ERG/AKR1C3/AR Constitutes a Feed-Forward Loop for AR Signaling in Prostate Cancer Cells

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Abstract

Purpose: Intratumoral androgen synthesis in prostate cancer contributes to the development of castration-resistant prostate cancer (CRPC). Several enzymes responsible for androgen biosynthesis have been shown to be overexpressed in CRPC, thus contributing to CRPC in a castrated environment. The TMPRSS2–ERG transcription factor has been shown to be present in primary prostate cancer tumors as well as CRPC tumors. We hypothesize that TMPRSS2–ERG fusions regulate androgen biosynthetic enzyme (ABE) gene expression and the production of androgens, which contributes to the development of CRPC.

Experimental design: We used a panel of assays, including lentivirus transduction, gene expression, chromatin immunoprecipitation and sequencing, liquid chromatography-mass spectrometric quantitation, immunocytochemistry, immunohistochemistry, and bioinformatics analysis of gene microarray databases, to determine ERG regulation of androgen synthesis.

Results: We found that ERG regulated the expression of the ABE AKR1C3 in prostate cancer cells via direct binding to the AKR1C3 gene. Knockdown of ERG resulted in reduced AKR1C3 expression, which caused a reduction in both DHT synthesis and PSA expression in VCaP prostate cancer cells treated with 5α-androstane-dione (5α-Adione), a DHT precursor metabolite. Immunohistochemical staining revealed that ERG was coexpressed with AKR1C3 in prostate cancer tissue samples.

Conclusions: These data suggest that AKR1C3 catalyzes the biochemical reduction of 5α-Adione to DHT in prostate cancer cells, and that ERG regulates this step through upregulation of AKR1C3 expression. Elucidation of ERG regulation of ABEs in CRPC may help to stratify TMPRSS2–ERG fusion-positive prostate cancer patients in the clinic for anti-androgen receptor–driven therapies; and AKR1C3 may serve as a valuable therapeutic target in the treatment of CRPC. Clin Cancer Res; 1–11. ©2015 AACR.

Introduction

The TMPRSS2–ERG fusion gene has been shown to be present in approximately 40% of prostate cancer tumors, including primary and advanced prostate cancer (1–6). The TMPRSS2–ERG fusion gene results in androgen receptor (AR)–derived overexpression of the ERG transcription factor (7). The presence of TMPRSS2–ERG in prostate cancer has been shown to be associated with poor clinical prognosis (2, 8–10). ERG fusion-positive prostate cancer patients had significantly lower disease-free survival in watchful waiting cohorts (11, 12), and significantly greater risk of biochemical PSA recurrence compared with fusion-negative prostate cancer patients (13–15).

ERG has been shown to have several biologic functions that facilitate its oncogenic properties in prostate cancer. It has been shown to regulate cellular migration and invasion, epithelial-to-mesenchymal transition, dedifferentiation, and AR signaling (16–19); however, the biologic functions of ERG contributing to the development of castration-resistant prostate cancer (CRPC) have not been fully elucidated. Interestingly, ERG fusion-positive prostate cancer patients responded better to abiraterone treatment, a CYP17A1 enzyme inhibitor used to treat CRPC, compared with ERG fusion-negative patients (5). These data are consistent with ERG fusion-positive patients having a higher PSA recurrence, and suggests that ERG may regulate the synthesis of intratumoral androgens, and AR activation in CRPC.

Upregulation of ABEs and intratumoral androgen synthesis have been shown to facilitate the development of CRPC (20–22). This can be seen with the ability of abiraterone treatment to reduce serum and intratumoral dihydrotestosterone (DHT) and testosterone levels in CRPC patients (23–25). One ABE that has recently become of particular interest is AKR1C3, because it has been shown to be highly upregulated in CRPC tumors (26). AKR1C3 enzyme functions downstream of CYP17A1 enzyme in the DHT synthesis pathway (22), and it may play a pivotal role in DHT synthesis in CRPC. Intratumoral DHT synthesis bypasses the synthesis of testosterone, and DHT is synthesized directly from androstanediol (5α-Adione) or androstanediol (22, 27, 28). Inhibitors specific for AKR1C3 are currently being developed (29–31), and may prove to be beneficial for treatment of CRPC.

This study is focused on TMPRSS2–ERG transcription factor upregulation of AKR1C3 expression and DHT synthesis in CRPC.
**Translational Relevance**

Intracellular androgen synthesis is a viable target for clinical management of patients undergoing traditional androgen deprivation therapies. Despite newer therapies such as abiraterone acetate, a drug that targets androgen biosynthetic enzyme (ABE) Cyp17, the disease eventually relapses (abiraterone resistance). Elucidating molecular mechanisms contributing to the expression of biosynthetic enzymes in androgen production helps to understand the biologic mechanisms contributing to the development of castration-resistant prostate cancer (CRPC). ERG factor regulates key enzymes that participate in DHT production in prostate cancer cells. ERG specifically binds to AKR1C3 gene, regulates its expression, promotes DHT production via 5α-androstanedione and results in androgen receptor (AR) activation. Further, both ERG factor and AKR1C3 are coexpressed in human prostate tumors and predict lower survival in patients. As TMPRSS2–ERG fusions are prevalent in prostate cancer, including CRPC, and our data present a link between ERG expression, androgen biosynthesis, and AR activation, this study suggests that TMPRSS–ERG fusion-positive prostate cancer patients toward anti-AR therapies may have favorable responses to anti-AR therapies.

We have evidence, suggesting that AKR1C3 functions as a key ABE responsible for DHT synthesis via biochemical reduction of 5α-Androide into DHT (bypassing testosterone). Our data indicate that 5α-Androide is the primary DHT precursor metabolite, and that 5α-Androide can induce high levels of AR activation in CRPC cells. Elucidation of TMPRSS2–ERG regulation of AKR1C3 may help to stratify ERG fusion-positive prostate cancer patients toward anti-AR-targeted therapies. In addition, our data support the notion that AKR1C3 is an attractive therapeutic target for CRPC treatment.

**Materials and Methods**

**Cell lines and treatments**

Prostate cancer cell lines VCaP, LNCaP, and HEK293T cells were obtained from the ATCC. BPH-1 cells were obtained from Dr. Shijie Sheng (Wayne State University). VCaP cells were maintained in ATCC DMEM media with 10% FBS (Thermo Fisher Scientific), and 1% penicillin–streptomycin (PS; Gibco). LNCaP and BPH-1 cells were maintained in Gibco RPMI media (Gibco) with 10% FBS and 1% PS. HEK293T cells were maintained in Gibco DMEM media with 10% FBS, 1% PS, and 1% sodium pyruvate. All cell lines were tested for contamination Mycoplasma and before use with the Venor-GeM Mycoplasma Detection Kit from Sigma Biochemicals. HPLC/MS-MS, immunocytochemistry, and PSA activation experiments were performed using Gibco DMEM phenol red-free media supplemented with 1% charcoal stripped serum (CSS) and 1% PS.

**Lentiviral plasmids and transduction**

Lentiviral plasmid selection and virus production were conducted as previously described with minor modifications (32). Briefly, the pGIPZ lentivector was used for shRNA ERG knockdown (5'-TGACACACGTCGCAAGATG-3') and shRNA AKR1C3 knockdown (5'-ACACCAGTGTGAAAAAGCTA-3'), and the pLOC lentivector was used for ERG overexpression (Open BioSystems). Truncated ERG and full-length ERG were cloned into the pLOC lentivector. Cloning primers are listed in Supplementary Table S1. Lentiviral particles were generated in HEK293T cells using a Trans-Lentiviral Packaging Kit (Thermo Fisher Scientific). VCaP cells were infected with pGIPZ lentiviral particles and selected with 0.3 μg/mL puromycin (Research Products International Corporation). LNCaP and BPH-1 cells were infected with pLOC lentiviral particles and selected with 2–4 μg/mL blastocidin (Research Products International Corporation). A pooled lentiviral cell population was used for all lentiviral experiments. Transient transfections were performed using Lipofectamine2000 Reagent (Invitrogen) in OptiMEM media (Invitrogen).

**Western blotting and antibodies**

Western blotting was performed using SDS-PAGE with gel transfer to a nitrocellulose membrane. Membranes were blocked with 5% non-fat milk and probed with primary antibody in 5% milk. Membranes were probed with horseradish peroxidase–linked secondary antibody in 5% milk. Protein bands were detected using enhanced chemiluminescence substrate and autoradiography film. Primary and secondary antibodies are listed in Supplementary Table S2. Densitometry was performed using ImageJ software (NIH).

**RT-PCR and RT-qPCR**

RNA was extracted from VCaP and LNCaP cells using the TRizol (Invitrogen) method. For RT-PCR experiments, cDNA was amplified using an Eppendorf Mastercycler Realplex2 qPCR machine. PCR products were loaded onto a 0.8% agarose gel containing ethidium bromide. For RT-qPCR experiments, cDNA was amplified with SYBR green from the SensiFAST SYBR Kit obtained from Bioline (Bio-98002). Gene expression was quantified with the previously described qPCR method (33). Fold changes in message levels were quantified using the comparative Ct method (34). PCR primers are listed in Supplementary Table S2.

**Chromatin immunoprecipitation PCR**

Chromatin immunoprecipitation (ChIP)-PCR was carried out using the ChIP-IT Express kit obtained from Active Motif as previously described with following modification (17). Briefly, five million VCaP cells were fixed with formaldehyde and chromatin was extracted according to the manufacturer's instructions. For immunoprecipitation, 15 to 25 μg of chromatin was incubated with 3 to 5 μg of anti-ERG primary antibody ERG1/2/3 (H-95)X or normal IgG antibody (Santa Cruz Biotechnology) and protein G agarose beads. Immunoprecipitated chromatin was reverse cross-linked with proteinase K. PCR was performed using 750 to 1,000 ng DNA template per sample and ran at 30 to 40 cycles using an Eppendorf Mastercycler PCR machine. ChIP-PCR primers are listed in Supplementary Table S1. PCR products were analyzed on a 0.8% agarose gel containing ethidium bromide. ChIP-seq methodology and data analysis were performed as previously described (35).

**Mass spectrometry (HPLC/MS-MS)**

Androgen metabolites obtained from Steraloids and Sigma-Aldrich (Supplementary Table S3) were used for MS standards
and in vitro steroid treatments. VCaP-shScrambled and shERG cells were plated at a cell density of 500,000 cells per well in a 6-well plate. Cells were serum starved for 24 hours using 1% CSS phenol red-free DMEM media. Cells were treated with androgen metabolites or 0.1% ethanol (vehicle control) for 24 hours in 1% CSS phenol red-free media. Cells were treated with (100 nmoL/L) androgen metabolite or a concentration gradient of (10 nmoL/L; 50 nmoL/L), or (100 nmoL/L) androgen metabolite. To serve as an internal control, 1 ng of DHEA-D2 and DHT-D3 was added to the media directly before cell lysis preparation. Cells and media were collected and probe sonicated on ice. Lipids were purified using a Sep-pak cartridge obtained from Waters Corporation (WAT023590). Lipid samples were eluted with acetonitrile into HPLC/MS-MS vials obtained from MicroSOLV Technology (9512S-0CV vials, 95025-10C-B tops). A cell count control plate was plated and cell number was determined on the day of sample collection. HPLC/MS-MS experiments and data analysis were performed at the Wayne State University Lipidomics Core Facility.

**Immunocytochemistry**

VCAp cells were plated on cover slips at a cell density of 400,000 cells per cover slip. Cells were serum starved for 24 hours using 1% CSS phenol red-free DMEM media. Cells were treated with (100 nmoL/L) 5α-Androstanediol (5α-Adione) or 0.1% ethanol for 24 hours in 1% CSS phenol red-free DMEM media. Cell coverslips were washed with 1X PBS, fixed with 4% formaldehyde, permeabilized with 0.5% Triton X-100, blocked with 2% horse serum, and incubated overnight at 4°C with either (i) AR antibody (rabbit) or (ii) AR antibody (mouse). 1:1000 in PBS (Santa Cruz Biotechnology). Cover slips were washed with PBS and incubated at room temperature in a dark box for 1 hour with either (i) Texas red antibody (rabbit; Vector Laboratories) or (ii) Alexa Fluor 633 antibody (mouse), 1:200 in PBS (Molecular Probes). Cover slips were mounted onto slides using Vectashield mounting medium with DAPI (Vector Laboratories). Nuclei were counterstained with Mayer’s hematoxylin (Sigma-Aldrich). Sections were then dehydrated by incubation with 3,3-diaminobenzidine tetrahydrochloride (Vector Laboratories). Images were captured using a Zeiss LSM 780 confocal microscope at a magnification of ×40.

**Immunohistochemistry**

Human prostate cancer tissues from patients undergoing radical prostatectomy were used for immunohistochemical analysis. Formalin-fixed, paraffin-embedded serial tissue sections from human prostate tumor tissue specimens and LuCaP xenograft tumors were deparaffinized with xylene and rehydrated in graded EtOH. Endogenous peroxidase activity was blocked by incubating in 3% H2O2 for 20 minutes. Antigen retrieval was performed with Antigen Retrieval Citra Plus Solution (BioGenex) in a steamer. Slides were then blocked with the Blocking Serum from ABC Antigen Retrieval Citra Plus Solution (BioGenex) in a steamer. To serve as an internal control, 1 ng of DHEA-D2 and DHT-D3 was added to the media directly before cell lysis preparation. Cells and media were collected and probe sonicated on ice. Lipids were purified using a Sep-pak cartridge obtained from Waters Corporation (WAT023590). Lipid samples were eluted with acetonitrile into HPLC/MS-MS vials obtained from MicroSOLV Technology (9512S-0CV vials, 95025-10C-B tops). A cell count control plate was plated and cell number was determined on the day of sample collection. HPLC/MS-MS experiments and data analysis were performed at the Wayne State University Lipidomics Core Facility.

**Gene expression omnibus database**

Gene expression omnibus (GEO) publicly available microarray data were used to analyze correlation between ERG expression and AKR1C3 expression. The 25 metastatic prostate cancer expression profiles were extracted from database GDS2545 using ERG accession ID 914_2_at and AKR1C3 accession ID 37399_at, and analyzed using "GEO2R." The metastatic samples were obtained from warm autopsy program. The in vitro cell line expression profiles were extracted from databases GSE22010, GSE39353, and GSE39354 using ERG accession ID’s 8070297, 211626_x_at, and 211626_x_at respectively, and AKR1C3 accession ID’s 7925929, 209160_at, and 209160_at respectively.

**Oncomine database**

The Oncomine database was used to extract survival data for 363 prostate tumor specimens from Setlur and colleagues “prostate cancer” (2008; ref. 36). Survival data were given as dead or alive at 1 year, 3 years, and endpoint. For survival data past 5 years, the last time to follow-up was used as the endpoint. Prostate tumor expression profiles were extracted from the GEO database GSE8402 using AKR1C3 accession ID DAP4_3222. AKR1C3 expression was determined as high or low by taking the upper and lower quartile expression value of 363 tumor specimens. This gave a sample size of 91 high tumors and 90 low tumors, with their respective available survival data taken from the Oncomine database. For ERG analysis the presence or absence of the TMPRSS2–ERG fusion gene was determined in the Setlur and colleagues study by FISH or PCR analysis, and these data were made available in the Oncomine database as well as the GEO database. Survival data and TMPRSS2–ERG fusion status data were available for analysis from 354 of the prostate tumor specimens.

**Statistical analysis**

Statistical analyses were performed using GraphPad Prism Version 5.0.

**Results**

**TMPRSS2-ERG regulates ABE expression in prostate cancer cells**

To determine ERG regulation of ABES in prostate cancer, we performed shRNA knockdown of ERG in TMPRSS2-ERG fusion-positive VCaP cells using lentivirus transduction. Lentiviral shRNA knockdown of ERG resulted in decreased ERG expression at the mRNA and protein levels compared with VCaP-shScrambled control (Fig. 1A). Using VCaP-shScrambled and shERG cells, we performed a screening of ABE gene expression. Among the tested genes, expression of AKR1C3, HSD17B4, and HSD17B6 was highly reduced in VCaP shERG cells, and expression of HSD3B2 and HSD17B10 was also reduced to some extent (Fig. 1B). Using quantitative PCR, we showed that AKR1C3, HSD17B4, and HSD17B6 expression was significantly reduced in shERG knockdown cells (Fig. 1C). ERG knockdown in VCaP cells resulted in reduced protein expression of AKR1C3 (Fig. 1D) and HSD17B4 enzymes (Supplementary Fig. SIA), whereas HSD17B6 protein expression was undetectable (data not shown).

Next, we overexpressed the truncated form of ERG that is most commonly found in prostate cancer patients, TMPRSS2 exon 1
fused to ERG exon 4 (T1-E4; ref. 37). T1-E4 is also the truncated form of ERG expressed in VCaP cells (Supplementary Fig. S1B). We termed this truncated form “ERG40” because it has a deletion of the first 39 amino acids from the N-terminus (38). Lentivirus was used to overexpress the truncated ERG40 in LNCaP prostate cancer cells, and in BPH-1 cells (benign prostatic hyperplasia). Overexpression of ERG40 resulted in a significant increase in AKR1C3 mRNA compared with empty vector control (Supplementary Fig. S1C). Overexpression of ERG40 caused an increase in AKR1C3 protein expression in both LNCaP cells and BPH-1 cells (Fig. 1E). Interestingly, similar results were seen in LNCaP cells overexpressing full-length (wild-type) ERG. LNCaP ERGwt cells showed an increase in AKR1C3 mRNA compared with empty vector control (Supplementary Fig. S1D). These data demonstrate that ERG positively regulates the expression of DHT synthesis enzyme, AKR1C3, in prostate cancer cells.

ERG regulates AKR1C3 expression via direct DNA binding to the AKR1C3 gene

To investigate whether ERG regulation of AKR1C3 expression in prostate cancer occurs through direct DNA binding, we performed ChIP-PCR in VCaP cells. Primers were used to access ERG binding to the AKR1C3 gene region, spanning from −2 kb upstream of the transcription start site (TSS) to +2 kb downstream of the TSS. Several ERG consensus–binding sequence sites (5′-GGAA/T-3′) were identified in the 2 kb 5′ untranslated region (UTR) and in the first intron of the AKR1C3 gene (Fig. 2A). Four primer sets were designed to span the −2 kb promoter region (P1–P4) and the intron 1 region (I1–I4; Fig. 2A). ERG was shown to bind directly to the intron 1 region of the AKR1C3 gene, at a site located +154 to +670 downstream of the TSS (Fig. 2B). The known ERG target gene Plasminogen Activator Urokinase (PLAU; ref. 39) was also enriched in anti-ERG antibody

Figure 1.
TMPRSS2–ERG regulates ABE expression in prostate cancer cells. A, RT-qPCR analysis of ERG in VCaP-shScrambled (shScr) and VCaP shERG lentiviral cells. Western blot analysis of ERG in VCaP shScr and shERG cells; MOI, multiplicity of infection for lentiviral transduction. B, RT-PCR analysis of ABE expression in VCaP shScr and shERG cells. PCR cycle numbers are indicated above each DNA gel. C, RT-qPCR analysis of HSD17B6, HSD17B4, and AKR1C3 in VCaP shScr and VCaP shERG cells. D, Western blot analysis of AKR1C3 in VCaP, VCaP shScr, and shERG cells. E, Western blot analysis of AKR1C3 in LNCaP ERG40 and BPH-1 ERG40 lentiviral cells. LNCaP Ctrl and BPH-1 Ctrl cells represent empty vector controls. For statistical analysis a two-tailed, paired, Student t test was performed (N = 3); \*P < 0.01; \**P < 0.001. Numbers above Western blots represent fold changes determined by densitometry. Representative of three independent experiments.
immunoprecipitates, suggesting the validity of the assay. To
determine the specificity of ERG’s interaction with the AKR1C3
gene, we designed negative control primers that span regions of
the AKR1C3 gene that do not contain putative ERG consensus–
binding sites. As expected, there was no ERG binding to these
regions of the AKR1C3 gene (Fig. 2C).

ChIP-Seq was performed in VCaP cells with two independent
experiments using anti-ERG antibody. ERG-binding enrich-
ment peaks were observed at three different sites along the
AKR1C3 gene. Two of the binding peaks were located far
upstream of the TSS in the 5'-UTR of AKR1C3; one at approx-
imately −25 kb, and another at −75 kb, relative to the TSS. The
third peak was shown to be located near the TSS and intron 1
region (Fig. 2D), consistent with the ChIP-PCR data. These data
demonstrate that ERG directly binds to the AKR1C3 gene and
regulates AKR1C3 gene expression in fusion-positive prostate
cancer cells.

Androstanedione is a precursor metabolite for DHT in
TMPRSS2–ERG fusion-positive cells
AKR1C3 participates in testosterone and DHT synthesis in the
androgen biosynthetic pathway (Fig. 3A). DHT can be produced
directly from testosterone and indirectly through androstenedi-
one without involving testosterone (testosterone bypass path-
way). Using HPLC/MS-MS analysis, we investigated the produc-
tion of DHT from its immediate precursors’ as shown in Fig. 3A.
Previous studies support the notion that androstendione to 5α-
Adione is the preferred pathway in prostate cancer cells for the
production of DHT (27). VCaP-shScrambled cells were treated
with (10 nmol/L; 50 nmol/L), and (100 nmol/L) of 5α-
Adione, androsterone, and androstanediol, and cells and media
were collected for MS analysis. A signifi-
cant dose-dependent increase
in DHT synthesis was observed following treatment with 5α-
Adione (Fig. 3B). These data show that in VCaP cells DHT is
produced from the 5α-Adione pathway.

Figure 2.
- ERG binds directly to the AKR1C3 gene. A, diagram illustrating the AKR1C3 gene located on chromosome 10. Black tick marks indicate putative ERG-binding sites (5'-GGAA/T-3') located in the region of −2 Kbp to +2 Kbp relative to the TSS. B, ChIP-PCR analysis of putative ERG-binding sites in the AKR1C3 gene. ChIP was performed in VCaP cells using anti-ERG antibody; IgG antibody was used as a control for nonspecific binding. NTC is non-template control. C, ChIP-PCR analysis of a known ERG-binding site in PLAU promoter region using VCaP cells. Negative control primers were used in VCaP cells to demonstrate specificity of the ChIP-PCR technique. D, ChIP-Seq analysis performed in duplicate using anti-ERG antibody in VCaP cells.
Androstane-3,17-dione is an enzyme that catalyzes the conversion of 5α-Adione to DHT. To study the direct role of 5α-Adione treatment induced a marked increase in AR translocation compared with vehicle-treated cells AR had a weak to moderate correlation with the nucleus (r = 0.38); however, in 5α-Adione–treated cells AR had a strong correlation with the nucleus (r = 0.72; Supplementary Fig. S3A). RT-qPCR analysis showed a significant increase in PSA expression in VCaP-shScr cells following treatment with (100 nmol/L) 5α-Adione compared with VCaP shERG cells (Fig. 4C). In addition, RT-PCR data showed that activation of PSA expression was abrogated in VCaP-shERG cells treated with 5α-Adione (Fig. 4D); this further supports the notion that AKR1C3 is the enzyme responsible for the conversion of 5α-Adione to DHT. To study the direct role of 5α-Adione synthesis to DHT in AR activation, we performed shRNA knockdown of AKR1C3 in VCaP cells using shAKR1C3 lentivirus (Supplementary Fig. S3C). RT-qPCR analysis showed a significant increase in PSA expression in VCaP-shAKR1C3 cells following treatment with (100 nmol/L) 5α-Adione compared with VCaP-shAKR1C3 cells (Fig. 4E). Taken together, these data show that ERG enhances 5α-Adione-induced AR activation through direct upregulation of AKR1C3 expression.

Androstane-3,17-dione induces AR activation through ERG regulated AKR1C3 expression

The data above show that androstane-3,17-dione (5α-Adione) treatment of VCaP cells caused an increase in DHT synthesis; therefore, we investigated whether this had any functional consequence on AR activation. AR activation can be determined by AR translocation into the nucleus, and by AR target gene expression. Immunocytochemistry in VCaP cells demonstrated that (100 nmol/L) 5α-Adione treatment induced a marked increase in AR translocation into the nucleus compared with vehicle controls (Fig. 4A and Fig. 4B). AR colocalization with the nucleus was quantified using Velocity software (PerkinElmer) analysis and represented as a global Pearson’s correlation coefficient. In vehicle-treated cells AR had a weak to moderate correlation with the nucleus (r = 0.38); however, in 5α-Adione–treated cells AR had a strong correlation with the nucleus (r = 0.72; Supplementary Fig. S3A). RT-qPCR analysis showed a significant increase in PSA expression in VCaP-shScr cells following treatment with (100 nmol/L) 5α-Adione compared with VCaP shERG cells (Fig. 4C). In addition, RT-PCR data showed that activation of PSA expression was abrogated in VCaP-shERG cells treated with 5α-Adione (Fig. 4D); this further supports the notion that AKR1C3 is the enzyme responsible for the conversion of 5α-Adione to DHT. To study the direct role of 5α-Adione synthesis to DHT in AR activation, we performed shRNA knockdown of AKR1C3 in VCaP cells using shAKR1C3 lentivirus (Supplementary Fig. S3C). RT-qPCR analysis showed a significant increase in PSA expression in VCaP-shAKR1C3 cells following treatment with (100 nmol/L) 5α-Adione compared with VCaP shAKR1C3 cells (Fig. 4E). Taken together, these data show that ERG enhances 5α-Adione–induced AR activation through direct upregulation of AKR1C3 expression.
ERG and AKR1C3 are coexpressed in human prostate tumor tissue specimens, and predict lower survival probability

To determine the expression of ERG and AKR1C3 in human prostate tumors, immunohistochemical (IHC) staining of ERG and AKR1C3 in 64 human prostate tumor tissues was performed. IHC staining revealed that ERG and AKR1C3 were coexpressed in human prostate tumor tissue (Fig. 5A). The distribution of 64 patient tumor tissue samples for the presence or absence of ERG and AKR1C3 showed that there was significant coexpression of the two genes (Fig. 5B). ERG and AKR1C3 were also coexpressed in TMPRSS2–ERG fusion-positive LuCaP xenograft tissue specimens (Fig. 5C). Analysis of 25 metastatic prostate tumor specimens extracted from GEO publicly available microarray data revealed a significant correlation (\(P < 0.001\)) between ERG and AKR1C3 expression (Fig. 5D). ERG and AKR1C3 expression also correlated in GEO microarray data from in vitro prostate cell line experiments (Supplementary Fig. S4B–S4D). Data extracted from the Oncomine database containing 363 prostate tumor tissue specimens were used to perform Kaplan–Meier survival plots of AKR1C3 low- versus high-expression tumors (Supplementary Fig. S4A), and TMPRSS2–ERG fusion-negative versus fusion-positive tumors. Analysis of 90 patients by low or high expression of AKR1C3 and ERG in prostate tumor tissues, showed that there was a significant decrease (\(P = 0.022\) for AKR1C3 and \(P < 0.0001\) for ERG) in survival for AKR1C3 high-expression tumors, and for TMPRSS2–ERG fusion-positive tumors (Fig. 5E). The median survival for AKR1C3 low tumors or TMPRSS2–ERG fusion-negative tumors was 12 to 13 years, whereas the median survival for AKR1C3 high or ERG-positive tumors was 7 to 10 years. Analysis of these patients by AKR1C3 low and ERG negative versus AKR1C3 high and ERG-positive showed that there was a significant decrease (\(P = 0.017\)) in survival for AKR1C3 high and ERG-positive tumors. The median survival for AKR1C3 low and ERG-negative tumors was 13 years, whereas the median survival for AKR1C3 high and ERG-positive tumors was 8.5 years.

Discussion

The TMPRSS2–ERG fusions persist in CRPC (low androgen state) and fuel tumor growth through oncogenic ERG mechanisms. This implies that in order for ERG to be expressed in tumors,
there should be at least some active androgen synthesis and AR signaling. As advanced tumors often have low systemic androgen exposure, it is well accepted that tumors gain the capability of androgen synthesis for tumor growth, but the transcriptional mechanisms contributing to the androgen biosynthetic machinery are not known. Here, we describe a model in which AR activates expression of the TMPRSS2–ERG transcription factor, which then activates androgen synthesis via regulation of ABE, AKR1C3. Under this model, AKR1C3 can use 5α-Adione as a substrate and synthesize intratumoral DHT to provide continual AR activation in a castrate environment. This can fuel AR signaling, as well as provide a feed-forward activation loop of TMPRSS2–ERG and AKR1C3 expression in prostate tumors (Fig. 6).

It has been shown previously that androgens can regulate AKR1C3 expression. Specifically, high androgen levels suppress activation of AKR1C3 expression, whereas androgen-starved conditions activate expression of AKR1C3 (22, 40). This provides negative and positive regulation where in the presence of high and low androgen, respectively, AKR1C3 expression is regulated as a means to balance intracellular androgen levels. Androgen inhibition of AKR1C3 is thought to be regulated, in part, by AR-induced recruitment of lysine-specific demethylase 1 (LSD1) to the AKR1C3 gene (40). Whether TMPRSS2–ERG plays a role in androgen-induced regulation of AKR1C3 remains unclear; although, microarray data from Supplementary Fig. S4B suggest that ERG positively regulates AKR1C3 expression independent of androgen status.

![Figure 5](image_url)

**Figure 5.**
ERG and AKR1C3 are coexpressed in human prostate tumor tissue specimens, and predict lower survival probability. A, immunohistochemical analysis of AKR1C3 and ERG in human prostate tumor tissue specimens. B, distribution of 64 patients by presence or absence of AKR1C3 and ERG in prostate tumor tissues, *P* < 0.0001. C, immunohistochemical analysis of AKR1C3 and ERG in LuCaP xenograft specimens. D, the correlation plot of AKR1C3 and ERG expression using microarray data from 25 metastatic prostate cancer samples. Data were extracted from GEO database. E, the Kaplan-Meier survival plot of (left) AKR1C3 low tumors versus AKR1C3 high tumors (middle), ERG fusion-negative tumors versus ERG fusion-positive tumors, and (right) AKR1C3 low and TMPRSS2–ERG-negative versus AKR1C3 high and TMPRSS2–ERG-positive tumors. Data were extracted from Oncomine database. For statistical analyses of Kaplan-Meier survival, a Mantel-Cox test and a Gehan-Breslow-Wilcoxon test were performed.
The ChIP and ChIP-seq data from our study (Fig. 2) show a novel transcription mechanism, whereby ERG transcription factor directly binds to the AKR1C3 gene locus and activates gene expression. We cannot rule out direct ERG factor regulation of AR activity, as Yu and colleagues (19) demonstrated that ERG can occupy AR targets and regulate their expression. In such cases, ERG can override AR repressive activity and directly regulate AKR1C3 expression. AKR1C3 genome analysis (Fig. 2A and B) supports this idea as shown by direct binding of ERG to AKR1C3 intron and 5′-UTR. Another implication of Yu and colleagues study is that ERG inhibits AR signaling involving prodifferentiation function and shifts cells to stem cell dedifferentiation and oncogenesis. As our data support the notion that ERG activates androgen synthesis through AKR1C3 expression, the tumor-expressed androgens can mediate growth function through AR activation. As ERG depends on AR for its own expression, ERG-induced androgens are a link for sustained expression of ERG in advanced tumors via a feed-forward loop (Fig. 6). Sustained expression of ERG, restored AR activity, and expression of ABEs exist together in CRPC (41); our study implicates the involvement of ABEs in DHT production (27). In this pathway 3α-hydroxysteroid dehydrogenase (HSD3B) catalyzes the rate-limiting step in conversion of adrenal steroids such as DHEA to androstenedione. Tumors have been shown to express a gain-of-function mutation in HSD3B1, which increases the stability of the protein and provides a higher influx of DHT production from adrenal steroid precursors (42). Our studies also show that, in VCaP cells, ERG regulates HSD3B2 (Fig. 1B) gene expression; thus, not only enzyme stability, but overexpression of this enzyme may contribute to DHT production. Taken together, our data demonstrate that ERG participates in the expression of multiple ABEs in the DHT biosynthetic pathway.

Our data support the hypothesis that, in TMPRSS2–ERG fusion-positive cells, DHT is produced from the 5α-Adione pathway, and this drives AR activation. However, the finding that AKR1C3 may catalyze 5α-Adione into DHT is a novel finding that lends further support for therapeutically targeting AKR1C3 in prostate cancer patients. It may be beneficial in the future to screen prostate cancer patients for levels of 5α-Adione and AKR1C3 in their tumor biopsies. This study suggests that TMPRSS2–ERG fusion-positive prostate cancer patients may have favorable response rates to anti–AR-targeted therapies, such as enzalutamide, abiraterone, or AKR1C3-specific inhibitors.

**Disclosure of Potential Conflicts of Interest**
I. Asangani is a consultant/advisory board member for Oncfusion. M.L. Cher reports receiving speakers bureau honoraria from Astellas-Medivation and is a consultant/advisory board member for Bayer, Dendreon, and Janssen Biotech. No potential conflicts of interest were disclosed by the other authors.

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**References**

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