Cross-talk between Paracrine-Acting Cytokine and Chemokine Pathways Promotes Malignancy in Benign Human Prostatic Epithelium

Mingfang Ao,1 Omar E. Franco,2 Dean Park,3 Dayanidhi Raman,1 Karin Williams,2 and Simon W. Hayward1,2,4

Abstract

The present study explores the mechanisms by which human prostatic carcinoma-associated fibroblasts (CAF) induce tumorigenesis in initiated but nonmalignant human prostatic epithelial cells (BPH-1). CAF express elevated levels of both transforming growth factor-β1 (TGF-β1) and stromal cell-derived factor-1 (SDF-1/CXCL12). TGF-β inhibits the growth of BPH-1 cells in vitro, but was found to be necessary for the tumorigenic response to CAF. This counterintuitive result suggested that the TGF-β signaling system was involved in other processes relating to tumorigenesis. The SDF-1 receptor, CXCR4, is expressed at low levels in benign prostate tissue and in BPH-1 cells in culture. However, CXCR4 levels increase during prostate cancer progression. CXCR4 was found to be induced and localized to the cell membrane in BPH1 cells by CAF-conditioned medium and by CAF cells in tissue recombinants. TGF-β was both necessary and sufficient to allow the detection of membrane-localized CXCR4 in BPH1 cells. Suppression of epithelial cell CXCR4 expression abrogated the tumorigenic response to CAF. SDF-1, secreted by CAF, acts via the TGF-β-regulated CXCR4 to activate Akt in the epithelial cells. This mechanism elicits tumorigenesis and obviates the growth-inhibitory effects of TGF-β. Thus, tumor stroma can contribute to carcinogenesis through synergism between TGF-β, SDF-1, and CXCR4. These experiments suggest mechanisms by which TGF-β can shift its role from an inhibitor to a promoter of proliferation during tumor progression. Both the TGF-β and SDF-1 pathways are targets of drug discovery efforts; these data suggest potential benefits in the cotargeting of these pathways. [Cancer Res 2007;67(9):4244–53]

Introduction

Because the bulk of human tumors are carcinomas, much attention has been paid to the epithelial cell type. However, inflammation and interactions with the surrounding stromal microenvironment are critical for cancer initiation and progression (1–3). Stromal alterations during tumorigenesis have been shown in tumors, including breast, colon, lung, and prostate (4). Compared with normal stroma, the tumor microenvironment often exhibits an increased number of fibroblasts, enhanced capillary density, and deposition of type I collagen and fibrin.

The fibroblasts within the tumor stroma commonly have a myofibroblastic phenotype similar to the granulation tissue seen in wound healing (5, 6) and have been designated as activated or carcinoma-associated fibroblasts (CAF; refs. 7, 8). The presence of a reactive stroma is most clearly evident, and generally best described, in tumors such as breast cancer, where myofibroblastic cells are not commonly seen in the normal stroma. Under these circumstances, the initiation of smooth muscle actin expression is obvious. In comparison, in an organ such as the prostate, the normal stroma is fibromuscular, and therefore, comparable changes are inherently less apparent. Despite these limitations, human prostatic stroma has been shown to be activated in response to cancer progression, resulting in the formation of a reactive stroma the presence and nature of which has a prognostic value (9–11).

Fibroblasts are recognized as prominent modifiers of cancer progression (12, 13). Using tissue recombination and renal capsule xenografting, Cunha’s group showed that human prostatic CAF induced tumor formation from initiated but nontumorigenic human prostatic epithelial cells, whereas normal prostatic fibroblasts (NPF) did not, although the mechanisms involved were unclear (7, 14).

Transforming growth factor-β (TGF-β) has been suggested to play an important role in the generation of the reactive stroma (9, 10). In prostatic CAF, TGF-β secretion is elevated compared with NPF (15). In an orthotopic xenograft model to reconstruct human mammary gland, Kupperwasser et al. (16) found that overexpressing TGF-β in mouse fibroblasts could induce the initiation of breast cancer from the normal human epithelium. A conditional knock-out mouse, in which fibroblasts lose TGF-β responsiveness by excision of TGF-β receptor II (TβRII) also supports the importance of TGF-β signaling in carcinogenesis. These animals exhibit elevated expression of mitogenic chemo-kines associated with intraepithelial neoplasia in the prostate and carcinoma in the gastrointestinal tract (17). Additionally, in a mammary tissue recombination model, fibroblasts from the same TβRII knock-out mice expressed elevated stromal hepatocyte growth factor (HGF), macrophage-stimulating protein (MSP), and TGF-α resulted in the activation of MET, RON, ERβb1, and ERβb2 in the adjacent epithelium (18).

In normal adult tissues, TGF-β is generally seen as a tumor suppressor, inhibiting cell growth and maintaining differentiation. However, as cancer progresses, TGF-β takes on a tumorigenic role, inducing angiogenesis, suppressing apoptotic activity, or enhancing cell motility (19–22). Target cells respond to TGF-β through a number of specific downstream signaling pathways. The overall nature of the response is determined by cellular integration incorporating data from different pathways, the cell context, and...
also the adjacent microenvironment (23). Our previous results showed that TGF-β may stimulate invasion via the induction of epithelial to mesenchymal transformation (EMT) in tumorigenic prostatic epithelial cells via phosphoinositide-3-kinase/Akt signaling (22). Collectively, these reports suggest that TGF-β plays an important bidirectional role in the communication between the epithelia and the stroma.

The present study aimed to investigate the mechanisms by which CAF induce tumorigenesis. To approach this question, we studied stromal-epithelial interactions in vivo and in vitro using a model of prostate cancer progression. The data show that TGF-β produced by CAF can induce tumorigenesis by modifying the response of adjacent epithelial cells to other aspects of the tumor microenvironment, specifically to elevated levels of stromal cell-derived factor-1 (SDF-1). This work provides a model for prostate cancer progression that fits well with previous observations of clinical samples and gives a mechanistic explanation for the switch from growth-inhibitory to growth-promoting effects of TGF-β, which are commonly associated with carcinogenesis.

Materials and Methods

**CAF and NPF cell generation.** Human prostatic CAF and NPF were prepared as previously described (7). For this study, CAFs and NPFs from three separate patients were used to ensure consistency. Following preparation, cells were qualified using a tissue recombination bioassay (7) to confirm that the CAF cells elicit tumorigenesis, whereas the NPF cells do not. Aliquots of CAF and NPF were frozen in liquid nitrogen. Cells were used at low passage (less than 10).

**Cell proliferation assay in cell culture.** A total of 3,000 cells per well were seeded in 24-well plates in serum-free RPMI 1640 (Life Technologies). After attachment and growth overnight, the culture medium was replaced, and the cells were treated with reagents diluted in conditioned medium (CM) collected from CAF or NPF cells or in serum-free RPMI. About 10 μg/mL TGF-β (1,2,3) blocking Ab (Clone 2G7), 5 ng/mL TGF-β1 ligand (R&K Systems, Inc.), and 100 ng/mL SDF-1 (Peprotech, Inc.) were added as indicated in the figure legends.

**Immunofluorescence staining.** Paraffin-embedded tissue samples were cut in 5-μm sections and then placed on glass slides. After deparaffinization with HistoClear (National Diagnostics), the antigen was unmasked by heating samples in unmasking solution (Vector Laboratories, Inc.), and the antigen was unmasked by heating samples in unmasking solution (Vector Laboratories, Inc.). This generated a gap in the monolayer, and the ability of cells to migrate into the cleared section was observed and recorded photographically at different times at fixed points in the wound (24). All the experiments were done in triplicate.

**Western blotting.** Cells were detached by trypsinization after washing with cold PBS, lysed with TNN buffer [50 mmol/L Tris-HCl, 150 mmol/L NaCl, 0.5% NP40 (pH, 7.4)] containing proteinase inhibitor (Roche) and phosphatase inhibitor I and II (Sigma). The whole cell lysates were quantified, and lysates were stored for use. About 20 μg proteins per well were loaded and electrophoresed through 10% NuPAGE Bis-Tris gel (Invitrogen) and electrophoretically transferred to nitrocellulose membranes. Membranes were blocked for 1 h in PBS-T (PBS, 0.1% Tween 20) containing 5% nonfat dry milk and incubated with primary antibody to CXCR4 (R&D Systems, Inc.) at a concentration of 1:1,000 and then with horseradish peroxidase-conjugated secondary antibody. Antibody bands were visualized with enhanced chemiluminescence. Antibodies against β-actin (Sigma) were used as loading control.

**Flow cytometry for CXCR4.** Cells were harvested and resuspended in 1×-binding buffer (BD Pharmingen) at a concentration of 1.0×10⁶/mL, and 50-μL cell suspension was incubated with 50 μL monoclonal mouse anti-human CXCR4 (BD Pharmingen) at a concentration of 1 μg/mL for 30 min on ice. After washing thrice, the cells were incubated with allophtocyanin (APC)-labeled secondary antibody (BD Pharmingen) at a concentration of 5 μg/mL for 30 min on ice. Washing thrice further, and analyzed using flow cytometry at the Vanderbilt-Ingram Cancer Center Flow Cytometry and Cell Sorting Core.

**Retroviral and lentiviral infections.** The BPH-1-DN cells were generated essentially as described in ref. (22) using the dominant negative TβRII (26, 27). Viral supernatant was generated, centrifuged at 3,000 rpm for 5 min, and passed through a 0.45-μm filter. Polybrene (Sigma) was added to the viral suspension at a concentration of 5 μg/mL and used to infect target cells. Successive rounds of infection over 5 days were employed. The infected cells were selected by fluorescence-activated cell sorting (FACS). Following selection, the activity of the dominant negative receptor construct was confirmed by transfection with a 3TP-luciferase reporter (28). The empty vector construct was used to generate a negative control.

**Transduction with a shRNA-CXCR4 or shRNA-GFP lentivirus.** shRNA-CXCR4 or shRNA-GFP lentivirus control plasmids (kindly provided by Dr. Robert Weinberg, Massachusetts Institute of Technology, Cambridge, MA) were engineered into BPH-1 cells by lentivirus infection as described in ref. (29). Activity of the construct was confirmed using Western blot analysis, which consistently showed a 73% to 76% reduction in CXCR4 expression compared with the levels seen in shGFP control cells.
Tissue recombinants and kidney capsule xenograft. All work involving animals was done under protocols reviewed and approved by the Vanderbilt Institutional Animal Care and Use Committee. Rat urogenital sinus mesenchyme (rUGM) was prepared from 18-day embryonic fetuses of pregnant Sprague-Dawley rats (Harlan) as previously described (30). UGM was then additionally reduced to single cells by a 90-min digestion at 37°C with 187 units/mL collagenase (Life Technologies). After digestion, the cells were washed extensively with RPMI 1640. Viable cells were then counted using a hemacytometer.

To prepare tissue recombinants, rUGM or CAF cells were mixed with BPH-1 cells at a ratio of 250,000 stromal cells to 100,000 BPH-1 cells in a sterile microcentrifuge tube in RPMI 1640. The cell mixture was pelleted and resuspended in 50 μL of rat-tail collagen (pretitrated to pH 7.4). After polymerization, the collagen was overlaid with growth medium. After incubation at 37°C overnight, the tissue recombinant was grafted under the renal capsule of intact male CB17/cr/Hsd-severe combined immune deficient (SCID) mice (Harlan). Hosts were sacrificed either 6 weeks (2G7 blocking antibody studies) or 8 weeks (all other studies) postgrafting. The kidneys were removed and imaged before processing for histology. The graft dimensions were measured, and tumor volume was calculated by the ellipsoidal formula: volume = width × length × 0.52. Note that this formula underestimates the volume of invasive tumors, and thus, we tend to underestimate the significance of size differences between small noninvasive and larger invasive tumors.

Treatment of the host mice with TGF-β neutralizing Antibody (2G7). Host SCID mice were ip injected with mouse monoclonal 2G7 (300 μg per mouse) in a 0.2-mL volume via a 26-gauge needle (31), starting 1 day before xenografting surgery and subsequently injected twice weekly at the same dose until sacrifice.

Results

TGF-β signaling is a critical component in the induction of a tumorigenic response to carcinoma-associated fibroblasts. Previous studies have shown that human prostatic CAF can elicit malignant changes in initiated but nontumorigenic human prostatic epithelium (7, 14). To investigate the mechanism underlying this process, we compared the effects of CAF and NPF populations on target epithelia in vitro. Initial studies (data not shown) showed that cells grown in NPF CM proliferated faster than cells grown in serum-free medium, and that proliferation was further increased in CAF CM.

In wound-healing assays, BPH-1 cells were grown in CM from either NPF or CAF until reaching confluence. The monolayers were then wounded with a pipette tip, and the rate of wound closure was recorded. In this case, wound closure was significantly faster in CAF CM than in NPF CM (Fig. 1A).

We examined the effects of abrogation of TGF-β signaling in these epithelial cells on wound healing. Cells expressing a dominant negative TβRII (DNTβRII) showed significantly reduced wound closure rates when grown in CAF CM (Fig. 1A), suggesting a role for TGF-β in this process. To confirm these data, we repeated the experiment in the presence of blocking concentrations of the antibody 2G7 to remove TGF-β ligand from the CM. Under these conditions, wound closure rate in CAF CM was reduced to that seen in NPF CM, whereas the rate in NPF CM was unaffected. Addition of TGF-β ligand to the CM did not affect the rate of wound closure in either NPF or CAF CM (Fig. 1B).

We examined the titer of secreted TGF-β1 in CM from CAF and NPF cells using ELISA. CAF cells secrete elevated TGF-β1 compared with NPF (mean values, 937 ng/mL versus 327 ng/mL, P < 0.01). This result is consistent in multiple groups of CAF and NPF derived from different patients and confirms observations by others (15).

To determine whether the observed effects of TGF-β on proliferation and motility in vitro could contribute to tumorigenesis in vivo, we used tissue recombination approaches. Consistent with our experience over many years, the take rate for all grafts was extremely high in both test and control groups (overall 97.5% (78/80) in this study).

First, as shown in Fig. 2A, BPH-1 cells were infected using retroviruses containing either DNTβRII or control empty vector (EV). Following selection of cells expressing stably integrated constructs, tissue recombinants were generated with CAF cells. In a complementary experiment, shown in Fig. 2B, CAF cells were infected with a human TGF-β1 ligand blocking antibody (2G7). In both cases, the overall tumor...
volume was significantly reduced, and invasive malignant histology ablated in situations where TGF-\(\beta\) signaling was suppressed (DN and 2G7). This contrasted sharply to EV and untreated controls, where (consistent with previous studies) rapidly growing tumors were produced. H&E staining showed that the control tumors were composed of poorly differentiated, irregular epithelia. In some areas, epithelium formed small glandular nests, whereas in other areas, epithelium appeared as single cells that were intermingled within fibrous stroma. Ku70 (which, in our hands, is human specific) and Hoechst33258 staining confirmed that the majority of the stromal cells in these tumors were of human origin, although occasional host-derived stromal cells could also be seen (data not shown). Most epithelia contained large, pleomorphic nuclei with large nucleoli. These data were consistent with the in vitro observations and showed that TGF-\(\beta\) signaling is necessary for CAF-induced tumorigenesis in this model.

We have previously shown that TGF-\(\beta\) acts upon BPH-1 cells to inhibit proliferation, but does not otherwise alter the motility or invasive potential of these cells (22, 32); however, the data presented here suggest a role for TGF-\(\beta\) signaling in tumorigenesis. This is consistent with previous observations of the role of this pleiotropic growth factor, which is known to play both tumor-suppressive and tumor-promoting roles at different disease stages (33). Our data clearly suggest that additional TGF-\(\beta\)-regulated pathways play a role in this model of tumorigenesis.

Both CAF CM and TGF-\(\beta\) can affect epithelial CXCR4. A preliminary analysis of pathways potentially regulated by TGF-\(\beta\) involving paracrine-acting factors thought to be up-regulated in CAF versus normal stroma suggested SDF-1 as a candidate for investigation. SDF-1 signals through the G-protein coupled receptor CXCR4. Induction of CXCR4 in prostatic epithelial cells has been correlated with malignant progression in the prostate, with little or
no expression in benign epithelium and elevated levels seen in cancer and particularly in bony metastases (34–36). TGF-β has been shown to play a role in the regulation of CXCR4 in macrophages and T cells (37, 38). SDF-1 is elevated in human breast cancer stroma where signaling through this pathway plays a role in tumor growth (8).

To determine whether a soluble factor could be involved in inducing expression or changing localization of CXCR4, we grew BPH-1 cells in CAF CM for 72 h. FACS analysis (which detects protein at the cell surface) showed an approximately 5-fold increase in CXCR4 under these conditions (Fig. 3A).

Given our suspicion that TGF-β might be sufficient to regulate CXCR4 action, we examined the expression of CXCR4 on BPH-1 cells grown in serum-free medium containing 5 ng/ml TGF-β for 0, 24, 48, and 72 h. This resulted in a time-dependent elevation in CXCR4 at the cell surface, as detected by FACS analysis, which was similar to that seen in CAF CM (data not shown). Following 72 h of TGF-β treatment, the percentage of cells expressing an empirically determined high level of CXCR4 on their surface membrane (as determined by FACS analysis) increased from <0.5% to nearly 14% (Fig. 3B). However, further analysis determined that CXCR4 mRNA
was detectable by reverse transcription-PCR analysis (data not shown), and protein was seen to be present by Western blot analysis.

Immunofluorescence analysis of BPH-1 cells in serum-free culture revealed a low-level diffuse expression of CXCR4 (Fig. 3C). This was consistent with our flow cytometry observations (which measure only receptor on the cell surface; Fig. 3B, control). Cells in serum-free culture in the presence of TGF-β had a slightly smaller area than untreated cells and showed concentration of stain along the cell membrane (Fig. 3C). This result was in agreement with the FACS analysis, which showed increased levels of the protein detected at the cell surface.

To examine whether TGF-β alters overall expression of CXCR4 mRNA and protein, we used RT-PCR and Western blot analysis. These techniques showed that CXCR4 mRNA (data not shown) and protein could be detected when BPH-1 cells were grown in the either CAF or NPF CM (Fig. 3D). Culture of the epithelial cells in CAF CM resulted in elevations of the total protein levels as compared with culture in NPF CM, and further culture for 72 h in the presence of the TGF-β blocking antibody 2G7 decreased the detectable amount of CXCR4 protein in either CM (Fig. 3D). Taken together, these data suggest that whereas TGF-β can exert some short-term effects on the quantity of CXCR4, it can also play a role in regulating the localization of the protein and, thus, its biological availability.

To examine whether CAF induce CXCR4 in vivo, we examined tissue recombinants prepared using BPH-1 cells recombined with CAF (malignant development) compared with either rUGM or NPF, which induce benign prostatic cords reminiscent of developing human prostate (7, 39). Immunofluorescence staining revealed minimal expression of CXCR4 in epithelial cells of the benign recombinants (Fig. 4A), in marked contrast to the widespread expression seen in the malignant recombinants involving CAF (Fig. 4B). These observations are consistent with published data relating to human clinical samples (36).

TGF-β is necessary for continued epithelial CXCR4 expression. The in vitro experiments described above show that whereas CXCR4 levels are decreased in the short-term absence of TGF-β, the protein does not disappear. To examine whether the elevated CXCR4 levels seen in recombinants with CAF is related to TGF-β

Figure 4. CXCR4 requires TGF-β and parallels malignancy in tissue recombination models in vivo. A, tissue recombinants of BPH-1 cells with either rUGM or NPF. CXCR4 expression was visualized using FITC, with nuclei marked by propidium iodide (rUGM recombinant) or DAPI (NPF recombinant). No widespread expression of CXCR4 was detected in these samples except in the host kidney tissue (*). B, tissue recombinants of BPH-1 and CAF cells were grafted into host mice with (right) or without (left) TGF-β blocking antibody (2G7) treatment. Top, CXCR4 expression was visualized using FITC, with nuclei marked by DAPI showing localization in the treated samples restricted to the host kidney (*). CXCR4 was seen throughout the epithelium of the control recombinant but was not seen in the presence of the TGF-β blocking antibody (2G7). Bottom, phosphorylated Smad2 staining confirmed a lack of signaling downstream of the TGF-β receptor in the 2G7-treated samples.
action, we did immunofluorescence staining in tissue recombinants from the 2G7-treated hosts described above. Under these circumstances, TGF-β1, TGF-β2, and TGF-β3 ligands are blocked by the neutralizing antibody. This experiment showed that in the presence of 2G7, the immunodetection of CXCR4 in the human epithelial cells was suppressed, although CXCR4 expression was still observed in the adjacent host kidney tissue (Fig. 4B). This is consistent with the in vitro data described above and suggests that paracrine TGF-β signaling is necessary for long-term maintenance of expression and membrane localization of CXCR4 in benign human prostatic epithelial cells. Confirmation of the activity of the 2G7 antibody in vivo was provided using staining against phosphorylated Smad2, which confirmed a lack of signaling downstream of the TGF-β receptor in the human cells (Fig. 4B).

SDF-1 contributes to protumorigenic responses in epithelial cells resulting from microenvironmental signaling. For SDF-1 to play a role in promoting carcinogenesis, it is reasonable to expect that its expression would be elevated in tumor stroma. An initial ELISA screen of CM showed that CAF CM contained approximately 3.7 times more SDF-1 than did comparable prepared NPF CM (Fig. 5A). As with all biomarkers, this elevation in CAF cells was always present, but varied somewhat between cell strains derived from different patients. This is consistent with previous studies in clinical samples showing that CXCR4 protein expression is significantly elevated in localized and metastatic prostate cancers, breast cancer, and thyroid cancer (36, 40, 41).

Phosphorylation of Akt is a downstream consequence of the activation of a number of chemokine and cytokine receptors, including TGF-β receptors and CXCR4. Uncontrolled activation of this pathway is linked to malignant changes. Specifically, in this model, as well as in others, elevated P-Akt has been linked to EMT and increased cellular invasion and to suppression of nuclear localization of Smad3 and p21, potentially allowing cells to acquire an ability to avoid the growth-inhibitory effects of TGF-β (22). CAF express a number of growth factors that can activate Akt. To determine whether SDF-1 signaling through CXCR4 contributes to Akt activation, we used an antibody (12G5) to the external domain of CXCR4 to block SDF-1 signaling. Following exposure to CAF CM, there was a steady increase over a 72-h period in the level of Akt caused by the CM. Blocking of CXCR4 activity showed 50% when SDF-1/CXCR4 signaling was blocked by 12G5. C. shRNA constructs targeting GFP (Control) or CXCR4 were retrovirally introduced into BPH-1 cells, which were then selected and used to generate tissue recombinants with CAF. Grafts were harvested after 8 wks, the tumor volumes were calculated, and histology was examined. Gross images show that the control tumors were well vascularized compared with the whiter appearing shCXCR4 tumors. Control tumors were significantly larger (P < 0.01, n = 11 for both test and control) than shCXCR4 tumors. D. histologically, the control tumors were invasive and malignant, with a predominantly squamous to adenosquamous phenotype, per previous descriptions and the controls shown in Fig. 2. In contrast, tumors containing shCXCR4-expressing cells had a well-defined noninvasive border with the adjacent host kidney (*) and contained small foci or cords of epithelium (arrows) with no obviously malignant phenotype.

Figure 5. SDF-1 expressed by CAF can elicit tumorigenesis in BPH-1 cells. A, ELISA was used to test SDF-1 in CAF and NPF CM. CAF CM has significantly elevated levels of SDF-1 compared with NPF CM (P < 0.01). The experiments were done in triplicate using three different CAF/NPF sets. Columns, mean; bars, SD. B, BPH-1 cells were cultured in CM collected from CAF cells with or without the CXCR4 blocking antibody 12G5. The whole cell lysate was probed with an antibody against phosphorylated Akt; β-actin was used as a loading control. CAF CM induced Akt phosphorylation in BPH-1 cells; this induction increased with time and was impaired by ~50% when SDF-1/CXCR4 signaling was blocked by 12G5. C. shRNA constructs targeting GFP (Control) or CXCR4 were retrovirally introduced into BPH-1 cells, which were then selected and used to generate tissue recombinants with CAF. Grafts were harvested after 8 wks, the tumor volumes were calculated, and histology was examined. Gross images show that the control tumors were well vascularized compared with the whiter appearing shCXCR4 tumors. Control tumors were significantly larger (P < 0.01, n = 11 for both test and control) than shCXCR4 tumors. D. histologically, the control tumors were invasive and malignant, with a predominantly squamous to adenosquamous phenotype, per previous descriptions and the controls shown in Fig. 2. In contrast, tumors containing shCXCR4-expressing cells had a well-defined noninvasive border with the adjacent host kidney (*) and contained small foci or cords of epithelium (arrows) with no obviously malignant phenotype.
this process. This supports the contention that TGF-β in CM can contribute to the activation of protumorigenic pathways (specifically by allowing CXCR4 activity), which can then contribute to suppression of the growth-inhibitory activities of TGF-β itself.

**SDF-1/CXCR4 signaling is required for CAF-induced tumorigenesis in vivo.** To examine SDF-1/CXCR4 in CAF-induced tumorigenesis, we used retroviral transduction of a shRNA construct (8) to suppress CXCR4 expression in BPH-1 cells. Western blot analysis showed that cells expressing the shRNA construct expressed ~25% of the CXCR4 seen in controls, FACS studies confirmed that these cells did not express detectable levels of membrane-localized CXCR4 following stimulation with either CAF CM or TGF-β (data not shown). The shRNA-expressing BPH-1 cells and control cells expressing a shRNA designed to target GFP were combined with CAFs and grafted to SCID mice. Two months after xenografting, the siCXCR4 BPH-1 cells formed significantly smaller grafts than controls (Fig. 5C). Histologic staining (Fig. 5D) revealed that the control grafts formed the typical adenosquamous tumors previously described. In marked contrast, there was no tumorigenic response in the siCXCR4-expressing cells. These data show that CXCR4 expression is required for CAF-induced tumorigenesis in this model.

**Discussion**

The data presented here provide important insights into the mechanisms by which paracrine signaling can promote tumorigenesis supporting the idea of TGF-β as a master regulator of intercellular communication. Cross-talk between cytokine and chemokine pathways can elicit stromally induced tumorigenic responses in genetically initiated epithelial cells. One important point is that the changes in protein concentrations and localization, which elicit these profound effects, are not massive. The combination of small alterations in a number of related pathways rather than a massive overexpression or loss of a single factor is important. The data also illuminate the change from tumor-suppressive to tumor-promoting actions of TGF-β.

A number of chemokines and cytokines have been proposed to play a role in the microenvironmental promotion of tumorigenesis. Loss of TGF-β receptor function in stromal cells has been shown to elicit malignant changes in some epithelial tissues (17), suggesting that stroma may contribute to, or suppress, tumorigenesis through paracrine interactions. We have shown that human prostatic CAF can induce initiated but nontumorigenic human prostatic epithelial cells to form tumors (7), and that epithelial cells can be permanently transformed by this process (42).

TGF-β has complex and often apparently contradictory effects depending on dose and context. In many normal tissues, TGF-β inhibits proliferation and enhances differentiation (43). In the prostate, TGF-β inhibits the growth of many nontumorigenic prostatic epithelial cell lines and is implicated in the differentiation of prostatic smooth muscle, a key component of prostatic development (22, 44). TGF-β also plays a key role in tumorigenesis where signaling, especially through non-Smad pathways, has been implicated in disease progression (3, 45, 46). We have recently shown that, following transformation caused by exposure to CAF, human prostatic epithelial cells can acquire an ability to ignore the growth-inhibitory effects of TGF-β as a result of elevated activated Akt, which inhibits nuclear translocation of p21 and Smad3 (22). Other published data support the proposal that interactions between Akt and Smad3 vary depending on the relative titers of these proteins. These interactions may be important in avoiding growth inhibition by TGF-β either as a result of changes in Smad3 localization, degradation, or by the inhibition of Smad3 phosphorylation by mTOR-dependent mechanisms (47–49). Given the pleiotropic nature of TGF-β signaling, it is possible, and indeed likely, that the variations noted between these studies reflect the specific details of the various models used.

Our initial findings of elevated expression of TGF-β by CAF were consistent with observations by others working in this field (15) and were of interest because of studies indicating the possible role of TGF-β in enhancing tumor progression (22). The *in vivo* and *in vitro* studies described here showed that TGF-β contributes to oncogenic effects on BPH-1 cells. TGF-β was shown to be necessary for CAF-induced tumor formation by BPH-1 cells. However, TGF-β per se is not tumorigenic to these cells. Previous studies showed that TGF-β acts upon BPH-1 cells to inhibit proliferation (22, 32). These observations set up a familiar apparent paradox mirroring that seen in a number of human tumors, where TGF-β is growth inhibitory for normal cells and yet promotes tumor progression (33).

SDF-1 is overexpressed in human breast (8) and prostate CAF (Fig. 5A). SDF-1 can contribute to both tumor growth and angiogenesis (8). We show here that TGF-β or CAF CM *in vitro* and CAF cells *in vivo* were able to increase expression and membrane localization of the SDF-1 receptor, CXCR4, by the epithelial cells. TGF-β was shown to be both necessary and sufficient for receptor expression in the nontumorigenic epithelial cells.

Elevation of CXCR4 expression is observed in human prostate cancer progression, with little expression in benign tissue and elevated expression seen in tumors (36). Elevated CXCR4 is also seen in other human tumors and is linked to increased tumor growth and poor prognosis. In this study, we show that SDF-1/CXCR4 signaling is required for CAF-induced tumorigenesis of BPH-1 cells. This work extends previous observations by establishing links between the TGF-β and SDF-1 pathways. The data presented here provide a mechanism by which epithelial cells can use elevated levels of TGF-β found in tumor stromal cells as a triggering mechanism to respond to the effects of elevated stromal levels of SDF-1 found in CA. As tumorigenesis progresses, tumor epithelial cells tend to express increased levels of TGF-β. Indeed, TGF-β secretion is elevated between 4- and 20-fold in the tumorigenic lines derived from BPH1 as compared with the parental cells. Such tumor cell–derived TGF-β could further contribute, by an autocrine route, to the total exposure of tumor cells from their microenvironment and, thus, enhance tumor promotion. In the model used here, epithelial cell–derived TGF-β would seem to be insufficient to trigger early malignant changes, but could certainly contribute to the overall growth and later progression of tumors.

Although BPH-1 cells show growth inhibition upon TGF-β treatment, the tumorigenic derivative BPH-1CAPTD lines avoid such inhibition via the effects of elevated levels of constitutively active Akt expression, which blocks nuclear translocation of Smad3 and p21 (22). We show here that during malignant transformation, SDF-1 signaling contributes significantly to the elevation of phosphorylated Akt in the target epithelial cells. These observations (summarized in Fig. 6) show a potential feedback loop.

---

5 O. E. Franco and S. W. Hayward, unpublished observations.
between the TGF-β and SDF-1 pathways. Elevated stromal TGF-β elicits epithelial CXCR4 expression, allowing stromal SDF-1 to activate Akt in the epithelial cells. P-Akt can then contribute to a loss of the growth-inhibitory response to TGF-β. Cells act as signal integrating centers, and this transition and continued activation of CXCR4 during tumor progression. This stylized and simplified diagram brings together the data from this study and others and presents a model illustrating how the TGF-β and SDF-1/CXCR4 pathways might interact initially to contribute to tumor formation and to set up conditions that would predispose cells to further malignant progression. In particular, this model suggests a mechanism by which TGF-β could switch from a tumor-suppressive to a tumor-promoting role, via a large increase in Akt activation brought about through TGF-β-induced CXCR4 activation. Activated Akt also induces Smad3 activity, allowing the cells to sidestep growth-inhibitory responses to TGF-β while continuing to retain a response to its growth-promoting activity.

Figure 6. Interactions of TGF-β and SDF-1 pathways in tumorigenesis and tumor progression. This stylized and simplified diagram brings together the data from this study and others and presents a model illustrating how the TGF-β and SDF-1/CXCR4 pathways might interact initially to contribute to tumor formation and to set up conditions that would predispose cells to further malignant progression.


Cross-talk between Paracrine-Acting Cytokine and Chemokine Pathways Promotes Malignancy in Benign Human Prostatic Epithelium

Mingfang Ao, Omar E. Franco, Dean Park, et al.


Updated version
Access the most recent version of this article at:
http://cancerres.aacrjournals.org/content/67/9/4244

Cited articles
This article cites 49 articles, 14 of which you can access for free at:
http://cancerres.aacrjournals.org/content/67/9/4244.full#ref-list-1

Citing articles
This article has been cited by 25 HighWire-hosted articles. Access the articles at:
http://cancerres.aacrjournals.org/content/67/9/4244.full#related-urls

E-mail alerts
Sign up to receive free email-alerts related to this article or journal.

Reprints and Subscriptions
To order reprints of this article or to subscribe to the journal, contact the AACR Publications Department at pubs@aacr.org.

Permissions
To request permission to re-use all or part of this article, contact the AACR Publications Department at permissions@aacr.org.