ABSTRACT
Castration-resistant prostate cancer (CRPC) is the most aggressive, incurable form of prostate cancer. MDV3100 (enzalutamide), an antagonist of the androgen receptor (AR), was approved for clinical use in men with metastatic CRPC. Although this compound showed clinical efficacy, many initial responders later developed resistance. To uncover relevant resistant mechanisms, we developed a model of spontaneous resistance to MDV3100 in LNCaP prostate cancer cells. Detailed characterization revealed that emergence of an F876L mutation in AR correlated with blunted AR response to MDV3100 and sustained proliferation during treatment. Functional studies confirmed that AR F876L confers an antagonist-to-agonist switch that drives phenotypic resistance. Finally, treatment with distinct antiandrogens or cyclin-dependent kinase (CDK)4/6 inhibitors effectively antagonized AR F876L function. Together, these findings suggest that emergence of F876L may (i) serve as a novel biomarker for prediction of drug sensitivity, (ii) predict a "withdrawal" response to MDV3100, and (iii) be suitably targeted with other antiandrogens or CDK4/6 inhibitors.

SIGNIFICANCE: We uncovered an F876L agonist-switch mutation in AR that confers genetic and phenotypic resistance to the antiandrogen drug MDV3100. On the basis of this finding, we propose new therapeutic strategies to treat patients with prostate cancer presenting with this AR mutation. Cancer Discov; 3(9); 1030–43. © 2013 AACR. See related commentary by Nelson and Yegnasubramanian, p. 971.
INTRODUCTION

Prostate cancer is one of the most commonly diagnosed cancers among men worldwide (1, 2). Although localized tumors are often successfully treated, distant metastases emerge in a significant fraction of patients (3, 4). Androgen-deprivation therapy is initially effective; however, almost invariably resistance emerges and results in a much more aggressive form of tumor referred to as castration-resistant prostate cancer (CRPC). CRPC is the second most common cause of cancer-related death in American men (5) and is currently incurable. A conserved feature of CRPC is the sustained expression of androgen receptor (AR)-signaling (6), by virtue of mechanisms including AR gene overexpression/amplification and AR gene mutations (3). These data have suggested that prostate cancer may largely remain dependent on AR signaling.

The continued reliance on AR signaling in CRPC has led to the development of CYP17 inhibitors (abiraterone) and improved antagonists that compete with androgens for binding to the ligand-binding pocket of AR. MDV3100 (enzalutamide) is a novel antiandrogen that was recently approved to the ligand-binding pocket of CRPC previously treated with docetaxel. Although MDV3100 has shown significant efficacy in clinical trials, many patients who initially responded favorably develop resistance to this second-generation antiandrogen (7). The molecular mechanisms driving resistance, however, are currently unclear, and a deeper understanding is critical for the rational development of alternate therapeutics.

In vitro and in vivo experimental models of resistance serve as useful tools for expeditious discovery of mechanisms that allow drug escape, and for the evaluation of alternate therapies. We here present the derivation of a model of spontaneous resistance in LNCaP cells, which led to the identification of a novel F876L mutation in AR that potently drives genetic/phenotypic resistance to MDV3100. This mutation allows AR-F876L to use MDV3100 as an agonist and ultimately promotes an addiction phenotype in vitro. These data continue to support the notion that despite improved AR antagonists, prostate cancer cells remain dependent on AR signaling, and hence evolve specific mutations to overcome antiandrogen therapies. Because we further show that the F876L variant retains sensitivity to bicalutamide, combination therapy with structurally distinct antiandrogens either in parallel or in series together with androgen deprivation may provide an appealing therapeutic strategy for combating AR-mediated resistance mechanisms in the clinic. Furthermore, in addition to targeting the hypermutable AR ligand-binding domain, we show that targeting downstream or interactive effectors of AR signaling, such as cyclin-dependent kinases (CDK)4/6, provides an alternative strategy for overcoming resistance mechanisms when AR-directed therapies become ineffective.

RESULTS

Development and Characterization of a Model of Spontaneous Resistance to MDV3100

To facilitate the discovery of resistance mechanisms, we generated a model of spontaneous resistance in LNCaP cells. Although short-term culture of LNCaP cells with MDV3100 (<1.5 months) induced population-wide stasis [Fig. 1A, fetal calf serum (FCS) + MDV3100 relative to FCS], long-term culture with 1 μmol/L MDV3100 led to the emergence of resistant clones (Fig. 1B). After isolation and expansion, resistant clones that displayed similar growth properties as the control populations (C1–C3; Fig. 1B) were chosen for further characterization. Short-term (Fig. 1C) and long-term (Supplementary Fig. S1) proliferation assays confirmed the resistance phenotype. Specifically, four of seven resistant clones (#1, 15, 19, and 24; strongly resistant, green curves and font) displayed significantly higher resistance to MDV3100 than weakly resistant clones (#9, 10, and 14; red curves and font) or the control lines (C1–C3; brown curves and font; Fig. 1C). In contrast, strongly resistant clones displayed sensitivity to bicalutamide (Fig. 1C), cumulatively suggesting that the mechanism(s) of resistance in strongly resistant clones may be fine-tuned to specifically promote resistance to MDV3100.

To elucidate mechanism(s) of resistance, we first analyzed expression levels of AR, as its overexpression has previously been shown to promote resistance to castrate levels of androgens (6) and the antiandrogen bicalutamide (1). Here, we did not observe a significant change in AR expression (Fig. 1D), and global gene expression analysis of AR pathway activity showed a lack of significant modulation of the AR pathway at baseline (Fig. 1E, beige bars).

Strongly Resistant Clones Show Blunted AR Pathway Response to MDV3100

To further explore the molecular mechanisms that drive resistance, we conducted gene-expression microarray analysis on RNA derived from three controls and seven resistant clones treated with dimethyl sulfoxide (DMSO) or MDV3100 for 24 hours. Unbiased hierarchical clustering of the transcriptional effects in response to MDV3100 treatment revealed that the strongly resistant clones clearly segregated from the weakly resistant and control lines (Fig. 2A, left), supporting the phenotypic differences described earlier (Fig. 1C). Further interrogation of the data revealed four distinct gene expression patterns (labeled I–IV). Although pathway enrichment analysis (8) failed to reveal a significant enrichment of pathway signatures in classes I, II, and IV, a strong enrichment of genes involved in AR pathway activation was observed in class III (Fig. 2A, middle and right, and Supplementary Table S1). These data suggested that strongly resistant cell lines could at least maintain AR pathway activity despite continuous exposure to MDV3100. In keeping with this notion, clustering (Supplementary Fig. S2A), pathway enrichment analysis (Fig. 2B and Supplementary Fig. S2B), and quantitative PCR (qPCR) analysis of three AR target genes (Fig. 2C) confirmed that MDV3100 treatment downregulated AR pathway activity in control and weakly resistant lines but not in the strongly resistant clones.

The mechanism by which MDV3100 inhibits AR signaling has been attributed partially to its ability to hinder nuclear translocation of AR (9). We therefore determined whether localization of AR was altered in the resistant clones in
response to MDV3100. To this end, cytoplasmic and nuclear protein fractions from a control (C1) and strongly resistant (clone #1) line treated with DMSO or MDV3100 were isolated. In contrast to C1, where MDV3100 significantly reduced (clone #1) line treated with DMSO or MDV3100 were isolated. It in C1, where MDV3100 significantly reduced nuclear AR localization (nuclear:cytoplasmic ratio: DMSO = 0.46, MDV = 0.07), MDV3100 treatment did not significantly alter AR nuclear localization in the strongly resistant clone (nuclear:cytoplasmic ratio: DMSO = 0.59, MDV = 0.49; Fig. 2D and Supplementary Fig. S3), supporting the notion that AR remains activated in the strongly resistant cell lines.

**Whole-Transcriptome Sequencing Uncovers a Novel AR Mutation Correlated with Resistance**

To define the mechanism(s) underlying resistance to MDV3100, we next conducted whole-transcriptome sequencing on nine of 10 lines described above. Expressed protein-coding sequence variants were identified and compared with sequences in parental control lines. Somatic mutations found in more than one clone, but with discordant genotypes across clones, were used to cluster the samples using hierarchical clustering (Fig. 3A). Although there were many recurrent mutations, only one candidate, a recurrent F876L mutation in the AR gene, was conserved among all four strongly resistant clones and not found in weakly resistant or control lines (Fig. 3A and Supplementary Table S2). Interestingly, clone #19 presented a very distinct mutational spectrum compared with other strongly resistant clones, likely suggesting that ARF876L occurred by independent mechanisms in these subclones (Fig. 3A).

The F876L mutation is localized to the ligand-binding domain of AR and is adjacent to the homozygous T877A mutation found in weakly resistant or control lines (Fig. 3A and Supplementary Table S2). Strikingly, whole-transcriptome sequencing revealed that three of four resistant tumors harbored the F876L mutation (Fig. 3D), with frequencies ranging from 46% to 52% of the total AR transcript reads (Fig. 3E). Interestingly, there were two unique nucleotide substitutions observed promoting
F876L Mutation in AR Confers Resistance to MDV3100

To assess the potential impact of the F876L mutation on MDV3100 response, we computationally modeled the binding of MDV3100 to the wild-type (WT) and mutant receptors. We found that in the docking modes of the antagonistic state of WT AR, MDV3100 displayed only a weak interaction with F876 (Fig. 4A, left). However, in the presence of the F876L mutation, the benzamide motif of MDV3100 can extend into the access channel created by the smaller leucine residue. This would potentially prevent the compound from clashing with helix-12 of the AR ligand-binding domain in the agonistic mode (Fig. 4A, right). Thus, computational modeling suggested that F876L mutation in AR may abolish the antagonistic activity of MDV3100 and could potentially allow agonist activity.

To functionally test the impact of the F876L mutation, we next assessed the transcriptional responses of the WT AR with F876 (Fig. 3D and E). Furthermore, we computationally modeled the interaction between AR and MDV3100 and found that the F876L mutation in AR may abolish the antagonistic activity of MDV3100 and could potentially allow agonist activity.

AR F876L Confers an Antagonist-to-Agonist Switch for MDV3100

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Figure 3. Whole-transcriptome sequencing analysis identifies a novel F876L mutation in AR in strongly resistant lines and xenograft tumors. **A**, top, unbiased hierarchical clustering of somatic mutations detected in controls (brown font), weakly resistant clones (red font), and strongly resistant clones (green font). Gray line represents lack of mutation; orange line represents single recurrent heterozygous mutation; red line represents recurrent homozygous mutation; green line represents recurrent mutation in AR, as indicated by green arrowhead. Bottom, schematic of human AR: NTD, N-terminal domain; DBD, DNA-binding domain; LBD, ligand-binding domain. Site of F876L mutation indicated by green line and green font. **B**, left, IGV plot showing heterozygous nature of F876L mutation in exon 8 of AR in strongly resistant clones (indicated by green arrowheads). F876L mutation is adjacent to a preexisting homozygous T877A mutation (orange shade) in LNCaP. Right, raw counts of WT (red shade) and mutant (Mut, green shade) AR alleles in strongly resistant clones. **C**, tumor growth kinetics of two vehicle-treated (red curves) and four MDV3100-treated (green curves) LNCaP tumors. **D**, IGV plot showing the relative position and frequency of nucleotide substitutions promoting F876L in MDV3100-resistant tumors. C1–C2, vehicle-treated tumors; R1–R4, MDV3100-resistant tumors. **E**, table summarizing data from IGV plot. Red shade represents tumors bearing WT AR, whereas green shade highlights tumors bearing F876L-mutant AR. **F**, bar graphs showing relative expression of AR target genes KLK3 and NKX3-1 in LNCaP tumors. Red bars, expression data from tumors expressing AR-WT; green bars, expression data from tumors harboring ARF876L. IGV, Integrative Genomics Viewer.
**Figure 4.** F876L mutation functionally confers an antagonist-to-agonist switch. 

**A,** comparison of the docking modes of MDV3100 in an inactivated state of WT AR (left) with a speculative model of MDV3100 bound to an activated state of mutant AR (right). 

**B,** bar graphs showing normalized AR reporter activity following transfection of 293T (top) and VCaP (bottom) cells with various AR expression constructs (ARWT, ART877A, ARF876L, and ARF876L/T877A) and subsequent treatment with vehicle (Veh), 0.1 nmol/L R1881 (R), 10 μmol/L MDV3100 (MDV), 10 μmol/L bicalutamide (Bic), 10 μmol/L MDV3100 + 0.1 nmol/L R1881 (M/R), or 10 μmol/L bicalutamide + 0.1 nmol/L R1881 (B/R) for 24 hours. All data are normalized to Renilla luciferase (RLUC) expression. Data represent mean ± SEM; n = 3. *, P < 0.05; **, P < 0.01 (Student t test). 

**C, qPCR analysis of KLK3 expression in a control line (C1), weakly resistant clones (red font), and strongly resistant clones (green font) following treatment with vehicle (V), 0.1 nmol/L R1881, 0.1 nmol/L R1881 + 10 μmol/L MDV3100 (MDV), 10 μmol/L MDV3100 + 0.1 nmol/L R1881 (M/R), and 0.1 nmol/L R1881 + 10 μmol/L bicalutamide (Bic) in 10% CSS for 24 hours. TBP used to normalize expression. Data represent mean ± SEM; n = 3. *, P < 0.05; **, P < 0.01 (Student t test).
AR, single mutants T877A, W741C, W741L, and F876L, and the double mutant F876L/T877A to the agonistic synthetic androgen R1881 and the antiandrogens bicalutamide and MDV3100 in transactivation reporter assays using HEK293T cells. The W741C/L mutant has previously been shown to confer an agonist switch specific for bicalutamide and was used as a control (13). Notably, we found that only ARF876L and ARF876L/T877A had a substantial transactivation response of an androgen response element (ARE)-driven reporter gene (+14) to MDV3100—comparable with 0.1 nmol/L R1881—suggesting an antagonist-to-agonist switch exclusively specific for MDV3100 (Fig. 4B and Supplementary Fig. S14). These findings were further validated in AR−/− PC3 (Supplementary Fig. S6) and AR+ VCaP prostate cancer lines (Fig. 4B).

In support of the transactivation data, a similar agonist switch was also observed in spontaneously resistant clones that harbored the F876L mutation when KLK3 expression was analyzed in response to MDV3100 in media stripped of endogenous androgens—a condition that minimized basal AR pathway activity and the response of endogenous WT AR to MDV3100 (Fig. 4C). Notably, although the most strongly resistant clones (#1, 19, and 24) expressed significantly higher levels of KLK3 in the presence of MDV3100 relative to vehicle, clone #15 showed similar sensitivity to MDV3100 as the control (C1) and weakly resistant clones, likely attributable to the low mutant allelic mRNA frequency (Fig. 3B, right). These data in aggregate strongly suggest that the F876L mutation in AR is a driver of an antagonist-to-agonist switch highly specific for MDV3100.

**The F876L Mutation Is Sufficient to Induce Genetic and Phenotypic Resistance to MDV3100 in Genetically Engineered LNCaP Cells**

Given that strongly resistant clones harbor several sequence variants in addition to the F876L mutation, we wanted to formally test whether the ARF876L variant is sufficient to promote an MDV3100-resistant growth phenotype. To this end, LNCaP cells were engineered to stably express the single-mutant ARF876L. Consistent with the transactivation data (Fig. 4B and Supplementary Fig. S6), ARF876L conferred genetic and phenotypic resistance to MDV3100, suggesting that F876L alone or in conjunction with T877A is equally capable of conferring an agonist switch (Supplementary Fig. S12A and S12B).

**The Resistance-Conferring Role of ARF876L Is Broadly Applicable to Several Prostate Cancer Lines**

Given that the F876L mutation in AR can promote resistance to MDV3100 in PTEN-null LNCaP cells, we next questioned whether this mutation is sufficient to broadly confer resistance in prostate cancer lines of various genetic backgrounds. To this end, human VCaP (harboring TMPRSS2-ERG fusion and AR amplification) and murine Myc–CaP (overexpressing Myc) lines were transduced to stably express the mutant AR. Consistent with the resistance phenotype observed in LNCaP cells, both lines also presented partial resistance to MDV3100 (Fig. 5D and Supplementary Fig. S13), suggesting that F876L mutation in AR has the potential for conferring resistance to MDV3100 under various genetic contexts.

Taken together, our data implicate a direct role for ARF876L, ARF876L/T877A, and potentially constitutively active AR variants, such as W741C/T877A, as drivers of resistance to MDV3100. Although constitutively active variants may promiscuously promote resistance to various classes of antiandrogens, we show that F876L mutation in AR selectively promotes resistance to MDV3100.

**ARF876L-Bearing Cells Are Resistant to MDV3100 in the Castrate Setting In Vivo**

Having shown that the F876L mutation in AR confers an agonist switch for MDV3100 that can promote resistance, we next asked whether F876L-bearing cells become dependent on this switch for cellular growth under androgen-deprivation conditions, a dependence that has been observed in the clinic for other antiandrogens such as flutamide (15). Interestingly, although the switch did not drive proliferation of F876L-bearing clones in vitro (Supplementary Fig. S14), we observed a marked dependence on MDV3100 for growth in vivo when the F876L-bearing cells were implanted into castrated male mice (Fig. 5E). Although control (C1) tumors showed immediate stasis upon MDV3100 treatment, resistant tumors (clone #1) failed to grow until stimulated by MDV3100 (Fig. 5E). Specifically, after a prolonged period of stasis, 10 of 15 mice treated with MDV3100 developed rapidly growing tumors compared with two of 15 in the vehicle group.
Figure 5. Prostate cancer cells engineered to overexpress AR\textsuperscript{F876L/T877A} are genetically and phenotypically resistant to MDV3100. A, qPCR analysis of KLK3 (top) and NX3-1 (bottom) expression in various engineered lines (vector controls (Vec), T877A, F876L, W741C, T877A, W741C). All lines were pretreated with vehicle (−) or doxycycline (+) for 3 days before treatment with DMSO or MDV3100 for 24 hours. β-Tubulin (β-Tub) and histone H3 (H3) were probed to validate purity of cytoplasmic and nuclear fractions respectively. B, colony formation assays of various engineered lines (Dox−/−) treated with DMSO (left wells) or 10 μmol/L MDV3100 (right wells) for approximately 14 days. Bottom, quantitation of CFA showing percentage of mice growing palpable tumors (numbers above bars represent number of mice presenting tumors). C, qPCR analysis of TMPRSS2 and SLC45A3 expression in control (C1) and resistant (#1) tumors treated with vehicle or MDV3100 (MDV). TBP was used to normalize expression. Data represent mean ± SEM; n = 3 for all groups except C1 vehicle treated, n = 2. *, P < 0.05; **, P < 0.01 (Student t test).
suggesting that AR F876L–bearing cells require MDV3100 for growth, as shown by AR target gene expression, relative to vehicle-treated resistant tumors, and significantly higher activity relative to vehicle-treated control tumors (Fig. 5G). These data cumulatively highlight the dependence of F876L-bearing cells to MDV3100 for in vivo growth under androgen-deprivation conditions.

Targeting CDK4/6 as a Therapeutic Strategy for Overcoming MDV3100 Resistance

Having established that AR F876L can promote resistance to MDV3100 under various genetic contexts in vitro and in vivo, we next aimed to develop rational strategies to antagonize the mutant allele. As an alternative to developing novel antiandrogens that continue to target the hypermutable ligand-binding pocket of AR (16), we aimed to identify therapeutic strategies that may be more sustainable in the clinic. To this end, we observed a significant enrichment for genes belonging to “cell cycle” and “E2F1 activation” gene sets in addition to “AR activation” in strongly resistant clones treated with MDV3100 (Fig. 2A), suggesting that these clones may potentially maintain proliferation under MDV3100-treatment conditions through continued expression of E2F1 target genes. This is an appealing hypothesis as androgen signaling, a critical regulator of G1–S transition, is known to promote active CDK4/cyclin D1 assembly and hence activation of E2F1 function (17). Consistent with this notion, we observed that MDV3100 treatment suppressed expression of the E2F1 target genes DHFR and TK1 in a control line, confirming AR signaling as a regulator of E2F1 function. In contrast, F876L-bearing cells were capable of maintaining higher expression of DHFR and TK1 under MDV3100-treatment conditions relative to a control line (Fig. 6A). On the basis of these data, we reasoned that E2F1 activity may serve as a downstream effector of AR signaling and, as such, regulators of E2F1 function may serve as critical therapeutic nodes when AR-directed therapies become ineffective. In agreement with this hypothesis, we found that the growth of strongly resistant clones (Fig. 6B) and LNCaP lines dependent on MDV3100 for growth upon MDV3100 treatment might benefit from drug withdrawal, and (iii) that all F876L-bearing patients (preexisting or acquired) might respond favorably to existing antiandrogens and CDK4/6 inhibitors (Fig. 7). Therefore, screening patients to identify this mutation will aid in predicting drug sensitivity and guide alternate clinical management strategies.

F876L: Hotspot Mutation in AR in Response to MDV3100 Treatment

The relatively quick emergence of the F876L mutation during in vitro selection (Fig. 3A and B) initially suggested that this mutation was likely preexisting at a low frequency. However, the fact that two independent nucleotide substitutions led to the F876L mutation during in vivo selection (Fig. 3D and E) implies that the mutation may have been acquired during treatment. Because LNCAp cells possess defects in the mismatch repair (MMR) mechanism, deficiencies found to also exist in a subset of prostate cancer (19), it is conceivable that they may more easily acquire this mutation (either with or without MDV3100 treatment). However, the fact that Balbas and colleagues (16) also reported the spontaneous emergence of F876L upon prolonged treatment of CWR22PC cells, a line that is believed to possess an intact MMR mechanism, suggests that F876L may truly be a hotspot mutation that may possess the capacity to confer resistance in prostate tumors irrespective of the MMR status.

Agonist Switch Suggests a Treatment Withdrawal Effect for MDV3100

In some patients that become refractory to antiandrogen therapy, discontinuation of treatment often leads to clinical improvement. This “antiandrogen withdrawal syndrome” has been reported for flutamide (20), bicalutamide (21), and other nonsteroidal and steroidal antiandrogens (22–24). In a subset of patients presenting “addiction” to antiandrogen therapy, mutations in AR that promote an agonist switch have been identified and considered to be one potential mechanism driving growth during treatment (15). In the current study, we also observed an “addiction” phenomenon as the growth of an F876L-bearing cell line (clone #1) became dependent on MDV3100 for growth in vivo (Fig. 5E). These parallels imply that refractory patients bearing the AR F876L variant may, at least temporarily, benefit from withdrawal of MDV3100 in the clinic.
F876L Mutation in AR Confers Resistance to MDV3100

Alternative Therapeutic Strategies

The frequent emergence of an agonist switch as a resistance mechanism to antiandrogens necessitates that (i) more potent compounds with better therapeutic indices be developed, (ii) alternate methods to target AR be sought, or (iii) non-AR-targeting therapeutic strategies be explored. To address the first point, Clegg and colleagues (4) recently developed ARN-509, an antiandrogen that is more potent, has a higher therapeutic index, and has a longer half-life than MDV3100, all of which might translate to less-frequent resistance. Interestingly, two independent groups recently reported the spontaneous emergence of the F876L mutation in AR as an agonist switch specific for both MDV3100 and ARN-509 (16, 25). To overcome this mutation, Balbas and colleagues (16) coupled modeling with focused chemical screens to discover novel antiandrogens that effectively antagonized AR-WT and AR-F876L. Although too early to predict, if agonist switch conferring mutations develop to these novel compounds, then applying strategies that may be less amenable to resistance by mutations in the AR ligand-binding pocket should be explored. Strategies such as combining two antiandrogens (in combination or sequentially), blocking activation function 1 (AF1; ref. 26) or AF2 (26, 27) functions of AR, or development of compounds that destabilize/degrade AR or hinder AR nuclear translocation might be also considered. Finally, non-AR-targeting therapies may also serve as a viable strategy. To this end, we found that inhibiting CDK4/6 potently targeted both strongly resistant clones (Fig. 6B) and LNCaPs engineered to overexpress AR F876L/T877A (Fig. 6C), implying that targeting downstream effectors of AR signaling may serve as a viable strategy for overcoming this mutation-based resistance mechanism. Even more generally, inhibition of CDK4/6...
also targeted weakly resistant LNCaP clones (Fig. 6B) and MDV3100-resistant 22Rv1 cells (Fig. 6E)—prostate cancer lines lacking AR<sup>F876L</sup>—implying that this therapy may be applied to overcome multiple mechanisms of resistance to MDV3100 and androgen-independence in general. In support of our findings, several reports have suggested that retinoblastoma (RB) loss plays a critical role in prostate cancer development and resistance to AR-directed therapies (28). More relevantly, consistent with our findings, a recent study has reported the use of CDK4/6 inhibitors as an effective therapeutic to target early- and late-stage prostate cancer that is mechanistically dependent on RB (29). Because a significant fraction of CRPCs maintain functional RB, we speculate that inhibition of CDK4/6 may serve as a viable approach for treating resistance to AR-directed therapies in a large subset of patients.

**METHODS**

**Cell Culture**

LNCaP-FGC and PC3 cells were maintained in RPMI-1640 media with 10% FCS (Hyclone) or 10% CSS (Omega; cat# fb-04) as indicated. 22Rv1 cells were maintained in RPMI-1640 media with 10% FCS. VCaP cells were maintained in Dulbecco’s Modified Eagle Medium (DMEM) with 10% FCS or 10% CSS. Myc-CaP cells were maintained in DMEM with 10% FCS. 293FT cells were maintained in DMEM supplemented with 10% FCS and 1 x Non-Essential Amino Acids (NEAA). All lines, except Myc-CaP cells, were obtained from the American Type Culture Collection and cells were tested and authenticated by single-nucleotide polymorphism fingerprinting. Myc-CaP cells were kindly provided by Dr. Charles Sawyers (Human Oncology and Pathogenesis Program, Memorial Sloan-Kettering Cancer Center, New York, NY) and were not further tested or authenticated.

**Generation of Spontaneous MDV3100-Resistant LNCaP Clones In Vitro**

Two million LNCaP cells were seeded into four 150-cm<sup>2</sup> tissue culture dishes in phenol red-free RPMI-1640 media supplemented with 10% FCS. The next day, DMSO and ethanol (control 1, C1), DMSO and 1.0 nmol/L R1881 (control 2, C2), 1 μmol/L MDV + 1.0 nmol/L R1881 (control 2, C2), 1 μmol/L MDV + 1.0 nmol/L R1881 (control 3, C3), and 1 μmol/L MDV3100 were added to dishes 1 to 4, respectively. Cells were reseeded into 150-cm<sup>2</sup> dishes supplemented with the appropriate treatments once each week. Media and compound were replaced for dish 4 once every week. Once resistant clones emerged, media was aspirated from dish 4. Trypsin-soaked 3-mm sterile cloning discs (Scienceware; cat# 17-2.X) were used to overlay the resistant clones and following a 1- to 2-minute incubation, cloning discs were transferred to 24-well plates with phenol red-free RPMI-1640 media supplemented with 10% FCS and MDV3100. Cells from control dishes 1 to 3 were maintained until resistant clones were cryopreserved to maintain a constant culture time for control and experimental lines.

**Generation of Stable Transduced Lines**

Codon-optimized cDNAs encoding WT or mutant ARs were synthesized (DNA2.0) and subcloned into the pLKO-TREX-HA-Neo (Invitrogen). Lentiviruses were produced by transfecting 293FT cells with VSVGdeltaR8.9: cDNA constructs at a ratio of 1:2.5:1.25. Virus
was harvested 2 to 3 days after transfection, filtered, and used to infect LNCaP, MyC-CaP, and VCaP cell cultures in the presence of 8 μg/ml polybrene. Infected cells were maintained in neomycin for 3 weeks. In all cases, at least 1,000 independent clones were pooled to generate stable cell lines to avoid clonal variations. Stable cell lines infected with control vectors were generated in parallel for use as experimental controls.

Microarray
A total of 3 × 10⁶ cells were seeded in 6-well plates 2 to 3 days before treatment with DMSO or 10 μmol/L MDV3100 for 24 hours. Total RNA was isolated from cells using the Qiagen RNeasy Kit. RNA integrity and purity were assessed with the RNA 6000 Nano LabChip system on a Bioanalyzer 2100 (Agilent Technologies). Generation of labeled cDNA and hybridization to Affymetrix GeneChip Human Genome U133 Plus 2.0 Array (Affymetrix Inc.) was conducted using standard protocols as previously described (8).

Expression Analysis
Probe sets from the Affymetrix gene expression datasets were normalized using MAS with a trimmed-mean target of 150 and log₂-transformed. Probe sets were then filtered for inclusion only if their maximum value over different samples was at least 5. Ordinary least squares was conducted using 0 to 1 indicator variables as the covariate; one indicator was used to represent the baseline (untreated sample) of each clone, and three indicator variables represented treatment with MDV3100 for each of the classes of samples (control, weakly resistant clones, and strongly resistant clones). This regression was used to generate nominal P values and regression coefficients (i.e., fold changes). Individual probe sets were considered significantly differentially expressed if their fold change was 1.5 or more, with a nominal P ≤ 0.05.

Gene Set Enrichment Analysis
GSEA was performed by calculating the AR gene signature (30) enrichment in the top-ranked genes following treatment of control, weakly and strongly resistant clones with MDV3100. Blue line represents expressed probe set position and is ranked by average fold change; only those probe sets expressed at a MAS-150 level of at least 32 in at least one sample are included. The red lines indicate where the probe sets mapping to genes in the AR gene signatures appear in our dataset, gray lines indicate probe sets that do not pass nominal significance, and the taller red line represents probe sets with a fold change of at least 1.5 and a nominal P value less than 0.05. The black curve shows the cumulative sum of the probe sets in the AR gene signature, and the dotted line represents the hypothetical cumulative sum for a random list of genes, which are unenriched.

Pathway Enrichment Scores
For the candidate signature (30), a two-tailed Fisher exact test was used to determine whether probe sets representing genes in those signatures were under- or over represented in the set of probe sets that were up- or downregulated at least 1.5-fold compared with expressed but nondifferentially expressed probe sets, with a nominal P value of 0.05 or less. For an unbiased approach, pathways derived from Gene Ontology (GO) terms and transcription factor networks were analyzed for overrepresentation via a one-tailed interpolated Fisher exact test, using genes that varied 1.5-fold or more with a nominal P value of 0.05 or less compared with all genes represented on the array; Benjamini-Hochberg correction was then applied to these P values (8).

Sanger Sequencing
Genomic DNA was isolated from various 1 μmol/L MDV3100-resistant clones and appropriate control lines using the Blood and Tissue DNAeasy Kit (Qiagen; cat# 69581) according to the manufacturer’s directions. Primers were used to amplify AR exon 8 (the site of the F876L mutation); forward: 5′-ATTGGAGAGAGTGCTGCATCA-3′; reverse: 5′-TTTCTGCTACATTGGCCCTC-3′ and the amplified cDNA was sequenced by Genewiz using the same primers. Trace files were analyzed to confirm the presence of the F876L mutation.

Quantitative Real-Time PCR
For spontaneous clones, 2 × 10⁶ cells were seeded in 6-well plates in RPMI-1640 supplemented with 10% FCS for 2 days before treatment with various compounds for 24 hours. Alternatively, for experiments involving androgen depletion, 2 × 10⁶ cells were seeded and grown in 6-well plates in phenol red-free RPMI-1640 supplemented with 10% FCS for 2 days. Media was aspirated and replaced with phenol red-free RPMI-1640 supplemented with 10% CSS for 3 to 4 days before treatment with various compounds for 24 hours. Similar protocols were applied for genetically engineered lines except that cells were pretreated with doxycycline (Dox) for at least 2 days before treatment with various compounds to allow sufficient transgene expression. Total RNA was extracted using the RNeasy Plus Mini Kit (Qiagen; cat# 74136) according to the manufacturer’s instructions. One to 2 μg of total RNA was used for cDNA synthesis using a high-capacity cDNA reverse transcription kit (Applied Biosystems; cat# 4368813). cDNA from each sample was diluted 15- to 20-fold and real-time PCR was conducted in triplicate using gene-specific primers and FastStart Universal Probe Master Mix (RoX; Roche Applied Science) on an ABI 7900HT series PCR machine. Expression levels were normalized to TBP expression. All analysis was conducted using the SDSS.3 software. The following gene-specific primers (Invitrogen) were used: AR (Hs0017172_m1), ALK3 (Hs02576345_m1), NKG2J (Hs00171834_m1), TMFR52 (Hs01120965_m1), SLC45A3 (Hs00263832_m1), TRIP (Hs00427620_m1), DHH (Hs00758822_s1), and TK1 (Hs01062125_m1).

In Vivo Tumorigenesis Assays
Ten million LNCaP cells (C1, clone #1) mixed 1:1 with Matrigel were injected subcutaneously into the flanks of castrated 7- to 8-week-old male nu/nu mice. Tumor-bearing mice (tumor volume = 150–300 mm³) were treated with vehicle or 30 mg/kg MDV3100 daily. Tumors were measured using calipers, and tumor volumes were calculated using length × width²/2. Data are expressed as mean ± SEM. All animal experiments were carried out in compliance with the guidelines of the Novartis Biomedical Research Animal Care and Use Committee protocols and regulations.

Statistical Analysis
Results were reported as the mean ± SEM. A two-sided independent Student t test without equal variance assumption was conducted to analyze gene expression levels and endpoints of in vitro luciferase assays. For gene set enrichment analysis, P values shown are based on a two-tailed Fisher exact test comparing probe sets in the gene signature that pass significance to those that do not, versus the significance/insignificance of all other probe sets. For animal experiments, a two-tailed Fisher exact test was conducted to determine the significance in percentage of mice growing palpable tumors in each group.

Accession Number
Gene expression microarray data used to analyze differential gene expression upon treatment with MDV3100 versus DMSO in spontaneous and engineered lines has been deposited at the National Center for Biotechnology Information (NCBI) Gene Expression Omnibus with the accession numbers GSE44924 and GSE44927, respectively. Additional experimental procedures are listed in the Supplementary Methods.
Disclosure of Potential Conflicts of Interest

M. Korpal has ownership interest (including patents) in Novartis Institutes for BioMedical Research. V.G. Cooke has ownership interest (including patents) in Novartis Institutes for BioMedical Research. T.M. Roberts has received a commercial research grant from Novartis and is a consultant/advisory board member of the same. W.R. Sellers is employed as VP/Global Head of Oncology at Novartis and has ownership interest (including patents) in the same. P. Zhu has ownership interest (including patents) in Novartis. No potential conflicts of interest were disclosed by the other authors.

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