TGF-beta antiproliferative effects in tumor suppression

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1. ABSTRACT

The TGF-beta signaling pathway controls multiple functions of cancer cells and the surrounding stromal tissue. Some TGF-beta actions suppress cancer formation, while others contribute to tumor progression. Evidence supporting a tumor suppressive role for the TGFbeta/Smad signaling axis is presented here. These data are compiled from cell culture studies, animal models, analyses of human tumors, and investigations of polymorphisms of TGF-beta pathway components and their associated cancer risk. Therapeutic strategies for cancer treatment involving either restoring or potentiating TGF-beta tumor suppressive activities, or blocking TGF-beta tumor promoting functions are considered.

2. INTRODUCTION

Transforming growth factor-beta (TGF-beta) is the prototypic member of an evolutionarily conserved superfamily of cytokines that regulate nearly every aspect of organismal development and function, including cell differentiation, proliferation, apoptosis, bone morphogenesis, angiogenesis, immune system regulation, and muscularity (reviewed elsewhere (1-6)). TGF-beta signals through two conserved families of transmembrane receptor serine/threonine protein kinases. Receptormediated phosphorylation and activation of the Smad transcriptional regulators plays a central role in transducing the biological responses to TGF-beta superfamily cytokines.

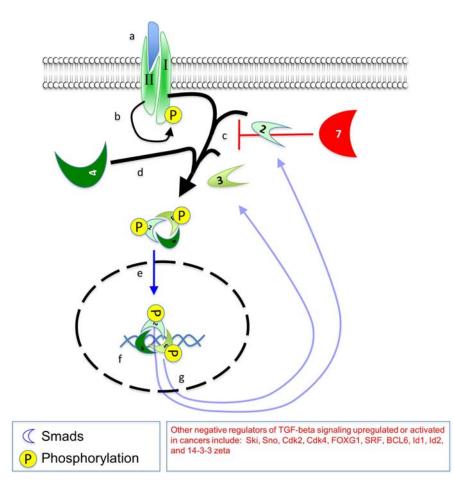


Figure 1. The TGF-beta/Smad signaling pathway. Binding of the TGF-beta ligand to the type II receptor (a) recruits the type I receptor to the complex. The type II receptor then phosphorylates and activates (b) the type I receptor. The type I receptor phosphorylates the receptor regulated Smads 2 and 3 (c). The R-Smads then bind to Smad4 (d), translocate to the nucleus (e), and bind to DNA and transcriptional coactivators and corepressors to control transcription (f). Smads become inactivated by dephosphorylation (g) and are exported out of the nucleus for additional rounds of receptor mediated phosphorylation. Elements downregulated or mutated in cancer are shown in green and elements overexpressed in cancer are shown in red.

TGF-beta inhibits the proliferation of nontransformed epithelial cells, but does not inhibit the division of certain carcinoma cell lines. This suggests that a normal function of TGF-beta is to restrain cell division. Since cancer is fundamentally a disease of uncontrolled cellular proliferation, and epithelial cells frequently secrete and respond to autocrine TGF-beta, the ability of TGF-beta to control cell replication was hypothesized to constitute a tumor suppressive mechanism (7-10). However, there is now a great deal of evidence indicating that depending on the molecular context within a given cell population and the microenvironment, TGF-beta can exhibit either tumor suppressive or tumor promoting activities. Several recent reviews focus on the tumor promoting actions of TGF-beta (11) as well as the numerous non-Smad signaling systems (12) whose effects are activated by TGF-beta. This review will summarize the data demonstrating TGF-beta anticancer activity obtained from in vitro experiments, studies of genetically modified animal models, analyses of mutations of TGF-beta pathway components discovered in human cancers, and the identification of polymorphisms of TGF-beta pathway components present in human populations and their association with tumorigenesis. Rational approaches for therapeutic targeting of the TGFbeta pathway to either restore its tumor suppressive functions in cancer, or to block TGF-beta tumor promoting activities are discussed.

3. TGF-BETA MEDIATED CELL CYCLE ARREST OF NONTRANSFORMED EPITHELIAL CELLS

In normal, non-transformed cells, TGF-beta acts as a potent suppressor of cell proliferation (7-8). The signaling mechanisms involved in this process have been extensively studied, and although TGF-beta signaling interacts with many intracellular pathways, the primary pathway involves the Smad proteins (Figure 1). In classic, Smad-dependent TGF-beta signaling, the cascade begins with a precursor of TGF-beta being processed extracellularly by Furin-type enzymes (13). Upon activation by cleavage, the dimeric TGF-beta cytokine binds to the type II TGF-beta receptor (TGF-betaRII) on

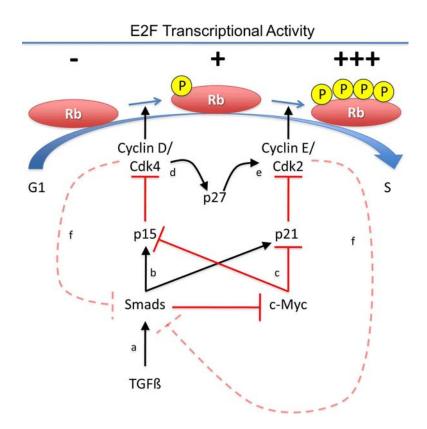


Figure 2. TGF-beta control of cell division. TGF-beta activates the Smad transcription factors (a) as detailed in Figure 1. The Smads activate the transcription of the Cdk inhibitors p15 and p21 (b). c-Myc antagonizes TGF-beta induction of p15 and p21, but TGF-beta represses the c-Myc promoter through a Smad-dependent mechanism (c). p15 inhibits the kinase activity of Cdk4 and displaces p27 from Cdk4 (d). The liberated p27, along with p21 that is transcriptionally upregulated by TGF-beta, inhibits Cdk2 kinase activity (e). Inhibition of Cdk4- and Cdk2-dependent phosphorylation of Rb and the related pocket proteins p107 and p130 maintains active repression of E2F-dependent genes and prevents the G1 to S-phase transition.

the cell surface. Once this interaction has occurred, the type I TGF-beta receptor (TGF-betaRI) is recruited to the complex. The close proximity of the type I and type II TGF-beta receptors results in the phosphorylation of the type I receptor by the type II receptor, thereby activating it. Activated TGF-betaRI recruits receptor-activated members of the Smad family (R-Smads) such as Smads 2 and 3, and subsequently phosphorylates them. In contrast, the bone morphogenetic proteins (BMPs) activate a distinct receptor complex containing different type I and type II receptors, and in this case the BMP type I receptor phosphorylates R-Smads 1 and 5. Phosphorylated R-Smads are then able to bind to the common mediator Smad, or co-Smad, Smad4. Once bound to the co-Smad, the R-Smads translocate to the nucleus where they, along with other nuclear co-factors, regulate gene transcription.

The core TGF-beta/Smad signaling system, as just described, is subject to regulation at multiple points. TGF-beta receptors and the Smad proteins are both subject to ubiquitin-mediated degradation in a ligand dependent manner (reviewed in (14)). Additionally, prolonged Smaddependent transcriptional control requires continuous Smad nucleocytoplasmic shuttling to maintain their receptordependent phosphorylation and overcome the effects of phosphatase-dependent inactivation of Smad signaling (reviewed in (15)). These mechanisms can be altered in cancer cells as compared with normal cells and contribute to the loss of TGF-beta tumor suppressor function in cancers.

A primary mechanism by which TGF-beta uses Smad signaling to induce a cell cycle arrest is through the upregulation of Cyclin dependent kinase (Cdk) inhibitory proteins (Figure 2). Cdks are a family of proteins whose activity controls passage through the cell cycle (reviewed in (16-17)). Cdks 1, 2, 4 and 6, along with their respective Cyclin binding partners, phosphorylate a wide variety of substrates involved in cell cycle progression. There are two families of Cdk inhibitory proteins (CKIs), the INK4 family, which includes p16^{ink4a}, p15^{ink4b}, p18^{ink4c}, and p19^{ink4d} (hereafter referred to as p16, p15, p18, and p19), and the Cip/Kip family, which includes p21^{Cip1/WAF1}, p27^{Kip1}, and p57^{Kip2} (hereafter referred to as p21, p27, and p57) (18-19). The INK4 proteins inhibit Cdks 4 and 6, while the Cip/Kip family primarily inhibits Cdks 1 and 2, but still bind to Cdks 4 and 6. There are a number of means by which TGF-beta signaling can cause an upregulation of CKIs, in both a Smad-dependent and a Smad-independent manner.

Active nuclear Smad complexes can associate

with the transcription co-factor Sp1 and bind to the p15 promoter, causing an upregulation in p15 mRNA and protein levels. Increased p15 levels have at least two main consequences. Firstly, p15 binds to, and inhibits Cdk4 and Cdk6. Secondly, this binding to Cdks 4 and 6 results in the release of p21 and p27 from these complexes, allowing them to inhibit Cdks 1 and 2 (20). The Smad/Sp1 complex can also bind to the p21 promoter and upregulate p21 protein levels directly (21-22).

The oncoprotein c-Myc is a transcription factor that is able to both activate and repress certain genes. By interacting with Miz-1, c-Myc represses the transcription of p15, p21 and p27, among other genes (23-25). As this is the case, in order for TGF-beta to achieve its antiproliferative effects, it must overcome this Myc induced repression. A complex containing Smad 3, E2F4/5, DP1, and p107 becomes activated upon stimulation by TGF-beta. This complex can bind to Smad4 in the nucleus and repress Myc expression by binding to its promoter (26). With Myc levels decreased, the Smad proteins are free to induce p15 and p21 expression.

Although Smad4 is the usual binding partner of the R-Smads, its presence is not absolutely necessary for upregulating p21. In Smad4 null cells, TGF-beta increases p21 levels, suggesting an alternative co-regulator of Smad activity (27). In another study, IKK-alpha, a kinase that regulates NF-kappaB, interacted with Smads 2 and 3, acting independently of Smad4 to control gene expression (28). The IKK-alpha/Smad complexes induced the expression of Mad1, Mad2, and Ovol1, all Myc antagonists.

Interestingly, like Smad4, Smads 2 and 3 are also not always necessary for upregulating p21 levels. Experiments performed in HaCaT human keratinocytes showed that the Map kinase pathway is required to increase p21 levels in response to TGF-beta (29). The MEK pathway was activated directly by the TGF-beta receptors. This led to an increase in the activity of Elk1, a transcription factor whose target genes include p21.

p53 also plays an important role in upregulating p21 in response to TGF-beta signaling. Smads 2 and 3 bind to p53, inducing p21 transcription in an Sp1 independent manner. Full transcription of p21 appears to require p53 activity, as p53 null cells do not respond as well to TGF-beta growth arrest signals (30). Recently, this pathway has been shown to become defective when p53 contains an *R175H* mutation (31). When this occurs, mutant p53 forms a complex with p63 and Smads 2 and 3. This complex not only fails to upregulate p15 or p21, but it also leads to increased invasion and metastasis.

TGF-beta can also induce cell cycle arrest independently of Smad activity. In cells treated with TGFbeta, protein kinase C-alpha (PKC-alpha) becomes activated. PKC-alpha then phosphorylates and activates S100C/A11, a Ca^{2+} binding protein (32). Upon activation, S100C/A11 translocates to the nucleus, activates Sp1, and induces p15 and p21 expression. Although p21 and p15 expression is the primary means by which TGF-beta induces cell cycle arrest, it is not the only mechanism. TGF-beta stimulation in some cell types induces plasminogen activator inhibitor-1 (PAI-1) expression (33). Rather than regulating p21 or p15 expression, increased PAI-1 activity suppresses signaling through the protein kinase B/AKT pathway.

4. MECHANISMS BY WHICH CARCINOMAS BECOME RESISTANT TO TGF-BETA CYTOSTATIC ACTIONS

During neoplastic progression, tumor cells frequently acquire resistance to the cytostatic effects of TGF-beta, thereby enhancing the development and progression of malignancies. The mechanisms by which tumor cells become resistant to TGF-beta are varied and unique to specific cancer types. As discussed below, these mechanisms range from defects in the TGF-beta receptor to influences of the tumor microenvironment on TGF-beta sensitivity.

4.1. Mutation or loss of TGF-beta receptors

Cells frequently lose sensitivity to TGF-beta mediated growth suppression early in carcinogenesis, with the loss of TGF-beta responsiveness occurring at the level of TGF-betaRII in certain types of cancers. The mechanism of silencing TGF-betaRII covers the spectrum from genetic to epigenetic changes. The most common mutational loss of TGF-betaRII occurs in hereditary nonpolyposis carcinoma (34-36). These tumors display microsatellite instability and a span of adenine nucleotides in the coding region of the TGF-betaRII gene that is subject to mutation, resulting in a truncated TGF-betaRII that does not activate downstream effectors (37). Interestingly, TGFbetaRII is mutated in >90% of colon cancers that display microsatellite instability and in 15% of microsatellite stable cancers (36, 38). In colon cancers that do not exhibit microsatellite instability, missense and inactivating mutations in the kinase domain of TGF-betaRII have been identified (34). Gastric cancers and gliomas with microsatellite instability also frequently display TGFbetaRII mutations (39-40). Furthermore, TGF-betaRII was mutated in 4% of pancreatic cancers and is often downregulated in breast and lung cancers, and was undetectable at the protein level in 24% of prostate cancers (41). In addition, frameshift mutations in the polyadenine tract of the TGF-betaRII gene occur in some endometrial cancers (42).

Cancer cells also use epigenetic mechanisms to inactivate TGF-betaRII. Aberrant patterns of histone methylation and acetylation/deacetylation contribute to silencing of the gene encoding TGF-betaRII in breast, ovarian, and pancreatic cancer cell lines (43-44). CpG methylation in the promoter of the TGF-betaRII gene is present in human B-cell lymphoma cell lines that lack a functional TGF-betaRII on the cell surface (45). The TGFbetaRII promoter is also silenced in several different lung cancer cell lines. Three distinct patterns of histone modification indicative of progressive degrees of TGFbetaRII silencing were identified in these cell lines (46). Furthermore, since the HDAC inhibitor Tricostatin A (TSA) induces TGF-betaRII expression in certain cell lines, it is thought that epigenetic silencing of TGF-betaRII occurs due to a compact nucleosome structure of the TGF-betaRII gene that is maintained by histone deacetylase and methyltransferase association (47).

In some cases, epigenetic silencing of the TGFbetaRII gene involves changes in promoter associated proteins. The activation of the TATA-less basal TGF-betaRII gene promoter is dependent on Sp1 binding to several sites within this promoter (47). Sp3 is a transcriptional repressor that also binds to this element, and there is evidence in certain cell lines that the ratio of Sp1/Sp3 affects whether the TGF-betaRII promoter is active or inactive (48-49).

Mutations in TGF-betaRI are less common than in TGF-betaRII, however TGF-betaRI mutations have been identified in ovarian, breast, head and neck cancers, and lymphomas (41). For instance, in human breast cancers a C to A transversion mutation resulting in a serine to tyrosine substitution at codon 387 (S387Y) of the TGF-betaRI gene was identified. This TGF-betaRI mutant is not as responsive to TGF-beta as compared with wild-type TGF-betaRI (50). Mutations of the TGF-betaRI signal sequence have been identified in B cell chronic lymphocytic leukemia. Although these mutant receptors were expressed at the cell surface and interacted normally with TGF-betaRII, their expression significantly reduced TGF-beta mediated gene expression (51). Reduced expression of TGF-betaRI has also been observed in the absence of mutation of the TGF-betaRI gene. For example, human papilloma virus (HPV)-19 oncogenes E6 and E7 have been found to repress TGF-betaRI gene expression in HPV-16 immortalized keratinocytes (52). Furthermore, hypermethylation of CpG islands in the 5' region of the TGFbetaRI gene decreases its expression in human gastric cancer (53).

Loss of growth inhibitory signaling by TGF-beta is common in the context of Ras-transformation, which can alter the expression of TGF-betaRI and TGF-betaRII. H-Ras^{G12V} induces a time-dependent switch in the ratio of TGF-betaRII to TGF-betaRI expression in rat intestinal epithelial cells. Furthermore, the levels of TGF-betaRII mRNA are approximately 5-fold lower in the Rasexpressing cells as compared with control cells. While H-Ras^{G12V} expression does not affect the binding of TGF-beta TGF-betaRII or TGF-betaRI, ligand-induced to internalization of TGF-betaRI is suppressed, suggesting a mechanism for the loss of TGF-beta anti-proliferative effects in the Ras-transformed cells (54). RhoB also represses the expression of TGF-betaRII, and RhoB expression causes resistance of human pancreatic carcinoma cells to TGF-beta growth inhibition. A RhoBresponsive region was identified in the TGF-betaRII promoter that contains an AP-1 site. AP-1 binding to this site is strongly inhibited by RhoB, thus decreasing TGFbetaRII gene expression (55).

4.2. Aberrant Smad activity

Mutations and deletions of the genes encoding Smads have been identified. In pancreatic and colon cancers, regions of the human locus 18q21 encoding Smads 2 and 4 are frequently mutated or deleted (56-58). While mutation of Smad3 has not been identified in specific cancers, the levels of Smad3 are altered in some cancers, including human gastric cancers, and gastric cancer cells that lack Smad3 are no longer growth inhibited by TGFbeta (59-60). Loss of one allele of Smad3 impairs the growth inhibitory effect of TGF-beta on normal T cells and works in tandem with inactivation of p27 to promote T-cell leukemogenesis in mice (61). A characteristic of pediatric T-cell acute lymphoblastic leukemia is the loss of Smad3 (41).

Smad3 is inactivated by other mechanisms as Several corepressors inactivate Smad3. well. Serum response factor (SRF) acts as a nuclear repressor and with Smad3, thus repressing associates Smad transcriptional activity and causing resistance to the TGFbeta mediated cytostatic response (62). Two other transcriptional corepressors of Smad3 include Ski and Sno (a novel Ski-related gene). Both Ski and Sno repress the antiproliferative effects of TGF-beta, and overexpression of Ski and/or Sno correlates with more advanced stages of melanoma, esophageal, and colorectal cancers (63-68). BCL6 is a transcriptional corepressor that interacts with Smad3 and Smad4, disrupts the Smad-p300 interaction, and represses Smad4 activity. B lymphoma cells that overexpress BCL6 are refractory to TGF-beta growth inhibition, whereas knockdown of BCL6 expression restores TGF-beta mediated cell cycle arrest (69).

Forkhead box O (FoxO) transcription factors, which are under negative control by the PI3K pathway, are key partners of Smad3 and Smad4 for the transcriptional activation of the p21 gene (70). FoxG1 inhibits FoxO-Smad complexes. The combined action of FoxG1 and PI3K mediate resistance of human glioblastoma cells to TGF-beta mediated growth arrest (70). Furthermore, FoxG1 contributes to resistance to TGF-beta-induced growth arrest through inhibition of p21 expression in ovarian cancer (71). Another transcription factor that regulates sensitivity to TGF-beta is inhibitor of differentiation or DNA binding-1 (Id1), which is a helixloop-helix transcription factor that lacks a DNA binding domain and acts as a dominant-negative regulator of basic helix-loop-helix transcription factors (72). Id1 modulates the sensitivity of prostate epithelial cells to TGF-betainduced growth arrest and loss of Id1 sensitizes cells to TGF-beta mediated growth inhibition (73).

The transcription factor c-Myc activates genes required to promote G1-S phase transition and inhibits the expression of p15, a Cdk4 and 6 inhibitor (74). TGF-beta downregulates c-Myc through a Smad-dependent pathway and overexpression of c-Myc inhibits TGF-beta mediated growth suppression (75). Ovarian cancer cells become resistant to TGF-beta mediated growth arrest through the loss of c-Myc repression in a manner independent of Smad activation (76). Besides overexpression of c-Myc, overexpression of E2F1 also confers resistance to TGF-beta growth inhibition. Overexpression of E2F1 by adenovirus in mink lung epithelial cells confers resistance to TGF-beta growth suppression (77).

The phosphorylation of the Smads also affects the ability of TGF-beta to induce cell cycle arrest. Cdk2and Cdk4-mediated phosphorylation of Smad3 on Thr⁸, Thr¹⁷⁸, and Ser²¹² reduces Smad3 transcriptional activity in nonhematopoietic cell lines, which leads to compromised p15 activation and c-Myc repression (78). Bone marrow myeloma cells are resistant to TGF-beta mediated growth suppression due to Smad2 phosphorylation on Thr⁸ by Cdk2 (79).

As mentioned above, H- Ras^{G12V} overexpression confers resistance to TGF-beta at the receptor level. Hyperactivation of Ras also inhibits Smad2 and 3 functions. SW480.7 colon carcinoma cells do not express Smad4 and contain activated K-Ras. Hyperactivation of Ras inhibits Smad2/3 nuclear localization by increasing their phosphorylation at MAPK sites (80). Furthermore, expression of activated H- Ras^{G12V} in intestinal epithelial cells decreases Smad4 nuclear translocation and TGF-betainduced formation of Smads 2, 3, and 4 complexes, and inhibits TGF-beta mediated growth suppression. PD98059, an inhibitor of MEK, prevents the Ras-induced decrease in Smad4 expression and complex formation, suggesting that Ras represses TGF-beta signaling in a MAPK-dependent manner (81).

Mammary epithelial cells transformed with oncogenic H-Ras are no longer sensitive to TGF-betameditated growth inhibition. These cells display increased expression of 14-3-3 zeta and decreased expression of 14-3-3 sigma, as compared with the parental cells. It was found that 14-3-3 sigma is required for TGF-beta mediated growth suppression, whereas 14-3-3 zeta negatively modulates this growth inhibitory response. Furthermore, overexpression of 14-3-3 zeta increases the level of Smad3 that is phosphorylated at linker regions and cannot mediate the TGF-beta growth inhibitory response (82).

Increased levels of Smad7, which suppresses TGF-beta-induced growth arrest, may also decrease Smad responsiveness and lead to resistance of cancer cells to TGF-beta mediated growth suppression. Smad7 is often overexpressed in pancreatic cancers, which are generally resistant to the growth inhibitory effects of TGF-beta (83). Downregulation of Zinc-finger E-box binding homeobox 1, which binds phosphorylated Smads 2 and 3 to enhance TGF-beta signaling, combined with overexpression of Smad7 also contributes to the resistance of TGF-beta mediated growth suppression in adult T-cell leukemia/lymphoma (84).

COLO-357 pancreatic cells that are engineered to overexpress Smad7 become resistant to TGF-beta growth inhibition (85). Interestingly, Smad7 overexpression interferes with TGF-beta mediated attenuation of Cyclin A and B levels, inhibition of Cdk1 dephosphorylation and Cdk2 inactivation, up-regulation of p27, and the maintenance of Rb in a hypophosphorylated state. Smad7 also suppresses TGF-beta mediated inhibition of E2F activity, yet does not affect the phosphorylation of Smad2 or nuclear translocation or DNA binding of Smads 2, 3, and 4. Smad7 is, therefore, able to functionally inactivate Rb and de-repress E2F without interfering with Smad2 and 3 activation. Smad7 thus exerts Smad2, 3, and 4 independent actions in cancer cells that are resistant to TGF-beta mediated growth suppression (85).

Viral proteins also interfere with Smad activity and are responsible for resistance to TGF-beta mediated cytostatic effects. Hepatitis C virus (HCV) core variants isolated from liver tumors interact with Smad3 and inhibit the Smad3/4 transcription factor complex, suggesting that during chronic HCV infection, there is a selection of viral variants that promote cell transformation by providing resistance to TGF-beta antiproliferative effects (86). The human T-cell leukemia virus type I (HTLV-1) protein, Tax, has been proposed to contribute to leukemogenesis in adult T-cell leukemia. Tax interferes with the recruitment of CBP/p300 to Smad transcriptional complexes, which may account for the resistance of HTLV-1 infected T-cells to TGF-beta mediated growth arrest (87). The human papillomavirus (HPV) E7 oncoprotein interacts with Smad2, Smad3, and Smad4, and prevents Smad3 from binding to DNA. This may account for HPV-associated acquisition of resistance to TGF-beta growth inhibition (88).

Viruses use alternative mechanisms to induce resistance to TGF-beta mediated growth suppression as well. The Epstein-Barr virus encoded protein, latent membrane protein 1 (LMP1), confers resistance to TGFbeta mediated growth suppression. LMP1 activates NFkappaB, which competes for a limited pool of transcriptional co-activators, thereby suppressing TGF-beta mediated transcriptional activity (89).

4.3. Dysregulation of cell cycle effectors

TGF-beta suppresses cell growth by downregulating components of the cell cycle, including Cyclin D1 and Cyclin E, and upregulating cell cycle inhibitors, including p15, p21, and p27 (90-91). Overexpression or activation of Cyclins or Cdks, or downregulation or inactivation of cell cycle inhibitors may ultimately lead to resistance of certain cancer cells to TGFbeta growth suppression.

Resistance to TGF-beta growth inhibition involves changes in Cyclin/Cdk/inhibitor complexes in certain cell types. The expression of Cyclin E is often increased in tumors, suggesting that it may contribute to abnormal growth and potentially to TGF-beta resistance. Along these lines, overexpression of Cyclin E is associated with increased resistance to TGF-beta mediated growth inhibition in two mammary epithelial cell lines (92). The overexpression of Cyclin D1 also contributes to TGF-beta resistance. For instance, overexpression of Cyclin D1 in several hepatocellular carcinoma cell lines is correlated with resistance to TGF-beta mediated growth inhibition, and suppression of Cyclin D1 expression with antisense Cyclin D1 in one of these cell lines partially overcame TGF-beta resistance (93). Primary keratinocytes derived from mice that overexpress Cyclin D1 are partially resistant

to TGF-beta mediated growth suppression (94).

Overexpression of Cdks also confers resistance to TGF-beta growth inhibition. Mink lung epithelial cells that overexpress Cdk4 are resistant to TGF-beta growth suppression (95). Cell lines derived from tumors engineered to express a constitutively active Cyclin D1-Cdk2 fusion protein secrete TGF-beta, yet are resistant to TGF-beta mediated antiproliferative effects, and mink lung epithelial cells stably expressing the Cyclin D1-Cdk2 fusion protein are also refractory to TGF-beta (96-97). These data indicate that constitutively active Cdk2 is sufficient to render cells resistant to TGF-beta cytostatic effects.

Activation of protein kinase B/AKT disrupts the actions of p27, which contributes to resistance to TGF-beta mediated growth suppression in human breast cancer cells (98-100). Thr¹⁵⁷ is a phosphorylation site for Akt and is within the nuclear localization site of p27. Akt-mediated phosphorylation of p27 causes cytoplasmic localization and accumulation of p27, which leads to resistance of cells to TGF-beta mediated G1 growth arrest. Cytoplasmic localization of p27 in conjunction with Akt activation correlates with a poorer prognosis in breast cancer patients (98-100). The Thr¹⁵⁷ p27 phosphorylation site is not conserved in rodents, however, revealing a potential limitation of the use of mouse models to study p27 function during tumorigenesis.

Regulation of p21 expression by microRNAs impairs TGF-beta-dependent cell cycle arrest. Two microRNAs, miR-106b and miR-93, suppress the ability of TGF-beta to increase p21 expression and inhibit cell cycle progression in gastric cancer cells (101). Regulation of p15 plays a role in resistance of melanoma cells to TGF-beta growth suppression. Id2 upregulation in melanoma cells, which is correlated with increased invasiveness, suppresses TGF-beta induction of p15, thus circumventing TGF-beta mediated inhibition of proliferation (102).

4.4. Tumor Microenvironment

Cross-talk between tumor cells and the surrounding stroma affects the ability of TGF-beta to mediate cytostatic activity. The autocrine and paracrine release of pro-inflammatory cytokines inhibits TGF-beta mediated growth suppression. For instance, interleukin-15 (IL-15) impairs TGF-beta cytostatic activity and Smad3dependent TGF-beta signaling in human T lymphocytes. IL-15-mediated inhibition of Smad3 is associated with c-Jun-N-terminal kinase activation and is reversed by c-Jun antisense oligonucleotides, consistent with the inhibitory effect of phospho-c-Jun on Smad3-DNA complexes (103-104). Furthermore, tumor necrosis factor-alpha (TNFalpha) interferes with Smad signaling through the induction of AP-1 components, which form complexes with Smad3 and prevent its binding to specific cis-elements. Additionally, Jun family members compete with Smad3 for binding to the co-activator p300, which may also explain suppression of Smad-dependent transcription by TNF-alpha (105).

Cyclooxygenase-2 is the key enzyme that converts arachidonic acid to several prostaglandins,

including prostaglandin E2 (PGE2). PGE2 promotes cancer progression by increasing cell proliferation and angiogenesis and by inhibiting apoptosis (106-108). PGE2 was recently found to inhibit the cytostatic effect of TGFbeta by binding to the EP2 receptor during mammary tumorigenesis (109).

In certain types of liver cancer cells, TGF-beta simultaneously activates Smads and induces phosphorylation of cytosolic phospholipase A_2 -alpha (cPLA₂-alpha) (110). While Smad activation inhibits tumor cell growth, phosphorylation of cPLA₂-alpha counteracts Smad-mediated inhibition of cell proliferation. cPLA₂-alpha increases the production of PGE2 for activation of the EP1 receptor and activates the eicosanoid receptor peroxisome proliferator-activated receptor-gamma, both of which counteract TGF-beta mediated growth suppression (110).

5. EVIDENCE FOR TGF-BETA ANTIPROLIFERATIVE EFFECTS FROM INTACT *IN VIVO* SYSTEMS

Understanding the role that TGF-beta signaling plays in inhibition of proliferation and tumor formation has been expanded greatly by studying polymorphisms that exist in the human population and the use of experimental animal models. In mouse models, all parts of the signaling cascade, including the ligand, the receptor, and the effector proteins have been manipulated to better understand their functions. The result has been strong *in vivo* evidence that TGF-beta signaling plays a crucial role in maintaining control over cell division.

5.1. Allelic variations in the TGF-beta signaling cascade

Plasma concentrations of TGF-beta are implicated in the pathogenesis of several diseases, including cancer, atherosclerosis, fibrotic disease and autoimmune disease (111-115). Polymorphisms of TGF*beta1* are present within the human populations that affect TGF-beta levels. For instance, individuals with an Arg²⁵ polymorphism in the TGF-beta1 gene have increased circulating levels of TGF-beta and an increased predisposition to hypertension (116-117). Polymorphisms are also present in the TGF-betaRI, TGF-betaRII and TGFbetaRIII genes that have the potential to regulate the activity of these gene products. Polymorphisms of TGFbeta1 and TGF-betaRII, for instance, are associated with a lower risk of certain cancers, including esophageal squamous cell carcinoma (118).

5.2. The TGF-beta1^{-/-} mouse

The use of a TGF-beta 1^{-/-} mouse to study the role of TGF-beta in growth suppression is complicated by the fact that these mice have a dysfunctional immune system, leading to organ failure and death approximately 20 days after birth (119). One method that has been used to obviate this problem is to knock out the gene in a severe combined immunodeficient (SCID) background. SCID mice are susceptible to *H. hepaticus* infection in the intestine, causing inflammation and a high rate of proliferation in the intestinal epithelium (120). However, this only progresses to tumorigenesis in mice that also lack the TGF-beta1 gene (121). It was later shown that TGF-beta1 exerts its growth suppressive role in this model by blocking the recruitment of the NF-kappaB transcription factor to the interleukin-6 promoter (122).

A second tactic that has been used is to generate a heterozygous knockout, which results in animals that do not show the early death phenotype of the homozygous knockout. Mice heterozygous for the TGF-beta1 gene show increased cellular proliferation in the liver and lung, and show greater susceptibility to tumorigenesis in the presence of carcinogens than do wild type mice. These tumors retain their intact allele, indicating that TGF-beta1 is a haploinsufficient tumor suppressor (123).

5.3. Targeted expression of TGF-beta

Targeted over-expression of TGF-beta1 has provided a valuable source of data supporting the growth inhibitory effects of TGF-beta. Expression of transforming growth factor-alpha (TGF-alpha) in the mammary gland under the control of the mouse mammary tumor virus (MMTV) promoter results in breast tumor formation (124). However, co-expression of TGF-beta along with TGFalpha greatly reduces the formation of tumors. The experiments also showed that TGF-beta expression blocks tumor formation induced by the carcinogen 7.12dimethylbenz-[a]-anthracene (DMBA) (125). Similar studies have shown that mammary TGF-beta1 expression blocks cancer formation due to either neu expression (126) or MMTV infection (127). The effect has also been seen in a mouse model of skin cancer where animals expressing TGF-beta1 specifically in keratinocytes show a reduction in benign tumor formation following topical application of DMBA (128).

5.4. Expression of mutant receptors

Manipulation of the TGF-beta receptors in vivo is a valuable tool as the targeted expression of dominant negative and constitutively active receptors allows the examination of both over- and under-active signaling. Expression of a dominant negative type II TGF-beta receptor (dnTGF-betaRII) in the mammary epithelium causes the formation of spontaneous tumors (129), increased tumor formation after DMBA treatment (130), and decreases the latency of TGF-alpha induced mammary tumors (131). Likewise, a TGF-betaRII knockout specific to the mammary epithelium leads to spontaneous hyperplasia and decreased latency in polyomavirus middle T antigen induced tumor formation (132). Conversely, expression of constitutively active TGF-betaRI decreases the incidence of MMTV-neu tumors, and those that form show a greater latency of formation (126).

Dominant negative TGF-betaRII receptors have also been used to show this effect in locations other than the mammary epithelium. Epidermal expression of *dnTGF-betaRII* approximately doubles the rate of papilloma formation in response to the tumor promoter 12-*O*-tetradecanolyphorbol-13-acetate (TPA) (133). Expression of *dnTGF-betaRII* in the intestine results in

greater azoxymethane induced carcinogenesis, while expression in the stomach increases tumor formation due to the bacterium H. pvlori (134-135). Conditional knockout of TGF-betaRII in the liver also cooperates with TGF-alpha overexpression to induce hepatocellular carcinoma (136). The tumor suppressive effects of TGF-beta were also shown using mice with a pancreas-specific knockout of TGF-betaRII (137). These mice develop pancreatic ductal adenocarcinoma at a rate of 100% when active K-Ras^{G12D} is also expressed in a pancreas-specific manner, whereas the TGF-betaRII knockout itself showed no phenotype and K-Ras^{G12D} expression only produced low-grade lesions with a much longer latency on its own. To date, there has been one report that TGF-betaRI loss causes tumor formation. Conditional knockout of the type-I receptor in the neurons caused spontaneous tumor formation in the periorbital and perianal areas of mice (138).

5.5. Studies with altered Smad signaling

The downstream effector proteins of TGF-beta signaling, the Smads, have also been utilized in mouse models to demonstrate the growth inhibitory effects of TGF-beta. The results of these experiments have been highly dependent on which Smad is altered and, in the case of intestinal carcinogenesis, the strain of mouse used. Homozygous deletion of Smads 2, 4, and 5 is embryonic lethal (139-141), while Smad3^{-/-} mice survive to adulthood. The original Smad3 knockout model showed an increased risk of colon cancer (142). Since that time, two additional Smad3 null mouse models have been developed and show no spontaneous tumor formation (143-144). The conflicting results may be due to the different mouse strains that were used (2).

Two separate lines of mice harboring heterozygous knockout of the genes encoding Smad2 and adenomatous polyposis coli (APC) have been generated, neither of which have shown an increased rate of colon carcinogenesis when compared to the APC heterozygote alone (145-146). Conversely, mice with heterozygous deletion of both APC and the co-Smad. Smad4. develop tumors that are more aggressive than those of the APC mouse (147) and mice with heterozygous Smad4 deletion develop spontaneous gastrointestinal polyps after one year of age (148). Likewise, a conditional knockout of Smad4 in the mammary epithelium results in squamous cell carcinoma (149). These results suggest that Smad4 may play a critical role in the anti-proliferative effects of TGFbeta, while Smad2 does not. Alternatively, this may reflect the role of Smad4 as a common mediator that relays signals from multiple cytokines including the BMPs. It also appears that Smad3 plays an important role in certain genetic backgrounds, or in a manner that is dependent on the bacterial flora present.

5.6. The use of TGF-beta decoy receptors

A fusion of the TGF-betaRII extracellular domain to the constant fragment (Fc) of immunoglobulin, Fc:TGFbetaRII, has also been used quite extensively in mouse models. Expression of this decoy receptor induces tumor cell apoptosis, decreases invasive characteristics, and blocks lung metastasis in MMTV-polyoma virus middle T antigen expressing mice (150). Similarly, expression of both Fc:TGF-betaRII and the neu proto-oncogene controlled by the MMTV promoter shows a reduced incidence of lung metastases when compared to mice expressing *neu* alone (151). Interestingly, in both studies, the decoy receptor had no effect on tumor latency or rate of incidence. The authors suggest that these data, which on the surface seem contradictory to other mouse models showing that lack of TGF-beta increases primary tumor formation, are explained by a selectivity that is inherent to this model (151). It is possible that the pro-invasive characteristics of TGF-beta are only seen when the ligand concentration in vivo is above a threshold value and that Fc:TGF-betaRII is able to reduce TGF-beta levels below that level but not low enough to block the tumorsuppressive effects. Although the process has not been well studied, TGF-beta has also been shown to exist in both active and inactive forms (152). If Fc:TGF-betaRII is selective towards one form or the other, either due to affinity or location, it could explain the observed results, which typify the complex and sometimes seemingly paradoxical role of TGF-beta in tumor development in vivo.

6. DIRECTIONS FOR FUTURE STUDIES

6.1. Abrogating TGF-beta signaling to block promotion of tumor invasion and metastasis

Many advanced human cancers retain a functional TGF-beta signaling pathway, although TGF-beta no longer arrests the cell cycle in these malignancies. With respect to breast cancer, while estrogen receptor (ER) positive tumors tend to exhibit decreased TGF-beta receptor expression, ER negative tumors frequently harbor an intact signaling pathway (153). In ER negative breast cancers this retention of TGF-beta signaling is thought to contribute to the invasive and metastatic properties that are characteristic of these tumors (154-156) and may confer increased cell survival (150). Despite these signaling responses, TGF-beta generally does not cause cell cycle arrest in ER negative tumors. These observations have led to the strategy of blocking TGF-beta signaling in advanced tumors in order to prevent autocrine or paracrine TGF-beta from promoting cancer invasion and metastasis. Approaches for abrogating TGF-beta signaling include the use of neutralizing antibodies, decoy receptors, and small molecule inhibitors of the serine/threonine kinase activity of the receptors (reviewed in (157-159)). Several studies indicate that these strategies can effectively block tumor metastasis in animal models, but convincing clinical evidence that these approaches significantly impact the progression of human cancer are lacking thus far. A recent article indicates that long-term treatment of tumor bearing mice with a TGF-beta receptor kinase inhibitor leads to the outgrowth of tumors with high levels of Smad phosphorylation that cannot be reversed by the kinase inhibitors (160). The authors cautioned against chronic treatment of patients with this class of drugs. Such treatment results in drug-resistant tumors were more aggressive, were associated with inflammation, and expression of markers consistent with an invasive phenotype and having undergone an epithelial to mesenchymal transition.

6.2. Restoring TGF-beta antiproliferative actions in tumors using rapalogs

Some tumor types, such as basal-like breast cancers, retain a subset of TGF-beta responses but are refractory to its cytostatic effects. This suggests that it may be possible to develop a pharmacological approach to restore or potentiate TGF-beta mediated cell cycle arrest. This approach has the advantage that cancers frequently secrete high levels of TGF-beta, and TGF-beta is a prominent component of the extracellular matrix and tumor microenvironment, so the putative therapeutic strategy would be to accentuate the anticancer effects of the preexisting TGF-beta ligand. Studies have demonstrated that the mTORC1 inhibitory rapamycin analogs, or "rapalogs," strongly cooperate with TGF-beta to arrest the proliferation of a wide array of cell lines (96, 161-166). This combined rapalog + TGF-beta effect correlated with inhibition of Cdk2 activity, an increase in p21 and p27 binding to Cdk2, and a corresponding decrease in Cdk2 association with complexes containing E2F4, p107, and p130. These changes in complex composition may also occur coincidently with Cdk2 translocation from the nucleus to the cytoplasm (164). It was proposed that TGFbeta and rapalogs cooperate to induce arrest of cancer cell proliferation by preventing Cdk2-dependent phosphorylation of p107 and p130, which actively repress E2F-dependent transcription in their hypophosphorylated states. Previous studies have shown that Cdk2-dependent phosphorylation of p107 and p130 requires the formation of transient but stable Cyclin/Cdk2/E2F4/DP1/pocket protein complexes (167). The extent to which potentiation of TGFbeta cytostatic action contributes to the anticancer activity of rapalogs in vivo is unknown at present.

Because of the plethora of biological activities attributed to TGF-beta, it may be difficult to completely extricate its tumor promoting effects from its tumor suppressive effects and to determine if in fact the TGF-beta axis is a useful therapeutic target in the treatment of cancer. It would be ideal if therapeutic strategies could be devised that simultaneously block TGF-beta tumor progression functions, while strengthening its tumor suppressive functions. Successful implementation of such a strategy will likely require sophisticated knowledge of the role of TGF-beta signaling in intact tumors encompassing all of the pertinent biological mechanisms. This strategy may need to be tailored to individual tumors in accordance with their particular pattern of oncogene activation and tumor suppressor gene inactivation. Despite these difficulties, the ability to therapeutically reprogram TGF-beta functions in tumors has the potential to significantly impact cancer therapy given the role of this factor in nearly every aspect of tumor initiation and progression including cell cycle control, chromosomal instability (168), apoptosis (169-171), tumor evasion of the immune response (172), and the epithelial to mesenchymal transition (173-175).

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Abbreviations: APC: adenomatous polyposis coli, BMPs: bone morphogenetic proteins, Cdk: Cyclin-dependent kinase, CKIs: Cdk inhibitory proteins, DMBA: 7,12dimethylbenz-[a]-anthracene, dnTGF-betaRII: dominant negative type II transforming growth factor-beta receptor, ER: estrogen receptor, FoxO: forkhead box O, HCV: hepatitis C virus, HPV: human papilloma virus, HTLV-1: human T-cell leukemia virus type I, Id1: inhibitor of differentiation or inhibitor of DNA binding-1, Id2: inhibitor of differentiation or inhibitor of DNA binding-2, IL-15: interleukin-15, LMP1: latent membrane protein 1, MMTV: mouse mammary tumor virus, PGE2: prostaglandin E2, cPLA₂-alpha: phospholipase A₂-alpha, PAI-1: plasminogen activator inhibitor-1, PKC-alpha: protein kinase C-alpha, R-Smads: receptor-activated Smads, SCID: severe combined immunodeficient, SRF: serum response factor, TGF-alpha: transforming growth factor-alpha TGF-beta: transforming growth factor-beta, TGF-betaRI: type I transforming growth factor-beta receptor, TGF-betaRII: type II transforming growth factor-beta receptor, TNFalpha: tumor necrosis factor-alpha.

Key Words: TGF-beta, Cell Cycle, Tumor Suppressor, Smad, Cyclin-dependent kinase, Review

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