SOX9 Elevation in the Prostate Promotes Proliferation and Cooperates with PTEN Loss to Drive Tumor Formation

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Abstract
Dysregulation of tissue development pathways can contribute to cancer initiation and progression. In murine embryonic prostate epithelia, the transcription factor SOX9 is required for proper prostate development. In this study, we examined a role for SOX9 in prostate cancer in mouse and human. In Pten and Akx3.1 mutant mice, cells with increased levels of SOX9 appeared within prostate epithelia at early stages of neoplasia, and higher expression correlated with progression at all stages of disease. In transgenic mice, SOX9 overexpression in prostate epithelia increased cell proliferation without inducing hyperplasia. In transgenic mice that were also heterozygous for mutant Pten, SOX9 overexpression quickened the induction of high-grade prostate intraepithelial neoplasia. In contrast, Sox9 attenuation led to a decrease proliferating prostate epithelia cells in normal and homozygous Pten mutant mice with prostate neoplasia. Analysis of a cohort of 880 human prostate cancer samples showed that SOX9 expression was associated with increasing Gleason grades and higher Ki67 staining. Our findings identify SOX9 as part of a developmental pathway that is reactivated in prostate neoplasia where it promotes tumor cell proliferation. Cancer Res; 70(3); 979–87. ©2010 AACR.

Introduction
Prostate cancer is a leading cause of mortality in older men of the western world (1). Understanding the processes that lead to prostate neoplasia is essential for the assessment of disease progression and choice of treatment. It is frequently the case that pathways involved in embryonic development are reactivated in cancer. Gene expression studies have indicated that programs that regulate prostate development and growth are reactivated in prostate cancer (2, 3).

The mouse has been used as a model for the study of prostate development and cancer. Although spontaneous prostate tumors do not arise in mice, several genetically modified mice have been shown to develop prostate intraepithelial neoplasia (PIN) and invasive carcinoma that is similar to the human neoplasia. An example of this is mice lacking the tumor suppressor gene Pten (phosphatase and tensin homolog deleted on chromosome 10) in the prostate that develop PIN at 6 weeks and invasive carcinoma after 9 weeks (4). Mutations in Pten have also been associated with prostate cancer in humans (5).

The transcription factor SOX9 has been shown to be essential for many processes during embryogenesis, including early prostate development (6). Studies on mice lacking Sox9 in the prostate showed a requirement in ventral prostate development and proper anterior prostate differentiation (7). High levels of SOX9 were associated with the prostate epithelia from the first stages of bud development from the urogenital sinus. In the ventral prostate, the absence of Sox9 gave rise to a decrease of proliferation within the epithelia and a lack of expression of genes specific to prostate bud development that led to a complete loss of the structure.

Studies on prostate cancer cell lines have implicated SOX9 in prostate cancer, although its role has not been clearly determined. One study showed that it can suppress growth and tumorigenesis (8). In contrast, other studies have shown that it can enhance the proliferation and invasion of prostate cell lines in a xenograft model (9, 10). Analysis of human tissue samples showed an association between SOX9 expression and prostate cancer, with a higher protein level in samples from patients with hormone-refractory cancer (2, 9). SOX9 expression has been associated with other cancers such as colorectal cancer and melanoma (11, 12). However, in some
cases expression is associated with tumor formation, but in others it is downregulated in neoplasia. This suggests that the role of SOX9 is distinct in different cancers.

In this study, we have performed an extensive analysis of the role of SOX9 in prostate cancer in mouse and human. We show that high levels of SOX9 associate with PIN lesions of all grades in mice and correlate with high Gleason score in prostate cancer in humans. Overexpression of SOX9 in adult mouse prostate epithelia gave rise to an increase in proliferation and induced early high-grade PIN lesions when mice were also heterozygous for Pten. Our studies show that high levels of SOX9 contribute to regulate proliferation within the prostate epithelia and can cooperate with PTEN loss to accelerate prostate neoplasia.

Materials and Methods

Mouse strains. The mouse strain containing the Sox9 conditional allele was kindly provided by Andreas Schedl (Institut National de la Santé et de la Recherche Médicale U470, Nice, France; ref. 7). Mice with the mutant Pten allele and the PbCre4 transgene were obtained from the Mouse Models of Human Cancers Consortium repository unit (13, 14), and mice with the conditional allele of Pten were obtained from The Jackson Laboratory (15). Mice deficient for Nkx3.1 were obtained from Michael Shen (Columbia University, New York, NY; ref. 7). The animals were bred on a mixed genetic background.

Human and mouse samples. Details of the human prostate samples used for immunohistochemistry were initially as described previously (16). Assignment of areas of cancer and noncancer in each core was carried out after antibody staining on the basis of histopathologic examination. The primary end points were time to death from prostate cancer and time to death from any cause. Univariate and multivariate analyses were done by proportional hazard (Cox) regression analysis (17). Assignment of areas of cancer and noncancer in each core was carried out after antibody staining on the basis of histopathologic examination. The primary end points were time to death from prostate cancer and time to death from any cause. Univariate and multivariate analyses were done by proportional hazard (Cox) regression analysis (17). All follow-up times commenced at the point of 6 mo following diagnosis as in the previous report (18). The association between SOX9 expression and Gleason score and Ki67 staining was examined using the χ² test. The following variables were included in the multivariate analyses: centrally reviewed Gleason score, baseline PSA (last PSA value within 6 mo of diagnosis), extent of disease, and age at diagnosis.

For the mouse studies, the histologic phenotypes of all samples used for immunohistochemistry were initially assessed on H&E-stained sections. The assessment was based on published guidelines and assisted by a pathologist (19, 20). PIN lesions noted as low grade were equivalent to PIN I to II and those noted as high grade were equivalent to PIN III to IV as defined by Park and colleagues (20).

Immunohistochemistry. Antibody stains were done on paraffin sections as described previously (7). The following antibodies were used: For SOX9, two antibodies were used with amplification protocols, one was a gift from Francis Poulat (Centre National de la Recherche Scientifique, Montpellier, France; 1/2000 dilution) and was used for the human tissue array samples and the other was a gift from Robin Lovell-Badge (National Institute for Medical Research, London, United Kingdom; 1/16,000); Ki67 (TEC-3, Dako) was used at 1/25 and 1/200 dilutions (with amplification protocols); pAKT (T636E11, Cell Signaling Technologies) was used at 1/25 and 1/200 dilutions (with amplification protocols); p63 (4A4, Santa Cruz Biotechnology) was used at 1/50 dilution; green fluorescent protein (GFP; ab290-50, Abcam) was used at 1/3,000 dilution. Secondary fluorescent antibodies were obtained from Molecular Probes and were used at 1/1,000 dilution. The ABC vector kit (Vector Laboratories) was used for amplification and stained with 3,3′-diaminobenzidine chromogen or with the use of the TSA kit for fluorescence (NEL741, Perkin-Elmer).

Quantification of proliferation. Ki67 staining was done on a number of sections per animal and positive cells were counted from four to six different fields from different sections. The number of total cells per animal ranged from 600 to 2,500.

Quantitative RT-PCR. Tissues from the distal regions of the different prostatic lobes were dissected and RNA was isolated using the Rneasy Micro Kit (Qiagen). cDNA synthesis was primed with oligo dT and done with Superscript II reverse transcriptase (Invitrogen). Real-time PCR was done using the TaqMan system (ABI7900) with the following primers/probe sets: Mm00448840_m1 for Sox9 and Mm00486906_m1 for e-cadherin. Relative mRNA accumulation was determined by the ΔΔCt method and Sox9 levels were normalized to E-cadherin levels.

Results

SOX9 expression in the adult mouse and human prostate. Using an antibody to SOX9 that showed high levels of protein in the prostate epithelia of mouse embryos (7), we investigated the expression of this factor in the adult mouse prostate. This analysis determined that SOX9 was expressed in the epithelia of the adult mouse prostate but at different levels between lobes. Highest levels were found in the lateral and ventral prostate (Fig. 1A). This difference was confirmed by real-time RT-PCR (Fig. 1B). SOX9 was expressed in both luminal and basal cells of the lateral and ventral prostate (Supplementary Fig. S1A). In contrast, all zones in the human expressed similar levels of SOX9. Basal cell staining was predominantly found, with all zones showing some luminal cell staining (Fig. 1A; Supplementary Fig. S1B). The mouse prostatic lobes can be divided into three regions relative to the urethra: distal, intermediate, and proximal. Recent studies have shown that the proximal region harbors cells that have properties of adult stem cells (21, 22). Staining with an antibody to SOX9 revealed high levels of this protein within the proximal region relative to the intermediate and distal regions (Fig. 1C). Higher levels of SOX9 were also found in the epithelia of all lobes of prostate from mice that had been castrated when compared with intact animals (Fig. 1D).

SOX9 expression in mouse models of prostate neoplasia. SOX9 has been implicated in human prostate cancer, and therefore, we investigated the levels of SOX9 in various mouse models of prostate neoplasia. Nkx3.1-deficient mice
have been shown to develop hyperplasia and dysplasia at 12 months that will progress to PIN in mice over 18 months old (23, 24). Sections of 12-month-old anterior prostates from these mice showed a general hyperplastic lobe with cells filling the lumen. SOX9 antibody staining of these samples revealed discrete areas of high SOX9 expression within the epithelia (Fig. 2A).

Mice heterozygous for a deletion in *Pten* develop spontaneous tumors in various organs (13, 25–27). Within the prostate, they show hyperplasia that progresses to PIN after 10 months. Staining with an antibody to SOX9 of 6-month-old anterior prostates from these mice showed that high levels of this factor were associated with areas of hyperplasia (Fig. 2A).

Mice with a conditional allele of *Pten* (*Ptenfl*) and the prostate-specific Cre expressing construct PbCre4 develop PIN at 6 weeks of age that progresses to invasive carcinoma after 9 weeks (4). Antibody staining showed high levels of SOX9 expression associated with low- and high-grade PIN (ref. 20; Fig. 2B). Therefore, these studies show that an increase in SOX9 levels was observed at early stages of prostate hyperplasia and was associated with progression to high-grade PIN lesions.

**Overexpression of SOX9 in prostate epithelia.** The association between increased levels of SOX9 and prostate neoplasia indicated that this factor may contribute to prostate cancer initiation and/or progression. To investigate this possibility, we created mice that overexpressed high levels of SOX9 in the adult prostate. For this, we used transgenic mice that were hemizygous for a construct where *Sox9* and GFP, through the use of an internal ribosomal entry site, were driven by the CAG (cytomegalovirus early enhancer/chicken β-actin) promoter in tissues where Cre recombinase is expressed (Z/Sox9 mice; see Supplementary Fig. S2 for details of the Z/Sox9 construct). These mice were mated to the PbCre4 mice, creating mice that expressed high levels of SOX9 within the adult prostate epithelia. A variable number of GFP positive cells could be found in all lobes in a mosaic pattern, with highest levels in the lateral and dorsal prostates. As expected, cells that expressed GFP showed high levels of SOX9 (Fig. 2A). These cells were mainly luminal, although some positive basal cells could be found (Fig. 3A; Supplementary Fig. S2A).

**Figure 1.** SOX9 expression in the mouse and human adult prostate. A, sections from mouse and human prostate were stained (brown) with an antibody to SOX9 and counterstained with hematoxylin. The different lobes and zones are indicated. AP, anterior lobe; DP, dorsal lobe; LP, lateral lobe; VP, ventral lobe; PZ, peripheral zone (10 mice and 4 human samples analyzed). B, quantitative RT-PCR for *Sox9* expression was done on RNA from the different mouse prostate lobes (4 mice per lobe analyzed). *, P < 0.05 (Student’s t test). C, SOX9 levels are highest in the proximal region. The dashed lines in the left image indicate the proximal (p), intermediate (i), and distal (d) regions of the dorsal lobe. Images (proximal region) and b (intermediate) show magnified pictures of the boxed regions in the left (10 mice analyzed). D, SOX9 levels are high in castrated mice. Staining of sections from the dorsal prostates from adult mice that were intact and castrated (10 mice analyzed).
To establish if high levels of SOX9 can contribute to the prostate neoplasia observed in Pten mutant animals, we created mice that overexpress SOX9 and are heterozygous for the conditional Ptenfl allele. Analysis of prostates from 6- to 7-month-old heterozygous Ptenfl mutant animals without the Z/Sox9 construct showed few areas of mild hyperplasia in the anterior prostate (six animals analyzed). In contrast, two of four mice containing the Z/Sox9 construct revealed areas of high-grade PIN in the anterior prostate (Fig. 3B). These areas showed high levels of GFP and Sox9 (Fig. 3C; Supplementary Fig. S2C). Staining with an antibody to Ki67 showed a clustering of positive cells associated with these areas (Fig. 3D). Homozygous loss of Pten is associated with high levels of phosphorylated AKT (pAKT) in prostate neoplasia (4). Therefore, to investigate if increased levels of SOX9 could contribute to a Pten loss of heterozygosity phenotype, we stained sections from the dorsal prostates of mice that were wild type (control) or mutant for the conditional allele of Pten (Ptenfl/fl;PbCre4; 10 mice analyzed). Areas of low- and high-grade PIN are indicated.

Effect of Sox9 deletion on normal and neoplastic prostate epithelia. Our studies on mice that overexpress SOX9 indicate a role for this factor in promoting proliferation. To investigate if absence of SOX9 in the adult prostate epithelium could lead to changes in cell proliferation, we created mice that contained the conditional loss-of-function allele of Sox9 (Sox9fl) and the PbCre4 construct. These mice showed no obvious phenotype in the lateral and ventral prostates, where SOX9 levels were highest in normal prostate. Analysis of Ki67 expression showed a significant 3.1-fold decrease in positive cells in the prostate epithelia of the mutant mice (Fig. 4A). Therefore, these studies show a strong correlation between SOX9 levels and the number of Ki67-positive cells within the prostate epithelia.

To establish if SOX9 can contribute to the phenotype observed in homozygous Pten mutant animals, the conditional allele of Sox9 (Sox9fl) was included in our breeding program. Two types of mice were generated that contained PbCre4 and were homozygous for Ptenfl (Ptenfl/fl): those that were heterozygous for Sox9fl (Sox9fl/+); those that were homozygous for Sox9fl (Sox9fl/fl). Histologic analysis of mice at 3 and 6 months showed no major difference in the overall prostate neoplasia phenotype between these two groups. Prostates from mutant Pten animals have been shown to have an increase in proliferation as measured by Ki67 antibody staining (4). Interestingly, we observed a difference in the number of Ki67-positive cells in the prostate between the two groups. The Sox9fl/fl-containing animals showed a reduction in the number of Ki67-positive cells (Fig. 4B). Consistent with previous studies, most of the Ki67-positive cells were found near the stromal compartment of the gland (28).

To confirm that Sox9 has been deleted in the Sox9fl/fl-containing animals, we stained prostate sections with an antibody to SOX9. As expected, most cells of the prostates of

Figure 2. Upregulation of SOX9 is associated with early and late stages of prostate neoplasia. A, sections from the anterior prostates of mice that were wild type (control), Nkx3.1 deficient (Nkx3.1−/−; 10 mice analyzed), and heterozygous for Pten (Pten+−; 5 mice analyzed) were stained (brown) with an antibody to SOX9 and counterstained with hematoxylin. Right, higher magnifications of the samples on the left. The ages of the animals are indicated. Dashed lines, regions of high SOX9 expression. B, SOX9 staining of sections from the dorsal prostates of mice that were wild type (control) or mutant for the conditional allele of Pten (Ptenfl/fl;PbCre4; 10 mice analyzed). Areas of low- and high-grade PIN are indicated.
these animals lacked SOX9; however, cells with high levels of SOX9 were found in the region near the stromal compartment of the prostates of these mice (Fig. 4B). Staining with an antibody to pAKT showed that the SOX9-positive cells in the Sox9fl/fl-containing animals lacked an upregulation of this protein in the plasma membrane (Fig. 4B). Upregulation of pAKT levels has been shown to be associated with loss of Pten in the prostate (4); therefore, these studies indicate that these cells did not express Cre recombinase, and no recombination between flox sites at the Pten and Sox9 loci had occurred. Double staining with Ki67 and either SOX9 or pAKT antibodies showed that most of the Ki67-positive cells in the Sox9fl/fl animals were also positive for SOX9 and negative for pAKT (Fig. 4B). Consistent with this, quantification of cells that were positive for Ki67 and negative for pAKT between the two groups showed a significant 2-fold decrease in proliferation in Sox9fl/fl animals compared with the Sox9fl/+ animals (Fig. 4B). These data show that loss of Sox9 does not inhibit neoplastic progression in the prostate of homozygous mutant Pten mice but leads to a reduction in the number of proliferating prostate epithelial cells that have retained phosphoinositide 3-kinase (PI3K) signaling.

SOX9 expression in human prostate cancer. Our studies in mice suggested that high levels of SOX9 in the prostate might be associated with prostate cancer. Therefore, to establish the relationship between SOX9 levels and prostate cancer in humans, we stained 880 prostate cancer cores with an antibody to SOX9. These cores were derived from 387 patients with localized disease and Gleason scores ranging from 4 to 10. In contrast to our mouse studies, not all cancer samples showed SOX9 expression, with 54% of cores (N = 478) showing no staining and the remaining cores showing either low or high levels of nuclear staining (Fig. 5A and B). The level of SOX9, either 0 or some positive staining (>0), was determined for each patient and used in statistical analysis. There was a significant positive correlation between SOX9 expression and Gleason score (46% of SOX9 positive for Gleason <7, 67% for Gleason 7, and 61% for Gleason >7; Pearson’s χ² = 13.6, P = 0.001; Table 1). In univariate analysis, SOX9 expression correlated with poorer prognosis and
Figure 4. Loss of Sox9 leads to a decrease in proliferation in normal and neoplastic prostate epithelia. A, immunofluorescent staining with antibodies to SOX9 (green) and Ki67 (red) of sections from the lateral prostates of mice that were homozygous for the conditional allele of Sox9 (Sox9<sup>fl/fl</sup>) and either contained the PbCre4 construct (+Cre) or did not (−Cre). Blue staining, nuclei stained with 4′,6-diamidino-2-phenylindole. The graph depicts the quantification of the number of Ki67 cells for each genotype (5 control and 6 mutant mice analyzed). *, P < 0.05. Cells that were Ki67 and SOX9 positive in the +Cre group were not counted. All Ki67 cells in the −Cre group were SOX9 positive. B, sections from the anterior prostates of mice that were mutant for the conditional allele of Pten (Pten Mut; Pten<sup>fl/fl</sup>;PbCre4) and were either heterozygous (Sox9 Het; Sox9<sup>fl/+</sup>) or homozygous (Sox9 Mut; Sox9<sup>fl/fl</sup>) for the conditional Sox9 allele were stained with antibodies to Ki67, SOX9, and pAKT, as indicated. The graph shows the percentage of the number of cells that were positive for Ki67 and negative for pAKT (six mice for each genotype analyzed). *, P < 0.05 (Student’s t test).
was significant for overall survival (Fig. 5C) but not for cause-specific survival (Fig. 5D). However, SOX9 expression did not remain significant independently of age, Gleason score, PSA, and extent of disease in a multivariate model \( \Delta \chi^2 (1 \text{ degree of freedom}) = 0.17, P = 0.19 \). Higher levels of Ki67 have been shown to correlate with lower chance of survival in this group of samples (29). Consistent with our mouse studies, expression of SOX9 was significantly positively associated with Ki67 in the prostate cancer samples \( (\chi^2 \text{ for trend} = 7.25, P = 0.007; \text{Table 1}) \). These studies indicate that expression of SOX9 correlates with increased proliferation and tumor progression and decreased survival in humans.

**Table 1.** Distribution of Gleason score categories and the percentage of Ki67-positive cells between SOX9-negative (0) and SOX9-positive (>0) cancer cores

<table>
<thead>
<tr>
<th>SOX9 level, n (%)</th>
<th>0</th>
<th>&gt;0</th>
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<tbody>
<tr>
<td><strong>Gleason score</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>&lt;7</td>
<td>93 (54)</td>
<td>79 (46)</td>
</tr>
<tr>
<td>7</td>
<td>36 (33)</td>
<td>73 (67)</td>
</tr>
<tr>
<td>&gt;7</td>
<td>41 (39)</td>
<td>65 (61)</td>
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<tr>
<td><strong>Ki67 staining (%)</strong></td>
<td></td>
<td></td>
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<tr>
<td>0–1</td>
<td>89 (53)</td>
<td>80 (47)</td>
</tr>
<tr>
<td>&gt;1–5</td>
<td>53 (39)</td>
<td>82 (61)</td>
</tr>
<tr>
<td>&gt;5–10</td>
<td>14 (29)</td>
<td>34 (71)</td>
</tr>
<tr>
<td>&gt;10–100</td>
<td>12 (40)</td>
<td>18 (60)</td>
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**Discussion**

Various studies have implicated SOX9 in prostate cancer. However, the data are in conflict with studies indicating that it can promote as well as repress cell proliferation, and that it is involved in metastasis and may be required in the early stages of prostate carcinogenesis (2, 8, 10, 30). Our results in mice show that SOX9 expression is upregulated within the epithelia in areas where neoplastic abnormalities are first observed, and high levels of SOX9 are associated with all stages of PIN progression. This is consistent with our data on human prostate cancer where SOX9 expression was more frequent in samples with higher Gleason score. Our functional data show that high levels of SOX9 in the prostate...
contribute to an increase in proliferation that can lead to PIN in certain mutant genetic backgrounds. Therefore, our results are consistent with a cooperative role for SOX9 in the progression of the early stages of prostate cancer formation.

Our expression data had suggested that high levels of SOX9 could promote early stages of prostate neoplasia. Our overexpression studies showed that a high level of SOX9 on its own is not sufficient to induce hyperplasia and neoplasia in vivo, although increased proliferation was observed. However, in the context where one allele of Pten was lost, focal areas of high-grade PIN were detected, where all cells showed high GFP and SOX9 expression. This indicates that cells with increased levels of SOX9 and decreased levels of Pten are more likely to become neoplastic. The focal nature of this event could be due to a stochastic process or the nature of the cell of origin, which, if relatively rare in Cre-expressing cells, would be made even more infrequent if both transgenic SOX9 expression and loss of one Pten allele needed to occur in the same cell. The areas of high-grade PIN in these mice showed increased pAKT in most cells. This phenotype was not observed in GFP-positive cells that were not part of the PIN lesion. This suggests that a high level of SOX9 does not directly regulate pAKT levels, rather it increases the likelihood of an event that leads to an increase in cells with high PI3K signaling. A similar situation occurs in mice that are heterozygous for Pten and Nkx3.1 mutations (31). Our data suggest that an increase in proliferation is a potential mechanism in which SOX9 can contribute to the acceleration of neoplasia progression. Overall, our studies indicate that SOX9 does not act like a classic oncogene, but rather it cooperates with other events such as the loss of Pten to induce carcinogenesis.

Our genetic data show that Sox9 deletion leads to a decrease in proliferation in wild-type and homozygous Pten−/− mutant mice. However, this decrease did not inhibit prostate neoplasia progression in the mutant animals. Presumably, other pathways regulating proliferation are also active in these mice and are sufficient to ensure neoplastic progression. In the Pten−/− mutant mice, the proliferating cells were more likely to harbor cells where Cre recombination had not occurred (see Fig. 4B) and therefore contained wild-type Pten and Sox9. This suggests that the neoplastic epithelia associated with Pten loss produce non–cell-autonomous factors that regulate proliferation in neighboring cells. Paracrine effects from the epithelia have been observed to control processes within the stroma in models of prostate cancer (32). Our results are consistent with a contribution of SOX9 to the regulation of the factors controlling proliferation. This effect was also observed in the early neoplastic lesions where Ki67-positive cells tended to surround the areas of high SOX9 in the prostates of Nkx3.1 mutant mice (Supplementary Fig. S3). This suggests that the production of paracrine factors regulating proliferation might be a general mechanism associated with the initial stages of carcinogenesis.

A striking difference between mouse and human in our studies is that we observed high expression of SOX9 in prostate neoplasia in mouse models, but only 46% of human cancer cores were positive for this factor. One technical explanation is that the SOX9 antibody we used did not react with all the samples in the same way due to the tissue array process. We do not think this is the case because our studies with a different SOX9 antibody and two other studies using different antibodies and samples found a similar percentage of cancer samples that were negative for SOX9 (2, 9). Cancer samples that were positive for SOX9 tended to have a higher Gleason score and increased Ki67-positive cells. A multivariate analysis of our human data shows that expression of SOX9 is not an independent prognostic factor of survival. Therefore, our analysis suggests that SOX9 expression correlates with disease progression in a subset of prostate cancers and that other SOX9-independent pathways can also lead to a low survival prognosis. Classification of prostate cancers into different subtypes may be required to uncover whether expression of SOX9 has any predictive value. Screening of other mouse models of prostate cancer for SOX9 levels may also uncover differences in the dependence of SOX9 in the different pathways that lead to neoplasia.

SOX9 has been implicated in other cancers such as melanoma in humans (12). In this example, higher levels of SOX9 were associated with normal melanocytes and were downregulated in premalignant and malignant cells. In addition, overexpression of SOX9 inhibited proliferation and led to cell cycle arrest. This shows that the function of this factor in cancer is context specific. This is consistent with its many roles during embryonic development, in which it can cooperate with tissue-specific factors to initiate different cell fates such as Sertoli cell differentiation, chondrogenesis, and neural crest development (33–35). This also highlights the value of in vivo studies to delineate the role of SOX9 in specific tissues.

In summary, this study identifies SOX9 as a factor involved in the regulation of proliferation of prostate epithelial cells, which can contribute to neoplastic transformation in specific contexts. Future identification of different prostate cancer subtypes may uncover the contributions of SOX9 to specific pathways that lead to neoplasia.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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References

Correction: Online Publication Dates for 
Cancer Research April 15, 2010 Articles

The following articles in the April 15, 2010 issue of Cancer Research were published with an online publication date of April 6, 2010 listed, but were actually published online on April 13, 2010:


Dudka AA, Sweet SMM, Heath JK. Signal transducers and activators of transcription-3 binding to the fibroblast growth factor receptor is activated by receptor amplification. Cancer Res 2010;70:3391–401. Published OnlineFirst April 13, 2010. doi:10.1158/0008-5472.CAN-09-3033.


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Cancer Res 2010;70:979-987. Published OnlineFirst January 26, 2010.

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