



Mechanisms of prostate cancer progression to androgen independence[☆]

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Prostate cancer is a major health problem in the United States and worldwide. In 2007, more than 27,000 men were estimated to have died from prostate cancer in the United States alone. Although important advances have been made in the diagnosis and treatment of prostate cancer, therapies focused on the removal or inhibition of androgen action remain the most important components of therapy for individuals with metastatic disease. Despite the application of such modalities, the vast majority of patients with metastatic disease progress with a median survival of less than 2 years. A number of different mechanisms have been identified that may potentially contribute to the progression of prostate cancer. These insights suggest that signaling via the androgen receptor (AR) – either via alternate signaling pathways impinging on the AR or through the in situ formation of androgens within progressive tumors – is an important contributor to such progressive disease. It is anticipated that such mechanistic insights will lead to the development of useful new therapies in the future.

Key words: prostate; cancer; androgen; androgen receptor; mutations; steroidogenesis; signalling.

Prostate cancer is a major health problem in the United States and worldwide. In 2007, in the United States alone, the American Cancer Society has estimated that more than 218,000 new cases of prostate cancer were diagnosed, while more than 27,000 men died of the disease.^{1,2} This problem is even more substantial when viewed from a global perspective, with prostate cancer accounting for more than 220,000 deaths worldwide annually.³

Significant changes have occurred in the way that prostate cancer is diagnosed and treated. Advances employing the use of serum markers have resulted in a shift toward

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more localized forms of the disease at the time of diagnosis. The development of more selective and sparing surgical techniques has substantially reduced patient morbidity and minimized patient mortality. Major advances have been made in hormonal and also to some extent in chemotherapeutic therapies. Despite these advances, patients with metastatic disease progress to the point where their tumors no longer respond to hormonal – or non-hormonal – based therapies. Such cancers do not respond to available modalities and have limited survival.^{4–6}

In the last two decades, an increased effort has been focused on understanding the biology of prostate diseases, particularly prostate cancer. As a result of these efforts, an immense body of work has emerged regarding the genetics and biology of prostate cancer development, metastasis, and progression. The present manuscript is focused principally on reviewing insights into the mechanisms by which prostate cancer progresses to exhibit androgen-independent growth.^a

THE ANDROGEN RECEPTOR, THE NUCLEAR RECEPTOR FAMILY, AND MECHANISMS CONTROLLING ANDROGEN ACTION

The nuclear receptor family is a gene family that contains 48 members in the human genome.⁷ Members of this protein family were originally identified on the basis of characteristically conserved protein motifs and overall protein sequence similarities.^{8,9} Each protein within this family is believed to serve as a regulator of gene expression. This group contains members that appear to display constitutive activities, as well as those that are regulated by specific ligands, including the androgen receptor.

The androgen receptor (AR) is a typical member of the nuclear receptor family (Figure 1). Like other members of this family, it contains specific domains that mediate the binding of high affinity ligands (ligand binding domain, LBD), and modulate its interaction with specific target DNA sequences within the genome (DNA-binding domain, DBD) (Figure 1). The androgen receptor is one of the larger members of the nuclear receptor family, with an amino terminus that comprises nearly half the coding sequence of the receptor protein. Of note, although a number of studies have demonstrated the importance of this amino terminal segment in the capacity of the receptor protein to regulate gene transcription, the mechanism by which the amino terminus contributes to gene regulation remains unclear.^{11–13} Several investigators have published work suggesting the importance of an interaction between the amino terminus and the ligand binding domain in modulating AR activity.^{14–17} A clear understanding of the nature of this interaction has been hampered by the lack of detailed structural analyses, as crystal structures have only been solved for individual DNA-binding and ligand-binding domains.

Within the amino terminus of the human AR are two repeated segments composed of repeated glutamine (glutamine repeat) and glycine (glycine repeat) residues. The length of these segments has been linked to variations in the activity of ARs containing varying length repeats.^{13,18–23} While still viewed by many as controversial, such variations have been linked to important biological phenomena, including alterations in fertility²⁴, serum

^a The terms androgen-independent, hormone-independent, castration-resistant, and hormone-refractory have all been used by different authors to describe prostate tumors that progress despite the application of available surgical or medical castration and anti-androgen therapy. None of these terms is satisfactory, as it is plausible that more than one mechanism may contribute to tumor growth. Despite these very real limitations, the term 'androgen-independent' is used in this review.

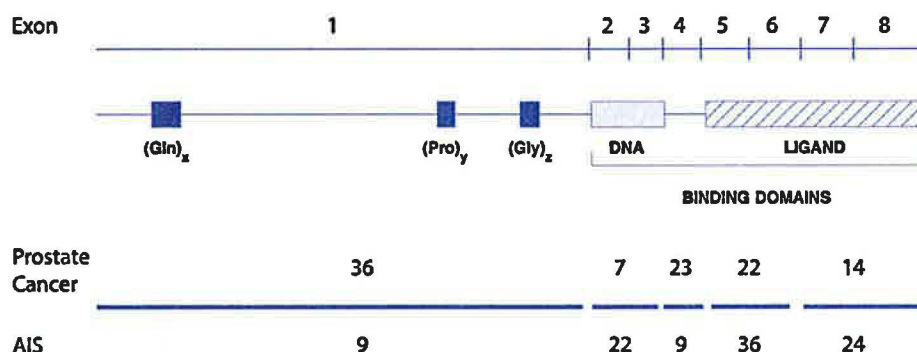


Figure 1. A schematic of the human androgen receptor (AR). Top: the AR is a typical member of the nuclear receptor family and is encoded by eight exons. It comprises segments that specifically recognize target DNA sequences (DNA-binding domain, DBD) and that bind specific ligands, such as testosterone and 5 α -dihydrotestosterone (ligand-binding domain, LBD). The AR possess a large amino terminus that comprises half of the open reading frame and contains repeated elements composed of repeated glutamine (Gln), proline (Pro), and glycine (Gly) residues. These segments are of different lengths in different individuals, and contain approximately 23, 8, and 23 residues in the respective regions. Bottom: the frequency of substitution mutation in the AR open reading frame is different in prostate cancer and syndromes of androgen insensitivity (AIS). For the purpose of this figure, the %age of total mutations within the amino terminus, DBD, hinge, and LBD are shown. Mutations within the amino terminus and hinge region (36 and 23%, respectively) have been identified more frequently in prostate cancer. This representation displays the distribution of 75 prostate cancer and 167 AIS AR mutations derived from the Androgen Receptor Database.¹⁰ This presentation does not take into account that some mutations are repeated within each group.

testosterone levels²⁵, and the clinical behavior of prostate cancers.²⁶ The recent creation of mice engineered to express androgen receptors with differing numbers of glutamine repeats offers the possibility of examining these phenomena in greater detail.²⁷

In vertebrates, testosterone and 5 α -dihydrotestosterone (DHT) are the principal androgens. Testosterone is the principal circulating androgen secreted by the testis and its synthesis is regulated by the action of luteinizing hormone (LH) on the Leydig cells of the testis. Although small quantities of DHT are secreted by the testes, much of the circulating DHT is formed in peripheral tissues by the action of two 5 α -reductase enzymes. Of note, distinctive pathways can give rise to androgens via selective steroidogenic pathways in specific tissues (Figure 2). Both testosterone and DHT bind to the same androgen receptor protein with high affinity. In many assays, DHT is a somewhat more potent androgen reflecting the higher affinity of the AR for DHT and the longer half life of the AR-DHT complex compared to the AR-testosterone complex.²⁸

The mechanisms by which nuclear receptors regulate genes transcription have been the subject of intense scrutiny for decades. Considerable progress has been made in the last twenty years that have contributed considerable detail to our understanding of the mechanisms by which these transcription factors regulate the activity of target genes. These insights have occurred in several waves, beginning in the early 1980s with the cloning of cDNAs encoding members of the nuclear receptor family, and progressing through the last twenty years as additional modulators and pathways have been identified.

Important efforts have centered on the definition of the intermediary factors affecting interactions between components of the general transcription machinery and

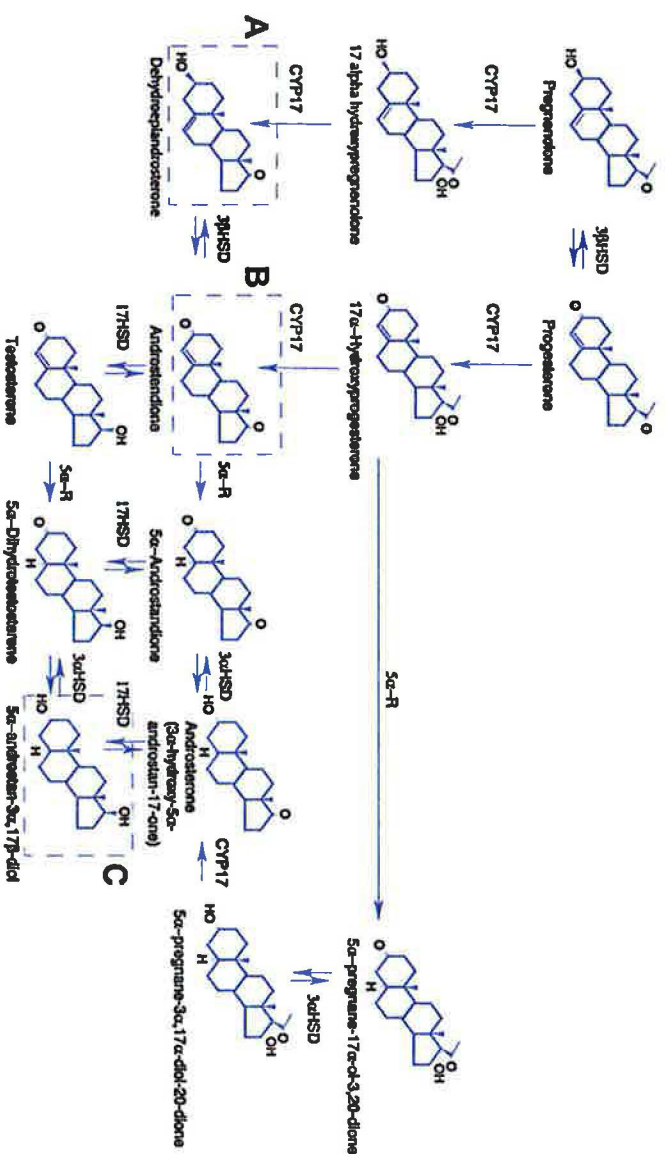


Figure 2. Interrelations and interconversions among androgens. Distinct pathways exist by which steroid precursors are converted to the active androgens, testosterone, and 5α-dihydrotestosterone. In the testis, the immediate precursor is androstenedione (box B). In the adrenal, conversion proceeds through the intermediate dehydroepiandrosterone. In the Tammam wallaby and the immature murine ovary, androgens are synthesized via 5α-androstan-3α,17β-diol. Potentially, any or all of these pathways might be the source of androgen synthesis during prostate cancer progression. These interconversions are catalyzed by families of enzymes: 17-hydroxysteroid dehydrogenases, 3α- and 3β-steroid dehydrogenases, and 5α-reductases. Reversibility or irreversibility is indicated by bi- or unidirectional arrows, respectively. Notably, synthesis of androgen via each of these pathways requires the formation of a 19-carbon steroid via the action of CYP17.

nuclear receptors themselves and the roles that these proteins play in the modulation of responsive genes.^{29,30} Broad groups of 'coregulator' proteins have been identified that either enhance or repress target genes, referred to collectively as 'coactivators' and 'corepressors', respectively. Each individual protein or protein complex possesses enzymatic activity which participates in the modulation of transcriptional complex stability and/or modification of the chromatin/surrounding regulated genes. In many instances, such proteins serve as coregulators for many members of the nuclear receptor family. The participation of such proteins in the regulation of AR function has been reviewed.³¹⁻³³

It has been clear for considerable time that members of the nuclear receptor family, including the androgen receptor, regulate gene transcription in response to ligands by alterations in the conformation of the ligand-binding domain. These changes in conformation dictate the patterns of cofactor recruitment and the subsequent patterns of gene expression. The binding of agonist ligands places the ligand binding domain of the receptor protein into a conformation that facilitates the recruitment of motifs within the primary sequence of coactivators to a specific hydrophobic cleft that is formed on the surface of the ligand-bound LBD. This recruitment facilitates the entry of proteins that enhance the stability of the transcription complex at the site of regulated genes and results in the enhancement of gene activation (Figure 3).

As was first elucidated for the estrogen receptor- α , the molecular basis of conformational changes centers on the creation of the hydrophobic cleft within the agonist-bound ligand binding domain surface that permits the recruitment of coactivators, such as members of the SRC-1 family of transcriptional coactivators.³⁴ The binding of antagonist ligands does not permit the formation of this coactivator cleft and instead facilitates the recruitment of proteins capable of repressing gene transcription. The molecular basis of agonism and antagonism has been observed in crystal structures of several members of the nuclear receptor family. Although it is felt that similar structural changes underlie the actions of AR antagonists, to date the crystal structure of the native androgen receptor ligand binding domain has only been solved when complexed to agonist ligands.³⁵⁻⁴⁰

In some instances, attempts have been made to map the complex interactions surrounding the regulation of responsive genes following the addition of steroid hormones. These studies have demonstrated a complex pattern of protein recruitment and dismissal from the regulatory elements within and adjacent to regulatory elements.⁴¹⁻⁴³ These changing patterns of promoter and enhancer occupancy have been associated with changes in the methylation, acetylation, SUMOylation, ubiquitination, and phosphorylation of the chromatin surrounding the regulated gene. These changes in the posttranslational modification of the chromatin are thought to mediate the state of the chromatin, permitting access to the transcription machinery and serving as a histone code.⁴⁴ Additional effects are thought to be mediated by the posttranslational modification of transcriptional machinery components themselves. Although this pattern has not been described in detail in many systems, it is anticipated that similar patterns of regulation occur at other regulated genes as well, including the AR. Importantly, it appears that patterns and gene regulation occur more broadly within regulated genes than anticipated from this study of specific model genes.^{45,46}

Just as pathways have been defined with respect to gene activation by agonist ligands, similar pathways have been identified that mediate the actions of antagonists of the androgen receptor and other nuclear receptors.⁴⁷⁻⁴⁹ The binding of androgen receptor antagonists to the ligand binding domain places the receptor into a conformation inconsistent with the recruitment of androgen receptor coactivators, and instead

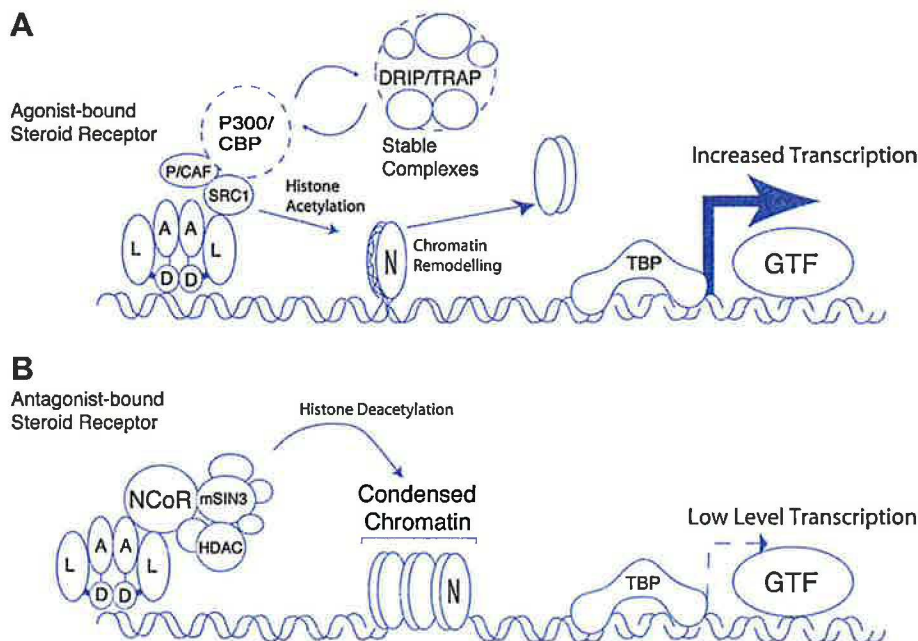


Figure 3. Coactivators and corepressors in the action of the androgen receptor and other nuclear receptors. A general model for the activities of coactivators and corepressors in the regulation of responsive genes by steroid receptors (A). The binding of a steroid receptor complexed to an agonist ligand to specific DNA sequence within or adjacent to the site of transcription initiation of a regulated gene recruits coactivator complexes containing proteins such as SRC-1, p300/CBP, and components of the mediator complex. Enzymatic activities of these proteins or by proteins within these complexes, such as histone acetyl transferase activity, modify the local chromatin structure. These changes make the transcription unit more accessible to the assembly and stability of transcription initiation complexes and results in an enhanced rate of transcription. (B) The binding of an antagonist to a steroid receptor results in the assumption of a different conformation of the receptor LBD and facilitates the recruitment of protein complexes containing corepressors such as NCoR and SMRT. The enzymatic activities associated with these corepressor complexes, such as deacetylation, leads to a condensation of chromatin structure and a decreased level of gene transcription. (A, amino terminus of NR with activation functions; D, DNA binding domain of NR; L, ligand binding domain of NR; N, nucleosome; TBP, TATA binding protein; GTF, general transcription factors.) Reprinted from Zoppi et al (2002, *Regulation of Gene Expression by the Nuclear Receptor Family in Genetics of Steroid Biosynthesis and Function* ed. J.I. Mason. Harwood Academic Publisher, pp 376–403) with permission.

places it into a conformation suitable for the recruitment of proteins that exhibit a repressive influence on the transcription of target sequences (Figure 3). As noted above, the precise structural correlates of these conformational changes remain undefined, as the crystal structure of antagonist-bound normal androgen receptor ligand binding domain has not yet been solved. Further, although most models would suggest the recruitment of coactivators such as NCoR and SMRT as a component of the action of AR antagonists, recent evidence has been presented suggesting that other pathways and mediators may be involved in the action of androgen receptor antagonists.^{49,50}

It is worthwhile to note that alterations in responsiveness to individual ligands – agonist or antagonist – may be altered by the levels of nuclear coregulators that are

present within individual cell types. Enhanced expression of AR coactivators might be anticipated to enhance the responsiveness of tumors to low levels of androgens and attenuate the responsiveness to AR antagonists. Similar responses might accompany decreased expression of AR corepressors. The importance of these changes has been demonstrated in a limited number of model systems.^{42,51-55}

Finally, in addition to pathways acting directly in the nucleus by the nuclear receptor activated by agonist ligands, it has become clear that alternative pathways exist in which the agonist-bound non-nuclear receptor activates alternate signaling cascade. Although these pathways have been more carefully defined with respect to the actions of estrogens and progesterone⁵⁶, similar rapid effects had been defined for androgens as well.^{57,58} In some cases, these alternate signaling pathways have been associated with changes in the hormone-dependent growth patterns of the cells under study.⁵⁹

CELL-CELL INTERACTIONS AND THE ACTIONS OF ANDROGENS IN VIVO

The biology of androgen action in the regulation of cell growth and function bears similarities to the actions of other steroid hormones. One line of evidence, however, has suggested that the actions of androgens maybe even more complex. These studies have demonstrated that androgens may not act simply within target cells, but may instead involve complex interactions between cells derived from epithelial cell populations and those derived from stromal cell populations.⁶⁰⁻⁶² Although such experiments have largely involved tissue reconstitution experiments conducted in mice, additional studies suggest that such interactions may play a role in other systems, including specific stages in development^{63,64} and in the evolution of human prostate cancer to more aggressive forms.⁶⁵

EVIDENCE THAT ALTERATIONS IN ANDROGEN ACTION MAY UNDERLIE THE PROGRESSION OF ANDROGEN-INDEPENDENT FORMS OF PROSTATE CANCER

Several lines of evidence have suggested that the androgen receptor may play an important role in the biology of progressive and recurrent prostate cancer. The demonstration that the androgen receptor is expressed in prostate cancer recurrence⁶⁶⁻⁶⁸, the frequent amplification of the androgen receptor in prostate cancer in progression^{69,70}, the enhanced expression of the AR in progressive prostate cancers⁷¹, and the emergence of mutations in the androgen receptor (see below) all have lent credence to its involvement in the progression of this disease.

Additional insights have come from examination of hormone levels in tumor samples expression and examination of gene expression patterns. In addition to demonstrating the continued expression of the androgen receptor protein in specimens of recurrent prostate cancer, Mohler and colleagues⁷² demonstrated the presence of levels of testosterone and DHT in tumors that would be expected to be capable of activating the androgen receptor. These authors suggested a 'paradigm shift', in that the prostate cancer which occurs following medical or surgical castration is 'recurrent' and not 'androgen-independent'.

These experiments have been reinforced by a number of lines of evidence of a similar nature. Page et al demonstrated in healthy subjects treated with a long-acting GnRH-antagonist to effect hypogonadism, that despite a 94% decrease in serum

testosterone concentrations, intraprostatic testosterone and dihydrotestosterone levels remained a level 20–30% of control values.⁷³ Similarly, Nishiyama and colleagues measured levels of dihydrotestosterone in patients treated with androgen deprivation therapy (castration + flutamide).⁷⁴ In these latter studies, the investigators found that the levels of prostatic dihydrotestosterone remained at approximately 25% following androgen deprivation therapy, compared to levels measured prior to androgen deprivation. By contrast, measurements examining serum levels of dihydrotestosterone in these same individuals demonstrated that DHT levels fell by over 90%.

Mostaghel et al examined intraprostatic androgen levels and patterns of androgen-regulated gene expression in normal men and in archival prostate cancer specimens following varying lengths of androgen deprivation therapy.⁷⁵ The results of these experiments demonstrated several major features. First, intraprostatic levels of testosterone and DHT showed marked variations between individuals following short-term medical castration. Second, androgen-regulated gene expression, as indicated by the levels of PSA expression, persisted and were substantially reduced only in those subjects with the most profound suppression of intraprostatic androgen levels. Finally, examination of the levels of androgen dependent gene expression in primary prostate cancers at different time points of the androgen deprivation revealed evidence that the expression of androgen-regulated genes persisted at each of the time points examined. Further, substantial heterogeneity was observed between the levels of androgen-regulated gene expression among different samples.

MUTATIONS IN THE ANDROGEN RECEPTOR IN THE EVOLUTION OF ANDROGEN-INDEPENDENT FORMS OF PROSTATE CANCER

As noted above, several lines of evidence have suggested the involvement of the androgen receptor in prostate cancer progression, including expression of the androgen receptor in metastatic prostate cancer deposits, the frequent amplification of the androgen receptor gene in advanced forms of prostate cancer, the continued expression of androgen-dependent genes in progress of prostate cancer. In addition to these observations, two observations have increased the interest in the potential role of mutations of the androgen receptor in prostate cancer growth and progression. First was the demonstration that constitutively active forms of the androgen receptor existed raising the possibility that mutations of the androgen receptor could contribute to the behavior of some progressive prostate cancers.^{76,77} The second was the identification of a mutation in the ligand binding domain of the androgen receptor expressed in the prostate cancer cell line, LNCaP, which conferred upon this cell line aberrant patterns of hormone responsiveness, including activation by anti androgens.⁷⁸

Subsequent work by a number of laboratories has contributed to our understanding of the frequencies and circumstances where such AR mutations may contribute to the behavior of prostate cancer. To this point, numerous mutations of the androgen receptor – somatic in nature – have been identified in clinical prostate cancer specimens.

The frequency and nature of AR mutations that have been identified in prostate cancers appear to be related principally to the stage of the disease and the selective pressure that have been exerted on the cancers.^{79,80} In localized primary cancers, AR mutations are believed to be uncommon and have been identified with the frequency of approximately 5%. As tumors become locally metastatic, the frequency with which AR mutations rises. In the series reported by Marcelli and coworkers,

mutations were identified in approximately 20% of microdissected locally metastatic tumor specimens.⁸¹ When samples were examined from distant metastatic sites, an even higher frequency was demonstrated (50%).⁸²⁻⁸⁴ Experiments examining the frequency and nature of mutations in distant metastatic sites in patients treated with androgen receptor antagonists showed an even higher frequency and a clustering of specific mutation types.⁸² Of interest, mutations of the AR have also been identified in murine models of prostate cancer.^{85,86} In some instances, mutations of the AR may themselves be oncogenic.⁸⁷

Unlike mutations that have been identified in genetic syndromes of androgen insensitivity (loss-of-function mutations), mutations that have been identified in clinical forms of prostate cancer exhibit a somewhat different distribution within the androgen receptor open reading frame. These mutations can be viewed as comprising at least two distinct groups. In the first of these, the mutation is localized at specific regions of the receptor protein that can be shown to result in alterations of androgen receptor function. Such mutations include those that alter the ligand-binding properties of the receptor (e.g. permitting its activation by a broader range of ligands, for example) or those that result in the production of receptor protein that displays constitutive activity (as a result of either receptor truncation or amino acid substitution). The study of these mutations has been completed for a number of different mutations of the androgen receptor, and support the possibility that these changes may play a role in the pathogenesis or behavior of the prostate cancer.^{82,88,89}

The second type of mutation that has been identified in the AR in prostate cancer specimens is more difficult to explain. These mutations are distributed differently in the AR open reading frame compared mutations causing AIS (Figure 1), often into regions of the receptor protein for which no clear-cut function has been identified or into segments that might be expected to lead to a loss of the androgen receptor function. These mutations may either represent disruptions of AR signaling pathways that have yet to be identified or for which the proper assay methods have not yet been tested or are not yet available.

EVIDENCE THAT ALTERNATIVE PATHWAYS MODULATE OR SUPPLANT THE REQUIREMENT FOR ANDROGENS TO STIMULATE THE ANDROGEN RECEPTOR

The demonstration that the chicken progesterone receptor could be activated in a ligand dependent fashion by cAMP dependent mechanisms⁹⁰ stimulated a large number of investigations to identify pathways capable of modulating the activities of the nuclear receptor family members, including the AR. Although early reports identified modulation of AR activity by cAMP and IGF-I signaling pathways^{91,92}, subsequent investigators have implicated other potential signaling pathways.⁹³⁻¹⁰⁰

In subsequent studies, a number of different pathways have been examined to assess their roles in modulating the activities of the AR in the regulation of androgen receptor function and of target genes.⁹⁴ In some instances, the effects seem most clearly to exert an effect in accentuating the activity of the AR in modulating target genes and proliferation in limiting androgen levels.⁹⁵ In other instances, these effects observed indicate that the effects may signal through mechanisms that obviate the need for androgens completely. The roles that these diverse pathways play in the emergence of androgen-independent prostate cancer remain uncertain.

EVIDENCE THAT PATHWAYS OF THE ANDROGEN-REGULATED PROSTATE GROWTH ARE INTACT AND MODULATED BY ALTERNATE SOURCES OF ANDROGENS

A variety of different models has been used to study the potential mechanisms by which prostate cancers make progress to androgen independence. Experiments have been conducted using both in vitro cultured cell lines and xenografts models of prostate cancer. Each of these approaches has produced a range of interesting experimental results. Nonetheless, each of these approaches has been limited by considerations relating to influences that may be absent in these models which may be present in human prostate cancers in vivo.

In this regard, a limited number of studies has attempted to explore the molecular basis of prostate cancer progression in vivo. One such study is that reported by Stanbrough et al.¹⁰¹ These intriguing experiments were conducted using bone-marrow aspirate samples obtained from individuals undergoing androgen deprivation as a part of their therapy for prostate cancer. In these studies, analyses of samples obtained from bone marrow biopsies performed in individuals with androgen-independent prostate cancer were compared to samples of primary prostate cancers following microdissection. Of note, the authors of this study took care to include in these analyses only samples that were comprised primarily of prostate cancer (i.e. with minimal contributions from bone marrow components). The results of these experiments were quite interesting. First, analysis of the microarray data permitted the grouping of the samples into metastatic androgen-independent prostate cancer groups. Inspection of the expressed genes in both groups of samples indicated that although androgen-regulated transcripts could be identified in both samples groups, the levels of these androgen-regulated genes were reduced in the androgen-independent samples. Inspection of the specific genes identified demonstrated a range of differentially expressed genes. Of particular note, was the increased level of androgen receptor expression which was noted in the majority of tumors. This finding was consistent with alterations of expression of the androgen receptor gene that have been observed in other analyses of human prostate cancers, as well as in xenograft models of prostate cancer progression.⁷¹

An intriguing attribute of these experiments was the identification of alterations in the expression levels of genes that would be expected to modulate the formation of androgens in situ within androgen-independent prostate cancer cells. Specifically noted were changes in the expression of genes involved in both androgen synthesis as well as breakdown. While the implications of the increase of several genes involved in the formation of androgens are obvious (HSD3B2, AKR1C3, SRD5A1 and 2) as they should lead to the formation of increased levels of active androgens within the tumors, the impact of increased levels of others are not (AKR1C1, AKR1C2, UGTB17).

The aforementioned experiments are largely consistent with the results of similar smaller trials, as well as experiments that have examined the importance of androgen levels in androgen action in prostate cancer progression. Additional support implicating in situ formation of androgens has come from additional directions as well. Some of the most compelling evidence is that centered on interim results employing agents that are capable of blocking the formation of steroid hormones that can be converted to androgens. Some of the most interesting results are the studies of Abiraterone, an inhibitor of CYP450c17 (CYP17), which blocks the cleavage of the 17/20 carbon-carbon bond that is required for the synthesis of both estrogens and androgens (Figure 3). Use of this agent in small, early stage clinical trials in patients with advanced prostate cancer who have failed

androgen deprivation and docetaxel-based chemotherapy have demonstrated that 2/3 of patients demonstrate a greater than 50% PSA decline and more than half have shown >90% PSA decline.^{102,103} Of even greater interest, of 8 pts with Response Evaluation Criteria in Solid Tumors (RECIST) evaluable disease, 5/8 showed radiological partial responses, 1/8 had stable disease (7 months+), and 2/8 displayed progressive disease.¹⁰⁴

Keeping in mind that conclusions cannot be reached due to the small number of patients, these results suggest that responses are likely to be heterogeneous. They also indicate that even among patients with advanced forms of prostate cancer, a substantial number of individuals with disease progressing while being treated with one type of androgen deprivation therapy could respond to therapies directed at the inhibition of the CYP17. These studies are consistent with the notion that biologically important levels of androgens are present in prostate tumors in the context of androgen deprivation therapies currently in use. These early findings suggest that these levels of androgens are important for continued tumor growth and progression and that therapies designed to further lower or eliminate them may have clinically important effects.

SUMMARY

An immense body of information has accumulated relating to the biology of human prostate cancer and prostate cancer models. Much of this information is consistent with the androgen receptor – and the gene networks that it regulates – being a central element in prostate cancer development and progression. A number of different distinct mechanisms have been identified which can participate in the modulations of prostate cancer progression (Table I). Although no individual pathway is likely to represent a single target by which prostate cancer progression might be interrupted, it is intriguing to note the recent evidence suggesting that the ablation of low levels of androgens detected in progressive tumor specimens is likely to have important therapeutic benefits.

Table I. Potential mechanisms of prostate cancer progression to androgen independence.

Growth mechanisms that employ the pathways that regulate prostate epithelial cell growth in normal tissues

Mutant androgen receptors

Emergence of signaling pathways that influence the androgen-regulated pathways

Augmenting the growth in response to androgens or in response to low levels of androgens

Increased expression of coactivators

Decreased expression of corepressors

Input from pathways that augment the effects of low levels of androgen

Signaling that requires the androgen receptor, but does not require hormone

Alterations in the complement of enzymes necessary to synthesize (increase) or degrade (decrease) active androgens

Emergence of growth mechanisms not normally regulated by androgen and supplanting those that are normally regulated by androgen in the prostatic epithelium

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