Suppression of Tak1 Promotes Prostate Tumorigenesis

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Abstract

Over 30% of primary prostate cancers contain a consensus deletion of an approximately 800 kb locus on chromosome 6q15.1. The MAP3K7 gene, which encodes TGF-β Activated Kinase-1 (Tak1), is a putative prostate tumor suppressor gene within this region whose precise function remains obscure. In this study, we investigated the role of Tak1 in human and murine prostate cancers. In 50 well-characterized human cancer specimens, we found that Tak1 expression was progressively lost with increasing Gleason grade, both within each cancer and across all cancers. In murine prostate stem cells and Tak1-deficient prostatic epithelial cells, Tak1 loss increased proliferation, migration, and invasion. When prostate stem cells attenuated for Tak1 were engrafted with fetal urogenital mesenchyme, the histopathology of the grafts reflected the natural history of prostate cancer leading from prostatic intraepithelial neoplasia to invasive carcinoma. In the grafts containing Tak1-suppressed prostate stem cells, p38 and JNK activity was attenuated and proliferation was increased. Together, our findings functionally validate the proposed tumor suppressor role of Tak1 in prostate cancer.
Introduction

Chromosome 6q14-21 is frequently deleted in the genome of prostate cancer (1) although specific prostate tumor suppressor genes have not been identified in this region. Recently, Liu et al. using SNP arrays identified an 870 kb consensus deletion located on chromosome 6q15 (2). The frequency of 6q15 deletion was significantly higher in tumors with Gleason score ≥ 8 (12 of 17 tumors, 71%) than in those of Gleason scores ≤ 7 (9 of 38 tumors, 24%). The association between 6q15 copy number changes and Gleason score was stronger than the association of any other common recurrent DNA copy number change identified, including PTEN, which had a similar prevalence of deletion but lower association with Gleason score. The majority of 6q15 deletions were hemizygous.

Five genes are deleted in the 6q15 consensus region; MDN1, CASP8AP2, CX62, BACH2, and MAP3K7, as well as one pseudogene (LOC644269). Four of these five genes are either required for cell viability [MDN1 (3) and CASP8AP2 (4, 5)] or are expressed in a tissue-specific manner that does not include the prostate [CX62 (6) and BACH2 (7)]. Therefore, these four genes are not good candidate prostate tumor suppressor genes.

The MAP3K7 gene encodes TGF-β activated kinase-1 (Tak1), a member of the MEKK family, which was identified for its role in non-canonical TGF-β receptor signaling through the MAP kinase pathway leading to JNK and p38 activation (8). Tak1 is also a downstream signaling molecule of numerous other pathways, including IL-1(9), TNF (10), Wnt/β-catenin (11), and Toll receptor (12) pathways. Cytokines such as TNFα and IL-1 activate signaling cascades in inflammatory cells that involve MAP kinase signaling and lead to activation of NF-kB and/or
June-N-terminal Kinase (JNK) (13). Tak1 has been found to be a central mediator of these signaling pathways (10, 12). Recent work has demonstrated a role for Tak1 in the activation of Snf1/AMP-activated protein kinase (AMPK) (14, 15) and in the activation of LKB1 (16). These studies demonstrate an important regulatory role of Tak1 in integrating multiple signaling pathways and suggest that MAP3K7 could function as a tumor suppressor.

Together, our previous genetic data that demonstrate frequent hemizygous deletion of MAP3K7 in prostate cancer and the known roles of Tak1 in integrating and regulating multiple signaling pathways important for prostate growth and differentiation support a role for Tak1 as a prostate tumor suppressor. However, the functional role of Tak1 as a prostate tumor suppressor has not been reported.
Materials and Methods

Human Samples

Formalin-fixed paraffin-embedded prostate tissues were from men who underwent radical prostatectomy at Stanford University Medical Center between 1983 and 1998. There is no information on race in this cohort. Historically during this period greater than 95% of men who underwent prostatectomy at Stanford University were Caucasian. This study received Institutional Review Board approval. Fifty prostate cancers were sectioned at Stanford University. The detailed information of staining and scoring TAK1 protein is described in Supplemental Materials and Methods and Supplementary Table 1.

Cell Culture

The isolation and characterization of the adult mouse prostatic stem/progenitor cell line, WFU3 was described previously in detail (17, 18). Tak1^{lox/lox} mouse prostate epithelial cells (MPECs) were isolated from the prostate of 8-week Tak1^{lox/lox} male mice as previously described (18). Generation and genotyping of Tak1^{lox/lox} mice were described previously in detail (12). To generate Tak1^{-/-} cells, Tak1^{lox/lox} MPECs were infected with self-deleting Cre-recombinase lentivirus (19). Individual clones from Cre or Mock-infected cells were isolated by limiting dilution. Both types of cells were maintained in 50:50 Dulbecco’s modified Eagle’s medium (DMEM)/ Ham’s F-12 Medium (F12) with supplements as previously described (17, 18).
Reverse Transcription-Polymerase Chain Reaction

Total RNA of WFU cells was isolated with TRIzol® Reagent (Invitrogen, Carlsbad, CA). RNA was quantified and treated with RQ1 RNase-free DNase (Promega, Madison, WI) to remove DNA contaminations. The detailed materials, methods and sequences of each primer used in PCR reactions are described in Supplemental Materials and Methods and Supplemental Table 2.

Lentivirus-mediated Gene Knockdown

The shRNA plasmids, pBS/U6/Map3k7 (target sequence GCCAGTGTTCGAACATT) and pBS/U6/shControl (GGGCCATGGCACGTAC GGCAAG) were constructed based on previously published work (20). The shRNA targeting sequences were cloned into a modified LentLox3.7 lentivirus vector (21, 22). Methods to generate lentivirus were described previously (23). Infection efficiency was detected by EGFP expression. Individual clones were isolated using cloning cylinders after cells were grown at clonogenic density.

Cell Growth Assay

Mouse shTak1 or shControl cells were inoculated onto 6-well culture dishes at 1 x 10^4 cells per well (n=3). At the indicated time points the cells were labeled with trypan blue and counted using Vi-CELL™ Series Cell Viability Analyzers (Beckman Coulter, Brea, CA) following the manufacturer’s instructions. Clonogenic assays were performed by inoculation of serial 0.5 fold dilutions (from 125 to 2000 cells per dish) of viable cells onto 60-mm dishes (n=3). After 10-days growth in culture, cells were fixed in 10% formalin and stained with 0.1% crystal violet/95% ethanol solution for 10 minutes. Colonies were counted manually.
Immunoblots

Protein lysates from cells or tissues were collected and quantified by following standard protocols. Approximately 25 μg of lysate were used for immunoblots. Protein resolving, membrane transferring, and blocking were performed following standard protocols. The membranes were incubated with primary antibodies for Tak1 (1:1,000), P-JNK (1:1,000), JNK (1:2,000), P-p65 (1:1,000), p65 (1:2,000), P-p38 (1:2,000), p38 (1:1,000), α-tubulin (1:4,000) (all from Cell Signaling, Danvers, MA), and β-actin (1: 100,000, Sigma-Aldrich) at 4 °C, overnight. Following washing, membranes were incubated for 1 hour at room temperature with rocking with a 1:2,000 dilution of horseradish peroxidase (HRP)-conjugated secondary antibody (Santa Cruz Biotechnology, Santa Cruz, CA). The HRP signal was detected using the ECL Plus Kit (Amersham Pharmacia Biotech, Buckinghamshire, England).

Immunofluorescence

Cells were inoculated at clonogenic densities in 6-well dishes containing glass coverslips (Carolina Biological, Burlington, NC). Twenty-four to 48 hours after inoculation the cells attached to coverslips were washed with 1 x PBS, fixed in 3% formaldehyde/PBS (Electron Microscopy Sciences, Hatfield, PA) and permeabilized in 0.1%Triton-x-100/PBS (Fisher Scientific). F-actin was labelled with Alexa Fluor 594 phalloidin conjugate (Molecular Probes, 1:250 in 5% donkey serum/PBS). Nuclei were labelled with Hoechst 33258 (Molecular Probes, 1:10,000 dilution in PBS for 5 minutes). All coverslips were mounted in ProLong Gold (Invitrogen).
Migration Assay

Cells were inoculated onto 60-mm dishes (1 x 10^6 cells per dish) and allowed to grow for 24 hours. After the incubation period a wound was made in the monolayer by scratching the dish with a 1 ml pipette tip. Cells were washed with HEPES-buffered saline (HBS) twice and cultured in complete growth medium. At time zero specific loci were marked for future reference and the closing of the scratches was observed at subsequent time points. Digital images of each indicated locus were taken every 10 hours. The distance of cell migration at a particular time point was measured with Photoshop CS3 (Adobe Systems Incorporated, San Jose, CA).

Invasion Assay

Invasion assays were performed using BD BioCoat™ Matrigel™ invasion chambers (BD Biosciences) following the manufacturer’s instructions. The detailed material and methods were described in Supplemental Materials and Methods.

Tissue Recombination

All procedures with animals were approved by the Wake Forest University Institutional Animal Care and Use Committee. Prostate tissue recombination was performed as described previously (17, 24-26). The detailed materials and methods are described in Supplemental Material and Methods.
Immunohistochemistry

Immunohistochemistry was performed by using SensiTek HRP (Anti-Polynalent) Ready-To-Use Lab Pack (ScyTek Laboratory, Logan, UT) by following the manufacturer’s instructions. Sections were incubated at 4 °C with primary antibodies: androgen receptor (AR) (1:500, Santa Cruz Biotechnology), p63 (1:500, Santa Cruz Biotechnology), CK5 (1:1,000, Covance), CK14 (1:500, Covance), CK8 (1:100, Abcam), CK18 (1:200, Abcam), and Ki67 (1:2,000, Abcam, Cambridge, UK). Detailed methods were described in Supplemental Materials and Methods.

Statistical Methods

Repeated measures ANOVA was performed that accounted for the within-clone correlation of repeated measures due to replicates or time points using a mixed-effects regression modeling approach to test for differences by group and clone. ANOVA and t-tests were used for analysis of cross-sectional data. More detailed information is described in Supplemental Materials and Methods. A two-sided p-value < 0.05 was considered statistically significant. All analyses were performed using SAS v9.2 (SAS Institute Inc., Cary, NC) and Stata v10.1 (StataCorp, College Station, TX).

RESULTS

Tak1 Expression Is Lost in High Grade Human Prostate Cancer

Figure 1A shows serial sections of prostate cancers of the indicated Gleason grades with hematoxylin and eosin staining (upper panels) and Tak1 immunohistochemistry (lower
panels). The numbers within images indicate the deduced score of staining. Note that the benign sample also contains a focus of cancer in the image presented, which is also scored for Tak1. Most slides contained some proportion of benign glands as well as multiple grades of tumor due to heterogeneity (Supplementary Table 1). Each slide was evaluated for Tak1 score for each Gleason grade of cancer in the section by two board certified human prostate pathologists, Joseph S. Sirintrapun and Adela Cimic (Supplementary Fig. S1, Supplementary Table 1). Tak1 expression was progressively lost with increasing Gleason grade both within each cancer and across cancers (Supplementary Table 1 and Figure 1B).

Gene copy number analysis demonstrated that only one copy of the MAP3K7 gene is retained in three prostate cancer cell lines (LnCaP, DU145, PC3, Supplementary Fig. S2A). No mutations were detected in the retained copy of the MAP3K7 gene in any of the three cell lines (Supplementary Fig. S2A). We analyzed the methylation of MAP3K7 promoter region by using bisulfite sequencing method. We found CpG islands in the promoter regions of DU145 were hypermethylated (Supplementary Fig. S2A and S2B), but not in LnCaP or PC3 cells.

**Deficiency of Tak1 Altered Growth of Mouse Prostate Cells In Vitro**

To model the role of Tak1 in prostate growth and development both *in vitro* and *in vivo*, we used a novel mouse prostate stem cell developmental model that we described (17). In this model, a stem cell line we developed (WFU3) (18) can be grown and manipulated *in vitro* and subsequently used for *in vivo* analysis of prostate glandular development. We explored the expression of the five genes, *Map3k7, Casp8ap2, Gja10, Bach2*, and *Mdn1*, whose homologs are deleted in prostate cancer at the human 6q15 locus, in the syntenic region of the mouse
genome (Ch4qA4) (Supplementary Table 2). Reverse transcription PCR of total RNA isolated from semi-confluent WFU3 cells is shown in Figure 2A. Negligible gene expression was detected for Bach2, Gja10 (the mouse CX22 homolog) and Mdn1. Both Map3k7 and Casp8ap2 exhibited robust expression. Given the recent literature that indicates an essential role of Casp8ap2 in histone gene expression (4, 5), we reasoned that the possibility of CASP8AP2 being a tumor suppressor gene was less likely than for MAP3K7. Therefore, the role of Tak1 as a tumor suppressor was explored further.

We knocked down the expression of Tak1 in WFU3 cells by infection with Tak1 shRNA lentivirus (shTak1). ShRNA lentivirus (shControl) that does not significantly recognize the sequence of any known gene, was used as control. To remove the uninfected cells from the pooled cell populations, we isolated individual clonal populations with high E-GFP expression. Immunoblots probed for Tak1 expression demonstrated that shTak1 shut down the expression of Tak1 protein to nearly undetectable levels (Fig. 2B). We assessed cell growth in presence or absence of Tak1. Interestingly, we found that shTak1 WFU3 cells exhibited faster kinetics of growth under monolayer conditions (Fig. 2C) and greater clonogenic survival relative to shControl cells (Fig. 2D). In parallel to these studies with WFU3 progenitor cells, we also generated mouse prostatic epithelial cells (MPECs) from Tak1lox/lox mice (12) and deleted the floxed allele in vitro with self-deleting Cre lentivirus (19) (Fig. 2E). Clonal populations were isolated from Cre lentivirus- and Mock-infected cells. Similar to what we found with shTak1 WFU3 cells, loss of Tak1 increased cell viability under monolayer growth conditions (Fig. 2F).
Deficiency of Tak1 Expression Promotes Cell Motility and Invasion In Vitro

During the course of generation and characterization of WFU3 cells with knockdown of Tak1, we noted a distinct morphological change in shTak1 cells relative to shControl cells. We found that shControl cells grew in clusters with extensive cell-cell junctions and presented a polygonal cobblestone-like shape (Fig. 3A). This pattern of growth is a normal phenotype for WFU3 cells grown under these conditions. In contrast, shTak1 WFU3 cells grew in a loosely scattered pattern, with very few cell-cell junctions and an elongated spindle-like shape (Fig. 3A). Cell-scatter assay demonstrated that more shTak1 cells underwent scattering and cell-cell disassociation compared with shControl cells (Supplementary Fig. S3A and B). To further evaluate the morphological difference between shTak1 and shControl cells, we labeled the cells with fluorescent phalloidin to visualize F-actin in cells growing in monolayer. shControl cells grew in clusters with F-actin staining concentrated at the cell interfaces, whereas shTak1 clones exhibited a reorganization of the F-actin away from the membrane into stress fibers with fan-shaped protruding edges (Fig. 3A). This morphological change was suggestive of a more motile phenotype. To test the motility of the cells we performed wound healing, or scratch assays, a scratch was made in a confluent monolayer and repeat images were captured from specific locations every 10 hours. The rate of cell migration into the “wound” was determined after calculation of the distance migrated at each time point. We observed enhanced migration of shTak1 cells at every time point (Fig. 3B). The migratory enhancement was evident for multiple clones and was reproduced in Tak1-null MPECs, relative to their floxed counterparts (Fig. 3C). We next measured the ability of shTak1 and shControl cells to migrate through an extracellular matrix using a Matrigel Boyden Chamber assay. Knockdown of Tak1 enhanced migration through Matrigel approximately 4-fold (Fig. 3D). In response to
TNFα Tak1 can activate JNK/p38 or NFκB which regulate the transcription of genes involved in apoptosis, survival, motility, or inflammatory response (10, 12, 13). We found that activation of both JNK and NFκB (p65) was attenuated in Tak1 null prostate epithelial cells upon the treatment of TNFα (Fig. 3E).

**Suppression of Tak1 in Prostate Stem Cells Promotes Prostate Tumorigenesis In Vivo**

We hypothesized that if the *in vitro* alterations we observed with shTak1 cells were manifested *in vivo*, then hyperplastic and possibly invasive developmental abnormalities would ensue. Three clones each of shTak1 cells and shControl cells were independently combined with UGM and grafted under the renal capsules of nude mice. For each clone, four independent grafts were prepared. After 10 weeks of *in vivo* growth the grafts were harvested, fixed, and sectioned for histology. The histological evaluation was done by a board certified veterinary pathologist, J. Mark Cline and by Scotrt D. Cramer. Grafts containing UGM alone exhibited small mesenchymal masses with no epithelium evident (Fig. 4A). Grafts from shControl cells only formed benign structures (Fig. 4A and B) with complete lineage differentiation into androgen receptor (AR), CK8, and CK18 positive luminal cells, p63, CK5, and CK14 positive basal cells, and secretion of mouse dorso-lateral secretory protein (mDLP) into the lumens (Fig. 4C). Three of the grafts from the shControl cells had small foci of benign hyperplasia (p63 and AR positive) with no evidence of nuclear atypia (Supplementary Fig. S4). These results are consistent with the benign phenotype of the parental WFU3 cells that we reported previously (17). In contrast, while all of the grafts formed from shTak1 cells had the presence of some benign glands, 80% percent showed dysplasia and/or high grade prostatic intraepithelial neoplasia (PIN) (Fig. 4A and B), and one had evidence of invasive carcinoma...
(Fig. 4A and B). The average weight of grafts formed either by shControl cells or shTak1 cells was not significantly different (Fig. 4D). To confirm the histopathological diagnosis we stained sections with lineage-specific markers AR, CK8, CK18 (luminal cell markers), p63, CK5, and CK14 (basal cell markers) (Fig. 5) (see (27)). Areas with morphologic features of high-grade PIN were confirmed by abundant luminal cell crowding, nuclear atypia, prominent nucleoli (arrow head in Fig. 5) and with retention of an intact p63, CK5, or CK14-positive basal cell layer (arrow in Fig. 5). We also observed basal cell hyperplasia characterized with crowding of basal cells and association with inflammatory cells (28), suggesting the histological transition to more proliferative phenotypes related to normal and nodular structures (circles in CK5 and CK14 staining, Fig. 5). Areas of invasive carcinoma were primarily composed of tightly packed small tubular structures either forming well-formed glands with lumens or poorly-formed glands without lumina. Immunohistochemically, invasive carcinoma showed strong AR, CK8, and CK18 positivity (arrow head in Fig. 5), with invasion confirmed by absence of p63, CK5, and CK14 positive basal cells (arrow in Fig. 5). Focal areas of p63 positive clusters were also observed, which may indicate areas of basal cell hyperplasia or stem cell clusters. We also evaluated expression of Tak1 in all grafts by using immunohistochemistry and immunoblot probed with Tak1. As expected, expression of Tak1 was diminished in grafts formed by shTak1 cells compared with grafts formed by shControl cells (Fig. 6A and B). Moreover, activation of p38 and JNK was demonstrated to be attenuated in the grafts containing shTak1 cells compared with shControl grafts, which was consistent with the in vitro results that activation of JNK was decreased in shTak1 cells when treated with TNFα (Fig. 3E).
Suppression of Tak1 Increases Cell Proliferation In Vivo

We measured in vivo cell proliferation in shControl or shTak1 grafts by Ki67 staining. We found that cell proliferation was increased between areas of benign glands, PIN and invasive carcinoma in shTak1 grafts (Fig. 7A and B). In vitro, we observed that suppression or loss of Tak1 increased cell proliferation in both monolayer and clonogenic growth conditions (Fig 2C, D and F). Therefore we compared cell proliferation by Ki67 staining in all benign regions from shControl and shTak1 grafts. Ki67 staining demonstrated a significant increase in proliferation in vivo by suppression of Tak1 (Fig. 7C and D). These data demonstrate that suppression of Tak1 in prostate stem cells leads to a high proliferation index in vivo.

DISCUSSION

This study investigated the tumor suppressor roles of Tak1 in prostate cancer. We demonstrated progressive loss of Tak1 expression in human prostate cancer with increasing Gleason Grade. We also found promoter methylation in the retained copy of MAP3K7 in DU145 cells. The data support previous genetic data that demonstrated deletion of the MAP3K7 locus. We used a novel developmental model, which has mouse prostate stem cells at its core, to assess the functional role of Tak1 expression on proliferation, motility, invasion, and morphological changes in vitro and in vivo. We found that loss of Tak1 in the prostate stem cell increased proliferation and invasion both in vitro and in vivo. In vivo, loss of Tak1 recapitulated developmental stages of human prostate cancer, with shTak1 cells producing benign glands, abundant PIN and frankly invasive carcinoma. These studies are important because they establish a causal role for loss of Tak1 expression in prostate tumor development.
Importantly, these studies establish a paradigm to functionally model putative prostate cancer genes using an *in vitro*/*in vivo* prostate developmental model.

Previous work by our group demonstrated somatic loss of 6q15.1 in human prostate cancer at rates approaching 40% (2). The loss of 6q15.1 was the most prevalent deletion in the genome. In addition, ≅ 70% of high-grade cancers showed loss of one copy. These studies suggested the presence of a tumor suppressor at this locus. Of the five genes in the locus of the consensus deletion, *Map3k7* and *Casp8ap2* were the only ones expressed in our mouse prostate stem cells. The lack of expression of the other three is consistent with previous literature.

*CASP8AP2*, Caspase 8 associated protein 2 (also known as FLASH), was identified as a homolog of the C elegans CED-4 protein (the mammalian ortholog of CED-4 is Apaf-1). *CASP8AP2* was originally described as a proapoptotic activator of caspase 8 (29). However, subsequent work has raised doubts about whether this protein is proapoptotic (30, 31). Given the contradictory findings on the role of FLASH in apoptosis, our studies focused on Tak1, encoded by *MAP3K7*, as the most likely tumor suppressor at this locus.

Tak1 is a prominent and important component of multiple signaling pathways including interleukin 1 and Toll receptor signaling, TRAIL and TNF signaling as well as modulation of the Wnt/β-catenin pathway through phosphorylation of nemo-like kinase. Here we demonstrated that loss of Tak1 attenuated TNFα mediated phosphorylation of p38 and p65. In the liver, loss of Tak1 leads to fibrosis, inflammation and carcinogenesis (32). Recent work has attributed the tumor suppressive role of Tak1 in liver cancer to its role in TNF-induced
NFκB activation and modulation of NEMO activity (33). Further work is needed to elucidate the role of Tak1 loss in these processes in prostate cancer.

Interestingly, loss of Tak1 expression in and of itself is sufficient to promote changes in morphology and invasion in vitro. These observed functions of Tak1 are not previously described and imply a basal role of Tak1 in the maintenance of a differentiated epithelial phenotype. In addition, this study demonstrates the utility of stem cell models to functionally validate prostate tumor suppressors, and by extension prostate oncogenes. Until recently, previous models relied on intact transgenic or knockout mice for specific target evaluation. These studies have been extremely informative and have validated such targets as c-myc (34), Pten (35), Nkx3.1 (36) and p27 (37). However, these models are time consuming, expensive, and become exponentially cumbersome when interrogating gene-gene and epithelial/mesenchymal interactions. The model described here is; 1) rapid ≅ 6 months from target identification to in vitro gene manipulation and in vitro/in vivo functional analysis; 2) comparatively inexpensive; and 3) uniquely suited for interrogating interactions between genes and tissue compartments. Primary isolation of mouse prostate stem cells by cell sorting has recently been used to evaluate the functional roles of stem cells in prostate tumor progression (38). Recently prostate stem cell models have been used as powerful screening tools to interrogate the functional role of putative prostate cancer genes (39-41).

In summary, we describe MAP3K7 as a prostate cancer tumor suppressor gene whose encoded protein, Tak1, has important roles in proliferation and invasion. We also describe the utility of a prostate developmental model for validation of prostate cancer genes.
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Reference


FIGURE LEGENDS

Figure 1. Expression of Tak1 Is lost in High Grade Human Prostate Cancer

(A) H&E and immunohistochemistry for Tak1 in representative prostate specimens. The numbers within images are the deduced expression score based on the expression matrix depicted in Fig. S1 for Tak1 expression. Note: The benign section contains a small focus of carcinoma with reduced expression of Tak1 relative to the benign tissue in the same section.

(B) The expression intensity of Tak1 was scored in each section based on the matrix presented in Fig. S1 and categorized based on tissue pathology. Each bar represents the mean ± SEM. Numbers in parentheses represent the sample size for that specific pathology that was scored. Bars with the same letter above them are not statistically significantly different from each other. Statistical significance was determined by ANOVA with post-hoc analysis by Sheffe’s multiple comparison test, P<0.05 was considered significant.

Figure 2. Deficiency of Tak1 in Mouse Prostate Stem Cells Promotes Growth

(A) Expression in normal WFU3 prostate stem cells of the five genes that are deleted at 6q15.1 in human prostate cancer. Note GJA10 is the mouse homolog of CX22.

(B) Immunoblot of Tak1 expression in individual clones from WFU3 cells infected with virus expressing Control shRNA (shControl) or Tak1 shRNA (shTak1).

(C) Kinetics of cell viability of shControl or shTak1 clones in monolayer growth.
(D) Clonogenic growth assay of shTak1 clones or shControl clones over a 10-day growth period. Results are mean ± SEM, n=3. A and B are significantly different at each time point, p<0.05. Two-group t-tests and repeated ANOVA were used to compare individual clones.

(E) Deletion of Tak1 in MPECs. Upper two panels, PCR results from DNA isolated from Cre lentivirus-infected cells and Mock-infected Tak1<sup>lox/lox</sup> cells. Bottom two panels, immunoblot of Tak1 in individual Tak1<sup>lox/lox</sup> or Tak1<sup>−/−</sup> clones.

(F) Loss of Tak1 increases cell proliferation in vitro. Trypan blue exclusion assay of Tak1<sup>lox/lox</sup> (n=3) or Tak1<sup>−/−</sup> (n=3) clones over 140-hour growth. Results are mean ± SEM. A and B are significantly different at each time point. P<0.05. Two-group t-tests were used to compare individual clones.

Figure 3. Suppression of Tak1 Promotes an Invasive Phenotype In Vitro

(A) Suppression of Tak1 alters cell morphology and arrangement of F-actin. Top panels: representative phase contrast images of shControl and shTak1 clones. These morphological differences were consistent across multiple clones for each background (not shown). Middle and lower panels, immunofluorescent visualization of F-actin. Red, Alexa Fluor 594 phalloidin labeling. Blue, Hoechst.

(B) Suppression of Tak1 promotes migration. Scratch assay with shControl or shTak1 clones to assess migration as a function of Tak1 status. Upper panel: Representative phase contrast images at the indicated time points. Black lines on images depict the location of the cell front. Lower Panel: Quantification of migration. Results are mean ± SEM. A and B are significantly different; P<0.05. Two-group t-tests were used to compare individual clones.
(C) Loss of Tak1 promotes migration. Scratch assay with Tak1<sup>lox/lox</sup> or Tak1<sup>−/−</sup> clone to assess migration. Upper panel: Representative phase contrast images at the indicated time points. Black lines on images depict the location of the cell front. Lower Panel: Quantification of migration as described in (B).

(D) Boyden chamber assay for evaluation of the invasive ability of shControl and shTak1 cells. Upper Panel: Images from crystal violet-stained chambers after invasion. Lower Panel: Quantification of invasive cell number. Bars represent the mean ± SEM, n=3 wells for each group. Statistics were described in (A).

(E) Immunoblots demonstrate that loss of Tak1 attenuates activation of JNK and NFκB in response to TNFα <i>in vitro</i>. Cells were starved by depletion of all supplements for 16 hours before treatment with TNFα (10 ng/ml). Lysates were collected at indicated time points.

Figure 4. Suppression of Tak1 Promotes Invasive Carcinoma <i>In Vivo</i>.

(A) Histology of representative grafts generated by recombination of UGM with shControl or shTak1 cells. Upper panels: representative gross morphology after 10 weeks <i>in vivo</i>. Lower panels: representative sections stained with hematoxylin and eosin. Scale bars: 10X=2000 μm, 400X=50 μm

(B) Distribution of phenotypes in shControl and shTak1 tissue recombinant grafts. Hematoxylin and eosin-stained sections from each graft were scored for the presence of benign, PIN, and carcinomatous structures by 2 observers who were blinded to the genotype of the graft. Each column represents pooled data for shControl clones and for shTak1 clones.

(C) Complete Lineage Differentiation of shControl Cells <i>in vivo</i>. Immunohistochemistry of AR, CK8, CK18, p63, CK5, CK14, and mouse dorsal-lateral secretory protein (mDLP) showing complete lineage differentiation of shControl cells <i>in vivo</i>.
(D) Quantification of average weight of grafts formed by shControl or shTak1 cells. Bars represent the mean ± SEM.

Figure 5. Suppression of Tak1 in PrP/SCs Leads to Heterogeneous Phenotypes Including Benign prostate, PIN, and Carcinoma in vivo.

Immunohistochemistry for AR, p63, CK8, CK18, CK5 or CK14 of representative areas of benign prostate, PIN, and carcinoma from shTak1 grafts. PIN areas show retention of intact basal layer (arrow), pleiomorphic nuclei, prominent nucleoli, and hyperplastic filling of lumen (arrow head). Carcinoma areas show lacking of intact p63, Ck5, or CK14 positive basal layer (arrow) and elevated AR, CK8, or CK18 expression (arrow head). All images were taken at 400X magnification. Scale bar = 50 μm.

Figure 6. Suppression of Tak1 attenuates activation of p38 and JNK in vivo.

(A) Expression of Tak1 is decreased in grafts containing shTak1 cells. Immunohistochemistry for Tak1 in benign, PIN, or carcinoma areas from grafts containing shControl or shTak1 cells.

(B) Suppression of Tak1 attenuates activation of p38 and JNK in grafts. Protein lysates were collected from grafts containing shControl or shTak1 cells. Immunoblots for phosph-p38 (P-p38) and phosph-JNK (P-JNK) were performed to evaluate activation of p38 and JNK, respectively.
Figure 7. Suppression of Tak1 Increases Cell Proliferation \textit{in vivo}.

(A) Immunohistochemistry for Ki67 of representative areas of benign prostate, PIN, and carcinoma from shTak1 grafts.

(B) Quantification of Ki67+ cells in representative areas of benign prostate, PIN and carcinoma from grafts containing shTak1 cells. Bar chat shows the significantly increase of percentage of ki67 positive cells in PIN and tumor areas. Expression of Ki67 was quantified with percentage of ki67 positive cells to the total cells in each area (n=10). Results are mean ± SEM. A, B, and C are significantly different; P<0.05, two sided. Non-parametric analysis was used.

(C) Immunohistochemistry for Ki67 in benign areas from shControl or shTak1 recombinants.

(D) Quantification of ki67+ cells from (C). Quantificational methods and statistics were described in (B).
Figure 1

A  Benign  Grade 3+3  Grade 3+4  Grade 4+4  Grade 5+5

H&E

Tak1

B

Tak1 Expression (arbitrary units)

A  B  B  C

(50) (45) (45) (15)

Benign  3  4  5

Gleason Grade
Figure 5

Benign | PIN | Carcinoma

H&E

AR

p63

CK8

CK18

CK5

CK14
Figure 6

A

Benign       PIN       Carcinoma

shControl

Tak1

shTak1

B

<table>
<thead>
<tr>
<th>shControl</th>
<th>shTak1</th>
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<td>Tak1</td>
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<td>α-tublin</td>
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</table>
Figure 7A: Benign, PIN, Tumor

Figure 7B: ki67 + (%)

Figure 7C: shControl, shTak1

Figure 7D: ki67 + (%)

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Suppression of Tak1 Promotes Prostate Tumorigenesis

Min Wu, Lihong Shi, Adela Cimic, et al.

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