Deregulation of a Hox Protein Regulatory Network Spanning Prostate Cancer Initiation and Progression

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Abstract

Purpose: The aberrant activity of developmental pathways in prostate cancer may provide significant insight into predicting tumor initiation and progression, as well as identifying novel therapeutic targets. To this end, despite shared androgen-dependence and functional similarities to the prostate gland, seminal vesicle cancer is exceptionally rare.

Experimental Design: We conducted genomic pathway analyses comparing patient-matched normal prostate and seminal vesicle epithelial cells to identify novel pathways for tumor initiation and progression. Derived gene expression profiles were grouped into cancer biomodules using a protein–protein network algorithm to analyze their relationship to known oncogenes. Each resultant biomodule was assayed for its prognostic ability against publically available prostate cancer patient gene array datasets.

Results: Analyses show that the embryonic developmental biomodule containing four homeobox gene family members (Meis1, Meis2, Pbx1, and HoxA9) detects a survival difference in a set of watchful-waiting patients (n = 172, P = 0.05), identify men who are more likely to recur biochemically postprostatectomy (n = 78, P = 0.02), correlate with Gleason score (r = 0.98, P = 0.02), and distinguish between normal prostate, primary tumor, and metastatic disease. In contrast to other cancer types, Meis1, Meis2, and Pbx1 expression is decreased in poor-prognosis tumors, implying that they function as tumor suppressor genes for prostate cancer. Immunohistochemical staining documents nuclear basal-epithelial and stromal Meis2 staining, with loss of Meis2 expression in prostate tumors.

Conclusion: These data implicate deregulation of the Hox protein cofactors Meis1, Meis2, and Pbx1 as serving a critical function to suppress prostate cancer initiation and progression. Clin Cancer Res; 18(16); 4291–302. ©2012 AACR.

Introduction

The prostate gland is the most predominant site of neoplasia in aging men. In the United States alone in 2011, approximately 240,890 men were estimated to be diagnosed with prostate cancer (1). Less than 14% (33,720) of men, however, actually died of the disease (1). Clearly the advent of more aggressive screening programs has reduced mortality from prostate cancer, but has concomitantly detected tumors that often have no impact on overall patient morbidity or survival. Our understanding of prostate cancer treatment traces back to the seminal discovery by Charles Huggins and Clarence Hodges in 1941 that castration significantly benefits patients with advanced prostate cancer (2). Researchers have since identified the critical role deregulations in the androgen receptor (AR) pathway play in both oncogenesis and eventual resistance to castration. Although there are newer and more effective strategies targeting the AR, the majority of men continue to have disease progression. Thus, it is critical to first identify novel molecular pathways which are deregulated within prostate tumors that will permit discrimination of low-grade tumors at risk of progression. Second, pharmacologic targeting of these pathways in prostate cancer may provide disease control in the advanced, metastatic setting.

As the AR pathway is developmentally critical, we hypothesized that other developmental pathways may also play a key role in oncogenesis and tumor progression. To provide us insight into what pathways may be deregulated, we took advantage of the unique similarities and differences between seminal vesicle and prostate tissues. In contrast to over 2 million U.S. cases of prostate cancer diagnosed in the past decade, there are fewer than 50 cases of primary seminal vesicle cancer in the English literature (3, 4). Similar
to the prostate, the development and maintenance of the seminal vesicles is androgen-dependent, and the seminal vesicles synthesize and secrete molecules and proteins that contribute to semen (5). This implies that there are unique differences between prostate and seminal vesicle tissues, which strongly predispose prostate tissue to neoplasia and cancer. These differences could be accounted for by their specific developmental differences and their distinct embryologic origins, as well as exposure to infectious and inflammatory agents, distinct secreted factors produced by their gland of origin, or differences in the kinetics of tissue turnover (6).

Here we report the identification of a developmental transcription factor biomodule that is unique to prostate epithelial cells when compared with patient-matched seminal vesicle epithelial cells. A “biomodule” is defined as a subnetwork of genes connected by their protein–protein interactions. The biomodule described here consists of the 3-amino acid loop extension (TALE) and homeodomain transcription factors Meis1, Meis2, and Pbx1, and the homeodomain-containing DNA-binding protein HoxA9. Meis1, Meis1, and Pbx1 are critical Hox gene cofactors which modify Hox gene specificity (7), and have critical roles during development (7–9). In addition, Meis proteins and Pbx1 have a well-defined role in promoting certain leukemias (10–14). The clinical relevance of this biomodule in prostate cancer was tested against multiple, comprehensive, and independent publically available prostate tissue databases. Aberrant expression of these 4 genes was significant in normal prostate as compared with tumor, predictive for both biochemical relapse (i.e., PSA recurrence) and overall patient survival.

Materials and Methods
Tissue preparation and cell culture
Fresh prostate and seminal vesicle cells were isolated from patients undergoing radical prostatectomy at our institution according to an Institution Review Board approved protocol. Dissociation of prostate tissue and growth of epithelial cells has been previously described (15, 16). Briefly, 4 mm biopsy punches were taken from prostate and seminal vesicle tissue; half of this tissue was fixed and analyzed by a pathologist to confirm the absence of tumor. The remaining portion was digested overnight at 37°C in collagenase solution (0.28% collagenase I [Sigma-Aldrich], 1% DNase I [Sigma], 10% FCS, 1× antibiotic/antimycotic [Life Technologies-Invitrogen], in RPMI-1640). The following day, the cell suspension was washed in PBS, and epithelial cell clusters were isolated by density sedimentation, whereby cells in 10 mL PBS were allowed to settle for 10 minutes at room temperature and the top 9 mL of medium (containing fibroblasts) were removed; this was repeated 2 more times. Epithelial cell clusters were further dissociated into single cells via treatment with DTT (1 mmol/L for 30 minutes at 37°C), a PBS wash, and trypsin/EDTA (0.25% for 30 minutes at 37°C). The trypsin was neutralized with RPMI 1640 plus 10% FCS, and the cells were washed twice in PBS. Prostate epithelial cell cultures (PrECs) and seminal vesicle epithelial cell cultures (SVECs) were established and grown using keratinocyte serum-free defined media supplemented with growth factors (GFs; standard K-SFM; Invitrogen Life Technologies). All cultures were screened for the absence of mycoplasma contamination using the ATCC Universal Mycoplasma Detection Kit (Manassas, VA).

RNA isolation and gene array analyses
Cells were plated at a density of 50,000 cells per cm², and after 48 hours mRNA was isolated using the Qiagen RNeasy Mini kit per the manufacturers’ instructions. All RNA used for analyses had an RNA integrity number (RIN) of 10 when measured using an Agilent 2100 Bioanalyzer. Double-stranded cDNA and cRNA synthesis was conducted according to the GeneChip Expression Analyses Technical Manual (Rev5), and samples hybridized to Affymetrix HG 133+2.0 Arrays (Lot #4087104 for all chips).

Analysis of epithelial tissue gene expression data
Affymetrix expression data was analyzed using BRB-ArrayTools developed by Dr Richard Simon and the BRB-ArrayTools Development Team (http://((linus.nci.nih.gov/(BRB-ArrayTools.html; ref. 17). We conducted standard RNA normalization. Probes were filtered based on the requirement of a 2-fold change in the dataset and no less than 50% normalization. Probes were filtered based on the requirement of a 2-fold change in the dataset and no less than 50% normalization. Paired analysis using significance analysis of microarrays (SAM; ref. 18) was done with a false discovery rate (FDR) of 0.05 over the dataset to generate an epithelial-specific gene signature. For purposes of this article, we define gene signature as any collection of genes, be they a collection of differentially expressed genes or a set of refined genes. We derived the final gene expression signature by converting the probes to their unique corresponding gene names.

Historical datasets used in the analyses
Six historical prostate cancer datasets were used in the analyses: Thompson (GSE11376; ref. 19), Cai (GSE32269; published online in 2004; ref. 20), Cai (GSE32270; published online in 2004; ref. 21), Delahanty (GSE32267; ref. 22), Thompson (GSE32268; ref. 23), and Cai (GSE32272; ref. 24).
Differential gene signature generation from historical datasets

GSE32269, GDS2545, and GSE11376 were loaded into BRB-ArrayTools. A 2-fold change filter was implemented. Paired SAM analysis was conducted on the GSE11376, and unpaired analysis on the GSE32269 and GDS2545 dataset samples. A FDR of 0.05 was used to control for multiplicity. Resulting genes in each signature were analyzed for their fold-change in the comparison conditions.

Protein–protein interaction network analysis and pathway enrichment

To evaluate whether distinct derived gene signatures connected to cancer-related genes greater than expected by chance, we used a single protein analysis of network (SPAN) methodology (25–27). As our reference cancer gene gold standard, we used the Wellcome Trust Sanger Institute Cancer Gene Census downloaded on August 5, 2011 from http://www.sanger.ac.uk/genetics/CGP/Census/ (28). The Cancer Gene Census contains a catalog of genes for which mutations have been causally implicated in cancer, acquired and updated through literature-based methods. SPAN analysis has been extensively previously described (26, 27). In brief, each gene expression signature was compared with the Sanger Cancer Gene set using SPAN. We compared the expected distribution of linkages between the gene expression signatures and the Sanger cancer genes through 10,000 permutation resamplings. The unadjusted P-value of each signature gene’s connectivity was further adjusted for multiplicity using a Bonferroni correction (29).

The SPAN method prioritizes genes at the protein level. We first evaluated whether there were cancer genes more connected to each gene signature than expected by conservative empirical controls. A converse calculation was then conducted where each single Sanger cancer gene was analyzed for its total number of interactions with each independent, unique gene in the gene signatures. Prioritized genes and their interactors that had a FDR < 0.05 were retained. The resulting statistically significant genes were then retained and deemed a “biomodule.” As each SPAN protein keeps an equal number of partners in the empirical distribution the network is conservatively prioritized. Visualization of the SPAN prioritized biomodule was then conducted using Cytoscape software (30). Biomodules were then enriched for Gene Ontology pathways using the Database for Annotation, Visualization and Integrated Discovery (DAVID) tool v6.7 (31).

Evaluation of clinical datasets

To test the clinical relevance of the cancer gene centered biomodules, we first examined the ability of individual biomodules to find a survival or recurrence difference in 3 independent retrospective datasets. This survival analysis using a separate dataset serves as a clinical evaluation of the biomodule signature. In the first dataset (Glinsky), we examined the disease-free interval after prostatectomy of 79 samples (24). This dataset contained 37 patients with recurrent and 42 patients with nonrecurrent disease. After loading the dataset into R/Bioconductor, we used the prediction analysis for microarrays (PAM; 32) algorithm for each biomodule gene list to provide an unbiased division of the prostate cancer cohort into 2 groups. Kaplan–Meier analysis was conducted using time from diagnosis until recurrence. We then validated the Glinsky results in a second dataset (Taylor) that contained 131 prostatectomy specimens with longitudinal data as to their PSA recurrence (27 recurrent, 104 nonrecurrent). We conducted a PAM analysis similar to the Glinsky procedure outlined earlier. The third dataset (Sboner) contained 281 Swedish men who underwent a course of “watchful waiting” after being diagnosed with prostate cancer (GSE16560; ref. 22). This set of 281 only included patients who were alive or had died from prostate cancer-specific causes. In addition to the PAM algorithm described previously, we also dichotomized the patient cohort into those who were above or below the average mRNA expression for each gene or gene set of interest. Kaplan–Meier analysis was conducted using time from diagnosis until death. In a subsequent analysis, we examined only the Gleason Score 6 and 7 cohorts (n = 83 and 117, respectively).

In a second analysis, we explored genes from relevant biomodules as possible independent predictors of recurrence or survival using Cox regression analysis. We again examined the datasets detailed earlier. Loading the datasets into R/Bioconductor, we explored biomodule gene expression levels first in a univariate analysis and then adjusted for Gleason score and age.

Biomodule classification ability in prostate cancer

To graphically evaluate the ability of a biomodule to classify prostate cancer, we computed the score of the used a large independent dataset of 185 gene expression profiles including normal tissue, primary prostate tissue, metastatic tumor specimens, and immortalized prostate cancer cell lines (23). A composite biomodule score was generated via the summation of the upregulated genes and subtracting sum of the scores of the downregulated genes. The unadjusted score for each sample was compared with the average score across the dataset to produce a percentage change from mean. Samples were ordered by percentage change from mean and graphed using Excel.
Immunohistochemistry

Immunostaining for Meis2 (63-T; Santa Cruz Biotechnology; mouse monoclonal) was conducted on formalin-fixed, paraffin-embedded sections managed either by the University of Chicago Human Tissue Resource Core facility or the Northwestern University/University of Chicago Prostate SPORE and their Specimen Procurement Program. Tissue samples were deidentified and there was no exclusion criteria applied toward sample selection. After deparaffinization and rehydration, tissues were treated with antigen retrieval buffer (S1699 from DAKO) in a steamer for 20 minutes. Anti-MEIS2 antibody (1:50 dilution) was applied on tissue sections for 1 hour at room temperature in a humidity chamber. After TBS wash, the antigen–antibody binding was detected with Envision + system (DAKO, K4001 for mouse primary antibodies) and DAB + Chromogen (DAKO, K3468). Tissue sections were briefly immersed in hematoxylin for counterstaining and were cover-slipped. Tissues were analyzed by a trained Genitourinary Pathologist and scored on percentage of cells with positive nuclear staining (0 = no staining; 1 = 1–10% positive cells; 2 = 11–50% positive cells; and 3 = >50% positive cells); as well as the intensity of staining (0 = no staining; 1 = weak staining; 2 = moderate staining; 3 = strong staining). For images, slides were digitized using a Pannoramic Scan Whole Slide Scanner (Cambridge Research and Instrumentation) and images captured using the Pannoramic Viewer software version 1.14.50 (3DHistech).

Statistical analyses

Gene expression profiling of the PrEC and SVEC samples were conducted using standard RMA normalization and SAM analysis to control for multiplicity as described earlier. SPAN analysis, described earlier, uses a permutation sampling methodology of the network controlling for connectivity. This permits us to derive empirical \( P \)-values for all SPAN results. Biomodule testing and statistical analysis was conducted using the PAM algorithm in the R/Bioconductor environment using the survival package. Meis protein module signature scores were generated simply by taking algorithmic sum of genes that were decreased in expression and subtracting from it the expression level of genes that were upregulated. No training algorithms were used. Descriptive statistics were used to summarize the TMA data. Yate’s \( \chi^2 \) test was then used to compare tumor versus normal tissue staining. Cox proportional hazards regression models were used to examine the effect of gene expression parameters as continuous variables, and to estimate hazard ratios. Kaplan–Meier analysis was used to estimate overall survival and disease-free recurrence in dichotomized patient cohorts. Kaplan–Meier analysis, Cox regression analysis, and proportional hazards assumption testing were conducted using the “survival” package in R.

Results

Comparison of prostate to seminal vesicle epithelium reveals widespread embryonic differences

Gene array analyses were conducted on a set of 3 matched normal human prostate epithelium (PrEC) and seminal epithelium (SVEC) cultures. For clarity, we define “gene signature” as any purposeful collection of genes. For example, the set of differentially expressed genes derived from the SVEC vs. PrEC epithelial comparison will be termed a signature in this article. An overview of our workflow is displayed in Fig. 1. The epithelium-only signature, after correcting for multiplicity, resulted in 447 differentially expressed genes (Supplementary Table S2). Strikingly, there were 15 homeobox (Hox) genes that were differentially expressed (HoxA13, B2-3, B5-9, B13, C6, D1, D3-4, and D10-11), as well as Meis1 and Meis2 which were 25.43 and 51.4-fold overexpressed in PrECs, respectively (Supplementary Table S2). Differential expression of both Meis1 and Meis2 was validated using quantitative real-time PCR (Supplementary Fig. S1). This observation was further evaluated using the functional enrichment formed using the Biological Process branch of Gene Ontology (GO; ref. 33). We used a FDR of 5% and the GO enrichment yielded annotations primarily involved in development (Supplementary Table S3). In fact, the top 5 branches related to embryonic development. In addition, we observed GO branches relating to epithelium development and differentiation, as well as urogenital system development.

Presence of homeobox and cell-cycle prioritized genes distinguish epithelial signature from mixed tissue gene signature

Previous studies have evaluated the difference between seminal vesicle and normal prostate using whole and unfractionated prostate and seminal vesicle tissue but did not report on a preponderance of homeobox proteins (19). We hypothesized that careful gene profiling of matched primary epithelial cultures from normal prostate and seminal vesicles would reduce confounding noise during analysis and provide a more robust pathway prioritization. To evaluate this difference more thoroughly, we reanalyzed the gene expression data from Thompson and colleagues and derived a gene signature (mixed tissue signature) in exactly the same manner (19). The resulting mixed tissue signature contained 502 probes that were significant by SAM analysis with a FDR of 5%. Of note, Gene Ontology enrichment did not significantly enrich for embryonic development within whole tissue analyses.

To see where our epithelium-only signature overlapped and differed with the whole-tissue signature, we used a validated methodology to compare them using SPAN. We have previously successfully analyzed both breast and prostate cancer signatures in this manner (27). The SPAN methodology relies on comparing gene signatures to a common background based on statistical prioritization of protein–protein interactions. For this analysis, we compared both the mixed tissue and epithelial signatures to the Wellcome Trust Cancer Gene Census (28). We asked whether there were members of each signature that were connected to known cancer genes more than expected by chance (FDR \( < 0.05 \)). The results of the comparison are represented graphically in Fig. 2A.
On the basis of each signature’s connectivity to the Wellcome Trust Cancer Gene Census, we noted excellent overlap between the 2 signatures in well-established cancer genes such as the Janus kinase (JAK) family, phosphatidylinositol 3-kinase (PI3K), and H-Ras. Of significance to the epithelium-only signature was the additional prioritization of 2 genes, Cdkn2c and Meis1. Cdkn2c is a cell-cycle gene whereas Meis1 is a homeobox gene cofactor and corresponded with our GO enrichment findings documenting significant differential Meis1 expression between prostate and seminal vesicle epithelial cells.

**Protein–protein network evaluation of epithelial-only signature confirms Meis biomodule**

Given our original hypothesis that differences in prostate versus seminal vesicle gene expression are important for oncogenesis, we conducted a second SPAN analysis. In contrast to our first analysis, we now asked whether there were individual Wellcome Trust Cancer Gene Census members that were connected to our epithelial-only signature more than expected by chance (false discovery rate < 5%). Each set (cancer gene and its connected differentially expressed genes) are termed biomodules. Step 3: To determine if these biomodules from Step 2 are clinically relevant and of prognostic import, we evaluated their ability to identify patients with poor prognosis using the prediction analysis for microarrays (PAM) algorithm in historical prostate cancer datasets. Biomodules that were prognostic were then retained. Step 4: Genes from the prognostic biomodule are then validated and refined in silico (using other independent historical datasets), in vitro (via protein and qPCR analysis of genes), and on tissue microarrays (TMA).

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**Figure 1.** Biomodule discovery and validation workflow. Step 1: We first examined the differentially expressed genes between normal prostate epithelium and seminal vesicle epithelium. Matched tissue samples were profiled using standard Affymetrix gene arrays. Genes with a false discovery rate < 5% were retained. Step 2: Using the protein-network prioritization algorithm single protein analysis of networks (SPAN), we compared our set of differentially expressed genes from Step 1 to a reference set of known cancer-related genes from the Wellcome Trust Sanger Cancer Gene Census. SPAN identifies Cancer Genes that are connected to the differentially expressed genes more than expected by chance (false discovery rate < 5%). Each set (cancer gene and its connected differentially expressed genes) are termed biomodules. Step 3: To determine if these biomodules from Step 2 are clinically relevant and of prognostic import, we evaluated their ability to identify patients with poor prognosis using the prediction analysis for microarrays (PAM) algorithm in historical prostate cancer datasets. Biomodules that were prognostic were then retained. Step 4: Genes from the prognostic biomodule are then validated and refined in silico (using other independent historical datasets), in vitro (via protein and qPCR analysis of genes), and on tissue microarrays (TMA).
and enriched for Myd88-dependent Toll-Like receptor signaling pathway. Second, Biomodule B centered on Eln (Elastin) and enriched for proteinaceous extracellular matrix. Third, Biomodule C centered on homeobox genes Pbx1 and Hoxa9 and enriched for embryonic skeletal system development. Consistent with our previous observations, Biomodule C also contained the homeobox genes Meis1 and Meis2. Thus, we observed involvement of Meis proteins using 2 different and independent prioritizations. We termed this biomodule the Meis biomodule.

The Meis biomodule genes are prognostic for both prostate cancer recurrence and survival

To explore and refine the revealed biomodules for their clinical relevance and potential clinical translation, we adopted a 2-step approach. First, we evaluated each biomodule’s ability to divide patients into statistically different cohorts based on Kaplan–Meier analysis using the Prediction Analysis for Microarrays (PAM) algorithm (32). PAM provides an unbiased, unsupervised approach to determining whether there are different cohorts based on gene expression patterns. If the PAM methodology showed
indications of curve separation with Chi-squared $P$-values $\leq 0.1$, we would then proceed with a second step—that of biomodule refinement. This second step is critical. As we have previously noted (27), the most informative (pathway-enriched) biomodules are not usually the most discriminatory (i.e., able to find survival/recurrence differences). Therefore, incorporation of mRNA data is needed to modify our informative biomodules into discriminatory biomodules. To conduct the refinement, we systematically evaluated the mRNA expression scale of biology gene combinations within the selected biomodules using independent datasets. We specifically trained in one dataset and validated our findings using independent datasets.

In particular, we initially examined 2 independent datasets: the first being a well-studied dataset of 78 patients status postprostatectomy (24) (Glinsky data set) where we evaluated their disease-free interval (i.e., PSA recurrence after treatment of the primary tumor). The second dataset was a cohort of 281 men who were diagnosed with prostate cancer who were treated with watchful-waiting in which we evaluated their overall survival (Sponer Swedish Watchful Waiting cohort; ref. 22). Of the biomodules evaluated, only the Meis biomodule showed an association in the disease-free interval dataset. Finally, we reverified our Meis biomodule in another recurrence dataset (Taylor) that contains 131 patients with biochemical recurrence data. Only PAM analysis with the Meis biomodule showed statistical significance ($\chi^2, P = 0.039$; Supplementary Fig. S2).

Because the Meis biomodule now had showed clinical import in the disease-free interval dataset, we proceeded to refine the biomodule using the same approach. Although the biomodule consisting of 5 genes (Meis1, Meis2, Pbx1, HoxA9, and HoxB7) approached statistical significance, we noted that a smaller combination of 4 genes (HoxA9, Meis1, Meis2, and Pbx1) provided the most significant $P$-value ($\chi^2$ of 0.02 (Fig. 3A). We then validated this refined biomodule in the independent Swedish Watchful Waiting dataset in an unbiased manner using PAM and found this biomodule to have a $P$-value of 0.05.

This same curve separation persisted when we examined low-grade prostate cancer tumors. In fact, when we looked at patients with Gleason 7 disease in the Swedish Watchful Waiting cohort, we saw marked differences in the 2 groups ($n = 117$, $\chi^2 P = 0.03$; ref. 22). Interestingly, the 4-gene signature was not able to split Gleason 6 tumors. However, when we examined the individual signature genes, we noted that decreased expression (less than the mean of all samples) of only Meis1 and Meis2 combined were able to define cohorts with differences in survival ($n = 83$, $P = 0.008$; Fig. 3B). Differential expression of HoxA9 and Pbx1 individually did not show any measureable survival difference among low-grade tumors and were only significant in disease recurrence and patient survival from advanced tumors. Impressively, patients with differential expression in both Meis1 and Meis2 Gleason 6 tumors showed an 18-month decrease in overall survival (157 months vs. 175 months, Fig. 3C), supporting a role for these proteins in the formation of poor-prognosis tumors. We saw a similar pattern among the Gleason 7 cohort with a 40-month survival difference ($n = 117$, $P = 0.01$, Fig. 3D).

We next asked whether Meis1, Meis2, or a combination could serve as independent predictors of recurrence and survival using Cox regression analysis. Recaptulating our Kaplan–Meier analysis experience, univariate analysis of Meis1 and Meis2 expression scores (or their combination) showed significant hazard ratios in all categories (Supplementary Table S4). Even after adjusting for Gleason score and age, elevated levels of Meis2 remained an independent predictor of decreased rate of recurrence ($HR = 0.69$, $P = 0.052$). Similarly, both elevated levels of Meis1 and the combination of Meis1 and Meis2 were highly associated with improved survival ($HR = 0.14$, $P = 0.017$ and $HR = 0.33$, $P = 0.025$, respectively).

**Decreased expression of Meis1, Meis2, Pbx1 and increased expression of HoxA9 characterize Meis biomodule**

Having established clinical relevance in this Meis-driven biomodule, we then set out to determine the changes in the biomodule within different clinical stages. To do this, we examined the fold-change of our genes of interest from 2 other independent datasets: the first compared primary tumor versus normal prostate (GDS2547: 64 vs. 18 specimens, respectively; ref. 34) and the second castrate resistant prostate cancer as compared with primary tumor specimens (GSE32269: 22 vs. 29 specimens, respectively; ref. 20). Table 1 provides a synopsis of our findings. These data document a consistent pattern of decreased expression of Meis1, Meis2, and Pbx1 during tumor initiation and progression. Indeed, from normal prostate to primary prostate tumor, the greatest decrease is in Meis1, suggesting that decreased expression of Meis1 plays a role in tumor initiation. HoxA9 showed a 1.1-fold increase (not significant). Although it exhibited only a subtle change, our initial Kaplan–Meier analysis of the recurrence dataset showed that HoxA9 was essential for proper separation of the population into 2 cohorts. When HoxA9 was left out of the PAM algorithm, no significant curve separation was seen. Therefore, we reasoned that subtle changes in HoxA9 seem to have profound changes in phenotype and have maintained it as part of the Meis biomodule. Given that these were prostatectomy specimens, we further reasoned that HoxA9 potentially is involved in tumor initiation. The fold-change comparing primary prostate tumor to castrate-resistant tumor documents the greatest decline in Meis2 and Pbx1, suggesting that these genes play a role in tumor progression and castration resistance.

**Meis biomodule signature effectively classifies prostate oncogenic states and is associated with Gleason grade**

Given that the 4-gene signature could, in an unsupervised fashion, identify cohorts of patients with decreased survival and decreased time to disease relapse, we tested the hypothesis that this 4-gene signature could indeed separate groups of patients based on their expression profile. To do this, we used another independent dataset of 185 gene expression...
profiles comprising normal prostate, primary prostate cancer, prostate metastasis, and immortalized prostate cancer cell lines (23). We computed a composite score by simply adding the normalized expression levels of Meis1, Meis2, Pbx1, and HoxA9. We subtracted HoxA9 because, when we examined the 2 cohorts identified by PAM in the relapse postprostatectomy dataset, we saw a nonsignificant trend toward an increase in HoxA9 as opposed to significant decreases in Meis1, Meis2, and Pbx1. We then ordered the specimens based on this composite signature score. Importantly, we did not employ any training algorithm that may influence or bias our analyses. Data shown in Fig. 4A shows that normal prostate was separated furthest from immortalized cell lines and metastatic disease. Although there was some overlap between the normal prostate and primary prostate tumor, they are graphically separated. Thus, without the use of a training algorithm, we are able to cluster prostate tissue in different stages of oncogenesis using our Meis1/Meis2/PBX1/HoxA9 biomodule.

We repeated this simple graphical analysis using only primary prostate cancer tumor specimens and grouped them based on Gleason score. The pattern that emerges is that Gleason 6 and Gleason 7 prostate cancers are quite heterogeneous with wide-ranging Meis module scores (Fig. 4B). As noted in the figure, the mean Meis module score

Figure 3. Changes in Meis regulatory biomodule is prognostic for PSA recurrence and patient survival. A, gene expression profiles from prostatectomy specimens of 79 patients (Glinsky dataset) using the prediction analysis for microarrays (PAM) algorithm to stratify patients into 2 groups based on changes in expression of Meis1, Meis2, Pbx1, and HoxA9. PAM computationally separates patients into 2 groups based on available gene expression data. The result is 2 computation clusters (PAM cluster 1 and PAM cluster 2). Time to PSA recurrence was analyzed using Kaplan–Meier analysis and detected an 8-month decrease in median disease-free interval (log-rank P-value = 0.02). B, gene expression profiles of biopsy specimens from 281 patients (GSE16560) who underwent watchful-waiting until death were analyzed using Kaplan–Meier techniques. Decreased expression of either Meis1 or Meis2 (below the mean Meis levels, green lines) significantly decreased patient survival compared with controls (at or above mean Meis levels, blue lines) and showed a 33-month difference in median survival (P = 0.01). C, gene expression profile of 83 Gleason 6 tumors biopsy specimens (GSE16560) for their changes in Meis1 and Meis2 using Kaplan–Meier techniques. Decreased expression of either Meis1 or Meis2 (below the mean Meis levels, green lines) significantly decreased patient survival compared with controls (at or above mean Meis levels, blue lines) and showed an 18-month survival difference (P = 0.009). D, gene expression profile of 117 men with Gleason 7 tumors biopsy specimens (GSE16560) analyzed using Kaplan–Meier techniques. Decreased expression of either Meis1 or Meis2 (below the mean Meis levels, green lines) significantly decreased patient survival compared with controls (at or above mean Meis levels, blue lines) and showed a 40-month difference in median survival (P = 0.01).
decreases with increasing Gleason with a Pearson correlation coefficient of 0.98 ($P = 0.02$).

**Immunohistochemical detection of Meis2 in prostate tissues**

To validate the bioinformatic analyses of our Meis module using clinical specimens, we evaluated the histologic pattern and prevalence of Meis2 expression in 110 prostate tissue specimens. We focused on Meis2 because mRNA expression appeared to decrease in 2 stages, first during oncogenesis and second during metastasis and castration-resistance, as shown in Table 1; this indicated that Meis2 has a role during both oncogenesis and tumor progression. Immunohistochemical analyses of normal human prostate

Table 1. Fold-change univariate analysis

<table>
<thead>
<tr>
<th></th>
<th>Epithelial-only signature (prostate vs. sem. ves.)</th>
<th>Primary prostate vs. normal tissue</th>
<th>CRPC vs. primary tumor</th>
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<tr>
<td>MEIS1</td>
<td>25.43</td>
<td>0.55</td>
<td>N.S.</td>
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<tr>
<td>MEIS2</td>
<td>52.63</td>
<td>0.64</td>
<td>0.09</td>
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<td>PBX1</td>
<td>2.78</td>
<td>0.69</td>
<td>0.28</td>
</tr>
<tr>
<td>HOXA9</td>
<td>N.S.</td>
<td>N.S.</td>
<td>N.S.</td>
</tr>
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Abbreviation: N.S., not significant (FDR > 0.05).
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Figure 5. Loss of Meis2 protein expression in prostate tumors. A, immunohistochemical detection of Meis2 in normal prostate tissue documented strong nuclear staining of basal-epithelial cells with weak luminal-epithelial cell staining (left). Furthermore, Meis2 was expressed in stromal fibroblasts. In all prostate tumors, Meis2 expression was undetectable (middle and right). Stromal and adjacent normal tissue retained Meis2 expression. B, summary of epithelial Meis2 staining of prostate tissues. Bars represent the percentage of normal glands (normal), tumors (GG3, GG4, GG5), or lymph-node metastases (LN-Met) which had more than 1% (gray bars) or 10% (black bars) of cells staining positive for Meis2. This loss of epithelial Meis2 expression from normal prostate tissue to tumor was highly statistically significant (P-value < 0.0001). C, changes in Meis1 and Meis2 are not associated with changes in basal and luminal epithelial cell–specific cytokeratins. To control for changes in basal and luminal epithelial cell content during tumor initiation and progression, we analyzed the associated expression of Cytokeratins 5 and 14 (basal, CK5, and CK14) and 8 (luminal, CK8) between patients separated via Meis expression within the Swedish Watchful Waiting Gleason 6 cohort. Decreased expression of either Meis1 or Meis2 (below the mean Meis levels, green lines, and bars) significantly decreased patient survival compared to controls (at or above mean Meis levels, blue lines, and bars).

The robust expression of Meis2 in the basal cell layer of normal prostate epithelia suggested that the observed decrease in Meis2 mRNA expression during cancer initiation and progression, as observed in our gene array analyses, may simply be because of the characteristic loss of basal cells and enrichment of malignant luminal epithelial cells in prostate tumors (35). To address this, we conducted further analyses of the expression of basal-specific Cytokeratins 5 and 14, and luminal-specific Cytokeratin 8 in patients split by Meis1 and/or Meis2 differences. These data document that, in Gleason 6 watchful waiting patients, there is no statistical difference in the expression of basal Cytokeratins 5 and 14, or luminal Cytokeratin 8 between tumors that were grouped based on Meis expression (Fig. 5C). Thus, decreases in Meis2 expression during cancer initiation and progression is not simply an artifact of changes in basal to luminal epithelial cell content. These data validate our...
bioinformatic analyses of mRNA data showing decreased expression of Meis2 in poor prognosis prostate tumor specimens, and confirm that deregulation of the homeobox gene cofactors Meis1, Meis2, and Pbx1 may be significant molecular events during prostate cancer initiation and progression.

Discussion

Here we document the identification of a single developmental signaling pathway that spans both prostate oncogenesis and progression. Our study documents molecular differences between seminal vesicle and prostate epithelial cells that highlight critical determinants in the vast disparity between cancer incidences for these sex accessory glands. The role of Meis1 and Meis2 in low-grade prostate tumors suggests that these genes play a critical function in the formation of poor prognosis tumors and may be a useful biomarker or therapeutic target.

Indeed, a recent study of familial prostate cancer identified a germ line mutation of HoxB13 (G84E) in men with early-onset, familial prostate cancer (36). The G84E mutation and other additional mutations frequently occurred within the Meis interacting domain of HoxB13. Thus, interference with appropriate Meis/Hox protein interactions, either by germ line mutation or decreased expression, is clearly a critical molecular event in prostate cancer etiology. As shown in the protein–protein network of Supplementary Fig. S3, our data shows a clear connectivity among the Meis and Pbx proteins and HoxB13.

Concordant to our observations, Meis2 was identified in an array screen as one of the top 50 downregulated genes in prostate cancer, and changes in Hoxa9 mRNA expression was reported in a prostate cancer cell line in response to selenium treatment (37). The relative weak DNA-binding specificity of Hox proteins themselves, along with their dependence upon cofactors to regulate gene targets, implies 2 critical points (7). First, Hox proteins may not be as important as the cofactors, which are expressed and which regulate Hox protein DNA-binding specificity and transcriptional activity. Second, changes in cofactor expression may profoundly alter the prostate gene-specificity of Hox protein transcriptional regulation. Hox proteins may function to promote differentiation and suppress proliferation of normal prostate epithelial cells or promote a less-aggressive cancer phenotype. Thus, compounds that restore Meis1, Meis2, and/or Pbx1 may be effective toward the prevention or treatment of aggressive prostate tumors.

In addition, our work provides a cautionary tale to the analysis of genomic profiling of unselected tumor tissue. The persistence of stromal Meis2 expression provides an explanation as to why previous gene array analyses comparing whole tissue prostate and seminal vesicle did not identify Meis2 as being differentially expressed (19). It may explain why Meis2 mRNA expression appeared to decrease further in metastatic tissues, as there was no longer any Meis2-positive stroma present. Thus, the overall decrease in Meis2 expression from gene array analyses of primary prostate tumors may be even more profound than observed as there is often contaminating stroma present during the tissue preparation.

From a translational standpoint, the Meis module is exciting on 2 counts. First, loss of the Meis1 and/or Meis2 expression may be a useful biomarker to discern patients with low-grade tumors that would benefit from treatment. PCR analysis of patient prostate needle biopsies may provide critical prognostic information as to the necessity of prostatectomy in low-risk disease. Indeed, patients who underwent radical prostatectomy for Gleason 6 prostate cancer trended toward an improvement in overall survival with an absolute risk reduction of 13% and absolute decrease in distant metastasis by 11.4% (38). Thus, it is clear that some patients are benefiting from treatment of their tumors, and proper selection of these low-risk patients may spare others undue morbidity. Second, targeting the Meis module could function as an efficacious clinical target for the development of new therapies to prevent prostate tumor initiation and treat aggressive prostate tumors.

Conclusion

Loss of Hox protein co-factors Meis1, Meis2, and Pbx1 are associated with both prostate cancer oncogenesis and tumor progression. Not only may these genes potentially serve as useful therapeutic targets, but they may also serve as powerful biomarker in identifying men for treatment of low-grade disease.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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