Prostate cancers become “addicted” to male hormones during the pathogenesis of the disease. In doing so, the cancer cells co-opt androgen receptor (AR) signaling, a driver of secretory cell differentiation in normal prostate cells, for maintenance of a malignant phenotype. Somatic chromosomal translocations and deletions, creating fusions between androgen-regulated differentiation genes and cancer genes, may enable this addiction (1). For more than 70 years, androgen signaling has been targeted for prostate cancer treatment. Initially accomplished via removal of the testes, therapeutic reduction of circulating androgens in men with advanced prostate cancer almost always leads to improvement in disease-related symptoms, to diminution in blood biomarkers of disease activity, and to improvement in radiographic images of disease sites. Unfortunately, for most men, this benefit is short-lived. The disease inevitably progresses despite low levels of circulating androgens to “castration-resistant prostate cancer” (CRPC). CRPC cells often remain addicted to AR signaling, fomenting a recent flurry of new drug discovery and development, already yielding two new approved agents targeting androgen action: the androgen biosynthesis inhibitor abiraterone and the AR antagonist enzalutamide (2). In the current issue of Cancer Discovery, both Joseph and colleagues (3) and Korpali and colleagues (4) report the detection of a missense mutation generating an F876L change in the ligand binding domain (LBD) in each of these sublines. AR F876L bound enzalutamide and ARN-509 with 48-fold and 30-fold greater affinity than wild-type AR. Forced expression of this AR mutant in LNCaP prostate cancer cell line and of an LNCaP/AR cell subline engineered to overexpress AR via chronic exposure to the second-generation antiandrogens in vitro. In three of 10 resistant variant sublines, both enzalutamide and ARN-509 exhibited partial AR agonist activity, stimulating both cell proliferation and target gene expression. AR sequencing revealed a missense mutation generating an F876L change in the LBD in each of these sublines. AR F876L bound enzalutamide and ARN-509 with 48-fold and 30-fold greater affinity than wild-type AR. Forced expression of this AR mutant in LNCaP prostate cancer cells was sufficient to confer agonist activity to the second-generation AR antagonists in vitro and in vivo, likely by permitting a homodimeric association of one N-terminus with the other C-terminus known to form an agonist conformation at AR DNA-binding sites.

Joseph and colleagues (3) then analyzed plasma DNA from a phase I clinical trial of ARN-509 for metastatic CRPC. Although more than 40% of men receiving ARN-509 showed declines in serum prostate-specific antigen (PSA), indicating response to treatment, of 29 men available for molecular analysis, 18 ultimately exhibited PSA increases, hinting at intrinsic or acquired resistance to the drug. Using a PCR-based BEAMing (Beads, Emulsions, Amplification, and Magnetics) method to detect F876L-encoding mutant AR variants, mutant AR sequences (C to A change at nucleotide 2628) were found in plasma
Figure 1. Mechanisms of resistance to AR-directed therapies. Despite treatment with androgen-deprivation therapy (ADT) or first-generation antiandrogens, prostate cancers progress to castration resistance, often with emergence of an AR-dependent resistant phenotype that is sensitive to treatment with second-generation antiandrogens such as enzalutamide or ARN-509. However, AR-dependent resistance emerges again, this time driven by mutant AR. This tendency to maintain AR addiction will permit treatment with next-generation AR antagonists. If prostate cancer clones that have escaped AR addiction appear at any time during disease progression, such treatments will prove ineffective.
DNA from three of the men with progressive cancer despite ARN-509 treatment, whereas no such variants were present in any of the men before treatment (3). When this association of ARF876L with prostate cancer progression despite ARN-509 treatment was considered in the context of the agonist activity of ARN-509 in prostate cancer cells expressing ARF876L, a compelling case for ARF876L mediating clinical resistance to second-generation antiandrogens could be made.

Using a similar approach, Korpal and colleagues (4) also generated LNCaP variant sublines using prolonged exposure to enzalutamide in vitro, isolating four sublines exhibiting resistance to the drug. For these sublines, enzalutamide was unable to prevent AR trafficking to the cell nucleus or to abolish expression of AR-regulated genes. Whole-transcriptome sequencing disclosed an F876L-encoding AR mutation in each subline, and transient transfection of cDNA for ARF876L and AR-dependent reporter constructs showed a switch from antagonist to agonist activity upon exposure to enzalutamide. Predictably, three of four LNCaP tumor xenografts with acquired resistance to enzalutamide also showed ARF876L expression. Forced stable expression of ARF876L conferred enzalutamide-resistant growth to LNCaP, VCaP, and Myc-CaP cells in vitro. Curiously, LNCaP variant sublines carrying ARF876L grew poorly, if at all, as xenograft tumors in castrated mice in vivo. The growth of such xenograft tumors was nonetheless stimulated by enzalutamide.

Examine gene expression data for enzalutamide-resistant sublines, Korpal and colleagues (4) speculated that persistent expression of "cell cycle" and "E2F1 activation" gene sets might nominate CDK4/cyclin D1 assembly as a candidate therapeutic target for prostate cancers progressing despite second-generation antiandrogen treatment. In support of this notion, the enzalutamide-resistant LNCaP sublines appeared sensitive to the CDK4/6 inhibitors LEE011 and PD033299.

The consistent finding of ARF876L in LNCaP sublines selected for resistance to second-generation antiandrogens in both reports, along with the propensity for ARF876L to mediate agonist responses to enzalutamide and ARN-509, strongly suggests this mutant receptor as a likely mediator of clinical resistance to this class of drugs. The detection of mutations encoding ARF876L in men progressing despite treatment with ARN-509 further supports this contention. Ready emergence of treatment resistance has long bedeviled inhibitory or toxic therapy of microorganisms and of human cancers. Luria and Delbrück (9) distinguished between spontaneous and induced mutations as a source of resistance using fluctuation analysis to study phage lysis of bacteria, a formalism recapitulated for cancer by Goldberg and Coldman (10).

For most acquired antineoplastic drug resistance, spontaneous mutation seems to account for genetic and phenotypic resistance to MDV3100 (enzalutamide). Cancer Discov 2013;3:1030–43.

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Resistance Emerges to Second-Generation Antiandrogens in Prostate Cancer

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