the C-terminus are replaced with the sequence of TGF-beta, indicating the C-terminus of TGFbeta isoforms contributes to distinct receptor affinities. Diverse effects may also occur with temporal and tissue specific secretions of the ligand due to control of expression by distinct promoters (45-48).

The activity of the TGF-beta ligand is tightly regulated by multiple mechanisms (reviewed in 49). TGFbeta is modified during secretion by the cleavage of the Cterminus at RRXR sequences by furin-like proteinases (50). The N-terminal region is designated the latency-associated peptide (LAP), while the C-terminus is the active TGFbeta. The LAP non-covalently associates with a 25-kDa active dimer to form a 100-kDa secreted inactive precursor (51). In most cell types, TGF-beta is translated and secreted in a large latent complex in which TGF-beta ligand is bound to the LAP molecule which is in turn associated covalently with one of four latent TGF-beta binding proteins (LTBPs). Interestingly, several human glioma cell lines secrete active TGF-beta ligand (52). Latent TGF-beta becomes bound to components of the extracellular matrix (ECM) through the LTBP to provide a source of readily accessible ligand. Disruption of LTBP expression in a murine model is linked to tumor formation associated with reduced deposition of TGF-beta (53). To elicit biological effects, the TGF-beta ligand must become activated after its initial secretion. An initial step involves proteolytic cleavage of the LTBP molecule by serine proteases, including plasmin. To become active TGF-beta, the latency-associated peptide must also be released or undergo a conformational change to expose the receptor binding site (reviewed in 54). Prominent mechanisms of

activation include acidic conditions (common in most malignant tumors), proteases, integrins, or thrombospondin.

Three classes of receptors mediate TGF-beta effects: type I, type II, and accessory receptors. The accessory receptors include betaglycan (termed the type III receptor) and endoglin. Each accessory receptor binds TGF-beta at low affinity and presents it to type I and II receptors to enhance signaling (55, 56). For example, binding of TGF-beta₂ to betaglycan appears to increase the affinity of the type II receptor for this isoform (57, 58). Another receptor type, endoglin, can bind TGF-beta ligands as well, but its exact function is unknown. Betaglycan also binds TGF-beta₁ and TGF-beta₃ (reviewed in 59), as does endoglin (55). However, endoglin has a very low affinity for TGF-beta₂.

Type I and type II receptors for TGF-beta belong to a family of transmembrane serine/threonine kinases that initiate a signal transduction cascade upon ligand binding. TGF-beta receptors are glycoproteins with short extracellular regions, a single transmembrane region, and longer cytoplasmic regions with kinase activity (see Figure 1). Both the type I and type II receptors have a kinase region that is consistent with the canonical sequence of serine/threonine kinases, but the receptor types can be structurally distinguished. Phosphorylation of the receptor regulation sequences and the kinase activities of both the type I and II receptors are critical to TGF-beta signaling (60).

The TGF-beta signal transduction cascade is initiated through the binding of the ligand to the type II receptor. Subsequently, the type I receptor is recruited and binds TGF-beta within a receptor complex with the type II receptor (61-65). Of note, the type I receptor cannot bind ligand in the absence of type II receptor. Since TGF-beta dimerizes and each TGF-beta monomer can facilitate the interaction between one type I and one type II receptor, the TGF-beta Receptor complex probably contains two type I and two type II receptors to form a heterotetrameric complex (61, 66-69). Complexes of both the type I and type II receptors are required for the type II receptor to phosphorylate the type I receptor. The type II receptor has constitutively active kinase activity and autophosphorylated on several serine and threonine residues (70-72). When type I and II receptors are in close proximity, serines of the type I receptor are phosphorylated by the type II receptor (60, 73). Phosphorylation of type I receptor is required for initiating the intracellular signaling cascade since type II receptor alone is incapable of transducing the signal but constitutively active type I receptor alone can (74).

Although several proteins have been determined to bind TGF-beta receptors, the TGF-beta signal transduction cascade from the cytoplasm to the nucleus predominantly involves a novel family of proteins called SMADs. The term SMAD is derived from the conjunction of two invertebrate homologues, SMA from C. elegans (75) and MAD (mother against decapentaplegic) in *Drosophila*(76, 77). The SMADs are classified into three groups based on their

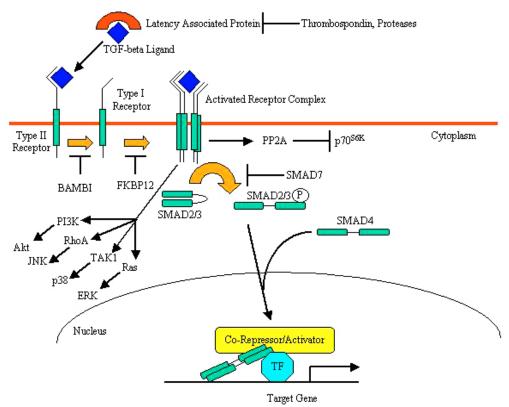


Figure 1. The Transforming Growth Factor Beta Signal Transduction Pathways. Transforming growth factor beta (TGF-beta) is secreted in an inactive latent form that can be activated by proteases. Dimerized TGF-beta ligand induces a heterodimerization of TGF-beta types I and II receptors that is associated with type I receptor phosphorylation and activation. Active TGF-beta type I receptors act on downstream effectors, including the receptor SMADs (R-SMADs) that are posphorylated on the carboxyl terminus to permit binding to the Co-SMAD, SMAD4, and nuclear localization. Nuclear SMAD complexes bind with low affinity to specific SMAD binding elements (SBEs) in the promoter sequences of regulated genes. Transcription complexes are formed with transcriptional binding partners and transcriptional activators/ inhibitors to specifically induce or repress gene expression.

structure and function: the receptor-regulated or pathway-specific SMADs (R-SMADs), the common SMADs (Co-SMADs), and the inhibitory SMADs (I-SMADs). The R-SMADs and Co-SMADs have Mad homology domains, designated MH1 and MH2 regions, joined by a proline-rich linker region. A MH2 region is also present in the carboxyl terminus of the I-SMADs that also have an amino terminus homologous among I-SMADs.

The R-SMADs function as the downstream effectors of TGF-beta receptors through a direct interaction with activated type I receptor. SMAD 2 and 3 specifically mediate the signals induced by TGF-beta and activin (78-84). Phosphorylation of R-SMADs induces release from the receptor, relief of auto-inhibitory folding, binding to SMAD 4 (the Co-SMAD), and translocation to the nucleus where transcription regulation is initiated. The I-SMADs (predominantly SMAD 7 in TGF-beta signal) appear to act predominantly in competition with the R-SMADs for receptor binding.

Nuclear localization of an active SMAD complex initiates the regulation of target genes. SMADs bind to

particular DNA sequences (CAGAC -- named SBEs, SMAD binding elements) (85). SMADs bind with low affinity to these sequences and SBEs are found throughout the genome. SMAD complex binding to particular promoter sequences is determined by transcriptional binding partners (e.g. AP-1 family members) with subsequent recruitment of co-activators and corepressors (reviewed in 86). In turn, transcription regulators such as HATs (histone acetyltransferases such as CBP/p300, which act to add acetyl groups to histones resulting in opening of genomic structure for increased transcription) or **HDACs** (histone deacetylases, which act to repress transcription through removal of acetyl groups on histones) are recruited. Thus, SMADs can act in either an activating or repressive fashion on gene expression dependent on other components of the transcription complex.

The activity of the SMAD pathway is terminated through a number of mechanisms including ubiquitinylation and proteosomic destruction of the SMADs. Specific E3 ligases including SMURF1 and SMURF2 act to increase SMAD and TGF-beta receptor degradation (87 - 91).

Table 1. The Biphasic Role of Transforming Growth Factor Beta in Cancer

Target Cell	Normal Epithelium (Tumor Suppression)	Cancer (Tumor Promotion)
Cell-of-origin (autocrine)	Growth inhibition	Epithelial-to-mesenchymal transition (EMT)
	Apoptosis	Growth stimulation
	Induced senescence	Increased motility
	Maintenance of tissue environment	Increased invasion
Stroma (paracrine)		Increased MMP expression
		Increased angiogenesis
		Immune suppression

The Biphasic Role of Transforming Growth Factor Beta in Cancer. In cancer formation, transforming growth factor beta (TGF-beta) plays a complex role with tumor suppressive effects at early stages of cancer development through growth suppression and tumor enhancement in malignant cancers with both autocrine and paracrine effects on growth, invasion, angiogenesis, and immunosuppression.

3.2. Regulation of TGF-beta Signal Transduction By Other Pathways

TGF-beta signal transduction is heavily influenced by many other cellular pathways (reviewed in 92) – including the Ras (93), Vitamin D (94, 95), wnt (96), phosphatidylinositol 3-kinase (97), interleukin-6 (IL-6) (98), interferon-gamma (IFN-gamma) (99, 100) among others. Non-TGF-beta pathways regulate TGF-beta §ignal intensity, selection of gene targets and biologic outcome. Of additional complexity, it appears that in some cell types in some cellular conditions, TGF-beta may activate SMAD-independent pathways permitting alternative physiological outcomes or self-regulation of the SMAD pathway.

Several of the pathways that interact directly with the TGF-beta signal pathway are prominent in oncogenesis of brain tumors, including the MAPK pathways. Activation of growth factor receptors increases Ras mediated pathway activity that acts in multiple ways to either increase or decrease SMAD-mediated transcription. MAPK can directly phosphorylate the R-SMADs on a middle, linker region (93). Additionally, MAPK plays a role in the DNA-binding partners of the SMADs through AP-1 family members, jun and fos, and can act to modulate TGF-beta receptor function. Other pathways, including the wnt (96), estrogen (101), interferon-gamma (102), and vitamin D (94, 95) pathways also directly influence TGF-beta function. Some of these pathways act through the induction of SMAD7 (102), one of the inhibitory SMADs.

TGF-beta receptor activation can induce activity of PP2A (103), RhoA (104), ERK, and p38 (105). These pathways have their own effects and can act on the transcription complex formed with the SMADs. Thus, TGF-beta can act by SMAD-independent mechanisms that can cooperate with, inhibit, or act separately from the traditional TGF-beta signal transduction pathways.

Finally, a number of oncogenes have been discovered that act on TGF-beta function, including Ski and SnoN (reviewed in 106). Ski and SnoN can directly interact with SMAD2 and SMAD3 to block TGF-beta-mediated transcriptional activity in two ways: Ski/SnoN displace other transcriptional partners from a transcriptional complex and Ski/SnoN recruit histone deacetylases (HDAC) to repress transcription (107). Ski and SnoN

levels exhibit a biphasic relationship with TGF-beta receptor activation – initially Ski and SnoN proteins are decreased through SMURF-mediated ubiquitinylation and proteasome degradation but transcriptional regulation increases levels later suggesting a role in signal termination (108 - 110).

3.3. TGF-beta: Tumor Suppressor or Tumor Enhancer?

The role of TGF-beta in cancer is complex and has been called "paradoxical" (111, 112). The TGF-beta ligand is a tumor suppressor gene early in cancer due to its ability to prevent cellular proliferation and induce apoptosis in some cell types (See Table 1). In malignant cancers TGF-beta acts as a tumor promoter as TGF-beta can mediate a number of effects that support tumor growth including angiogenesis, increased cell matrix component elaboration, and immunosuppression. The switch of the dominant effects caused by TGF-beta has been the subject of a tremendous amount of study. No one mechanism appears to explain the mechanism by which cancers lose their growth inhibitory response to TGF-beta. Rather, the large number of detailed mechanisms suggests that the inactivation of the tumor suppressive aspects of TGF-beta is critical in a broad range of cancers.

In general, disruption of the normal TGF-beta function can either completely block TGF-beta signaling or selectively target aspects that are growth suppressive. The complete loss of TGF-beta signal transduction is uncommon in most cancers and has not been shown to occur in brain tumors. A mechanism by which TGF-beta function can be disrupted in some cancers, such as colon cancer, involves the loss of expression of the type II receptor (113). This occurs frequently in tumors with abnormal mismatch repair mechanisms. Interestingly, tumors with loss of type II TGF-beta receptor expression often have a favorable prognosis (114).

Most types of cancer employ mechanisms that partially disrupt the normal signaling of TGF-beta, including hyperactive MAPK activity, altered SMAD expression or function, and alterations in target genes (reviewed in 115). Each of these mechanisms may play a role in brain tumors, particularly gliomas. Malignant gliomas have increased Ras/MAPK activity due to increased activity of tyrosine kinase growth factor receptors

not mutant forms of Ras. SMAD mutations have not been found in brain tumors but expression may decline with increasing tumor grade in gliomas. Finally, the genes that are transcriptionally regulated by TGF-beta canbe targeted for deletion or mutation. This will be discussed in the following sections.

3.4 TGF-beta Components in Primary Brain Tumors

Primary brain tumors include a broad range of over one hundred tumor types. These tumors are generally named based on the presumed cell of origin: gliomas (including astrocytomas and oligodendrogliomas) from glia, ependymomas from ependymal cells, meningiomas from arachnoid cap cell lining the meninges. The cell-of-origin of medulloblastomas and primitive neuroectodermal tumors (PNETs) remain unclear. Although there are many phenotypic differences between these cancer types, primary brain tumors share many common traits among themselves and with other cancer types. Prominent among the requirements for cancer formation and growth include the abilities to avoid growth inhibitory signals, escape immune responses, invade normal structures, and form new blood vessels (reviewed in 1). Each of these functions is impacted by TGF-beta signal transduction. It should, therefore, be expected that many primary brain tumors have altered TGF-beta activity.

All three TGF-beta ligands are expressed in malignant brain tumors, including gliomas, medulloblastomas, ependymomas, and meningiomas (2 - 7, 116 - 118). It is unclear which isoform(s) is most important in brain tumor pathophysiology but most studies have examined the beta1 and beta2 ligands. Interpretation of TGF-beta expression in studies using only cell lines can falsely overestimate TGF-beta expression as one study found that passage of astroglial cell lines increased TGFbeta₂ expression levels (119). TGF-beta is also expressed by areas of normal brain in response to the formation of gliomas as measured in a C6 glioma model (120). This reaction by the normal brain is not surprising as TGF-beta is an important regulator of the activity of reactive astrocytes. TGF-beta expression by reactive astrocytes appears to permit an increase in the invasion of these cells and elaboration of new extracellular matrix components while blunting the immune response and astrocyte proliferation (121, 122). Both thrombospondin, which acts to activate latent TGF-beta, and TGF-beta expression have been linked to increased tumor malignancy in gliomas (123). Other mechanisms of TGF-beta activation also are activated in glioma cell lines - the furin-like proteases process pro-TGF-beta to an active form and can be blocked with specific inhibitors (124). TGF-beta-binding protein expression is increased in a carmustine-resistant cell line (125).

Expression of TGF-beta cell surface receptors has been studied in a number of brain tumors. Gliomas, medulloblastomas, primitive neuroectodermal tumors (PNETs), meningiomas and ependymomas tumor samples and cell lines express the TGF-beta type I and II receptors as well as the ligand, which suggests the presence of an autocrine loop (2-7, 117, 126, 127). The accessory receptor

endoglin is expressed in tumor endothelium, including gliomas and medulloblastomas (128, 129). No clear link exists between glioma receptor expression level and the tumor malignancy. It does not appear that loss of receptor expression is an important mechanism of resistance to TGF-beta-mediated growth inhibition in glioma cell lines (126, 127).

Smad mutations have not been found in gliomas or medulloblastomas (130, 131) and no systematic evaluation of SMAD expression has found a strong relationship between SMAD expression and response to TGF-beta (126, 127)? One recent study of different glioma grades by RT-PCR suggests that the expression of SMAD2, 3, and 4 may decrease with increasing glioma tumor grade (5). In an experimental glioma model, we found that the stable expression of a constitutively active form of TGF-beta₁ ligand induced decreased expression of SMAD2 and SMAD3 with retained expression of SMAD4 and TGF-beta receptors (J. Rich, unpublished observations).

Ras activity is increased in malignant gliomas in the absence of Ras mutations (132). The relationship of Ras activation in gliomas and resistance to TGF-beta growth inhibition has not been evaluated. Other oncogenes — Ski, SnoN, BF1 — that impact on TGF-beta function have not been evaluated in brain tumors.

4. TGF-BETA AND CELLULAR PROLIFERATION

TGF-beta inhibits the growth of most types of epithelial cells while increasing the proliferation of mesenchymal cells. Thus, the frequent epithelial-tomesenchymal transition (EMT) associated with cancer development may play an important role in modulating the response to TGF-beta (112). In fact, TGF-beta can induce EMT itself. TGF-beta generally induces a G₀/G₁ cell cycle arrest in most epithelial cell types through the ability to increase the expression or activity of particular cyclindependent kinase inhibitors that act to bind and inactivate the cyclin-cyclin dependent kinase (CDK) complexes that regulate cell cycle progression. In some cell types, TGFbeta can induce either cell cycle arrest followed by apoptosis or apoptosis as a primary response. Immune system components are the most prominent cell type in which apoptosis plays a dominant role.

Most primary cell types in the central nervous system are growth inhibited by TGF-beta and may be induced to undergo apoptosis. Astrocytes, the presumed precursor cell of the majority of gliomas, are significantly growth inhibited by TGF-beta treatment (126, 133). This growth inhibition is associated with the induction of the cyclin-dependent kinase inhibitor p15 $^{\rm INK4B}$ and a G0/G1 cell cycle arrest (126). Further, TGF-beta inhibits astrocyte cell proliferation largely through a SMAD3 pathway as astrocytes derived from mice with disrupted SMAD3 expression failed to exhibit full growth inhibition when treated with TGF-beta (126). Oligodendroglial precursors can undergo apoptosis upon TGF-beta treatment associated with induction of the cyclin-dependent kinase inhibitors p21 $^{\rm Waf1}$ and p27 $^{\rm Kip1}$ (134). FGF can protect these cells

from the TGF-beta induced apoptotic (134). The role of TGF-beta in neuronal survival or apoptosis is dependent on cellular context. Cerebellar granule neurons undergo apoptosis when exposed to TGF-beta except when exposed to high potassium concentrations (135). Differentiated neurons may actually be protected from apoptotic stimuli by TGF-beta (136). Additionally, TGF-beta can potentiate the neural cell survival mediated by other growth factors (reviewed in 137).

Most glioma cell lines have lost TGF-betamediated growth inhibition and some are growth stimulated in response to TGF-beta (126, 127, 138, 139). Two studies have shown that some glioma cell lines may undergo apoptosis if treated with or expressing TGF-beta although this appears to be an exception (140, 141). The loss of growth inhibitory response to TGF-beta in gliomas is associated with increased grade of malignancy (142, 143). Most glioma cell lines do not growth inhibit upon TGF-beta treatment and this is associated with the mutation or promoter methylation of p15INK4B (126), which is frequently codeleted with the p16INK4A tumor suppressor gene. Many gliomas appear to have a critical target gene (p15INK4B) disrupted as a mechanism of TGF-beta resistance (126). A subset of glioma cell lines is growth stimulated upon TGF-beta treatment. These lines may be hyperdiploid and the resistance may involve PDGF elaboration (144) although other studies have not found this link (126, 127). Other brain tumor cell lines (medulloblastoma, PNET, ependymomas) exhibit resistance to TGF-beta growth inhibition and can be stimulated in their growth as well (7). A study of meningiomas revealed expression of TGF-beta ligand and receptors yet continued sensitivity to TGF-beta-mediated growth inhibition (117). Many issues regarding TGF-beta effects of cell survival remain unanswered. For example, TGF-beta downregulates expression of the tumor suppressor gene Pten/MMAC1/TEP1 (145). It is possible that TGF-beta plays a role in suppressing PTEN function in tumors that retain a wild-type Pten genotype.

5. TGF-BETA AND TUMOR MICROENVIRONMENT

There is an increasing recognition of the critical role that the microenvironment plays in the development and growth of nascent tumors (reviewed in 146). Surrounding stromal elements including normal stromal cells, extracellular matrix, and blood vessels largely dictate the survival and growth characteristics of tumors. TGFbeta plays a central role in the regulation of the relationship between a cell and its environment. TGF-beta induces the expression of many components of the extracellular matrix (ECM) as well as cellular adhesion factors. TGF-beta acts in ECM remodeling through regulation of matrix metalloproteinases (MMPs). Additionally, TGF-beta acts in a paracrine fashion to regulate stromal cells, blood vessels, and local immune response. The net result of these interactions in malignant cancers is increased tumor cell invasion and angiogenesis.

5.1. Tumor Cell Invasion

Tumor invasion and metastasis play critical roles in most types of brain tumors. Gliomas rarely metastasize outside of the central nervous system (CNS) but these

tumors are highly invasive. Glioma invasion into normal brain prevents curative surgical resection and ultimately leads to failure of "local" therapies directed at the control of the primary site of tumor occurrence. Invasion occurs at an early stage in glioma development. Medulloblastomas, PNETs, and ependymomas are frequently invasive into normal brain and can metastasize both within and outside of the CNS. Invasion into normal brain is a hallmark of the conversion of a meningioma to a malignant phenotype. Although many of the genetic alterations that dysregulate the cell processes of growth and death involved in tumor initiation have been elucidated in recent years, less progress has been made in the complex but critical processes of tumor invasion, metastasis, and angiogenesis. Study of TGF-beta, however, has led to increased understanding of many of these processes. Of note, the regulation of the tumor microenvironment by TGF-beta can permit increased tumor invasion either directly or indirectly.

Experiments with glioma cell lines have generally shown that TGF-beta treatment mediates an invasive glioma phenotype (140, 147). TGF-beta₁ induces glioma invasion more readily than TGF-beta2, likely due to differential receptor binding. The effects of TGF-beta involve multiple related mechanisms. upregulates the expression of many components of the ECM that act in tumor invasion, including plasminogen activator inhibitor-1 (PAI-1) (126) and secreted protein, acidic and rich in cysteine (SPARC) (1148) among others. PAI-1 expression has been linked to increased tumor grade in gliomas (149) as well as tumor cell invasion and angiogenesis. SPARC has been linked to a role in glioma cell invasion (150 and J. Rich, unpublished observations) and metastases in medulloblastoma (151). TGF-beta can also act to remodel the ECM through the induction of the matrix metalloproteinases (MMPs), MMP-2 (gelatinase A) and MMP-9 (gelatinase B), in gliomas (152). MMPs can breakdown component of the ECM and cell adhesion molecules, e.g. E-cadherin, permitting increased tumor invasion and motility. The TGF-beta also acts to increase expression of regulators of cell adhesion in gliomas including neural cell adhesion molecule L1 (153) and integrin alpha_vbeta₃ (the vitronectin cellular receptor) (154). Each of these molecules can mediate an invasive phenotype in gliomas. Integrin alpha_vbeta₃ is expressed at the leading edge of invading tumors (155), and inhibition of alpha_vbeta₃ can prevent glioma invasion (154, 156). Integrin alpha₂ may also mediate aspects of TGF-beta regulation of glioma invasion as blocking antibodies to alpha₂ integrin reversed TGF-beta-mediated invasion (157). TGF-beta can also regulate intracellular pathways that regulate cellular response to interactions with the cellular environment. For example, TGF-beta treatment of U-251MG cells plated on fibronectin increased the expression of paxillin (158), which acts as an adaptor molecule at focal adhesions.

While many studies examine the function of TGF-beta on isolated tumor cell lines, a dominant role of TGF-beta in mediating a tumorigenic phenotype may come from the ability of TGF-beta to alter the behavior of surrounding cells via paracrine mechanisms. For example,

stromal cells secrete much of the tumor-associated MMPs. In fact, the stromal elements may be the primary target of tumor-generated TGF-beta.

5.2. Angiogenesis

Malignant gliomas represent one of the most vascularized cancers with vascular proliferation a hallmark of malignancy. The process of new blood vessel formation is called angiogenesis. The importance of angiogenesis in glioma outcome has been recognized and has been a recent target of therapeutic intervention. In fact, there is mounting evidence that many traditional cancer therapies – including radiation and chemotherapy – target blood vessels. Thus, it is important to increase understanding of the mechanisms regulating vascular proliferation.

TGF-beta has long been recognized to play a role in angiogenesis. The role of TGF-beta in angiogenesis was first recognized after a study in which injection of TGFbeta into newborn mice caused collagen deposition and new blood vessel formation at the site of injection (14). However, the effect of TGF-beta on blood vessel growth is complex with very different effects on measures of angiogenesis in different assays. Endothelial cells are directly growth inhibited by TGF-beta (159). In twodimensional cultures that mimic microvascular cells at the distal tip of blood vessels, TGF-beta₁ inhibits proliferation, increases fibronectin and collagen expression, and decreases tight junction formation. On the other hand, three-dimensional cultures that mimic more mature vessels show that TGF-beta₁ has little effect on proliferation but increases tight junction formation and deposition of matrix components (reviewed in 160). Thus, TGF-beta may permit the selective maturation of blood vessels. It is important to remember, however, that most angiogenic assays are not performed from tumor-derived endothelium that may have different biological properties.

The role of TGF-beta in regulating pericyte behavior is less well understood. The co-culture of pericytes and endothelial cells induces the expression of activated TGF-beta (161). Treatment of mesenchymal cells with TGF-beta induces a differentiation towards pericytes (162).

TGF-beta regulates angiogenesis also through the regulation of multiple angiogenic factors. Prominently, TGF-beta can induce VEGF in human glioma cell lines (126). Additionally, expression of MMPs, integrins, PAI-1, and ECM proteins (collagen, fibronectin, laminin, von Willebrand Factor, and vitronectin) as a result of exposure to TGF-beta can induce angiogenesis.

6. TGF-BETA IMMUNE SUPPRESSION

Despite the fact that the brain is an immune privileged organ, CNS neoplasms initiate both local and systemic immunosuppression in the course of their development (reviewed in 163 - 165). The systemic immunosuppressive effects of gliomas in particular have been recognized for decades (166 - 168). Patients with malignant gliomas have decreased cell-mediated immune

responses with T-cell lymphopenia, signaling defects in Tcell signaling, and impaired monocytic function associated with low class I and II MHC expression (reviewed in 163 -165). Patients diagnosed with medulloblastomas have also been found to have systemic lymphopenia associated with tumor recurrence (169). In addition to the systemic immune dysregulation associated with these tumors, local immune reactions are altered despite the presence of infiltrating immune cells. The mechanisms involved in this immunosuppression are likely multi-factorial – including interleukin-10 (IL-10), prostaglandin E₂ (PGE₂), sialic acidcontaining glycosphingolipids termed GANGs, and HLA-G (reviewed in 163 - 165) -- but also appear to involve TGFbeta. In fact, the recognition of the role of TGF-beta₂ in glioma-mediated immunosuppression antedated identification as a specific protein (170). TGF-beta plays a pleiotropic role in regulating the immune system including B and T cell, macrophage, and dendritic cell involvement (reviewed in 171). Genetic models have provided evidence of TGF-beta function in immune development. example, disruption of TGF-beta₁ expression is associated with a severe, multi-organ inflammatory process in mice that survive past birth (29, 32). Disruption of TGF-beta effector SMAD3 function leads to inappropriate local immunity (172). As a general concept, TGF-beta induces a block on immune cellular proliferation and differentiation with a particular effect on T cells.

The immune reaction to a tumor is a complex, multi-step process. The initial arm of immune attack on tumors involves the presentation of tumor-associated antigens by antigen presenting cells (APCs) that include dendritic cells, microglia, and macrophage. Naïve, immature APCs are highly efficient in endocytosis but are poor presenters of antigen due to low expression of surface MHC I and II molecules and of co-stimulatory molecules. As APCs mature, they acquire improved capabilities in antigen presentation but lose efficient endocytosis capabilities. APCs can then present antigen to and activate CD4+ helper T lymphocytes. Activated helper T cells elaborate critical cytokines, including interleukin-2 (IL-2), interferon-gamma (IFN-gamma), and tumor necrosis factoralpha (TNF-alpha) that can activate CD+ cytotoxic T lymphocytes that act as an effector arm to mediate tumor killing.

TGF-beta can act at multiple stages in the cellular immune response process to inhibit the appropriate immune response. TGF-beta inhibits the activation of macrophages and their elaboration of pro-inflammatory cytokines (173). TGF-beta can also inhibit the maturation of dendritic cells into their activated forms (174). Thus, T cells exposed to TGF-beta are not appropriately activated (174) and may undergo apoptosis. TGF-beta also blocks migration of immature dendritic cells in the epidermis known as Langerhans cells from the skin to the lymph node preventing initiation of systemic antigen presentation (175). In addition, the normal upregulation of MHC class II molecules in antigen presentation is blocked with TGF-beta treatment (176).

T cells represent a prominent target of TGF-betamediated immune regulation. TGF-beta derived from gliomas can decrease the function of glioma-derived lymphocytes (177). TGF-beta inhibits the proliferation of T cells in vitro (28), in part through the inhibition of IL-2 expression (178). TGF-beta also prevents the activation of naïve T cells in the presence of low levels of antigen. Importantly, TGF-beta can block the differentiation of naïve T cells exposed to optimal levels of antigen into appropriate helper CD4⁺ and cytotoxic CD8⁺ cells (179). Thus, these cells are not permitted to adopt a functional state to initiate the full immune response. In particular, a subset of helper T cells critical to initiation of the humoral response designated T_H2 cells are prevented from developing in the presence of TGF-beta. T_H2 cell development is controlled by the expression of Gata-3, the expression of which is inhibited by TGF-beta (179, 180). $T_{\rm H}1$ cells that are involved in the cellular immune arm are also inhibited in development by TGF-beta but somewhat less significantly (180).

Thus, multiple arms of the immune response to tumors can be blocked by TGF-beta. Of interest, not only do cancers such as gliomas secrete TGF-beta, but also apoptotic cells and regulatory T cells can secrete TGF-beta. Immune dysfunction has been detected in patients with malignant gliomas consistent with TGF-beta-mediated effects (166- 168). Overall patients can exhibit a systemic immune dysfunction associated with a T cell lymphopenia (166, 181). Further, glioma cells express low levels of MHC class II molecules in response to TGF-beta (182). The role of TGF-beta function in glioma-associated immunosuppression has been shown by studies using antisense oligonucleotides. Gliomas with disrupted TGFbeta expression induce an increased response to lymphokine-activated killer (LAK) cells and tumor control (183, 184).

7. THERAPEUTIC IMPLICATIONS OF TGF-BETA

TGF-beta plays an important tumorigenic role in many of the behaviors of primary brain tumors. Therefore, it is to be expected that neutralizing TGF-beta function will likely offer several advantages in tumor control: decreasing invasion and angiogenesis and inducing an increased immune response. Several interventions have been developed to target TGF-beta activity. Current studies have involved three general approaches: decreasing TGFbeta expression, inhibiting TGF-beta release, or binding active TGF-beta. Expression of antisense oligonucleotides can decrease RNA translation and protein production of the targeted sequence. Constitutive antisense treatment to TGF-beta in a 9L glioma rat model permitted increased tumordirected immune response and tumor control (183). An antisense oligonucleotide directed to TGF-beta1 has shown preclinical efficacy to increase immunological response to the treated glioma but increased glioma invasion in vitro (147, 184). A clinical phase I/II dose escalation trial of antisense oligonucleotide directed to TGF-beta2 (AP12009) determined that the therapy is tolerated and may offer some efficacy with intratumoral injection (185).

Additional therapies involve indirect methods to target TGF-beta secretion or removal. TGF-beta is a

common end pathway in many fibrotic diseases. Thus, several agents that have been used in fibrotic diseases appear to function through effects on TGF-beta production. TGF-beta secretion or responsiveness may be modulated by the angiotensin system. Angiotensin-converting-enzyme inhibitors (186) and angiotensin II receptor blockers (187) may offer the ability to block TGF-beta activity but treatment of a renal cell carcinoma cell line with captopril did not alter TGF-beta production but reversed resistance to TGF-beta growth inhibition (188). Captopril treatment decreased glioma cell line invasion in vitro associated with a decrease in MMP-2 and MMP-9 expression but the role of TGF-beta in these effects is unclear (189). An antiallergic agent, N-[3,4-dimethoxycinnamoyl]-anthranilic acid (tranilast), acts to block TGF-beta1 production and blocks growth factor effects on stromal tissues. Treatment of glioma cell lines with tranilast decreases TGF-beta production and in vitro measures on glioma invasion (190).

Multiple proteins have been utilized to bind and prevent formation of active TGF-beta complexes. These include soluble type II and III receptors and decorin. Soluble receptors are the extracellular portions of the native receptors. They function by competing with the full-length receptor (191, 192). Decorin and biglycan are both small leucine-rich proteoglycans found in the cartilage (193). Both decorin and biglycan bind TGF-beta but only decorin decreased TGF-beta-mediated fibrosis in a lung fibrosis model (194). Decorin expression in a C6 glioma cell line abrogated tumor growth due at least in part to an immune response as corticosteroid treatment reversed the decorinmediated effects (195). Decorin may mediate its effects through a non-TGF-beta dependent pathway as neutralizing anti-TGF-beta antibodies failed to recapitulate the results of tumor control achieved with decorin (196).

Small molecule kinase inhibitors are an exciting novel therapeutic modality in oncology. Inhibitors of the TGF-beta receptors are in early preclinical development (197, 198) and may offer the best option in targeting TGF-beta function in chronic therapy, as delivery may be significantly less of a problem than some of the other mentioned therapies. Some caution to all anti-TGF-beta therapies is warranted as they may cause significant systemic side effects due to the critical role that TGF-beta plays in many normal physiological processes.

8. CONCLUSIONS

The complexity of TGF-beta signal transduction and biological activities is daunting but TGF-beta is a critical target in multiple CNS malignancies. The components of the TGF-beta pathway and other signal transduction pathways that interact with TGF-beta signal are rapidly being elucidated and are frequently expressed in human brain tumors. The cell specific nature of the TGF-beta pathway and function demands a thorough examination of TGF-beta pathway components in primary nervous system tissues and the corresponding malignancies. Activation of the TGF-beta pathway in malignant brain tumors is associated with a variety of effects conducive to tumor growth, including tumor cell

invasion, neoangiogenesis, and immune suppression. The future may hold significant advances in brain tumor control through targeted therapies of TGF-beta function likely in combination with other therapeutic modalities.

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