Rapid Induction of Androgen Receptor Splice Variants by Androgen Deprivation in Prostate Cancer

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Abstract

Purpose: Mechanisms mediating androgen receptor (AR) reactivation in prostate cancer that progresses after castration (castration-resistant prostate cancer; CRPC) and subsequent treatment with abiraterone (CYP17A1 inhibitor that further suppresses androgen synthesis) remain unclear.

Experimental Design: Prostate cancer xenografts were examined to identify mechanism of progression after castration and abiraterone.

Results: AR reactivation in abiraterone-resistant VCaP xenografts was not associated with restoration of intratumoral androgens or alterations in AR coregulators. In contrast, mRNA encoding full-length AR (AR-FL) and a constitutively active splice variant (AR-V7) were increased compared with xenografts before castration, with an increase in AR-V7 relative to AR-FL. This shift toward AR-V7 was due to a feedback mechanism whereby the androgen-ligated AR stimulates expression of proteins that suppress generation of AR-V7 relative to AR-FL transcripts. However, despite the increases in AR-V7 mRNA, it remained a minor transcript (<1%) relative to AR-FL in resistant VCaP xenografts and CRPC clinical samples. AR-V7 protein expression was similarly low relative to AR-FL in castration-resistant VCaP xenografts and androgen-deprived VCaP cells, but the weak basal AR activity in these latter cells was further repressed by AR-V7 siRNA.

Conclusions: AR-V7 at these low levels is not adequate to restore AR activity, but its rapid induction after androgen deprivation allows tumors to retain basal AR activity that may be needed for survival until more potent mechanisms emerge to activate AR. Agents targeting AR splice variants may be most effective when used very early in conjunction with therapies targeting the AR ligand-binding domain.

Clin Cancer Res; 20(6); 1590–600. ©2014 AACR.
androgen synthesis versus alternative mechanisms, including expression of alternatively spliced AR isoforms, in progression to abiraterone resistance.

Materials and Methods
siRNA and transfection analysis
The siRNAs specific for full-length AR (AR-FL; siExon 7, siEx7) and for AR-V7 (siCryptic Exon 3; siCE3) were described previously (17). The siRNA targeting AR exon 1 (siEX1) was described previously (21). Transfection of siRNA was performed using Lipofectamine RNAiMax (Invitrogen) in OptiMEM according to the manufacturer’s protocol. The final siRNA concentration was 20 nmol/L. A scrambled nontargeting control siRNA (Qiagen) was used as a negative control. Sixteen hours later, transfection medium was replaced with medium containing 5% charcoal-dextran stripped serum. Another 24 hours later, transfected cells were stimulated with DHT at 10 nmol/L or vehicle (ethanol) for 16 hours.

Immunoblot and steroid analyses
Whole-cell lysates were prepared using lysis buffer containing 2% SDS and subjected to immunoblotting. The antibodies against human AR (N20 and C19) were obtained from Santa Cruz Biotechnology. The antibodies against AR-actin (AC-15) and β-tubulin were from Millipore. The results from a minimum of three experiments were subjected to densitometry and normalized to β-actin or β-tubulin loading control and the mean values relative to control empty vector cells (set to 1.0) are given. AR immunoblot analyses were further quantified by comparison with blots containing serial dilutions of AR protein. Steroid extractions from xenografts and mass spectrometry were performed as described previously (5).

RNA sequencing
Total cellular RNA was extracted and purified from tissues using the RNeasy Mini Kit (Qiagen). One microgram of RNA was treated with DNase in-solution (Qiagen) and purified with the RNeasy MinElute Cleanup Kit (Qiagen). DNA-free RNA was then depleted of ribosomal RNA using the Ribo-Zero rRNA Removal Kit (Epigenetec). The remaining fraction of RNA was prepared into an indexed, strand-specific library using the Script-Seq v2 RNA-Seq Library Preparation Kit (Epigenetec), pooled, and then clustered and sequenced on a HiSeq 2000 (Illumina) with 100-base paired-end reads (100 × 100) and seven indexing cycles. Demultiplexed FASTQ files were aligned to the human genome and genetic features were quantified with the RNA sequencing (RNA-seq) Unified Mapper (http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3167048/). Data were visualized using the Integrative Genome Viewer (22). Data were submitted (SRP019503).

Reverse transcriptase PCR analysis
RNA was isolated using the RNeasy Mini Kit (Invitrogen). Superscript III reverse transcriptase (Invitrogen) was used for reverse transcription with 500 ng RNA in the presence of 100 ng of random primers (Invitrogen). For conventional PCR, the primers for AR-V7 were described previously (17). Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) primers were as follows: Forward: 5'-tcaccttccagggata-3', Reverse: 5'-gctccacattcttcgttga-3'. For quantitative reverse transcriptase PCR (qRT-PCR), the AR-V7 TaqMan primers and probe were as follows: Forward: 5'-cgaaatgttagagcagggatga-3', reverse: 5'-gctcatttgatgcagctcacta-3', probe: 5'-FAM-gggagaaatatcggggt-3'. The specific TaqMan primer probe sets for AR-FL, PSA, FKBPS5, TMPRSS2-ERG, PLZF, and GAPDH were as described previously (2, 21). KLK2 and NKX3.1 primer and probe sets were purchased from Applied Biosystems. qRT-PCR was performed in an ABI7900 thermal cycler.

Results
Expression of AR-stimulated genes in abiraterone-resistant VCaP xenografts
We previously reported a castration-resistant VCaP xenograft model that responds initially to abiraterone and then relapses after approximately 6 weeks of abiraterone treatment (2, 12). It should be noted that the abiraterone response in these castration-resistant xenografts primarily reflects blockade of de novo androgen synthesis by intratumoral CYP17A1, as the murine adrenal gland does not synthesize the substantial levels of androgens precursors that are produced in humans and are hence a major target of CYP17A1 inhibitors in men with CRPC. AR activity, based on expression of a small panel of AR-regulated genes, was lowered in abiraterone-resistant VCaP xenografts is not associated with restoration of intratumoral androgens. Moreover, we find that increases in the major AR splice variant (AR-V7) occur rapidly through a feedback mechanism and can mediate low-basal AR activity immediately after androgen deprivation, but cannot mediate the high-level AR activity in relapsed tumors. These results indicate that agents targeting AR splice variants may be most effective when used very early in conjunction with therapies targeting the AR LBD before the emergence of additional resistance mechanisms.
we used Affymetrix oligonucleotide microarrays to compare expression of AR-regulated genes in biopsies from CRPC xenografts before starting abiraterone and at relapse. This analysis showed that expression of multiple well-recognized AR-stimulated genes, including ERG from the TMPRSS2:ERG fusion gene and the recently reported AR and ERG-dependent oncogene SOX9 (23), was not significantly higher in the tumors before therapy than at relapse, supporting the conclusion that AR transcriptional activity was restored (Fig. 1A).

To more systematically identify alterations in the spectrum of AR-regulated genes, we also examined expression of all genes shown previously to be induced at least 2-fold by androgen in VCaP cells (21). Figure 1B shows a plot of their fold induction by DHT in VCaP cells versus the ratio of their expression in the xenografts before abiraterone and at relapse. These results show that expression of androgen-stimulated genes, whether they are weakly or strongly androgen induced, was broadly restored in the abiraterone-relapsed tumors, with no significant trend toward lower expression in the relapsed tumors.

**Androgen synthesis in abiraterone-resistant VCaP xenografts**

Consistent with our previous report, expression of CYP17A1 and AKR1C3 were increased in three of the four abiraterone-relapsed xenografts, and there were variable changes in other androgen synthetic enzymes (Fig. 1C). To determine whether restoration of intratumoral androgen synthesis may be mediating relapses, we performed mass spectrometry to examine intratumoral androgens in biopsies from these xenografts before starting abiraterone and at relapse. Significantly, we could readily detect DHT, testosterone, and androstenedione in the relapsed tumors. However, in all cases their levels were markedly lower than those in biopsies from the matched tumors before starting abiraterone treatment (Fig. 1D). These findings are consistent with recent clinical studies showing sustained suppression of testosterone in both blood and bone marrow in patients relapsing after abiraterone treatment (24). Therefore, although AR activity may still be dependent on residual androgen synthesis, it seemed that additional mechanisms must also be driving AR activity at low androgen levels.

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**Figure 1.** Expression of AR-stimulated genes and androgen synthesis in abiraterone-resistant VCaP xenografts. A, mice bearing recurrent VCaP xenografts were treated with abiraterone until relapse (0.5 mg/mL in drinking water for 4–6 weeks). RNA extracted from four sets of tumor samples pretreatment (Pre-abi) or posttreatment (Abi-resistant) was analyzed by microarray (Affymetrix HuGene 1.0 ST). Expression of 12 androgen-stimulated genes is shown as heatmap (red, high expression; green, low expression). B, the log2 ratio for expression of androgen-stimulated genes (>2-fold) in abiraterone-relapsed versus pretreatment xenograft is plotted versus their fold androgen induction. R² is presented as an indication of the correlation between androgen induction and change induced by abiraterone treatment, and showed no trend toward lower expression in the relapsed tumors. C, expression of nine genes involved in androgen synthesis is shown as heatmap. D, DHT, testosterone, and androstenedione levels in six sets of abiraterone-relapsed VCaP xenograft tumor samples versus pretreatment levels in tumor biopsies were measured using mass spectrometry. Each sample was measured in duplicate.
Genes and pathways altered in abiraterone-relapsed xenografts

We next did an unbiased analysis and identified all genes with significant ($P < 0.05$) changes in expression in the abiraterone-resistant xenografts versus the matched pre-treatment xenografts. A total of 181 genes were upregulated in abiraterone-resistant tumors and 132 genes were downregulated (Fig. 2A and B, and Supplementary Table S1). Amongst the 30 most upregulated and downregulated genes, only GATA2 has been shown to associate with AR and may contribute to enhancing AR activity, and we did not observe consistent increases in any established AR coactivator proteins or decreases in AR corepressors (Fig. 2A and B). Gene ontology analysis using the Database for Annotation, Visualization and Integrated Discovery system showed only weak enrichment for genes associated with histone acetylation amongst the genes that were upregulated in the abiraterone-resistant xenografts (Fig. 2C). In contrast, the downregulated genes were most strongly associated with mitosis (Fig. 2D). This latter finding indicated that although the relapsed tumors were growing, the abiraterone was still slowing their proliferative rate relative to the CRPC tumors before starting abiraterone.

We reported previously that AR functions directly as a transcriptional repressor on a subset of genes, including the AR gene itself and multiple genes involved in nucleotide and DNA synthesis (21). Interestingly, 10 of the 30 most upregulated genes in the abiraterone-resistant xenografts were genes we found previously to be AR repressed in VCaP or VCaP-derived CRPC cells (Fig. 2A, in bold and colored green, as an example). These included genes involved in nucleotide metabolism, fatty acid synthesis, and transcriptional regulation.

Figure 2. Genes and pathways altered in abiraterone-relapsed xenografts. A and B, heatmap presentations of expression of top 30 most consistently upregulated genes (A) or downregulated genes (B) in abiraterone-resistant tumors. Genes shown in bold and red in (A) were shown previously to be repressed by DHT in VCaP cells. C and D, gene ontology analysis on 181 upregulated genes (C) or 132 downregulated genes (D; $P < 0.05$). E, expression of 13 androgen-suppressed genes shown as heatmap.
Structural alterations in AR in abiraterone-resistant xenografts

VCaP cells have an amplified AR that is wild-type (25), and Sanger sequencing of AR from the abiraterone-relapsed xenografts did not reveal any AR mutations (not shown). To identify mutations that may be present in a subset of resistant cells or in only one of the amplified AR genes, and therefore present in a minority of AR transcripts, we also performed RNA-seq on three abiraterone-resistant xenografts. However, this analysis only identified AR mutations at low frequencies that were not shared amongst the xenografts and were of unclear functional significance (Supplementary Table S3; RNA-seq data are available in the NCBI Sequence Real Archive: SRP019503).

Previous studies have shown that AR can undergo alternative splicing from exon 3 in the DNA-binding domain (LBD) to cryptic exons in intron 3 or to exon 8 (14–20). These AR isoforms lack the carboxyl-terminal (C-terminal) LBD and can have ligand-independent constitutive activity that may mediate resistance to androgen deprivation therapy and to AR antagonists that target the LBD. Using RT-PCR with primer sets specific for AR-V1 to V7 and V12 in the VCaP xenografts, the only variant we could consistently detect was AR-V7 (not shown). Consistent with this result, using paired-end RNA-seq in three abiraterone-resistant VCaP xenografts, the only AR variant we detected was AR-V7. Relative to transcripts containing exon 3 spliced to exon 4, the abundance of transcripts containing exon 3 spliced to the V7 cryptic exon was 1.0% (1/99), 0.9% (48/5,323), and 0.2% (5/2,223).

As shown in Fig. 3A, AR-V7 was readily detectable and consistently increased in the abiraterone-resistant xenografts relative to levels in biopsies from the matched CRPC xenografts before starting abiraterone. AR-FL was also increased, but the increase in AR-V7 expression seemed to be greater. This was confirmed by qRT-PCR for AR-V7 versus AR-FL in the pre- and postabiraterone-treated tumors (Fig. 3B). We further assessed expression of AR-V7 and AR-FL in a series of previously described VCaP xenografts that were biopsied before castration (androgen dependent), at 4 days postcastration, or at relapse after castration (12). AR-V7 expression was increased at 4 days, was further increased in the relapsed castration-resistant xenografts, and these fold increases in AR-V7 were greater than those of AR-FL (Fig. 3C). As summarized in Fig. 3D, the mean increase of AR-V7 expression was 53-fold during the development of castration resistance, whereas AR-FL was increased to a lesser extent (10-fold). Similarly, AR-V7 was increased approximately 3-fold in abiraterone-resistant xenografts relative to levels in castration-resistant xenografts before abiraterone, whereas AR-FL was less increased (1.4-fold).

Androgen preferentially suppresses expression of AR-V7 versus AR-FL

We reported previously that AR gene transcription is rapidly repressed by the androgen-ligated AR through AR binding to a site in intron 2 of the AR gene (21). Therefore, we next addressed whether the increase in AR-V7 may reflect this feedback mechanism, versus selection for subpopulations of cells expressing higher AR-V7. Consistent with our previous results, VCaP cells cultured in steroid-depleted medium expressed high levels of AR-FL mRNA that were substantially decreased after 24 hours treatment with DHT (Fig. 4A, right). AR-FL mRNA was similarly decreased by DHT in VCS2 cells, which were derived from a castration-resistant VCaP xenograft (2). Significantly, DHT treatment caused an even greater decrease in the levels of AR-V7 in both the VCaP and VCS2 cells (∼20- and ∼80-fold in VCaP and VCS2 cells, respectively; Fig. 4A, left). AR-V7 is also expressed in high passage LNCaP cells (LNCaP) and in the LNCaP-derived C4-2 line. Although its levels are lower than in VCaP, DHT in both of these lines similarly decreased AR-V7 expression to a greater extent than AR-FL (Fig. 4B).

Examining a DHT dose response in VCaP cells, we found that AR-V7 was decreased by approximately 80% at 0.1 nmol/L DHT versus approximately 60% for AR-FL, and that AR-V7 was further markedly decreased by >95% at 1 to 10 nmol/L DHT versus approximately 80% for AR-FL (Fig. 4C). To confirm that the effects of DHT were mediated by the AR-FL, we used an siRNA targeting exon 7 (siEX7; which is not present in AR-V7) to selectively deplete the AR-FL. As expected, the siEX7 markedly decreased AR-FL, but not AR-V7 (Fig. 4D). Moreover, depletion of the AR-FL by siEX7 prevented the DHT-mediated decrease in AR-V7. To determine whether DHT may be preferentially enhancing degradation of the AR-V7 transcript, we assessed AR-V7 and AR-FL mRNA levels after treatment with actinomycin D to block new mRNA synthesis. Consistent with our previous results (21), DHT did not increase degradation of AR-FL mRNA (Fig. 4E, bottom). Significantly, DHT similarly did not increase degradation of the AR-V7 transcript, which instead seemed to be somewhat more stable in the presence of DHT (Fig. 4E, top). These results indicate that increased mRNA degradation does not account for the relative decrease in AR-V7 versus AR-FL in response to DHT.

Interestingly, examination of AR-FL versus AR-V7 transcripts over a 24-hour time-course showed that both declined similarly in response to DHT for approximately 8 hours, and that there was further loss primarily of AR-V7 between 8 to 24 hours (Fig. 4F; DHT+DMSO). Treatment with DHT and cycloheximide (CHX), which blocks new protein synthesis, abrogated the decline in AR-V7 at 24 hours (Fig. 4F; DHT+CHX), indicating that an androgen-stimulated increased in the synthesis of one or more proteins...
mediates the preferential decline in AR-V7 versus AR-FL mRNAs. These may be splicing factors, but also may be proteins that enhance RNA II polymerase elongation and thereby prevent stalling and premature chain termination in intron 3. In any case, our overall conclusion from these data is that the increased expression of AR-V7 in the castration-resistant and abiraterone-resistant xenografts reflects a feedback mechanism that rapidly increases AR-V7 relative to AR-FL at low androgen levels, rather than selective pressure for subsets of cells expressing higher AR-V7.

**AR-V7 contribution to AR activity after androgen deprivation**

AR-V7 has been detected in prostate cancer cell lines as well as in clinical samples, and higher AR-V7 staining has been associated with progression to CRPC (16–19, 26–28). Functional analyses based on ectopic expression demonstrated that AR-V7 is constitutively active and can induce CRPC growth (16, 29). However, the contribution of endogenous AR-V7, which seems to be expressed at low levels relative to AR-FL, to AR activity remains to be clarified. As noted above, despite the marked increases in AR-V7 mRNA in the castration-resistant VCaP xenografts, and further increases in the abiraterone-resistant xenografts, RNA-seq indicated that AR-V7 mRNA in the abiraterone-resistant xenografts was still only a small fraction (<1%) of total AR mRNA. However, as AR-V7 protein could be higher than suggested by the mRNA levels, we next assessed AR-V7 protein. Immunoblotting of proteins extracted from biopsies of androgen-dependent VCaP xenografts and the matched castration-resistant VCaP xenografts showed only a very minor band migrating at the predicted position of AR-V7, consistent with the low mRNA levels (Fig. 5A). Quantitative analysis of the AR-V7 and AR-FL bands indicated that AR-V7 protein was expressed at approximately 1.0% to 1.5% of the AR-FL levels in castration-resistant xenografts, which was at least 10-fold higher than the AR-V7 to AR-FL ratio in the androgen-dependent xenografts.
Immunoblotting of VCaP cells cultured in vitro in androgen-depleted medium similarly showed low levels of a protein that migrated at the predicted position of AR-V7 (Fig. 5B). Consistent with this protein being AR-V7, it was not detected by an antibody directed against the AR C-terminus, and its expression was markedly decreased by treatment with DHT (Fig. 5B). To confirm VCaP expression of AR-V7 protein, VCaP cells in androgen-depleted medium were treated with siCE3. This markedly decreased the faster migrating AR band without decreasing AR-FL (Fig. 5B). In contrast, both the AR-FL and AR-V7 bands were decreased by siEX1. Finally, immunoblotting with an AR-V7–specific antibody further supported the conclusion that the lower AR band was AR-V7 (Fig. 5B, AR-V7). The AR-V7 and AR-FL bands were quantified and AR-V7 versus AR-FL ratio was approximately 1.6% in the negative control siRNA (siCtrl), and was markedly decreased by addition of DHT (siCtrl+DHT). Overall these results indicate that AR-V7 protein, although increased after androgen deprivation, is still expressed at low levels.

Figure 4. Androgen preferentially suppresses expression of AR-V7 versus AR-FL. A, VCaP or VCS2 cells were treated with 10 nmol/L DHT or vehicle (ethanol) for 24 hours and mRNA for AR-V7 or AR-FL were measured using qRT-PCR (GAPDH as internal normalization control). B, C4-2 and high-passage LNCaP (LN-HP) cells were androgen deprived for 3 or 10 days, respectively, before being treated with 10 nmol/L DHT for overnight. RNA samples were subjected to qRT-PCR for AR-V7 and AR-FL. C, VCaP cells were treated with increasing doses of DHT (0–10 nmol/L) for 24 hours. RNA samples were subjected to qRT-PCR for AR-V7 and AR-FL expression, and the levels shown are normalized to the levels in the absence of added DHT. D, VCaP cells were transfected with siRNA against exon 7 of AR-FL (siEX7) for 48 hours and then treated with 0 to 10 nmol/L DHT for 24 hours. RNA samples were subjected to qRT-PCR. E and F, VCaP cells were pretreated with/out DHT for 2 hours followed by addition of actinomycin D (10 μmol/L) for 0 to 6 hours (E) or cycloheximide (10 μg/mL) for 0 to 24 hours (F). Note: all cells were androgen starved by culturing in steroid-depleted medium before treatments.
low levels compared with AR-FL, and that this is consistent with the low levels of AR-V7 mRNA.

Culturing VCaP cells in steroid-depleted medium markedly reduces their AR transcriptional activity compared with androgen-stimulated VCaP cells, but they still retain basal AR activity that can be further reduced by blocking de novo androgen synthesis with abiraterone or other agents (2). To assess whether AR-V7 contributes to this basal AR transcriptional activity, we transfected VCaP cells in steroid depleted with siRNA targeting AR-V7 (siCE3). Compared with the control siRNA (siCtrl), depletion of AR-V7 decreased mRNA for a series of AR-regulated genes by approximately 30% (Fig. 5C, left). An siRNA targeting AR-FL (siEX7) decreased these AR-regulated genes to a similar degree (Fig. 5C, middle). Expression of these genes was not substantially further decreased by transfecting the cells with an siEX1 to knockdown both AR-FL and AR-V7, which may reflect an inability to adequately downregulate AR in a subset of the cells (Fig. 5C, right). In contrast, when we used enzalutamide to block activation of the AR-FL by residual androgens, we found that expression of AR-regulated genes could be further reduced by knockdown of AR-V7 (Fig. 5D). Taken together these findings indicate that the rapid induction of AR-V7 protein, although still expressed at low levels, can contribute to maintaining a low basal level of AR transcriptional activity immediately after androgen deprivation therapy. However, these findings further indicate that AR-V7 expressed at these levels is not a major contributor to the high-level AR activity observed in castration-resistant or abiraterone-relapsed tumors.

**AR-V7 mRNA expression in CRPC clinical samples**

We previously analyzed RNA from a series of CRPC bone marrow metastases and showed that AR-regulated genes were highly expressed, although their levels were not fully restored to those in primary prostate cancers before castration (6). To determine the potential contribution of AR-V7 to this AR activity, we used qRT-PCR to assess expression of AR-V7 and AR-FL in these clinical samples relative to VCaP cells. Significantly, AR-V7 mRNA in some clinical samples
Discussion

Intratumoral androgen synthesis is now well established as a mechanism that contributes to AR reactivation after castration, but its role in resistance to CYP17A1 inhibitors or AR antagonists is not clear. Results in this study show that intratumoral levels of androstenedione, testosterone, and DHT are not restored in abiraterone-resistant VCaP xenografts. A recent study similarly found that androgen levels remained low in bone marrow aspirates from patients with abiraterone-resistant tumors (24). Importantly, although these findings indicate that full restoration of androgen synthesis is not a common mechanisms of abiraterone resistance, the AR may remain dependent on the low levels of androgen that are still being produced. Indeed, previous studies have shown that AR may become sensitized to low levels of androgen through a variety of mechanisms (30). Amongst the genes that were increased in the abiraterone-resistant VCaP xenografts, GATA2 was previously shown to cooperate with AR in the activation of multiple androgen-regulated genes (31). However, we did not observe increases in other well-characterized AR coactivators or decreases in AR corepressors. Interestingly, a negative regulator of the phosphoinositide 3-kinase pathway (PIK3IP1) was one of the most upregulated genes in the abiraterone-resistant xenografts. Recent studies show that the PI3 kinase pathway inhibition may enhance AR signaling (32, 33), but the basis for this effect seen in PTEN-deficient mouse models is not clear and studies in other models have yielded conflicting results (34–36). We also observed increased expression of BMX, a nonreceptor tyrosine kinase shown previously to enhance AR activity and to be increased in CRPC (37, 38). We recently reported that BMX enhances the activity of multiple receptor tyrosine kinases by phosphorylating a regulatory site in their kinase domains, but its role in CRPC remains to be established (39). Finally, expression of the mineralocorticoid receptor (NR3C2) was also increased, but its potential contribution to AR signaling remains to be determined.

A further mechanism implicated in resistance to androgen deprivation therapies is increased expression of constitutively active AR splice variants that have deleted the LBD (10, 14–20). Indeed, as observed here, previous reports found that AR variants were increased in prostate cancer xenografts after treatment with abiraterone or enzalutamide (10, 40). Analyses of our abiraterone-resistant VCaP xenografts showed that AR-V7 was the only consistently expressed AR variant. Expression of both AR-FL and AR-V7 transcripts were increased in the castration-resistant VCaP xenografts, and were further increased in the abiraterone-resistant xenografts. Significantly, the fold increase in AR-V7 was markedly more than for AR-FL, which suggested that there may be positive selection for cells with increased AR-V7. However, further studies showed that the increase in AR-V7 reflected rapid feedback mechanisms rather than selection for subclones with increased AR-V7. Consistent with our report showing that AR gene transcription is negatively regulated by agonist-liganded AR (21), we found that DHT rapidly decreased expression of both AR-FL and AR-V7. Moreover, we found that generation of AR-V7 was further suppressed by DHT through an additional mechanism that was dependent on AR-FL and required new protein synthesis. Significantly, a report that came out while this study was under review found that androgen deprivation could increase recruitment of certain splicing factors that enhanced splicing of AR pre-mRNA to AR-V7 (41). Further studies are needed to determine whether new proteins synthesized in response to DHT impair the recruitment of these splicing factors or suppress AR-V7 by other mechanisms, and whether they have broader roles in AR function.
Despite the marked fold increase in AR-V7 mRNA during the development of castration and abiraterone resistance, AR-V7 mRNA remained at low levels compared with that of AR-FL (<1%). Moreover, although AR-V7 protein may be somewhat more stable than AR-FL under some conditions (29, 42), we found that AR-V7 protein was similarly present at very low levels relative to AR-FL in castration-resistant VCaP xenografts and in androgen-starved VCaP cells in vitro. As AR activity in the androgen-starved VCaP cells in vitro is markedly decreased, these observations indicate that AR-V7 expressed at these low levels is unlikely to be the major factor driving high-level AR activity in the castration- or abiraterone-resistant xenografts. Nonetheless, the functional analysis of AR-V7 in androgen-starved VCaP cells showed that it could make a substantial contribution to the residual basal AR activity under conditions where AR-FL is impaired. Therefore, we hypothesize that the rapid induction of AR-V7 immediately after androgen deprivation, mediated by both an increase in AR gene transcription and a decrease in androgen-regulated factors that suppress generation of the AR-V7 splice variant, represents a mechanism by which tumor cells retain low levels of AR activity needed for survival until more potent mechanisms emerge. Importantly, this would suggest that agents targeting AR splice variants may be most effective when used early in conjunction with androgen deprivation or antagonists that target the LBD, and that their efficacy may be markedly diminished if used later at relapse when additional mechanisms are driving AR activity. An exception may be in tumors expressing very high levels of AR splice variants relative to AR-FL. Although these tumors currently seem to be infrequent, and may occur primarily due to structural alterations in the AR gene (14, 18, 27, 43), they may become frequent as patients become resistant to more potent agents targeting the AR LBD.

Acknowledgments
The authors thank Drs. Brett Mark and Alvin Matsumoto (University of Washington, Seattle, WA) for mass spectrometry assays, and Dr. Jun Luo (Johns Hopkins University, Baltimore, MD) and Dr. Chen-Lin Hsie (Dana-Farber Cancer Institute, Boston, MA) for AR-V7-specific qRT-PCR primers.

Grant Support
This work was supported by a Department of Defense Prostate Cancer Research Program Postdoctoral Training Award (W81XWH-12-PCRP-PTA to Z. Yu and A. Sowalsky), Idea Development Awards (W81XWH-11-1-0295, W81XWH-08-1-0414, and W81XWH-07-1-0443 to S.P. Balk), DF/HCC-Prostate Cancer SPORE P50 CA93811 (to C. Cai and S.P. Balk), NIH K99 award CA166507 (to C. Cai), NIH P01 CA163227-01A1, and Prostate Cancer Foundation Challenge Award (S.P. Balk, E. Mostaghel, and P.S. Nelson). PNW Prostate SPORE P50CA097186 and DOD PC095359 (P. Nelson and E. Mostaghel).

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Received July 7, 2013; revised December 20, 2013; accepted January 9, 2014; published OnlineFirst January 21, 2014.

Disclosure of Potential Conflicts of Interest
P.S. Nelson is a consultant/advisory board member for Janssen (Johnson and Johnson). S.P. Balk is a consultant/advisory board member for Astellas, Johnson and Johnson, and Tokai. No potential conflicts of interest were disclosed by the other authors.

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