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The AR dependent cell cycle: Mechanisms and cancer relevance

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Abstract

Prostate cancer cells are exquisitely dependent on androgen receptor (AR) activity for proliferation and survival. As these functions are critical targets of therapeutic intervention for human disease, it is imperative to delineate the mechanisms by which AR engages the cell cycle engine. More than a decade of research has revealed that elegant intercommunication between AR and the cell cycle machinery governs receptor-dependent cellular proliferation, and that perturbations in this process occur frequently in human disease. Here, AR–cell cycle interplay and associated cancer relevance will be reviewed.

Keywords

Androgen receptor; Cell cycle; Prostate cancer

1. Androgen receptor function and prostate cancer progression

The androgen receptor (AR) is a ligand-dependent transcription factor that elicits context specific effects in the prostate. In the developing gland, active AR acts as a differentiation factor that is requisite for prostate function and maintenance. However, in prostate cancer (PCa), AR acquires a cell-autonomous function in actively promoting cancer cell growth and survival, mediated in part through exquisite dependence of this tumor type on AR function to induce cell cycle progression (Balk, 2002; Balk and Knudsen, 2008; Culig and Bartsch, 2006; Evans, 1988; Klotz, 2000; Knudsen and Penning, 2010; Knudsen and Scher, 2009; Shand and Gelmann, 2006). Prior to ligand (testosterone or dihydrotestosterone, DHT) binding, the receptor is present diffusely throughout the cytoplasm and is held inactive through association with heat shock proteins. Ligand binding induces rapid nuclear translocation and accumulation, chromatin association at multiple sites that govern gene expression (including those that contain canonical androgen response elements, AREs), recruitment of cofactors that influence downstream gene expression events, and initiation of a gene expression program that promotes tumor phenotypes (Gelmann, 2002;

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Gnanapragasam et al., 2000; Heinlein and Chang, 2002, 2004; Marivoet et al., 1992; Trapman and Brinkmann, 1996). In addition, the product of a prostate-specific AR target gene (KLK3/PSA, prostate specific antigen), is used clinically to monitor prostate cancer development and progression (Nash and Melezinek, 2000; Riegman et al., 1991; Ryan et al., 2006). As PSA is secreted into and detected in human serum, quantification of serum PSA provides a clinical means to assess prostate cancer tumor burden. Prostatic adenocarcinomas respond poorly to standard chemotherapy (including both cytostatic and cytotoxic agents); therefore, AR-directed therapeutics are utilized as the first line of intervention for non-organ confined disease (Chen et al., 2008; Knudsen and Penning, 2010; Knudsen and Scher, 2009). At the biochemical level, suppression of AR function is readily achieved through pharmacological methods that ablate testicular androgen synthesis (androgen deprivation therapy, ADT) and therefore deprive AR of circulating ligand. Such modalities are frequently accompanied by adjuvant use of direct AR antagonists (e.g. bicalutamide), which not only compete with androgens for AR binding, but also induce recruitment of corepressors to the bicalutamide-bound AR complexes on chromatin (Chodak, 2005; Klotz, 2006; Shang et al., 2002). Efficacy is monitored biochemically through marked reduction of serum PSA levels, and clinically through radiographic evidence of tumor regression. Although the vast majority of patients respond to ADT and AR-directed therapeutics, these responses are transient – within a median time of 2–3 years (Chen et al., 2008; Knudsen and Penning, 2010; Knudsen and Scher, 2009), recurrent tumors develop which are almost invariably preceded by a rise in detectable PSA (referred to as “biochemical failure”). This stage of disease, for which there is no durable cure, is known as castrate-resistant prostate cancer (CRPC), and arises as a result of restored AR activity that is refractory to ADT and AR-directed therapeutics (Chen et al., 2004, 2008; Knudsen and Penning, 2010; Knudsen and Scher, 2009).

An extensive body of literature has addressed the multiple mechanisms by which AR is reactivated to promote therapeutic bypass, and these pathways have been recently reviewed (Knudsen and Penning, 2010). At least five major, non-mutually exclusive categories have been identified through which cells adapt to ADT and AR-directed therapeutics. Most frequently, deregulation of AR is observed, as can be achieved through amplification of the AR gene locus, alternative mechanisms that induce high level AR gene expression, and/or mechanisms that induce AR protein stabilization. Significantly, it has been shown in multiple model systems that up-regulation of AR alone is sufficient to drive the transition to CRPC, and high nuclear AR levels are predictive for increased risk of death from prostate cancer (Chen et al., 2004; Donovan et al., 2010). Secondly, it has been recently shown that prostate cancers up-regulate enzymes that convert weak adrenal androgens to testosterone, and thus engage in intracrine androgen synthesis (Labrie et al., 1995, 2000; Locke et al., 2008; Montgomery et al., 2008; Penning et al., 2006; Stanbrough et al., 2006; Tran et al., 2009). These events therefore supply the receptor with sufficient ligand to outcompete AR antagonists, restore AR activity, and promote CRPC growth (Locke et al., 2008; Montgomery et al., 2008; Stanbrough et al., 2006; Tran et al., 2009). New pharmacological agents (e.g. abiraterone acetate) directed against this pathway show positive results in clinical trials (Attard et al., 2009, 2008; Pal and Sartor, 2011). Third, somatic mutation of AR, or development of splice variants, are known to facilitate CRPC. ADT is known to select for AR mutations that broaden the spectrum of ligands able to be utilized as agonists and/or convert antagonists into agonists (Brooke and Bevan, 2009; Knudsen and Penning, 2010; Steinkamp et al., 2009; Yuan and Balk, 2009). Not surprisingly, these mutations generally cluster to the ligand binding domain (Knudsen and Penning, 2010). Alternatively, production of constitutively active AR splice variants that lack the ligand binding domain occurs in CRPC; these variants are not amenable to inhibition by ADT or established AR antagonists (Dehm et al., 2008; Guo et al., 2009; Hu et al., 2009; Knudsen and Penning, 2010). Fourth, alterations in pathways that regulate AR post-translational modifications that

alter AR activity in a no or low ligand environment have been observed, and are thought to promote CRPC (Faus and Haendler, 2006; Knudsen and Penning, 2010; Yuan and Balk, 2009). Finally, alterations in the levels and/or action of cofactors that modulate AR function have been reported, and play diverse roles in CRPC (Heemers et al., 2009; Knudsen and Penning, 2010). Irrespective of the mechanism(s) utilized to bypass therapeutic intervention, AR activity resumes the capacity to drive cellular proliferation in CRPC. As such, it is imperative to delineate the mechanisms by which AR governs cell cycle transitions in both early stage and castrate-resistant disease. As will be discussed herein, investigation of the mechanisms by which AR controls the cell cycle led to discovery of elegant crosstalk between the AR signaling axis and the cell cycle machinery that, when altered, significantly influence tumor cell phenotypes and disease progression.

1.1. AR regulates cell cycle control

The means by which ligand-activated AR initiates the cell cycle has been generally defined. ADT-sensitive cells deprived of androgen exit the cell cycle and arrest in G0 (Agus et al., 1999; Huggins and Hodges, 1972; Knudsen et al., 1998). Transitions into and within the cell cycle are controlled by cyclin/cyclin-dependent kinase (cdk) complexes, which act sequentially to maintain ordered progression from G1 to mitosis (Lee and Sicinski, 2006; Malumbres and Barbacid, 2007; Sherr and Roberts, 2004). Typically, cdk activity is influenced by limited availability of the required cyclin subunit and/or the presence of cdk-inhibitors, and both processes assist in controlling androgen-dependent cell cycle progression (Fig. 1). In early G1, cdk4 or cdk6 activity is induced in most cell types, as achieved by growth factor-mediated D-type cyclin accumulation (Lee and Sicinski, 2006; Sherr and Roberts, 2004). Indeed, expression of major D-type cyclins (cyclins D1 and D3) is suppressed in ADT-responsive prostate cancer cells after steroid deprivation, and contributes to cell cycle arrest (Knudsen et al., 1998; Xu et al., 2006). There is little evidence that androgen deprivation alters p16^{ink4a} levels, a known cdk4/6 inhibitor. As such, it is thought that androgen regulation of D-cyclin accumulation serves as the major underpinning means by which AR regulates cdk4/6 activity and early G1 transitions. Accordingly, androgen stimulation induces mTOR-dependent translation of D-cyclins, resulting in protein accumulation sufficient to activate cdk4/6 (Xu et al., 2006). These events are independent of D-cyclin gene expression; distinct from what is observed in breast cancer cells, D-cyclin mRNA levels are unchanged by hormone deprivation in prostate cancer cells (Comstock et al., 2009, 2011). Thus, AR regulates early G1 progression primarily through controlling D-type cyclin protein levels.

Activated D-cyclin/cdk4 or 6 complexes initiate phosphorylation/inactivation of the retinoblastoma tumor suppressor (RB), which negatively regulates cell cycle transitions and the onset of DNA replication (Knudsen and Knudsen, 2008). RB function is envisaged as a “rheostat” to govern all stages of the cell cycle, wherein cdk4/6-mediated phosphorylation events compromise RB activity, and subsequent cdk5 increase RB phosphorylation status as a function of cell cycle progression (Knudsen and Knudsen, 2006). Active RB is recruited to chromatin at sites that regulate expression of genes important for cellular proliferation, including genes essential for DNA replication (*e.g.* MCM7) and S-phase entry (*e.g.* cyclin A2). Many RB-regulated genes are activated by the E2F family of transcription factors, and RB counterbalances E2F-mediated gene expression by assembling transcriptional repressor complexes that dampen transcriptional transactivation. Thus, a major function of G1 cdk complexes is to attenuate these functions of RB through direct phosphorylation and inactivation (Burkhart and Sage, 2008; Knudsen and Knudsen, 2008).

Toward this end, cdk2 activity promotes completion of G1 and transitions into S-phase, as mediated by sequential partnering with cyclins E1 and A2 (Knudsen and Knudsen, 2008). Similar to what is observed with cdk4/6, androgen ablation or stimulation has little influence

on cdk2 protein levels (Knudsen et al., 1998). However, at least two gatekeepers place cdk2 activity under AR control. First, while cyclin E1 protein levels are unchanged by the presence or absence of androgen, cyclin E1/ckd2 activity is strongly suppressed by ADT *in vitro* (Knudsen et al., 1998). This effect is likely attributed to androgen-mediated regulation of p27^{kip1}, a potent suppressor of cdk2 activity and bona fide tumor suppressor protein. p27^{kip1} levels are induced by androgen deprivation (Knudsen et al., 1998); conversely, androgen stimulation is known to promote rapid p27^{kip1} degradation (Lu et al., 2002). Although the mechanisms by which androgen promotes p27^{kip1} degradation and subsequent cdk2 activity is incompletely defined, it is thought that these events serve to promote G1 progression and commitment to the mitotic cell cycle. A related protein with no known tumor suppressor function, p21^{cip1}, exerts both pro-proliferative effects (as mediated through its capacity to assist in assembly of D-cyclin/ckd4 complexes) and anti-proliferative effects (through association with and suppression of cdk2 complexes) on the cell cycle (Alt et al., 2002; Balk and Knudsen, 2008; Cheng et al., 1999; LaBaer et al., 1997; Sherr and Roberts, 1999). Interestingly, p21 levels are directly up-regulated by androgen, indicating that p21^{cip1} may serve to facilitate G1 progression in this tumor type (Lu et al., 1999). Second, androgen deprivation reduces cyclin A2 levels, as a result of ADT-mediated suppression of cdk4/6 function and resultant engagement of RB transcriptional repressive capacity (Knudsen et al., 1998). Recently, it has been shown that the DNA replication factor Cdc6 is under direct control of AR activity, indicating that both G1 and S-phase components of the cell cycle machinery may be under AR regulation (Jin and Fondell, 2009; Mallik et al., 2008). Based on these collective findings, it is evident that a major function of AR is to control the G1-S transition. Additionally, AR could potentially serve to assist in DNA replication licensing, as in some systems, AR is degraded in mitosis (Litvinov et al., 2006). Whether the putative link between AR and the mechanics of DNA synthesis control impinge upon cell cycle transitions mediated by endogenous AR or in an *in vivo* setting will be of interest to discern.

While androgen utilizes divergent mechanisms to induce cdk4/6 and cdk2 activation, suppress RB activity, and thereby permit commitment to the mitotic cell cycle in ADT-sensitive cells, distinct mechanisms may be invoked in CRPC which further enhance AR-dependent cell cycle progression. Through genome-wide analyses of AR binding in CRPC cells, novel AR occupancy sites were observed near the regulatory loci of genes associated with mitotic progression (Wang et al., 2009). Consistent with the postulate that the AR program is altered in CRPC so as to strengthen the capacity of AR to drive cellular proliferation, AR was shown to up-regulate expression of UBE2C, whose gene product has been associated with regulation of cyclin levels. Upregulation of UBE2C was not sufficient to induce castrate-resistant cell growth in ADT-responsive cells, but silencing of UBE2C slowed cell proliferation rates in CRPC cells (Wang et al., 2009). These findings suggest that CRPC cells develop additional means to foster AR-dependent cell cycle control, and further delineation of these mechanisms may be of benefit for the design of novel therapeutic agents.

2. Cell cycle feedback regulation of AR activity

Investigation of the mechanisms by which AR governs cell cycle control led to the unexpected discovery of feedback pathways that influence AR activity (Fig. 2). Delineation of the interplay between AR and cell cycle machinery has both illuminated the cellular consequence of pathway crosstalk and underscored the importance of cdk and cyclin functions in transcriptional control.

2.1. cdks

A subset of cdks proximal to cell cycle regulation have been shown to enhance AR activity, thus indicating that initiation of the androgen dependent cell cycle engine may induce signals that further support AR-dependent cellular proliferation. In early G1, cdk6 has been shown to associate with AR in prostate cancer cells and to enhance ligand-dependent AR activity as monitored by reporter assays (Lim et al., 2005). These effects of cdk6 do not require cyclin D1 or intrinsic kinase activity, and are not shared by cdk4. Subsequently, cytoplasmic localization of the p44 AR cofactor was shown to up-regulate cdk6 levels, and it would be of interest to determine if the co-activator functions of p44 require cdk6 action (Peng et al., 2008). In latter phases of the cell cycle, expression of the G2/M kinase cdk1 has been shown to promote phosphorylation of AR at multiple sites including Ser-81, which has been implicated in bolstering AR stability and function (Chen et al., 2006). It will be intriguing to determine whether the effects of cdk1 on AR phosphorylation are direct, and whether cdk1 function alters cell cycle stage-specific AR signaling and/or resultant cell cycle progression. In addition, it may be of benefit to determine what phosphatases may counterbalance cdk1-mediated AR activity, whether cdk1-dependent phosphorylation events are up-regulated in human disease, and to assess whether or not this pathway could be developed as a means to suppress AR activity in human tumors. Finally, cdk5 was predicted (based on cdk1 homology) to harbor potential catalytic activity utilizing AR as a substrate, yet was shown in ectopic expression studies to function in a manner distinct from that of cdk1 (Chen et al., 2006). Independent mass spectrometry studies subsequently confirmed association of AR with both cdk1 and cdk5 (Gordon et al., 2010). Thus, it is apparent that cdks differentially regulate AR, and may compete for phosphorylation sites and result in divergent biological outcomes.

2.1.1. Transcriptional cdks—Distinct from the cdks proximal to cell cycle control, several cdks associated with transcriptional regulation (cdk9, cdk7, and cdk11) have been shown to modulate AR activity. Serine 81 of AR is phosphorylated by ectopic expression of cdk9 in AR-negative cells re-engineered to express the receptor (Gordon et al., 2010). In this model system, mutation of Ser81 to alanine resulted in decreased cell proliferation, consistent with the observation that Ser81 phosphorylation is important for AR activity. In cells with endogenous AR, ectopic expression of the S81A mutant similarly inhibited cell growth, even in the presence of AR agonists; conversely, the pan-cdk inhibitor flavopiridol suppressed cell proliferation in AR-positive cells, and cdk9 silencing decreased AR phosphorylation (Gordon et al., 2010). Less is known mechanistically about how cdk7 impinges on AR phosphorylation, but this transcriptional cdk has also been shown to heighten AR function. cdk7 is part of the CAK (cdk activating kinase) complex, which modulates both cdk function and general transcriptional activity. Over-expression of cdk7 in AR-negative cell lines enhanced AR activity in transient assays, thus implicating the alterations in the general transcription machinery as a putative means to alter AR activity (Lee et al., 2000). Finally, cdk11, which is involved in diverse biological functions including RNA processing and apoptosis, exists in two isoforms that can bind cyclin D3 (p58 and p110). Intriguingly, each isoform regulates AR but yields opposing effects on receptor function; cyclin D3/cdk11^{P58} phosphorylates the AR N-terminus at Ser-308, suppresses AR activity, and dampens prostate cell proliferation, whereas cdk11^{P110} activates AR function and lacks the ability to phosphorylate AR (Zong et al., 2007). To further advance these findings, delineation of the mechanisms that control the “switch” between the cdk11 isoforms would be relevance, as would assessment of cdk11 function during disease progression.

2.2. Effectors of cdk activity

Consistent with the concept that cdks can modulate AR activity, there is evidence that positive regulators of cdks can further enhance AR function. Cdc25b, a phosphatase that primarily acts in G2/M to dephosphorylate and activate cdk1, was shown in mammalian 2-hybrid assays to interact with AR, and in transient transcriptional assays to induce AR activity (Chua et al., 2004; Ma et al., 2001). As Cdc25b is a proto-oncogene and is upregulated in a number of tumor types, it would be of interest, to determine whether Cdc25 protein alterations affect AR phosphorylation status, alter function of AR at endogenous sites of action, and/or contribute to AR-mediated cell cycle control. Whether other Cdc25s with proto-oncogenic activity serve to facilitate AR function or the transition to CRPC remains unaddressed. Delineation of overall Cdc25 action should be discerned more rigorously, as opposing functions were observed with Cdc25a (Chiu et al., 2009); this Cdc25 family phosphatase was found to bind to AR *in vitro* and inhibit endogenous AR activity.

2.3. G1 cyclins

A rich body of evidence supports the concept that AR is modulated by G1 cyclins, resulting in both positive and negative effects on AR function (Burd et al., 2005, 2006; Knudsen, 2006; Knudsen et al., 1999; Kobayashi et al., 2009; Olshavsky et al., 2008; Petre et al., 2002; Petre-Draviam et al., 2003, 2005; Reutens et al., 2001; Schiewer et al., 2009; Yamamoto et al., 2000; Zong et al., 2007). The most widely studied cyclins that modulate AR belong to the D-cyclin family, and are negative regulators of ligand-dependent AR activity (Burd et al., 2005, 2006; Knudsen et al., 1999; Kobayashi et al., 2009; Olshavsky et al., 2008; Petre et al., 2002; Petre-Draviam et al., 2003, 2005; Reutens et al., 2001; Schiewer et al., 2009; Zong et al., 2007). *In vivo* analyses of cyclin D1 function confirmed that cyclin D1 not only associates with cdks, but is associated with a large number of transcriptional modulators (Bienvenu et al., 2010). Strikingly, the ability of cyclin D1 to alter transcription factor activity appears to underpin major cyclin D1 functions. For example, loss of cyclin D1-mediated Notch1 activity results in the long-observed retinal hypoplasia of the cyclin D1 knockout mouse. Moreover, ChIP-promoter chip analyses determined that cyclin D1 is found on chromatin at a large number of regulatory loci (Bienvenu et al., 2010). Thus, it is apparent that cyclin D1 harbors significant functions independent from cdk control that serve to modulate transcription factor activity. With regard to AR, cyclin D1 interacts directly with the receptor N-terminal domain, requiring the FxxLF motif (Burd et al., 2005). This motif mediates ligand-dependent N-to-C terminal interactions that facilitate chromatin binding and resultant AR activity (He et al., 1999; Wong et al., 1993); cyclin D1 association suppresses both events (Burd et al., 2005). In addition, cyclin D1 has been shown to associate with a number of histone deacetylases (HDACs) (Fu et al., 2005; Li et al., 2002; Lin et al., 2002; Petre et al., 2002), thus providing a means of transcriptional repression (Bienvenu et al., 2010). Accordingly, the ability of cyclin D1 to dampen ligand-dependent AR function is partially reversed by HDAC inhibitors (Petre et al., 2002). These combined functions of cyclin D1 put forth a model of elegant cell cycle control, wherein androgen up-regulates cyclin D1 through mTOR-dependent mechanisms, thus allowing for cdk4 activation and initiation of the cell cycle engine (Knudsen et al., 1998; Xu et al., 2006). However, as cyclin D1 levels rise, cdk4-independent binding to AR provides a negative feedback switch to govern subsequent AR-dependent signaling and cell cycle transitions. The ability of cyclin D1 to bind HDACs and negatively regulate AR is dependent on a defined motif, deemed the repressor domain (RD) (Petre-Draviam et al., 2005). Introduction of the RD domain allows for separation of the cyclin D1 cdk4-modulatory and AR-modulatory functions, and leads to not only suppression of AR-dependent cell growth but also triggers loss of cell viability, thus illustrating the importance of cyclin D1 on cellular outcomes (Schiewer et al., 2009). As will be discussed below, the ability of cyclin D1 to dampen AR activity appears to be altered in prostate cancer, as mediated by down-

regulation of cyclin D1 expression, mislocalization, and/or a shift to production of the cyclin D1b variant, which is compromised for AR-regulatory functions (Burd et al., 2006; Comstock et al., 2009, 2007; Knudsen, 2006; Olshavsky et al., 2010). As would be expected based on conservation of the RD domain, cyclin D3 elicits similar functions with regard to AR control (Olshavsky et al., 2008); in addition, cdk11-mediated functions of cyclin D3 also contribute to negative regulation of AR (Zong et al., 2007). Although limited in study, preliminary findings indicate that cyclin D2, which is silenced in a subset prostate cancers, also negatively regulates AR activity (Henrique et al., 2006; Kobayashi et al., 2009; Padar et al., 2003). Collectively, these observations strongly suggest that a function of D-cyclins is to control AR output, and that these functions are dysregulated. Given these observations, it will be of relevance to further delineate the overall impact of D-cyclin mediated AR regulation, in the context of both the untransformed and tumorigenic cells.

Distinct from the functions of D-cyclins, up-regulation of cyclin E can enrich AR activity both in transient assays as well as at endogenous sites of action. Cyclin E also binds the AR N-terminus, and therefore could conceivably compete with D-cyclins for controlling AR (Yamamoto et al., 2000). Accordingly, in the TRAMP (T-antigen driven) model of prostate cancer, development of prostatic intraepithelial hyperplasia (PIN) is associated with down-regulation of D-cyclins and up-regulation of cyclins E1 and A2 (Maddison et al., 2004). A tempting hypothesis is that a shift in cell cycle control toward dependence on the later G1 cdk-cyclin complexes facilitates both rapid cell cycling and aberrant AR activity.

2.4. RB: gatekeeper of G1/S control

Recent evidence demonstrates that RB is a major effector of AR levels, AR function, and the ability of prostate cancer cells to transition to the CRPC stage. Initial studies with RB suggested that transiently over-expressed RB and AR (in cells with no endogenous AR), can allow for formation of a complex between the transcriptional regulators and enhanced AR activity in reporter gene assays (Lu and Danielsen, 1998; Yeh et al., 1998). These initial findings prompted further analyses of RB function in an endogenous setting, which yielded surprising outcomes. Remarkably, it was found that RB is lost in the transition to CRPC with high frequency, whereas there was low evidence of RB loss in primary disease (Sharma et al., 2010). Mimicry of this event in prostate cancer cells demonstrated that silencing of RB resulted in marked up-regulation of AR mRNA and AR protein sufficient to drive castration resistance both *in vitro* and *in vivo* (Sharma et al., 2010). Mechanistically, it was found that the AR locus is under RB/E2F1 control; loss of RB results in E2F1 deregulation and resultant upregulation of AR and AR activity. The importance of this event was evident in exploration of CRPC specimens, wherein loss of RB was significantly associated with high AR levels (Sharma et al., 2010). Thus, in AR-positive PCa cells, RB serves not only to suppress cell cycle progression in the absence of androgen, but actively attenuates AR expression (Sharma et al., 2010). These findings identify RB as utilizing pleiotropic mechanisms to suppress tumor progression in prostate cancer. Further interplay between the RB/E2F1 axis and AR may alter the activity of EZH2, a polycomb group associated transcription factor that is deregulated in human disease. Specifically, androgens repress EZH2 expression in concert with RB family members (including p130), thereby altering phenotypes associated with cell migration (Bohrer et al., 2010). These combined observations illustrate the importance of delineating the underlying mechanisms and consequence of crosstalk between the RB/E2F axis and AR.

Collectively, these studies provide strong evidence that interplay between the cell cycle machinery and the AR signaling axis leads to profound cellular outcomes using *in vitro* and *in vivo* models of human disease. The contributions of these interactions to disease development and progression in human prostate cancer have only begun to be explored. Early advances toward this end will be discussed below, and lay the foundation for future

studies directed at harnessing this information for the purpose of identifying new nodes of therapeutic intervention.

3. Clinical relevance of cell cycle-AR crosstalk

Assessment of AR–cell cycle crosstalk in the context of clinical samples has been limited. The current state of the field is summarized in Tables 1, 2 and 3 and Supplementary Table 1, and reveals open questions germane to human disease. Those studies that examined any part of AR biology are highlighted in light gray with dark borders, demonstrating how few studies have actually examined AR in the context of cell cycle effector perturbation. For example, cell cycle-associated and transcriptional-regulatory cdks have been scantily examined in clinical specimens; given the depth of *in vitro* and *in vivo* studies that illustrate putative pathway and disease relevance of these players, these effectors should be prioritized for further investigation. A preliminary resource to potentially assist in this endeavor is the Human Protein Atlas, which provides useful but limited insight into the relative expression profiles (including frequency and distribution) in human disease (Uhlen et al., 2010). Similarly, the clinical relevance of the Cdc25 proteins should be determined, given the putative divergent roles of individual isoforms on AR regulation and cell cycle progression and dearth of information regarding the impact of Cdc25s on disease phenotypes (Ozen and Ittmann, 2005; Ngan et al., 2003). With regard to the cyclins, it remains unclear whether the E-, A-, and B-family cyclins merely serve as indicators of increased cellular proliferation, or hold predictive value beyond that of proliferative indices. Evidence to date with the D-type cyclins demonstrate roles for these proteins that are distinct from mere cell cycle control, as may be mediated through functions in transcriptional regulation. Discerning the proximal targets of cyclin D action and the resultant impact on human disease behavior is of the utmost importance.

By contrast, much emphasis has been placed on understanding the impact of cdk inhibitors in the context of both ADT-sensitive and castrate resistant disease. With few exceptions, clear and diverse clinical correlates are associated with alterations of p27^{kip1} (Ben-Izhak et al., 2003; Chang et al., 2004; Cheng et al., 2000; Cheville et al., 1998; Claudio et al., 2002; Cordon-Cardo et al., 1998; Cote et al., 1998; De Marzo et al., 1998; Doganavsargil et al., 2006; Dreher et al., 2004; Drobnjak et al., 2003; Erdamar et al., 1999; Fernandez et al., 1999; Freedland et al., 2003; Guo et al., 1997; Halvorsen et al., 2003; Huang et al., 2008; Kibel et al., 2001, 2000, 2003; Kuczyk et al., 1999, 2001; Li et al., 2006; Nguyen et al., 2009; Nikoleishvili et al., 2008; Ribal et al., 2003; Romics et al., 2008; Thomas et al., 2000; Tsihlias et al., 1998; Vis et al., 2000, 2002; Wolters et al., 2010; Wu et al., 2007; Yang et al., 2002, 1998; Zeng et al., 2004) versus p21^{cip1} (Aaltomaa et al., 1999; Baretton et al., 1999; Cheng et al., 2000; Facher et al., 1997; Lacombe et al., 2001; Matsushima et al., 1998; Omar et al., 2001; Sarkar et al., 1999). As detailed in Supplementary Table 1, low or no p27^{kip1} is generally associated with poor outcomes, including shorter time to biochemical recurrence and reduced survival. These observations are consistent with the well-known and validated role of p27^{kip1} as a tumor suppressor. Conversely, cytoplasmic p27^{kip1}, which has oncogenic functions associated with metastasis, is associated with poor outcome in human disease (Claudio et al., 2002; Dreher et al., 2004; Li et al., 2006). Based on these findings, it will be critical to determine the overall impact not only of p27^{kip1} levels on clinical outcomes, but the utility of assessing p27^{kip1} sub-cellular distribution in prognostic or predictive studies.

Despite conservation of cdk2 inhibitory functions, the related protein p21^{cip1} shows remarkably distinct expression profiles and association with clinical correlates as compare to p27^{kip1}. These observations may not be surprising, as p21^{cip1} holds no validated tumor suppressive activity in any tissue type. In the context of prostate cancer, p21^{cip1} is generally

associated with proliferation, higher grade, and poor outcomes (Aaltomaa et al., 1999; Baretton et al., 1999; Lacombe et al., 2001; Matsushima et al., 1998; Omar et al., 2001; Sarkar et al., 1999), consistent with the *in vitro* observation that p21^{cip1} levels are increased upon AR activation. Thus, prostate cancer provides an intriguing platform with which to study divergent roles of cdk2 inhibitors on cellular and tumor outcomes, and the mechanisms underlying differential effects on cellular proliferation should be discerned. Finally, the role of p16^{ink4a} remains an enigma. While p16^{ink4a} shows clear tumor suppressor function in a number of tissue types, p16^{ink4a} levels in prostate cancer show a wide range of expression (Cairns et al., 1995; Chakravarti et al., 2007, 2003; Chen et al., 1996; Chi et al., 1997; Cho et al., 2007; Faith et al., 2005; Gu et al., 1998; Halvorsen et al., 2000; Heidenreich et al., 2000; Henshall et al., 2001; Iemely-nova et al., 2009; Jarrard et al., 1997, 2002; Jeronimo et al., 2004; Komiya et al., 1995; Konishi et al., 2002; Lee et al., 1999; Maruyama et al., 2002; Nguyen et al., 2000; Perinchery et al., 1999; Roach et al., 2009; Tamimi et al., 1996; Zhang et al., 2006). Moreover, no clear patterns of associated clinical correlates have emerged from studies to date. This lack of clarity may be attributed to the confounding effects of the RB pathway on p16^{ink4a} expression, as loss of RB function typically results in marked up-regulation of p16^{ink4a}. Up-regulation of p16^{ink4a} in the absence of functional RB does not impinge on cell cycle progression (since p16^{ink4a} requires RB to elicit cell cycle arrest); therefore, the cellular or tumor relevance of this event remains uncertain and needs to be explored (Knudsen and Knudsen, 2008).

Finally, the role of the RB family members in prostate cancer progression has been recently addressed. While there is little evidence that p107 and p130 are altered in prostate cancer, recent findings implicate alternation of the RB/E2F1 axis as playing major roles in human disease. As described above, tracking RB expression and RB loss of function (as achieved through a well established RB loss gene signature) in human specimens revealed that inactivation of the RB axis is highly overrepresented in castration resistant disease, and is strongly associated with AR deregulation (Sharma et al., 2010). Since perturbation of RB function can lead to AR-dependent castration resistance (Sharma et al., 2007, 2010), it will be imperative to discern the mechanisms underlying this event, and to determine alternative mechanism(s) for treating RB-deficient tumors. Further underscoring this postulate, recent findings in genetically engineered mice suggested that RB can control progression to invasive carcinoma (Sun et al., 2011). Collectively, these findings identify disruption of RB tumor suppressor and AR regulatory functions as significantly contributing to disease progression.

4. Conclusion and future directions

Inability to durably control AR activity plays a major role in the transition to lethal prostate cancer. While it has been long understood that AR activation drives prostate cancer cell proliferation, the realization that significant cross-communication between AR and the cell cycle machinery modifies this process has been only recently brought to light. Gains in our understanding of AR–cell cycle interplay not only bring new appreciation of the mechanisms that support AR function in human disease, but raise important questions that should be prioritized for future study. *First, are the mechanisms by which AR promotes cell cycle control altered in castrate-resistant disease?* Most studies to date have examined the impact of AR on cell cycle control in hormone-therapy sensitive systems, wherein AR requires ligand for activation. As a subset of CRPC demonstrates AR activity in the absence of ligand or in the presence of alternative ligands, it will be imperative to assess the impact of these events on AR crosstalk with the cell cycle machinery. *Second, given the number of cell cycle alterations observed in human tumors, it will be essential to determine whether these events alter AR function or AR regulation in the clinical setting.* Precedent has been established in tumors exhibiting loss of RB or expression, for which tumor suppressor loss

results in AR deregulation. *Third, data in model systems suggest that cell cycle regulation of AR may result in cell cycle phase-specific AR activity.* It is tempting to speculate that AR function (with regard to both chromatin binding and downstream signaling) is altered as a function of cell cycle position, and preliminary studies support this concept (Knudsen et al., in preparation). *Fourth, numerous mouse models of cell cycle alterations have been generated which perturb factors important for AR–cell cycle crosstalk, yet few studies have addressed the impact of these events on prostate-specific AR function.* It will be of interest to determine the *in vivo* impact of these events on AR activity and AR-dependent tumor development using these defined genetic systems. *Finally, and perhaps most importantly, current understanding of AR–cell cycle interplay affords the possibility for therapeutic intervention, so as to determine whether cell cycle alterations that promote AR activity can serve as targets to prevent tumor development or progression.* Such studies are increasingly tractable, as new agents for therapeutic modulation are in advanced stages of development or in clinical trial. Overall, it is apparent that cross-communication between AR and the cell cycle machinery plays a significant role in controlling hormone-dependent cellular proliferation; next steps will be to obtain greater mechanistic understanding of these events, discern specificity, and leverage this combined information for therapeutic gain.

Supplementary Material

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at doi:
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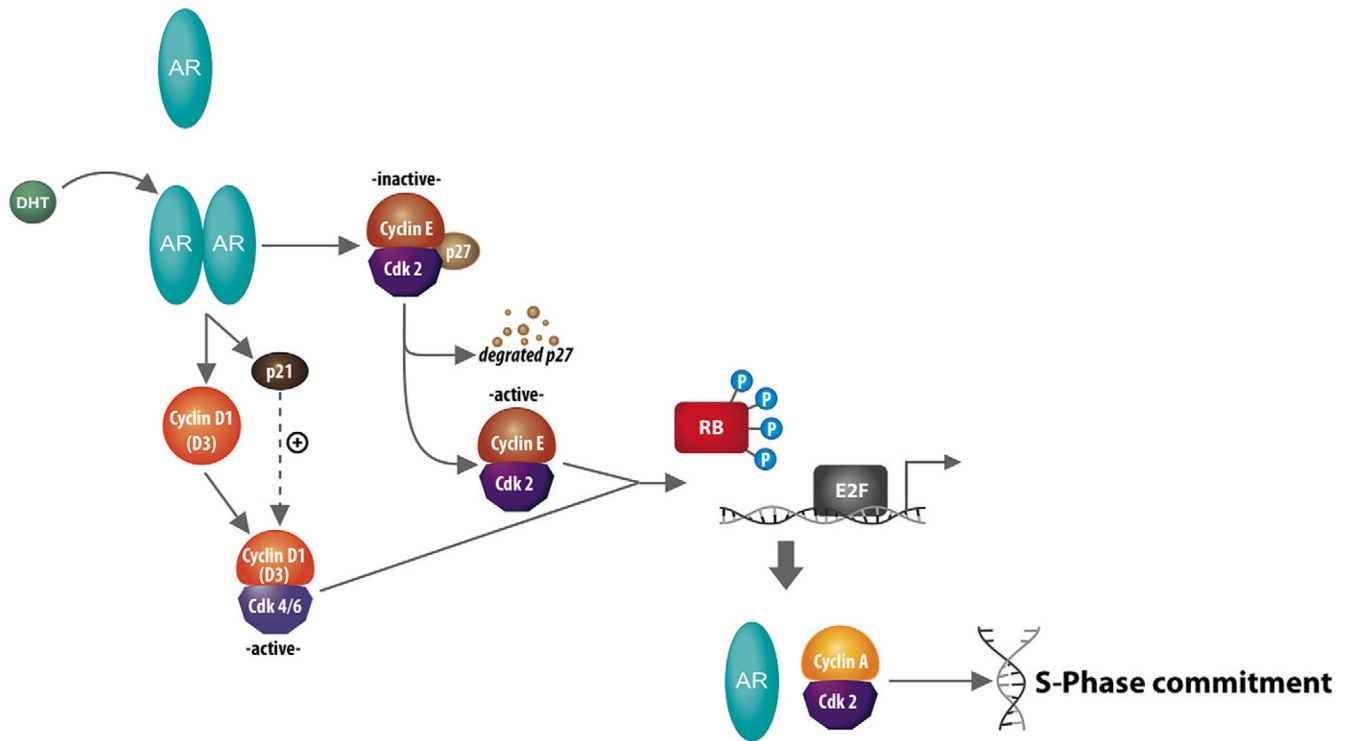


Fig. 1. Regulation of cell cycle by the androgen receptor. Liganded AR induces the translation and accumulation of D-type cyclins by engaging the mammalian Target of Rapamycin (mTOR) complex, which mediates cdk4/6 activation and subsequent phosphorylation and inactivation of the retinoblastoma tumor suppressor (RB). Concomitantly, AR further impinges on G1-S progression by inducing expression of p21^{cip1} and degradation of p27^{kip1}, promoting enhanced cdk4/6 and cdk2 dependent inactivation of RB and progression through G1. Pathways requisite for entry into S phase are initiated upon RB inactivation, which induce the activity of the E2F family of transcription factors responsible for the production cyclin A, activation of cdk2 (via cyclin A binding), and entry into S-phase. Additionally, E2F1 directly induces the expression of AR itself, potentially enhancing progression through the cell cycle.

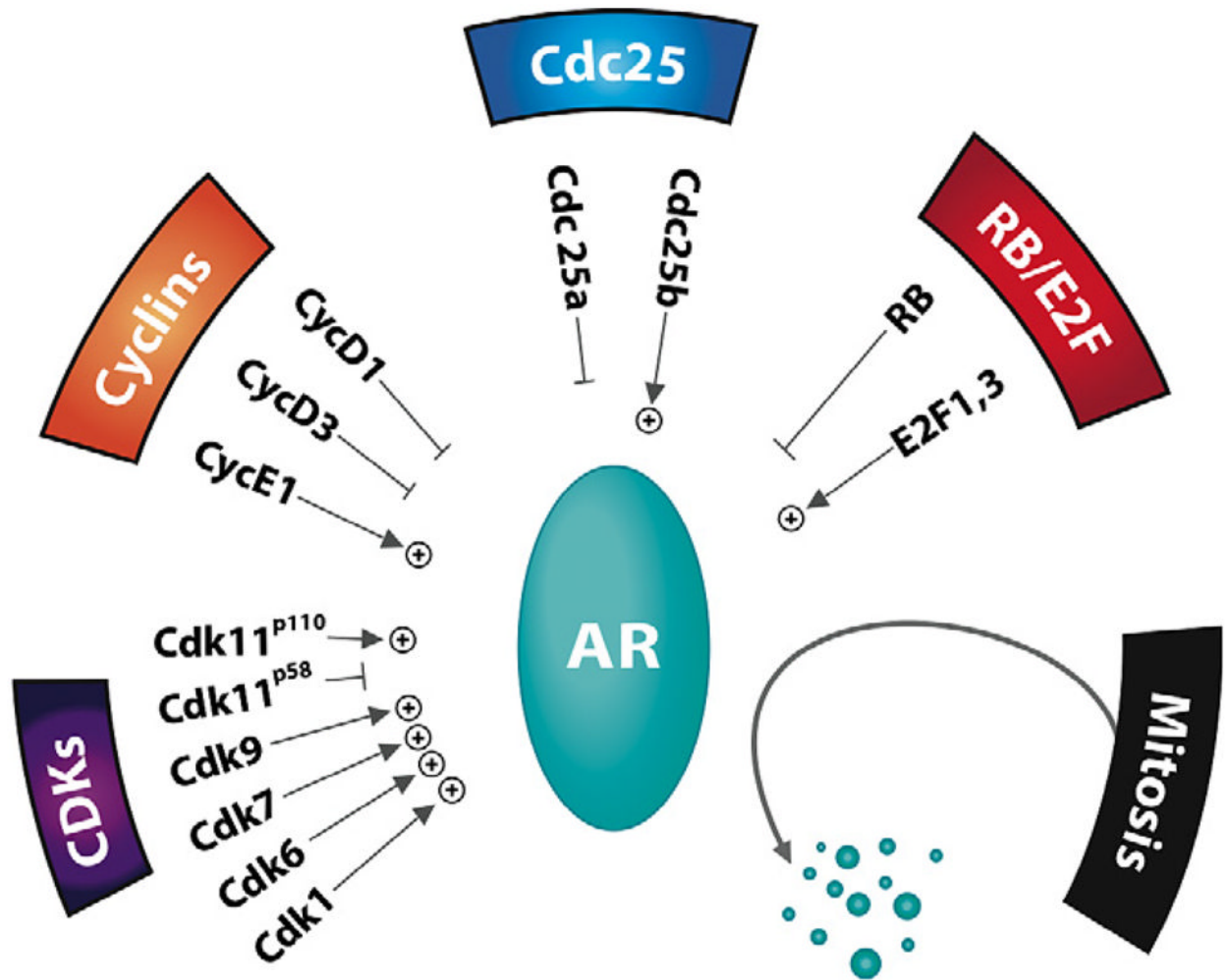


Fig. 2. Contribution of cell cycle machinery to androgen receptor activity. The androgen receptor (AR) is regulated by many factors whose functions are also responsible for modulating cell cycle control. Cyclin-dependent kinases (CDKs), cyclins, members of the Cdc25 family of phosphatases, and the RB/E2F axis all contribute to this regulation. AR is degraded as cell progress through mitosis. Arrows terminating in “+” indicate activities resulting in upregulation of AR activity, while negative regulation is indicated by “-”.

Table 1

CDKs.

Cell cycle factor	Study size (n)	Change observed	Impact on AR activity or PSA levels	Clinical correlates	Citation
CDK4	n = 104	No change from BPH to PCa	No correlation	No correlation	Halvorsen et al. (2000)
CDK1	n = 140	60% positive for high cdk1		Associated with increased grade, stage, DNA ploidy, and disease recurrence	Kallakury et al. (1997)

Table 2

Cyclins.

Cell cycle factor	Study Size (n)	Change observed	Impact on AR activity or PSA levels	Clinical correlates	Citation
Cyclin D1	n = 140	78% showed no or low cyclin D1		No correlation with grade, stage, or DNA ploidy	Kallakury et al. (1997)
	n = 66	70% no or low cyclin D1 staining		No correlation with Gleason	Shiraishi et al. (1998)
	n = 86 PCa n = 22 Met	11% with >20% cyclin D1 positive in primary and 68% in bone metastases		<ul style="list-style-type: none"> High cyclin D1 in bone metastases, associated with high Ki67 No association with Gleason score or time to PSA Failure 	Drobnjak et al. (2000)
	n = 156	<ul style="list-style-type: none"> No or low cyclin D1 was associated with reduced survival Overexpression rate and observed only in advanced disease states 			Dunsmuir et al. (2000)
	Not specified	mRNA trends lower in primary and CRPC as a function of progression		No correlation with Ki67	Linja et al. (2004)
	n = 68	<ul style="list-style-type: none"> Reduced expression Cytoplasmic localization 	Low cyclin D1 associated with high pre-operative PSA		Comstock et al. (2007)
	n = 1600 PCa, PIN, normal	<ul style="list-style-type: none"> Reduced expression (1°PCa) Splice to produce cyclin D1b 		No correlation with Ki67	Comstock et al. (2009)
	n = 79			High expression (along with low PTEN and SMAD4, and high SPP1) separated patients into low and high risk for biochemical recurrence	Ding et al. (2011)
	n = 600			This four gene signature improves the prognostic value of Gleason score	
Cyclin D2	n = 101 PCa	32% show CCND2 methylation		Increased methylation correlated with higher Gleason score	Padar et al. (2003)
	n = 74 PCa	Methylation observed		If co-observed with APC methylation, correlates with decreased time to progression	Rosenbaum et al. (2005)
	n = 118 PCa n = 38 PIN n = 11 Normal	Cyclin D2 encoding gene (CCND2) is methylated in all tissues, but is hypermethylated in cancer		Higher methylation associated with increased grade and non-organ confined disease	Henrique et al. (2006)

Cell cycle factor	Study Size (n)	Change observed	Impact on AR activity or PSA levels	Clinical correlates	Citation
	<i>n</i> = 4 cell lines				
Cyclin D3	<i>n</i> = 32 BPH <i>n</i> = 20 PCa <i>n</i> = 10 hormone treated <i>n</i> = 67 PCa	Increased expression in PCa vs. BPH		Cyclin D3 correlates with Ki67	Nikolaishvili et al. (2008)
		Expression decreased as a function of disease progression		High cyclin D3 inversely correlates with Ki67	Olshavsky et al. (2008)
Cyclin E1	<i>n</i> = 28 PCa	Low expression (14% pos, 86% negative)		None	Mashal et al. (1996)
Cyclin A2	<i>n</i> = 28 <i>n</i> = 132	100% positive 35% positive		Correlated with Ki67 expression (0.71)	Mashal et al. (1996)
				Cell-cycle-associated markers and clinical outcome in human epithelial cancers: a tissue microarray study.	Kallakury et al. (1999)
Cyclin B1	<i>n</i> = 28 <i>n</i> = 132	71% positive 46% positive		Correlated with Ki67	Mashal et al. (1996)
				Correlated with ploidy and grade $p < 0.05$ and PCNA $p < 0.0001$	Kallakury et al. (1999)

Table 3

The RB/E2F axis.

Cell cycle effector	Study size (n)	Change observed	Impact on AR activity or PSA levels	Clinical correlates	Citation
RB	n = 41 PCa	27% show loss of a single Rb1 allele			Brooks et al. (1995)
	n = 40 PCa	<ul style="list-style-type: none"> 48% showed allelic loss of Rb1 22% showed no RB detection LOH did not correlate with low RB expression 			Cooney et al. (1996)
	n = 26 localized stage B PCa	<ul style="list-style-type: none"> 35% showed LOH of the Rb1 locus 33% of specimens with LOH showed low or no RB protein 			Ittmann and Wicczonek (1996)
	n = 36 PCa	<ul style="list-style-type: none"> Analyzed for 13q deletions Found in 50% tumors Deletion did not correlate with absent RB protein 		<ul style="list-style-type: none"> 13q deletion did not correlate with grade, stage, or DNA ploidy Tetraploidy found in 56% tumors with altered RB expression 	Li et al. (1998)
	n = 81	Low expression observed in 36% of tumors from patients treated with combined androgen blockade, as compared to 13% in tumors from untreated patients		Low RB correlated with higher Gleason grade	Mack et al. (1998)
	n = 63 tumors after ADT n = 22 matched pre-ADT controls	FISH analyses showed that loss of the Rb1 locus was four times more frequent after ADT failure			Kaltz-Wittmer et al. (2000)
	n = 72 PCa	19% showed low RB expression		<ul style="list-style-type: none"> RB status did not correlate with p16 Loss of either p16 or RB found more commonly in metastatic disease (55%) 	Jarrard et al. (2002)
	n = 156 CRPC specimens n = 22 human xenografts (LuCaP) gene expression assays	RB loss is highly overrepresented in CRPC		<ul style="list-style-type: none"> RB loss associated with hormone therapy failure RB loss associated with poor outcome 	Sharma et al. (2010)
	n = 218 prostate cancers	Downregulation of RB gene expression observed in 5% of primary but 37% of metastatic samples			Taylor et al. (2010)

Cell cycle effector	Study size (n)	Change observed	Impact on AR activity or PSA levels	Clinical correlates	Citation
p130	n = 24 matched normal PCa	Low expression in cancer			Claudio et al. (2002)
p107	n = 24 matched normal and PCa			Low p107 showed an inverse correlation with Ki67	Claudio et al. (2002)