Tumor and Stem Cell Biology

TGF-β and ανβ6 Integrin Act in a Common Pathway to Suppress Pancreatic Cancer Progression

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Abstract

The TGF-β pathway is under active consideration as a cancer drug target based on its capacity to promote cancer cell invasion and to create a protumorigenic microenvironment. However, the clinical application of TGF-β inhibitors remains uncertain as genetic studies show a tumor suppressor function of TGF-β in pancreatic cancer and other epithelial malignancies. Here, we used genetically engineered mouse models to investigate the therapeutic impact of global TGF-β inhibition in pancreatic cancer in relation to tumor stage, genetic profile, and concurrent chemotherapy. We found that ανβ6 integrin acted as a key upstream activator of TGF-β in evolving pancreatic cancers. In addition, TGF-β or ανβ6 blockade increased tumor cell proliferation and accelerated both early and later disease stages. These effects were dependent on the presence of Smad4, a central mediator of TGF-β signaling. Therefore, our findings indicate that ανβ6 and TGF-β act in a common tumor suppressor pathway whose pharmacologic inactivation promotes pancreatic cancer progression. Cancer Res; 72(18): 4840–5. ©2012 AACR.

Introduction

The transforming growth factor-β (TGF-β) signaling pathway is an evolutionarily conserved regulator of embryonic patterning and cell differentiation, and has central roles in wound healing and inflammation (1). The activated TGF-β receptor (TGF-βR1/R2) phosphorylates the Smad2 and Smad3 proteins, which modulate transcription in association with Smad4. This pathway has been the subject of intense investigation in cancer due to its potential to act in both a pro- and antitumorigenic manner (2). Depending on cross-talk with other pathways, TGF-β can inhibit proliferation and suppress transformation by modulating expression of cell-cycle regulators. Alternatively, TGF-β can promote malignant growth through multiple mechanisms including enhanced cancer cell invasion, survival, matrix remodeling, fibrosis, and immunosuppression.

As in other epithelial cancers, TGF-β pathway function in pancreatic ductal adenocarcinoma (PDAC) seems complex. Inactivating mutations in SMAD4 and other pathway components are present in approximately 50% of human PDAC and cooperate with activated KrasG12D to promote PDAC in mouse models (3–6). However, TGF-β ligands are commonly overexpressed in PDAC, and can promote epithelial-to-mesenchymal transition (EMT) and invasion in cell lines (7, 8). TGF-β can also induce angiogenesis, activate tumor-promoting myofibroblasts (stellate cells), and attenuate immune surveillance (9, 10). In light of these observations, TGF-β inhibitors are under investigation as PDAC therapeutics and have shown efficacy in xenograft studies (11, 12).

The multifaceted and cell-type specific effects of TGF-β inhibition present problems in fully assessing the clinical utility of drugs against this pathway. Such effects are likely to be best-understood using native cancer models that appropriately recapitulate tumor–stroma interactions as well as the multi-stage progression that defines human cancers. Here, we investigated the upstream regulation of TGF-β signaling in the pancreas to establish new strategies to target the pathway, and we examined the impact of pharmacologic inactivation of multiple TGF-β signaling components using genetically engineered mouse (GEM) models of PDAC. These studies, carried out in the context of sequential tumor stages, different genetic lesions, and combined treatments with cytotoxic chemotherapies, failed to reveal a therapeutic window. Instead we found multiple settings in which disease was exacerbated by TGF-β inhibition. This preclinical information does not presently support the utility of broadly targeting this pathway in PDAC.

Materials and Methods

Mouse models

All treatment studies were conducted in accordance to UCAR and institutional standards using previously described mouse strains (5). Littermates were distributed among 1D11
Animals showing signs of illness and with concomitant comparisons were determined using the Log-rank test. Statistical analysis of neoplastic cells with positive staining was quantified by pathologic evaluation as the percent of pancreas occupied by nodules of PanIN/PDAC tumor burden was determined by serial analysis of more than 3 H&E sections through the longitudinal plane of the pancreas. A gastrointestinal pathologist (V. Deshpande) determined percentage of pancreas occupied by normal tissue, PanIN, and PDAC, in a blinded fashion.

### Antibodies
For αvβ6, the mAb 6.2A1 (14) used at 1:100 in human tissue or the human/mouse chimeric form of 6.2A1 (ch6.2A1) in mouse tissue (15) used at 1:100; for phospho (Ser465/467)-Smad2, catalog number AB3849 (Millipore Corporation); for endothelial cells, the rat endomucin v.7C7 (Santa Cruz) used at 1:50; for pericytes, NG2 catalog number AB5320 (Chemicon) used at 1:200; for Ki-67, NCL-Ki67p (Novocastra); for macrophages, the anti-CD68-M antibody, MCA1957T (Serotech); for total T-cells, the anti-CD3 antibody, Catalog number RM-9107S (Lab vision/Neomarkers); for Foxp3, catalog number 14-5773 (eBioscience).

### Quantification of IHC/IF
Staining for CD68, FoxP3 and phospho-Smad2 was quantified by scanning slides at 20× using the Aperio-XT automated imaging system. Regions of interest were identified within the tissues for quantification of DAB positive CD68 and Foxp3 stained cells. For phospho-Smad2 quantification, we used an automated algorithm to quantify the level of nuclear DAB staining on a scale ranging from 0, +1, +2, and +3. Ki-67 staining was quantified by pathologic evaluation as the percent of neoplastic cells with positive staining.

### Statistical analysis
Survival was determined using the Kaplan–Meier method and comparisons were determined using the Log-rank test. Animals showing signs of illness and with confirmed cancers were included as events, whereas animals that died for reasons other than cancer were censored. Histologic scores for disease burden, Ki67, and P-smad2 staining between treatment groups compared using t-tests, β6 IHC scoring was compared by the Mann–Whitney test.

### Results
PDAC evolves from premalignant lesions including acinar-to-ductal metaplasia (ADM) and pancreatic intraepithelial neoplasia (PanIN; ref. 16). We evaluated the activation status of the TGF-β pathway during PDAC progression via immunohistochemical staining for Serine465/467-phosphorylated Smad2 (phospho-Smad2) in the Ptf1-CreLSL-Kras(G12D); p53flox/flox model. Phospho-Smad2 was elevated in ADM and early PanINs compared to normal ductal and acinar cells, and remained at high levels throughout PDAC progression (Fig. 1A, upper panels, yellow arrowheads). Stromal fibroblasts also showed strong nuclear P-Smad2 staining (Fig. 1A, red arrowheads).

Previous studies have documented increased expression of TGF-β ligands in PDAC progression (5). Because TGF-β is produced as a latent complex, additional processes such as proteolytic cleavage or conformational changes are required to activate signaling. To determine the basis for TGF-β activation, we examined the expression pattern of αvβ6, a candidate activator of latent TGF-β that is upregulated in advanced tumors (15, 17). In mice, αvβ6 was absent in islet and acinar cells and at low to moderate levels in normal ducts, whereas expression was increased throughout each stage of PDAC progression (Fig. 1A, lower panels). Expression of αvβ6 was restricted to transformed pancreatic ductal epithelium with no evidence of staining in the stromal microenvironment. Human specimens showed a similar αvβ6 expression profile, with staining in low- and high-grade PanIN lesions and most PDAC, with normal human ducts showing only weak staining (Fig. 1B). The correlation between induction of αvβ6 expression and phospho-Smad2 in PanIN and PDAC suggests this integrin may be important in local activation of TGF-β signaling in ductal lesions.

To examine the relationship between αvβ6 function and TGF-β signaling, we treated Kras-p53flox/flox mice with an αvβ6 blocking IgG monoclonal antibody (3G9; ref. 14), a pan-TGF-β blocking IgG monoclonal antibody, ID11 (13), or an isotype control antibody (13C4). Anti-αvβ6 treatment strongly decreased phospho-Smad2 expression in PanIN and PDAC lesions as well as surrounding stroma (Fig. 1C). Collectively, our data indicate that αvβ6 is critical for activation of TGF-β signaling in the neoplastic epithelium.

Targeting TGF-β signaling could limit PDAC growth by blocking TGF-β-mediated protumorigenic effects on the microenvironment and on the invasiveness of cancer cells. Moreover, αvβ6 inhibition could serve to inactivate TGF-β signaling in a restricted manner, limiting the effects of a pharmacologic blockade to the diseased pancreas. To test these possibilities, we used the anti-TGF-β, anti-αvβ6, and isotype control antibodies in the Kras-p53flox/flox model. To evaluate the impact of treatments on progression of preinvasive lesions antibodies were administered at 5 weeks of age—when the pancreas is largely normal but contains focal early stage PanINs (schematic in Fig. 2A). Pancreases were evaluated for the presence of gross tumors and by correlative histologic and immunohistochemical analysis at 12 weeks. Anti-αvβ6 treated animals had increases in the proportion of the pancreas exhibiting PanIN or PDAC lesions compared with controls (mean = 73% in 3G9 vs. 45% control: P = 0.04; Fig. 2B, upper row), as well as a higher frequency of invasive PDAC (66%, vs. 33% in controls). Comparable increases in neoplasia were observed in anti-Tgf-β–treated mice. Therefore, blocking αvβ6 accelerated the course of PanIN initiation and progression.
leading to a larger burden of disease and more advanced tumors.

Acceleration in progression of PanIN lesions among anti-Tgf-β and anti-αvβ6–treated mice was associated with an increase in proliferation as reflected by Ki67 staining (Fig. 2B, lower row). Consistent with this we observed that 4/5 primary pancreatic ductal cell cultures with activated Kras showed growth inhibition in responses to TGF-β treatments. We failed to observe significant alterations in stromal components that can be activated by TGF-β, including the stellate cells (smooth muscle actin), Tregs (FoxP3), macrophages (CD68), the desmoplastic stroma (qRT-PCR analysis for collagen-1) and vasculature (endomucin and NG2; Supplementary Fig. S1A–C). Thus, these data indicate that the αvβ6-TGF-β pathway has a primary role in restraining proliferation and malignant progression of PanIN epithelial cells.

Because both TGF-β and αvβ6 signaling have been implicated in the induction of EMT and invasive growth of established cancers, we next sought to test whether the anti-TGF-β and anti-αvβ6 antibodies had a differential impact at later disease stages. *Kras-p53<sup>Lox/+</sup>* mice were treated beginning at 9 to 10 weeks of age, when either high grade PanINs (PanIN-3) or locally invasive PDAC were present (schema in Fig. 2C, upper). Mice were treated until signs of illness necessitated euthanasia. Notably, overall survival was significantly diminished in the anti-TGF-β and anti-αvβ6 groups demonstrating a persistent role for TGF-β in suppressing growth at later stages of disease (Fig. 2C, lower left). Histopathologic analysis revealed treated tumors to be invasive PDAC showing a range of histologic differentiation. Blocking antibodies did not produce significant differences in the spectrum of tumor grade and histologic subtypes (Supplementary Fig. S2A and B).

The PDAC stroma is a potential barrier to effective delivery of chemotherapeutic agents to tumor cells (18). Based on the potential function of TGF-β signaling in activating stromal fibroblasts, we tested whether TGF-β blockade influenced the response of the *Kras-p53<sup>Lox/+</sup>* model to gemcitabine, a standard chemotherapy. The addition of αvβ6 or TGF-β blocking antibodies to standard gemcitabine treatment led to a diminished survival as compared with gemcitabine alone (Fig. 2C,

Figure 1. αvβ6 activates TGF-β in the pancreatic epithelium. A, IHC staining for phospho-Smad2 (top row, ×400) and integrin β6 (bottom row, ×200), during multistage progression of the *Kras-p53<sup>Lox/+</sup>* PDAC model. Duct (D), acinar (A), islet (I), metaplastic acini (M), and PanIN (P) cells indicated. Phospho-Smad2<sup>+</sup> neoplastic and stromal cells designated by yellow and red arrowheads, respectively. B, IHC for integrinβ6 in normal human pancreas and in multistage PDAC progression. C, left, phospho-Smad2 IHC in PanIN and PDAC from *Kras-p53<sup>Lox/+</sup>* mice treated with αvβ6 blocking antibodies or control. Right, phospho-Smad2<sup>+</sup> nuclei quantified by automated analysis.
Inactivation of TGF-β at early stages of PDAC progression. To examine this question, we carried out IHC analysis across a set of PDAC specimens derived from Smad4 null mouse models using antibodies to αvβ6. Although all the tumors with Smad4 mutations expressed αvβ6 at higher levels in invasive tumors compared with PanINs, we found that approximately 26% of Smad4 wild-type tumors lost αvβ6 expression, suggesting that inactivation of TGF-β pathway may have a less prominent impact on tumorigenesis.

Our work shows that αvβ6 is a critical component of the TGF-β-Smad4 tumor suppressor pathway in PDAC. Correspondingly, reduced αvβ6 expression could serve as an alternative mechanism to Smad4 mutations as a means to inactivate the TGF-β pathway during PDAC progression.
expression (Fig. 3A). Importantly, the absence of αvβ6 staining correlated with SMAD4 status (P = 0.01). The spontaneous loss of expression of αvβ6 among Smad4 wild-type tumors, but never in combination with Smad4 mutation, supports the view that αvβ6 is a central activator of the TGF-β-SMAD4 tumor suppressor pathway, and suggests that molecular alterations of both upstream and downstream components promote PDAC tumorigenesis.

To test more directly whether αvβ6 acts in a common TGF-β/Smad4 tumor suppressor pathway, we assessed the impact of 3G9 on a Kras-driven PDAC model that also has an engineered homozygous deletion of Smad4 and therefore has defective TGF-β signaling in the pancreatic epithelial cells (5). Treatment was started at the time when focal PDAC is present, and maintained until signs of illness required euthanasia. In contrast to their effects in the Smad4 wild-type Kras-p53 mutant model, αvβ6 blocking antibodies did not alter the latency or histopathologic features of Smad4 null tumors (Fig. 3B). Therefore, genetic inactivation of TGF-β signaling obviates the effect of αvβ6 blockade on tumorigenesis, consistent with a predominant action of the blocking antibodies in inhibiting epithelial TGF-β-Smad4 signaling.

Discussion

Here, we show that TGF-β pathway blockade with specific monoclonal antibodies to αvβ6 or TGF-β1-3 accelerated PDAC progression in GEM models. This effect was observed when using antibodies at early and later disease stages, and as a single agent or in combination with gemcitabine. Although tumorigenesis was not accelerated in a GEM model lacking Smad4, αvβ6/TGF-β inhibition did not provide any appreciable benefit in this setting. Although it is possible that αvβ6/TGF-β pathway inhibition may restrain aspects of malignancy such as metastatic spread, our data indicate that there may be risks in broadly targeting this pathway given its primary function as a tumor suppressor.

Recent findings have supported the ability of GEM models to recapitulate therapeutic responses seen in patients (19). Our experiments illustrate a number of potential advantages of GEM models, such as the capacity to evaluate the impact of an intervention at different disease stages including preinvasive disease, and in defined tumor genotypes. Whereas preclinical studies in xenografts have supported the use of TGF-β pathway inhibitors in the treatment of PDAC, our work indicates this strategy carries risk in the context of autochthonous tumors.

It remains possible that there may be contexts in which inhibition of components of the αvβ6-TGF-β pathway may prove beneficial in PDAC treatment. Both αvβ6 and TGF-β have been implicated in metastasis, which we were not able to address definitively in our studies (1/7 controls and 1/15 treated mice exhibited metastasis, which was insufficient to provide statistical significance). In addition, while direct targeting of αvβ6 or TGF-β may carry risks, it is possible that signaling receptors or downstream effectors of the pathway have strictly tumor-promoting effects, and thus may be effective targets for pharmacologic blockade. Along these lines a recent study showed TGF-β activates CXC chemokine signaling in a PDAC GEM model and that inhibition delays tumor progression (20).

Our studies also reveal new insights into the mechanisms of TGF-β activation in the pancreas and the contributions of this pathway in multistage PDAC progression. We show that global inactivation of TGF-β signaling promotes increased proliferation of the PanIN epithelial cells and enhances PDAC initiation and progression in a Smad4-dependant manner. Although TGF-β likely has additional functions in regulating the PDAC microenvironment, these functions do not seem essential for either the tumor promotion or tumor suppression.

Figure 3. αvβ6 functions through Smad4 tumor suppressor in the pancreas. A, the relationship between Smad4 and αvβ6 expression was evaluated in Smad4 wild type and mutant PDAC models. Percentage of αvβ6-negative cells in individual tumors (left) and representative IHC images (right) are shown. All Smad4 null tumors retain αvβ6 expression (left), whereas subsets of Smad4 wild-type tumors either lose (middle) or retain (right) Smad4 expression (*, P < 0.05). Insets show higher magnification. B, impact of anti-αvβ6 treatment on PDAC progression in the Kras-Smad4Lox/−; Ink4a/ArfLox/− model. Left, schematic showing experimental design. Right, Kaplan–Meier analysis showing that αvβ6 blockade does not affect survival (n.s. = not significant).
We also identify αvβ6 as a critical upstream regulator of TGF-β signaling in the ducal epithelium and show that αvβ6 has a previously unanticipated function in tumor suppression. αvβ6 blockade attenuated Smad2 activation, produced similar biological effects to TGF-β blockade in our mouse models, and did not affect the progression of Smad4 null tumors. Thus, although αvβ6 has been shown to promote invasive growth of advanced cancers, our data indicate that the primary function of αvβ6 in the pancreas is to serve as an upstream component of the TGF-β tumor suppression program. It is worth noting that PDAC in the Kras-Smad4 model arise from cystic precursors rather than PanIN (3, 5), which could also contribute to the differential response to pathway inhibition in this setting.

In summary, this series of experiments highlight the use of GEM cancer models to guide in the clinical development of novel therapeutics and to elucidate signaling pathway circuitry in vivo. We show that αvβ6 and TGF-β act in a common Smad4-dependent PDAC tumor suppressor pathway. Moreover, we conclude that broad use of TGF-β inhibitors in unselected populations of PDAC patients could have detrimental consequences, and in particular, that there is potential for disease acceleration in cancers with an intact TGF-β/SMAD4 signaling pathway.

References

Disclosure of Potential Conflicts of Interest
R.A. Breken received commercial research support from ImClone Systems. N. Bardeesy received commercial research grant from Genzyme and Stromedix.

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