

Regulation of Androgen Receptor Levels: Implications for Prostate Cancer Progression and Therapy

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Abstract Androgen deprivation has been the standard therapy for advanced and metastatic prostate cancer for over half a century, as prostate tumors are initially dependent on androgens for growth and survival. Unfortunately, in most patients undergoing androgen ablation, relapse (recurrent tumor growth) eventually occurs. The actions of the principal androgens, testosterone and dihydrotestosterone (DHT), are mediated via androgen receptors (ARs), ligand-activated transcription factors that belong to the nuclear receptor superfamily. Because of the presence of transcriptionally active ARs in tumors from recurrent or androgen-independent disease, there is a heightened interest in new therapeutic paradigms that target the AR and its regulatory pathways. The regulation of AR levels is highly complex with control exerted by several pathways and in a cell-, tissue-, and developmental-stage specific manner. Androgens are important regulators of AR mRNA and protein through transcriptional and post-transcriptional mechanisms. This article reviews the evidence implicating the AR in recurrent prostate cancer and discusses the multiple mechanisms that regulate AR levels in normal and neoplastic cells. The complexity of AR regulation suggests that there will be an ample array of potential new drug targets for modulating levels of this receptor, a key signaling molecule in prostate cancer. *J. Cell. Biochem.* 95: 657–669, 2005. © 2005 Wiley-Liss, Inc.

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The androgen receptor (AR), like other steroid hormone receptors, is a ligand-activated transcription factor that belongs to a large family of nuclear receptor proteins, sharing a similar organization of functional domains [reviewed in Tsai and O'Malley, 1994]. AR comprises a divergent amino-terminus that contains a strong transcriptional activation function, a well-conserved DNA binding domain, and a large C-terminal ligand binding domain, which contains a second activation function [Kokontis and Liao, 1999; reviewed in Roy et al., 1999; reviewed in Gelmann, 2002]. Testosterone is the predominant circulating androgen in mammals and is converted to dihydrotestosterone (DHT) by 5 α -reductase in certain tissues of the

male urogenital tract, skin, and other target cells. DHT binds with highest affinity to AR and together with testosterone promotes AR transcriptional activity thereby ensuring the development and maintenance of male reproductive functions. Androgens also exert rapid effects initiated at the cell membrane but the physiologic significance of these actions is incompletely understood [reviewed in Heinlein and Chang, 2002b]. The unliganded AR resides predominately in the cytoplasm as a heteromeric complex with hsp90 and other chaperone proteins. These chaperone proteins maintain AR in a form that is receptive to ligand binding. Regulation of gene expression by androgen-activated AR occurs through receptor nuclear translocation, dimerization, and binding to androgen response elements (AREs) in the DNA of target genes. AR homodimers recruit a panoply of factors including coactivators and mediator proteins whose enzymatic activities promote chromatin remodeling and transcriptional regulation of target genes leading to cell differentiation, survival, and proliferation [reviewed in Heinlein and Chang, 2002a].

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Androgenic stimulation of the AR is not only essential but is also sufficient for the generation of the prostate gland [Marker et al., 2003] and is strongly implicated in development of prostate adenocarcinoma. Based on the suspected role of AR in prostate cancer initiation and progression, the regulation of AR transcriptional activity in prostate cancer cells and animal models has received substantial research attention and is the subject of several excellent, recent review articles [Culig et al., 2000; Balk, 2002; Heinlein and Chang, 2004; Santos et al., 2004; Taplin and Balk, 2004]. This article will focus on the more poorly understood mechanisms that control AR levels in target tissues and in prostate neoplasia. Recent findings from gene expression profiling analyses in advanced prostate cancers as well as from prostate cell and transgenic mouse models expressing AR strongly support the significance of AR expression and regulation in prostate adenocarcinoma [Stanbrough et al., 2001; Berger et al., 2004; Mellinger et al., 2004; Shah et al., 2004].

IMPORTANCE OF AR IN PROSTATE CANCER

Prostate Gland Architecture, Cell Types, and AR Expression

The human prostate gland consists of epithelial-lined acini with an underlying fibromuscular stromal layer. The epithelial cell compartment consists of slow growing well-differentiated secretory (luminal) cells, which are positive for both AR and prostate specific antigen (PSA), and a basal epithelial layer comprised of rapidly proliferating cells expressing low levels of AR and a small number of AR-negative, neuroendocrine cells [Bonkhoff et al., 1994]. Stem cells are presumed to exist within the basal cell population and these progenitors differentiate into basal, secretory, or neuroendocrine lineages. Androgen-directed development of the prostate initiates in the stromal compartment, which contains AR and produces paracrine factors that regulate growth and differentiation of the prostatic epithelium. In contrast, prostate cancer but not normal prostatic epithelial cells xenografted into AR-null nude mice grow in response to androgens suggesting that cancer development may result from an autocrine mechanism [Gao et al., 2001]. However, the cellular origins of prostate adenocarcinoma are unknown.

Androgen Dependence of Prostate Cancer

The dependence of prostate cancer on androgens was established more than half a century ago following Dr. Charles Huggins' Nobel prize-winning discovery that castration results in prostate cancer regression. Androgen deprivation therapy in its various surgical and medical forms continues to be the mainstay treatment for advanced prostate cancer with 80–90% of men undergoing a clinical remission. Complete androgen blockade is often instituted and consists of drugs to decrease testicular testosterone synthesis in conjunction with an AR antagonist. Androgen deprivation therapy is also under investigation in earlier stages of prostate adenocarcinoma in the adjuvant and neoadjuvant settings [reviewed in Hellerstedt and Pienta, 2002]. Despite an initial favorable response to androgen deprivation therapy, nearly all prostate cancer patients progress to androgen-independent or hormone refractory prostate cancer. This form of prostate cancer is incurable.

Because androgen-independent prostate cancer grows in the absence of testicular androgens and prostatic AR levels decrease following androgen ablation in rodents [Prins and Birch, 1993], it was assumed that AR protein would be downregulated in androgen-independent disease. Thus, it was unanticipated that locally progressed and metastatic prostate cancer specimens from patients with androgen-independent disease express AR protein [van der Kwast et al., 1991; Ruizeveld de Winter et al., 1994; Hobisch et al., 1995]. The maintenance of AR in androgen-independent prostate cancer is further supported by a recent study that assessed AR and other markers from metastatic, androgen-independent prostate cancer samples obtained from 30 men as part of a rapid autopsy program [Shah et al., 2004]. Although a high degree of heterogeneity was observed for all markers including AR, the majority of metastatic specimens express AR. Increased expression of AR in advanced prostate cancer can result from AR gene amplification, which occurs in approximately 30% of advanced prostate cancers [Visakorpi et al., 1995]. AR expressed in recurrent cancer appears to be functional based on its nuclear localization and the reacquisition of AR-regulated gene expression such as PSA [Gregory et al., 1998, 2001].

Experimental Models Demonstrate a Central Role for AR in Prostate Cancer Development and Androgen-Independence

To evaluate the role of AR in prostate growth and cancer development, Stanbrough et al. [2001] generated transgenic mice targeting AR (regulated by the prostate-specific probasin promoter) to prostate secretory epithelial cells. Overexpression of AR in prostatic epithelial cells of these mice resulted in enhanced cell proliferation. Although prostate adenocarcinoma did not develop, aged transgenic mice exhibited dysplastic prostate lesions, resembling high-grade human prostatic intraepithelial neoplasia (PIN). PIN is strongly suspected of being the precursor to prostate adenocarcinoma. This study provides direct evidence for the growth-promoting actions of AR and suggests that AR overexpression in prostate initiates oncogenic processes.

Greenberg and colleagues [Han et al., 2005] took a related approach to investigate the potential of AR to initiate prostate cancer. These investigators identified a highly conserved "signature motif" within the amino terminal region of the AR that is implicated in AR interactions with coregulatory proteins. ARs harboring a substitution in this region (E231G) exhibit higher transcriptional activity in the absence of ligand and increased sensitivity to coregulators [Han et al., 2001]. Strikingly, 100% of transgenic mice expressing AR-E231G in prostatic epithelium rapidly exhibited PIN that became invasive and metastatic. These studies demonstrate the critical role played by a variant AR, with a gain-of-function phenotype, in the initiation of aggressive prostate cancer.

The effects of introducing AR into immortalized, normal prostate epithelial cells lacking AR were recently investigated [Berger et al., 2004]. The AR-expressing prostate epithelial cells were tumorigenic when implanted into prostates of nude mice, whereas orthotopically implanted control prostate epithelial cells failed to produce tumors. The immortalized prostate epithelial cells were phenotypically basal cell-like; however, the AR-expressing cells had features of secretory cells when grown orthotopically. In addition, tumors formed from the AR-expressing cells were androgen-dependent for growth. Progression to androgen-independence was not assessed. Together, these studies support a central role for AR in prostate cancer development.

Progression to androgen-independence can be demonstrated experimentally in cell culture and in vivo. The human prostate cancer cell line LNCaP has proven valuable for studies of prostate cancer progression [Kokontis et al., 1994, 1998; Wu et al., 1994; Lu et al., 1999; Igawa et al., 2002]. LNCaP are AR-positive and exhibit growth stimulation at low concentrations of androgen [reviewed in Sobel and Sadar, 2005a]. Androgen induces PSA secretion in these cells. Further, since LNCaP are poorly tumorigenic in castrated nude mice, they are considered androgen-dependent. Extended culture of these cells in androgen-depleted media (or propagation as xenografts in castrated nude mice) results in the emergence of androgen-independent cells. The androgen-independent LNCaP cells express higher levels of AR than the parental LNCaP line, exhibit hypersensitivity to androgens and are tumorigenic in castrated mice [Kokontis et al., 1994, 1998; Umekita et al., 1996]. Disruption of AR by microinjection of hammerhead ribozymes or AR antibodies decreases the growth rate of androgen-independent LNCaP cells in the absence of androgens [Zegarra-Moro et al., 2002]. This study shows that proliferation of androgen-independent cells requires AR signaling.

A variety of prostate xenograft models are currently available that reproduce the transition from androgen-dependence to -independence [reviewed in Sobel and Sadar, 2005b]. A pivotal study by Chen et al. [2004] defined global gene expression changes associated with prostate cancer progression. Seven isogenic pairs of androgen-sensitive and androgen-refractory human prostate cancer xenografts were compared. Androgen-independent sublines were derived from their hormone-sensitive counterparts following serial passaging of xenografts in castrated nude mice. Remarkably, AR was the only gene (of >12,000 probe sets) that exhibited differential expression between all seven hormone-sensitive and refractory human prostate xenograft pairs. AR mRNA and protein were increased in each of the androgen-independent xenografts compared to its parental hormone-sensitive line. This upregulation of AR activity in hormone-refractory cancer is a necessary event in prostate cancer progression as knock-down of AR by RNA interference in refractory sublines dramatically reduced tumor growth in castrated mice. In the reciprocal experiments, introduction of AR into hormone sensitive

sublines resulted in a significantly shorter latency for tumor growth in castrated mice. Thus, AR is sufficient to confer androgen-independence in these model systems. These AR effects were dependent on AR nuclear localization and an intact receptor hormone binding domain. Further, upregulation of AR not only allowed cells to respond to very low levels of androgen but also resulted in limited agonistic action of a clinically used AR antagonist. This study strongly supports the therapeutic goal of reducing AR levels in advanced prostate cancer.

Proposed Mechanisms for Continued AR Function Under Conditions of Androgen Deprivation

As discussed above, androgen-independence results from upregulation of AR in the xenograft models. Clinical data including those showing the striking heterogeneity of metastatic prostate cancer [Shah et al., 2004] suggest that there are multiple mechanisms of androgen-independence. Functional inactivation of AR through mutation was initially proposed to explain maintenance of AR expression but loss of androgen-dependent growth. While somatic mutation of AR occurs with frequencies ranging from 20% to 40% in androgen-independent prostate cancer (particularly in men treated with antiandrogens), the vast majority of these mutations are gain-of-function, not inactivating [reviewed in Taplin and Balk, 2004]. In particular, many AR mutations, including the codon 877 threonine to alanine mutation found in LNCaP cells as well as in clinical samples, occur in the ligand binding domain of the receptor and result in a broadened range of ligand specificity. These mutations thus permit AR to regulate targets genes in response to other hormones or even AR antagonists [reviewed in Feldman and Feldman, 2001]. Additional mechanisms that enhance AR signaling have been proposed including increased levels of AR coactivators or decreased AR corepressors. Crosstalk between AR and other signaling pathways may increase AR sensitivity to low androgens or promote ligand-independent activation of AR. The AR gene contains a CAG repeat in exon 1 whose length is polymorphic (mean length is 21 repeats). Expression of AR containing shorter CAG repeat tracts has been correlated with earlier onset [Hardy et al., 1996] or increased risk of aggressive prostate cancer [Giovannucci et al., 1997]; however, recent

reports based on large, prospective studies do not support a significant or strong association between this AR gene polymorphism and prostate cancer risk [Zeegers et al., 2004; Freedman et al., 2005]. Finally, another model suggests that AR may be bypassed in favor of other signaling pathways that drive growth and survival of prostate cancer cells.

The results from experimental models of prostate cancer progression and from analysis of androgen levels in human prostate cancer clinical samples have prompted a reconsideration of terminology [Mohler et al., 2004]. Local levels of androgens in androgen-independent tumors may be sufficient to activate AR, made hypersensitive as a result of mechanisms discussed above. Because of this finding the term androgen-independence will be considered synonymous with recurrent or hormone-refractory prostate cancer.

REGULATION OF AR LEVELS

AR levels vary during development and aging (e.g., see Takane et al. [1991a]; Prins et al. [1996]) and these fluctuations are significant as sensitivity of cells and tissues to androgens is directly related to AR content [Takane et al., 1991a,b; McPhaul et al., 1993]. As discussed above, upregulation of AR can drive progression to androgen-independent prostate cancer [Chen et al., 2004]. Thus, elucidating the varied and cell-specific mechanisms that regulate AR mRNA and protein is essential to understanding hormonal responsiveness and may provide novel therapeutic targets.

AR Promoter

The human AR gene contains a single promoter that lacks typical TATA or CAAAT box motifs [Tilley et al., 1990]. This promoter is utilized in a variety of cell lines and AR-expressing tissues [Tilley et al., 1990]. Cis-acting sequences that contribute to AR promoter activity in humans or rodents include binding sites for Sp1 [Faber et al., 1993; Chen et al., 1997], NF κ B [Supakar et al., 1995; Zhang et al., 2004], cAMP response element binding protein [Mizokami et al., 1994], NF1 [Song et al., 1999] as well as sites for unidentified proteins including an age-dependent [Supakar et al., 1993], and a negative regulatory factor(s) that binds in conjunction with NF1 to a composite element [Song et al., 1999]. Two

uncharacterized, single strand DNA binding proteins, mARs [Grossmann and Tindall, 1995] and ssPyrBF [Chen et al., 1997], influence basal mouse AR promoter activity. The human AR gene also contains a suppressor element (ARS); however, this site is located in the 5'-untranslated region. Loss of protein binding to ARS is associated with increased levels of AR mRNA in one model of androgen-independent LNCaP cells [Wang et al., 2004]. Although androgen is a major regulator of AR mRNA levels, no functional AREs have been identified in the AR gene promoter or its 5'-flanking region [Blok et al., 1992; Takane and McPhaul, 1996].

Androgen Regulation of AR Gene Expression

Androgen regulation of AR mRNA levels (autoregulation) occurs in virtually every target tissue and cell line examined. Androgen downregulates AR mRNA in most cells and tissues [Tan et al., 1988; Quarmby et al., 1990; Shan et al., 1990; Krongrad et al., 1991] although there are several examples of androgen-mediated AR mRNA upregulation [Takeda et al., 1991; Nastiuk and Clayton, 1994; Takeuchi et al., 1994; Wiren et al., 1997]. The molecular basis for this differential regulation is unknown but appears to be cell- and tissue-specific. The dynamics of androgen-mediated AR mRNA regulation in target tissues was examined by comparing intact and castrated rats [Quarmby et al., 1990]. Northern blot analysis revealed that levels of AR mRNA in rat kidney, brain, epididymis, and anterior prostate were increased in castrated animals. Testosterone administration to castrated rats caused AR mRNA to decrease to levels lower than those observed in the intact control animals. Since estradiol had no effect on AR mRNA levels, androgen-mediated downregulation of AR mRNA is not due to testosterone conversion to an active estrogen. Consistent with AR-mediation of this autoregulatory process, testicular feminized (*tfm*) mice, which express a truncated, non-functional AR, showed no androgen regulation of AR mRNA.

Studies in LNCaP cells on the mechanism of androgen-mediated AR mRNA downregulation showed that this response is due to decreased transcription of the AR gene [Blok et al., 1992; Wolf et al., 1993]. Despite the transcriptional mode of AR mRNA regulation, neither the 5'-upstream region (including 7 kb of upstream sequences) nor the promoter or 5'-untranslated

region of the human AR gene confers androgen regulation [Blok et al., 1992; Mizokami et al., 1994; Takane and McPhaul, 1996]. The lack of autoregulatory sequences in the AR promoter and flanking region in conjunction with the demonstration of steroid receptor autoregulatory sequences represented in the cDNAs of the glucocorticoid and estrogen receptor [Burnstein et al., 1990; Kaneko et al., 1993] led us to ask whether sequences involved in AR mRNA autoregulation are present in the AR coding region. We demonstrated that androgen-mediated up- and downregulation of AR mRNA is reproduced in different cell lines expressing the human AR cDNA and this autoregulation occurs through transcriptional mechanisms [Burnstein et al., 1995; Dai and Burnstein, 1996; Dai et al., 1996]. AREs present within the AR cDNA confer this androgen-mediated upregulation of AR mRNA.

To establish definitively the role of these exonic AREs in autoregulation of AR mRNA, we generated silent mutations of the AREs, which resulted in a functional receptor that is resistant to androgen-mediated upregulation of AR mRNA. AR mRNA autoregulation is due to four AREs, which function synergistically with a myc site (E box) [Grad et al., 1999]. Myc and Max interaction with the E box cooperates with ARs bound to the exonic AREs and is required for androgen regulation of AR mRNA in this model. These regulatory elements are located within exons D and E of the human AR gene. A 6.5-kb genomic AR fragment (or androgen responsive region) encompassing the exonic AREs and myc site is regulated by androgens in cells that exhibit androgen-mediated upregulation of AR mRNA suggesting that these elements participate in the regulation of AR gene expression (Fig. 1) [Grad et al., 1999]. While the DNA region containing these AREs is responsible for

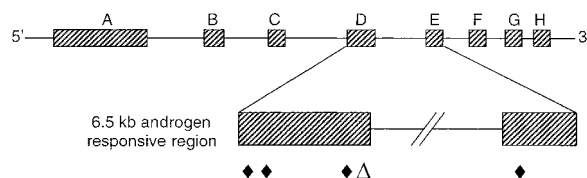


Fig. 1. Schematic of the human androgen receptor gene. The exon/intron structure of the human androgen receptor gene is shown (not to scale) emphasizing the exonic cis elements that are involved in autoregulation of AR mRNA [Dai and Burnstein, 1996; Grad et al., 1999]. Exons are depicted by hatched bars, introns by thin lines, closed diamond symbols represent AREs, and the open triangle is a Myc/Max binding site (E box).

androgen-mediated upregulation of AR mRNA, this region is not involved in AR mRNA downregulation. The finding that mRNA encoded either by the AR cDNA or the native AR gene is subject to differential autoregulation in distinct cell lines and tissues supports the existence of cell-specific factors that dictate this response. Further, we have observed that upregulation of AR mRNA in osteoblastic and some prostate cancer cells is associated with sensitization to hormone, whereas downregulation of AR mRNA is observed in LNCaP cells that undergo desensitization ([Dai et al., 1996] and unpublished data). Thus the identification of the cell-specific factors that participate in androgen-mediated autoregulation is vital to understanding mechanisms of androgen sensitivity.

Transcriptional Regulation of the AR Gene by Signaling Pathways

Androgens regulate gene expression in the liver of the male rat but this hormonal control subsides in aged animals. The decreased androgen responsiveness correlates with downregulation of AR mRNA. Because NF- κ B increases with age in the male rat liver and suppresses AR promoter activity, NF- κ B may account for decreased levels of AR and diminished hepatic androgen sensitivity in aged rats [Supakar et al., 1995]. The mechanism for transcriptional repression of the AR gene by NF- κ B (well-known for transcriptional activation of genes involved in immunity and inflammation) may be due to increased levels and preferential binding of NF- κ B subunit p50 homodimers to the AR gene promoter [Supakar et al., 1995; Zhang et al., 2004]. This form of NF- κ B can serve as a transcriptional repressor through recruitment of histone deacetylase-1 [Zhong et al., 2002] and/or by competing for DNA binding with NF- κ B p65/p50 heterodimers, which have high transcriptional activity [Saccani et al., 2003].

NF- κ B also regulates the AR promoter in Sertoli cells, which line the seminiferous tubules of the testis. AR levels in Sertoli cells vary during the spermatogenic cycle and dictate androgen regulation of gene transcription required for spermatogenesis [Isomaa et al., 1985; Vornberger et al., 1994]. In contrast to rat liver, NF- κ B (p65/p50) increases transcription from the rat AR gene promoter in Sertoli cells of prepubertal [Delfino et al., 2003] and adult

rats [Zhang et al., 2004]. Specific binding of the NF- κ B heterodimer to an NF- κ B consensus sequence was shown using nuclear extracts from adult rat Sertoli cells [Zhang et al., 2004]. NF- κ B signaling is also postulated to play a role in prostate cancer as the p65 subunit is overexpressed in human PIN and cancer compared to benign prostate tissue [Sweeney et al., 2004]. It is not known whether NF- κ B regulates human AR gene expression.

Post-Transcriptional Mechanisms of Androgen Regulation of AR mRNA

In addition to transcriptional mechanisms of AR mRNA autoregulation, an androgen effect on AR mRNA degradation is implicated in studies of the individual lobes of the rat prostate and in certain cancer cell lines [Prins and Woodham, 1995; Yeap et al., 1999]. Examination of AR mRNA by *in situ* hybridization and Northern blot analysis of rat prostatic lobes in response to castration revealed increases in AR mRNA in all lobes. While the effect of androgen withdrawal was transient in the dorsal and ventral lobes, the LP2 ducts of the lateral lobe exhibited prolonged elevation in AR mRNA. Nuclear run on assays revealed that increased transcription of the AR gene accounted for the maintenance of AR mRNA in the LP2 ducts. In contrast, castration had no effect on AR gene transcription in the other lobes suggesting that androgen withdrawal influences AR mRNA stability [Prins and Woodham, 1995]. In ventral prostate, testosterone may influence AR mRNA stability through effects on sequestration of AR mRNA on polyribosomes [Mora and Mahesh, 1999].

Yeap et al. [1999] made the intriguing observation that androgen promotes divergent effects on AR mRNA stability in LNCaP cells and in a breast cancer cell line, MDA453. Concurrent with androgen-mediated transcriptional downregulation of the AR gene, AR mRNA half-life is prolonged in LNCaP cells. In contrast, AR mRNA is destabilized in MDA453 cells following androgen treatment. Although the molecular basis for this differential effect on AR mRNA stability is not known, a highly conserved UC-rich sequence was identified in the AR 3'-UTR, which is bound by several widely expressed RNA-binding proteins including HuR (a member of the Elav/Hu family), CP1 and CP2 (heterogeneous nuclear RNP K-homology proteins) [Yeap et al., 2002].

Androgen Binding Stabilizes AR Protein

Discordance between androgen regulation of AR mRNA and protein levels in LNCaP cells [Krongrad et al., 1991], prostatic epithelium as well as certain other target tissues and cell lines prompted investigators to examine androgen effects on AR translation and degradation. While there is limited evidence for androgen regulation of AR protein synthesis [Syms et al., 1985; Mizokami and Chang, 1994], unliganded ARs undergo rapid turnover [Kemppainen et al., 1992]. Ligand binding profoundly increases AR stability thus providing an explanation for the divergent effects of androgen on AR mRNA versus protein levels in some cells and tissues. Ligand-mediated stabilization is relatively unique to AR as other steroid receptors undergo hormone-mediated downregulation. AR protein stabilization can be attributed, at least in part, to the ability of ligand to promote interaction between the AR amino and carboxyl termini [Langley et al., 1995; Zhou et al., 1995; He and Wilson, 2002].

Unliganded ARs appear to be rapidly degraded via the ubiquitin/proteasome system based on studies using the proteasome inhibitor MG132, which causes AR to accumulate in LNCaP and in an AR-expressing human hepatoma cell line, HepG2 [Sheflin et al., 2000]. MG132 had little effect on AR levels in the presence of androgen [Lin et al., 2002a]. In contrast, several steroid and nuclear receptors are subject to ligand-mediated degradation by the proteasome system [Nawaz et al., 1999; Lange et al., 2000; Wallace and Cidlowski, 2001]. For these receptors, including estrogen and progesterone receptors, ligand-mediated transcriptional activity is coupled to proteasomal degradation [reviewed in Nawaz and O'Malley, 2004]. While MG132 did not affect AR levels in the presence of hormone, MG132 reduced AR transcriptional activity, which correlated with decreased AR nuclear translocation and decreased AR-coactivator interactions. Thus, AR transcriptional activity may also be dependent on the proteasome [Kang et al., 2002; Lin et al., 2002a] but ligand-mediated AR degradation may not be linked to this process.

These studies show that androgens can promote up- and downregulation of AR mRNA and protein in a tissue-, cell- and/or developmental stage-specific manner. This autoregula-

tory process is achieved through a variety of mechanisms even within the same cell type. Since AR levels dictate hormonal sensitivity during development as well as in normal and neoplastic adult tissues, AR autoregulatory mechanisms will affect androgen responsiveness. What factors dictate upregulation versus downregulation of AR mRNA and protein and how do these processes influence AR transcriptional activity? These questions are significant from both a developmental perspective as well as the obvious implications for prostate cancer.

Regulation of AR Degradation by Non-Androgenic Steroids and Signaling Pathways

AR degradation is emerging as a common target for key signaling pathways in prostate epithelial cells although the mechanisms and role of specific AR phosphorylation sites in this process is unclear. As mentioned earlier, unoccupied AR is degraded via the proteasome system [Sheflin et al., 2000]; however, there is evidence for signal-mediated AR degradation as well. Chang and colleagues [Lin et al., 2002b] reported the phosphorylation of AR by Akt in the presence of hormone leading to AR ubiquitylation by the E3 ligase Mdm2 and subsequent proteasome-mediated degradation. This AR degradation correlated with decreased AR transcriptional activity. The opposite effects of PI3-kinase/Akt on AR levels were observed by Manin et al. [2002]. While Akt signaling influences AR degradation, the precise role of Akt in this process requires further study as Gioeli et al. [2002] provide strong evidence that Akt does not directly phosphorylate native or transfected AR *in vivo*.

The rat prostate gland is sensitive to estrogenic exposure during the neonatal period of prostate development resulting in abnormal patterns of growth, differentiation, and androgen-responsiveness in adult animals [Rajfer and Coffey, 1978; Prins and Birch, 1995]. This imprinting is mediated, in part, through permanent downregulation of AR in epithelial and stromal cells of the ventral lobe of the rat prostate [Prins, 1992; Prins et al., 1993; Prins and Birch, 1995]. This process of AR downregulation in prostates from estrogenized animals is due to increased AR degradation that is proteasome-dependent. Interestingly, prostatic AR degradation in estrogenized

animals is accompanied by decreased Akt activity [Woodham et al., 2003].

AR degradation in prostate cancer cells was recently found to be a downstream event following inhibition of EGFR/HER2 by the small molecule inhibitor, PKI-166 [Mellinghoff et al., 2004]. This exciting finding stemmed from studies addressing the growth stimulatory effects of the EGFR/HER2 receptor tyrosine kinases in prostate cancer xenografts and androgen-independent prostate cancer cells [Mellinghoff et al., 2002]. While targeting HER2 has had a significant impact on breast cancer, this strategy has proven to be more elusive in prostate cancer. Mellinghoff et al. [2004] showed that the dual EGFR and HER2 inhibitor, PKI-166, reduces AR transcriptional activity by promoting AR degradation and decreasing DNA binding by AR. These effects are mediated by inhibition of HER2 and not EGFR and do not involve the downstream kinase, Akt. PKI-166 causes AR degradation in AR-expressing breast cancer cell lines as well.

CONCLUSIONS AND PROSPECTS

The finding that androgen-independent prostate cancer is predominantly AR-dependent has heightened interest in decreasing AR content therapeutically. AR levels can be targeted through several regulatory pathways (Fig. 2). For example, ribozymes, antisense oligomers, and small interfering RNAs directed against AR are being tested in prostate cancer models [Eder et al., 2000; Zegarra-Moro et al., 2002; Wright et al., 2003; Ko et al., 2004]. AR degradation has been achieved using drugs such as geldanamycin that affect hsp90, the AR chaperone [Solit et al., 2002]. Interestingly, COX-2 inhibitors caused decreased levels of AR and several other key proteins in TRAMP mice [Narayanan et al., 2004], a well-characterized transgenic model for prostate cancer [reviewed in Huss et al., 2001]. However, the mechanisms responsible for these effects are unclear. Collectively, these studies illustrate that AR content can be depleted by various means in prostate cancer preclinical models resulting in decreased cell proliferation

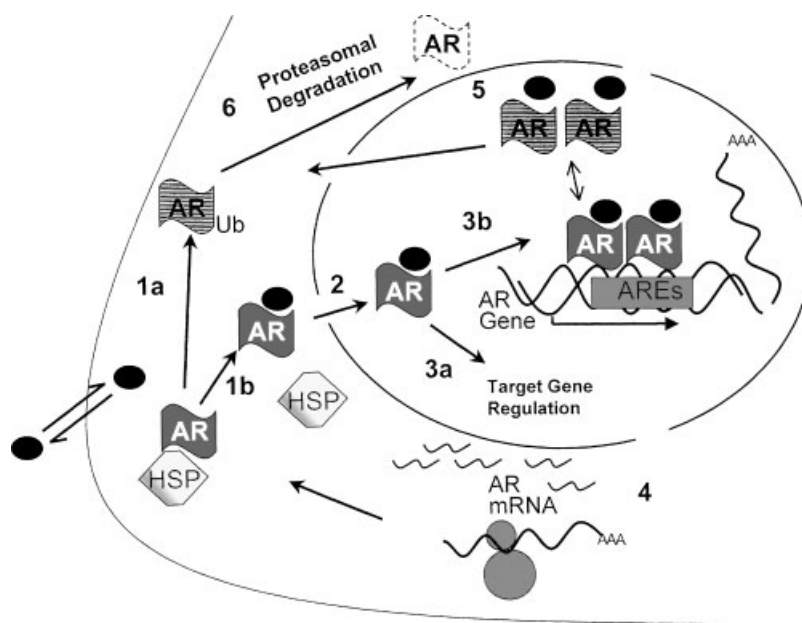


Fig. 2. AR regulation occurs at multiple steps. Prior to androgen binding, ARs exist in complexes (primarily cytoplasmic) containing hsp90 (HSP) and other chaperones (not shown). Unliganded receptors are susceptible to ubiquitylation (Ub) and proteasomal degradation (1a). Hormone that freely transverse the plasma membrane binds AR (1b) and causes a conformational change that releases hsp90 and reveals nuclear localization signals that mediate nuclear import through nuclear pore complexes (2). AR interaction with coactivators (not shown) may occur in sub-nuclear foci and during chromatin binding. AR homodimers bind AREs associated with target genes (3a) [including exonic AREs

within the coding region of the AR gene (3b)]. AR gene transcription is up- and downregulated by AR and by other factors. AR mRNA stability is influenced in a cell-specific manner by androgens via unknown mechanisms (4). ARs are exported from nuclei and this process may be coupled to receptor transcriptional activity (5). While ligand-occupied AR protein is more stable than the aporeceptor; signal-mediated proteasomal degradation of AR has been demonstrated in the presence of hormone although the mechanisms are not well-understood (6). Each of these steps represents a potential target for reducing AR levels or bioavailability.

and tumor growth. A concern with this strategy is the possible detrimental outcomes that may be associated with relieving the pro-differentiation functions of AR. Another potential therapeutic target is AR bioavailability. ARs, like other steroid receptors, shuttle between nuclear and cytoplasmic compartments [reviewed in DeFranco, 1999]. Recent work shows that AR resides transiently within subnuclear foci where interactions with coactivators occur prior to chromatin binding [Black et al., 2004]. Thus, AR nucleocytoplasmic trafficking presents further opportunities for modulating AR action.

There is substantial experimental as well as clinical evidence that AR mRNA and protein levels increase during prostate cancer progression to androgen-independence. However, like other tumor markers, AR expression is heterogeneous in tumor foci of advanced and metastatic cancer [Ruizeveld de Winter et al., 1994; Magi-Galluzzi et al., 1997; Shah et al., 2004]. In the majority of prostate cancer cases, increased AR is not due to AR gene amplification, although this occurs in a significant number of androgen-deprived patients. Since increases in AR mRNA and protein accompany progression to androgen-independence in all prostate xenograft models examined [Chen et al., 2004], androgen deprivation may initiate AR autoregulatory processes. An important consideration is that androgen regulation of AR may be secondary to effects on cell proliferation [Martinez and Danielsen, 2002]. Nevertheless, the pathways leading to AR upregulation in prostate cancer may provide new therapeutic targets. This strategy will require identification of the cell-, tissue- and/or stage-specific factors involved in the regulation of AR mRNA and protein levels in normal cells and elucidation of their dysregulation in neoplasia.

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