



## Review

## Therapy escape mechanisms in the malignant prostate

Frédéric R. Santer<sup>a,\*</sup>, Holger H.H. Erb<sup>b</sup>, Rhiannon V. McNeill<sup>c</sup><sup>a</sup> Medical University of Innsbruck, Division of Experimental Urology, Department of Urology, Anichstrasse 35, A-6020 Innsbruck, Austria<sup>b</sup> Yorkshire Cancer Research Unit, University of York, York YO10 5DD, United Kingdom<sup>c</sup> Jack Birch Unit for Molecular Carcinogenesis, University of York, York YO10 5DD, United Kingdom

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## ABSTRACT

Androgen receptor (AR) is the main target for prostate cancer therapy. Clinical approaches for AR inactivation include chemical castration, inhibition of androgen synthesis and AR antagonists (anti-androgens). However, treatment resistance occurs for which an important number of therapy escape mechanisms have been identified. Herein, we summarise the current knowledge of molecular mechanisms underlying therapy resistance in prostate cancer. Moreover, the tumour escape mechanisms are arranged into the concepts of target modification, bypass signalling, histologic transformation, cancer stem cells and miscellaneous mechanisms. This may help researchers to compare and understand same or similar concepts of therapy resistance in prostate cancer and other cancer types.

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## 1. Introduction

## 1.1. Prostate tissue architecture

The prostate is an exocrine gland of the male reproductive system surrounding the prostatic urethra [1] and composed of acini, which are formed by a pseudo-stratified columnar epithelium comprising a terminally differentiated, secretory layer and a less differentiated basal compartment with regenerating cells [2]. A basement membrane separates the epithelial cells from the surrounding fibro-muscular stroma. Within the secretory layer, neuroendocrine cells represent a rare lineage, lack expression of androgen receptor (AR) and are thus not growth-dependent on androgens [3]. However, the prevalent lineage consists of AR-positive, luminal cells whose secretome is rich in prostate acid phosphatase (ACPP), kallikrein-related peptidase 3 (KLK3; also known as prostate specific antigen, PSA) and  $\beta$ -microseminoprotein (MSMB) [4].

Adult tissue stem cells (SC) reside within the basal layer and are able to regenerate the prostate through a differentiation process into secretory cells [2]. SC with a high expression of prominin 1 (PROM1) and integrin  $\alpha_2$  (ITGA2) give rise to rapidly proliferating, transit amplifying cells (PROM1<sup>-</sup>, ITGA2<sup>hi</sup>), which can further

differentiate into committed basal cells (PROM1<sup>-</sup>, ITGA2<sup>lo</sup>) with a slower cell cycle. *In vitro* terminal differentiation of basal cells to a luminal phenotype is mainly triggered by androgens [5]. Additionally, basal cells can be differentiated into neuroendocrine cells *in vitro* [6].

## 1.2. Prostate cancer: Treatment options

The vast majority of all prostate cancer (PCa) cases are acinar adenocarcinomas and histologically appear as hyperplasia of luminal cells. Deferred treatment, radical prostatectomy, androgen deprivation therapy (ADT) and external beam radiation therapy are current options for localised PCa [7]. At a metastatic stage (M1), the disease becomes incurable and the mean survival is 21–54 months, depending on the treatment response [7]. A common first-line therapy option at this stage of the disease is androgen deprivation therapy (ADT), based on initial findings by Huggins and Hodges [8] helping to understand that PCa growth and progression is dependent on androgens. AR inactivation can be accomplished by several means. Surgical castration (orchiectomy) is only rarely performed these days. Chemical castration can be achieved by interfering with the hormonal signalling pathway of the hypothalamic–pituitary–gonadal axis, which regulates the production of testosterone. This consequently leads to hypogonadism with castrate testosterone levels below 20 ng/dl (1 nmol/l). Complete androgen blockade (CAB) can be reached in combination with chemical castration by the use of non-steroidal anti-androgens (e.g.

\* Corresponding author. Tel.: +43 0 512 504 81801; fax: +43 0 512 504 24817.  
E-mail address: [frederic.santer@i-med.ac.at](mailto:frederic.santer@i-med.ac.at) (F.R. Santer).

hydroxyflutamide, bicalutamide) that compete with the natural ligand dihydrotestosterone (DHT) for binding to the AR.

Recurrence after ADT/CAB is termed castration-resistant prostate cancer (CRPCa) and is concurrent with a reactivation of the AR signalling axis. Treatment options at this stage of the disease include taxane-based chemotherapy, dendritic cell vaccination-based immunotherapy, the calcium mimic <sup>223</sup>Radium dichloride targeting bone metastases, and second-generation AR-targeting therapies [9,10]. However, resistance to therapy invariably occurs at these advanced stages of the disease, including *ab initio* resistance and/or cross-resistance to previously used drugs [11,12].

### 1.3. AR: Main target in PCa therapy

Luminal cells are essentially dependent on androgens for survival, or more precisely, dependent on active AR signalling. Inactivation of this signalling axis is the primary goal of ADT, CAB and second-generation agents enzalutamide and abiraterone. It is therefore not surprising that in the past most work elucidating resistance mechanisms against this therapy was focused on the AR signalling axis.

The gene encoding AR on Xq12 is organised into 8 exons [13] and structurally belongs to the nuclear steroid hormone receptor family. Exon 1 encodes the aminoterminal domain (NTD) and contains activation function 1 (AF-1; transcriptional units (TAU)-1 and -5). The DNA binding region consists of two zinc finger motifs, is encoded by exons 2 and 3, and is responsible for binding to androgen response elements (ARE) in promoter and enhancer regions of target genes. It is followed by a hinge region where a nuclear localisation signal is located, that is sterically unmasked upon ligand binding. Exons 4–8 comprise the ligand binding domain (LBD), as well as AF-2, which has only minor transcriptional activity [14]. AR interacts with an important number of co-integrators via the LXXLL motifs in the amino- and carboxy-terminal domains, controlling the full transcriptional activity/repression of AR [15].

The present review will summarise known therapeutic resistance mechanisms in the secretory and the basal prostatic layer and classify the therapy escape routes in the categories target modification, bypass signalling pathways, histologic transformation, cancer stem cells and miscellaneous mechanisms. This categorisation of tumour escape mechanisms has been adapted for PCa according to a recent publication based on resistance mechanisms to kinase inhibitors [16].

## 2. Target modification

### 2.1. Target overexpression and hypersensitive pathway

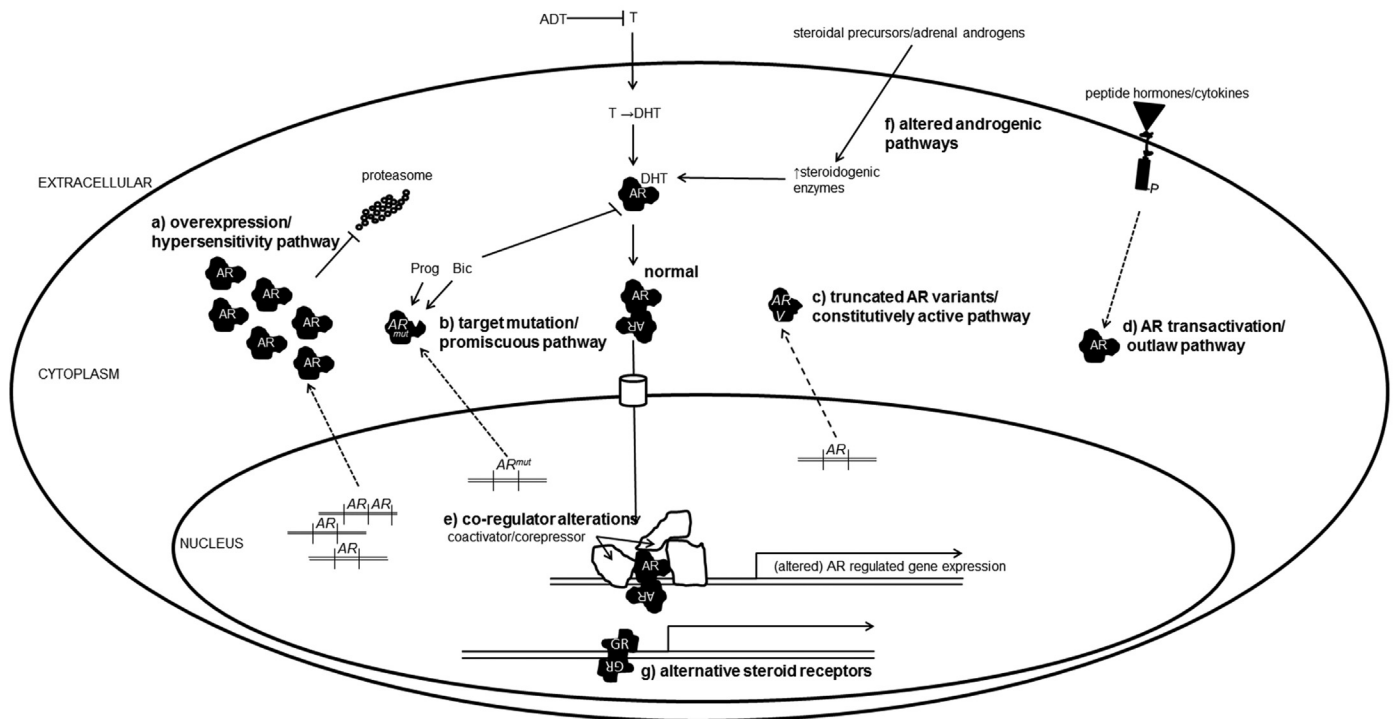
The most common molecular mechanism of endocrine therapy resistance is amplification of the AR gene locus. A number of studies have analysed paired patient biopsies before therapy, and after acquisition of castration resistance [17,18]. Amplification of the Xq12 locus, but also X-chromosome polysomy, have been documented in about 30% of all patients progressing to CRPCa, but were absent in the hormone-naïve specimens. These multiple copies of the AR gene result in high expression of AR mRNA and protein [18,19]. *In vitro* studies showed that AR transcriptional activity is regulated not only by the expression levels of both ligand and the receptor [20], but also as a consequence of increased receptor binding to chromatin [21]. In other words, ADT causes an amplification of the AR locus, in which a disturbed ratio of AR and its ligand results in a hypersensitive AR signalling pathway. Cells with such a high AR expression can deal with the low androgen concentrations during ADT, and give rise to new clonal outgrowth of castration resistant cells. However, AR gene amplification might

not be exclusively driven by ADT. A recent study discovered an amplification of the AR locus in small foci of cells in hormone-naïve patients suggesting that ADT could select for the clonal expansion of an already existing *ab initio* resistant cell population [22]. Of clinical interest is the fact that patients with AR amplification and thus high AR levels could take advantage of a CAB approach, inhibiting AR directly instead of following a standard ADT protocol only [23]. Interesting to note is that selection of patients for this purpose could be done on the detection of AR amplifications in circulating tumour cells isolated from the patients' blood, thereby possibly eliminating the need for biopsies [24].

Another mechanism leading to a highly expressed and hypersensitive AR pathway is the stabilisation of AR, i.e. a longer half-life of the protein through decreased degradation or through increased translation. The Cullin-based E3 ligase SPOP can promote polyubiquitination and subsequent proteasomal degradation of AR, as well as of its co-activator NCOA3 [25,26]. Mutations in the substrate-binding cleft of SPOP impair ubiquitination of AR and NCOA3, thereby extending the turnover and leading to an accumulation of these proteins. PCa-specific mutations of SPOP are found in up to 15% of analysed specimens [27]. However, the frequency of SPOP mutations (3 out of 50 cases) seems to be lower in CRPCa [28], raising the question whether this mechanism contributes to castration resistance. Another E3 ligase, SIAH2, was found increasingly expressed in CRPCa and to selectively regulate the transcriptional activity of AR [29]. MID1, which is known to interact with active polyribosomes, has been shown to associate with AR mRNA [30]. Negative regulation by the AR signalling axis leads to high MID1 expression under androgen deprived conditions, favouring increased AR translation and expression. Usually, AR is a negative regulator of its own transcription under normal androgen concentrations [31]. However, the castrate androgen levels in CRPCa are sufficient to stimulate AR activity on enhancer elements, but not suppressor elements, resulting in an increased expression of AR and AR-repressed genes, which may drive progression to CRPCa [32]. In conclusion, multiple mechanisms can eventually result in high expression levels of AR, which are transcriptionally hypersensitive to the residual amounts of DHT in castrate patients (Fig. 1a).

### 2.2. Target mutation and promiscuous pathway

Base substitutions in the coding sequence of the AR gene are less frequently observed than amplifications of the locus. The latest study using exome sequencing revealed a mutation frequency of 10% in CRPCa specimens ( $n=50$ ) [28]. Clinically relevant mutations occur in the ligand-binding pocket [33]. For instance, a recent study discovered H874Y and T877A mutations in circulating cell-free DNA from patients that no longer responded to treatment with abiraterone, and a F876L amino acid substitution in one enzalutamide-resistant patient [34]. The latter mutation, F876L, was found in earlier experimental approaches to confer resistance to enzalutamide and ARN-509, an anti-androgen undergoing clinical trials [35,36]. The T877A mutation can also be detected in CRPCa patients that progressed on abiraterone treatment [37]. The driving force for the occurrence of many AR mutations in the LBD is broadened ligand specificity. Promiscuous activation of mutant AR by adrenal androgens, progesterone, cortisol and cortisone,  $\beta$ -estradiol, testosterone metabolites, and moreover, the anti-androgens hydroxyflutamide, bicalutamide and enzalutamide has been documented [36,38–43]. These agonistic properties of the AR antagonists may be the basis of the anti-androgen withdrawal syndrome described for all three drugs [44–46]. Furthermore, T877A generates an androgen-independent gain of function for nuclear import [47] and H874Y enhances binding to the co-activators NCOA1–3 [48]. Thus, base substitutions in the AR can be responsi-



**Fig. 1.** Molecular mechanisms of AR-targeting therapy escape. Several molecular mechanisms leading to a reactivation of the AR-signalling axis and a progression to CRPCa have been described. These can be grouped in target modification (overexpression/hypersensitivity (a); target mutation/promiscuous (b); truncated AR variants/constitutively active (c) and bypass (AR transactivation/outlaw (d); co-regulator alterations (e), altered androgenesis (f), alternative steroid receptors (g)) pathways. ADT, androgen deprivation therapy; T, testosterone; DHT, dihydrotestosterone; Bic, bicalutamide; Prog, progesterone.

ble for a reactivation of the AR signalling axis, through alternative steroidal and non-steroidal ligands under conditions where DHT is restricted (Fig. 1b).

### 2.3. Truncated AR variants and constitutively active pathway

C-terminal truncated AR variants may arise through proteolytic cleavage of full length AR, AR gene rearrangement, and by alternative splicing of the AR gene transcript [49–52]. To date, around 20 AR variants have been documented, which lack the LBD rendering these variants constitutively active even in the absence of its ligand [53]. Although there are conflicting reports whether AR variants require dimerisation with the full length receptor for nuclear import and transcriptional activity [54,55], there is consensus that resistance against the currently available therapies targeting the LBD of AR can be mediated by truncated AR variants [56,57]. The best investigated AR variant, AR-V7, can be increasingly detected in CRPCa tissues using AR-V7 specific antibodies [58,59]. Its expression is induced by ADT and predicts progression to CRPCa [60]. Furthermore, AR-V7 mRNA expression in circulating tumour cells correlates with primary resistance to abiraterone and enzalutamide [61]. These AR variants may induce a distinct gene expression signature compared to the full length receptor [62]. The transcriptional program of AR-Vs preferentially leads to expression of cell cycle regulatory genes, while full length AR represses that program and favours transcription of genes related to macromolecular synthesis, metabolism and differentiation. The recognition that LBD-deficient AR variants drive CRPCa has prompted the development of anti-androgens targeting the NTD of AR, which possesses the highest transcriptional activity [14]. In conclusion, truncated AR variants are constitutively active and can promote AR signalling without the need for a ligand (Fig. 1c).

## 3. Bypass signalling pathways

### 3.1. AR transactivation and outlaw pathway

Several studies show that AR can also be transactivated by growth factors, neuropeptides and cytokines. For instance, IL6 can cross-talk to the AR signalling axis and lead to the transcription of KLK3 under castrate androgen conditions [63]. AR transactivation in response to IL6 can be mediated by MAPK and STAT3 pathways, whereas signalling through PI3K-Akt suppresses this interaction [64]. Interestingly, STAT3 is able to heterodimerise with the N-terminal domain of AR upon IL6 signalling in LNCaP cells [65]. Activation of the MAPK pathway by IL6 leads to phosphorylation of the AR co-activator NCOA1 thereby enhancing AR transcriptional activity [66]. In addition, the kinase FER may phosphorylate AR at tyrosine 223 and participate in the crosstalk with AR in response to IL6/STAT3 signalling [67]. The IL6 transactivating effects on AR can be reversed by MAPK inhibition or with the anti-androgen bicalutamide [68]. Another example is the tyrosine kinase SRC which can phosphorylate AR thereby regulating AR's nuclear translocation, chromatin recruitment and transcriptional activity [69]. SRC is known to play important roles in the progression and recurrence of a number of cancer types [70]. SRC plays also a role in AR transactivation by the neuropeptide bombesin and promotes an overlapping but not identical AR transcriptional program [71]. Earlier it was shown that EGF, keratinocyte growth factor (KGF) and insulin-like growth factor-1 (IGF1) are also able to transactivate AR in the absence of androgens, which, like IL6 can be blocked by bicalutamide treatment [72]. In conclusion, several signalling pathways can cause transactivation of AR in the absence of its ligand or under low androgen concentrations and thus contribute to PCa progression (Fig. 1d).

### 3.2. Co-regulator alterations and aberrant transcription

AR transcriptional activity is controlled by numerous co-regulators, i.e. co-activators and co-repressors [15]. Aberrant expression of co-regulators has been associated with PCa progression, and in addition the expression of various co-regulators is directly regulated through androgenic action [73]. For instance, increased expression of the histone (lysine) acetyltransferase (HAT) EP300 has been detected in PCa cells after androgen deprivation [74]. EP300 is involved in transactivation of the AR through IL6 [75]. Moreover, bombesin is able to activate EP300 HAT activity via SRC and PRKCD pathways. This results in AR protein acetylation and an increased expression of AR-regulated genes [76]. A similar role has been documented for the close EP300 homologue CREB-binding protein (CREBBP), which is also increased after androgen withdrawal [77]. Protein kinase A (PKA), which is frequently over-expressed in PCa, leads to the transcription of AR regulated genes in response to cAMP [78]. This involves the phosphorylation of cAMP responsive element-binding protein (CREB) through PKA and the recruitment of EP300 and CREBBP. In cells with a high expression of CREBBP and EP300, the co-activators may act as a bridging molecule between AR and CREB, resulting in an enhanceosome-based cooperation [79]. Interestingly, PKA can also phosphorylate and enhance nuclear translocation and repressive function of the nuclear receptor co-repressor NCOR1 [80]. Although this would usually favour AR transcriptional inactivation, the situation may be different in a particular cellular context; exogenous overexpression of NCOR1 and NCOR2 can increase AR transcriptional activity, possibly due to an impaired AR/co-repressor interaction [81]. Another study found altered recruitment to AR but also loss of expression of NCOR1/2 in CWR22R castration-resistant cells compared to the androgen-dependent CWR22 [82]. BAG1 is an AR co-regulator whose expression levels are also increased in CRPCa [83]. Amplification of its locus was found in 7.4% of CRPCa samples, while analysis of treatment-naïve samples did not reveal gene aberrations. BAG1 binds to a novel identified sequence adjacent to the AF-2 of AR, termed binding function 3 (BF-3) [84]. BAG1 is important for fine-tuning AR transcriptional activity and for suppressing a sub-set of AR responsive genes. In conclusion, the changed expression profile of AR co-regulators caused by ADT has implications for the transcriptional activity and program of AR and can result in an aberrant expression of AR downstream genes promoting survival of the malignant cells (Fig. 1e).

### 3.3. Altered androgenic pathways

AKR1C3 encodes for an aldo-keto reductase that converts androstenedione, a weak adrenal androgen, into testosterone [85]. This steroidogenic enzyme, among others of androgen metabolism, was increasingly detected in mCRPCa bone samples compared to primary treatment-naïve PCa [86]. In other words, intra-tumoural upregulation of androgenic enzymes enables conversion of adrenal steroids into testosterone and DHT with levels that are sufficient to activate transcription through AR and drive castration resistance (also known as the front-door, conventional pathway, Fig. 1f) [87,88]. Interestingly, this intra-tumoural conversion of adrenal steroids is not only a mechanism of resistance against ADT; upregulation of AKR1C3 was also found in cells that are resistant to the second-line anti-androgen enzalutamide [89]. A recent study has shown that the transcription factor ERG, which is fused to the androgen-responsive TMPRSS2 in about 50% of PCa patients [90], is a direct positive regulator on the AKR1C3 promoter [91]. ERG is co-expressed with AKR1C3 in PCa tissue samples. This could have clinical implications and explain why TMPRSS2-ERG in circulating tumour cells is a predictive biomarker of sensitivity for CRPCa patients treated with the CYP17A1 inhibitor abiraterone

acetate, which inhibits the formation of adrenal androgens [92]. Studies with a newly developed AKR1C3 inhibitor, SN33638, have been conducted in cell culture models [93]. However, the authors conclude that only a subset of CRPCa patients with high AKR1C3 expression could possibly benefit from such a therapy. Other steroidogenic enzymes may also be implicated in progression to CRPCa. A gain-of-function mutation in the HSD3B1 enzyme has been discovered in some CRPCa tissue specimens, which controls the rate-limiting step from dehydroepiandrosterone into DHT [94]. This mutation renders the enzyme resistant to ubiquitin-mediated proteasomal degradation, leading to its accumulation and accelerated synthesis of DHT. The expression levels and isozyme activity of 5 $\alpha$ -steroid reductase, which converts testosterone into DHT, is shifted from isoform 2 (SRD5A2) to isoform 1 (SRD5A1) and 3 (SRD5A3) in CRPCa [95,96]. The mineralocorticoid deoxycorticosterone is also reduced by SRD5A1 and is able to activate the AR [97]. 5 $\alpha$ -Dehydro-deoxycorticosterone was detected in eight out of 13 CRPCa tissues.

Another alternative steroidogenic route resulting from high expression and activity of SRD5A1 and AKR1C3 involves the conversion of androstenedione to 5 $\alpha$ -androstenedione, and finally into DHT. This pathway bypasses the formation of testosterone (5 $\alpha$ -androstenedione pathway). The shift from SRD5A2 to the SRD5A1 isoform in CRPCa samples may be a consequence of the fact that SRD5A1 has much higher affinity for androstenedione compared to SRD5A2 [98]. This pathway was shown to be the dominant pathway in CRPCa cell line models and metastatic tissue samples.

DHT may also be synthesised from cholesterol via the metabolites progesterone, allopregnanolone, androsterone and androstenediol, again by circumventing testosterone (back-door pathway) [99]. DHT synthesis through the back-door pathway requires the enzymes CYP17A1 and SRD5A, as well as a reverse oxidative step of androstenediol to DHT [100]. However, expression of CYP17A1 in PCa tissues seems to be low and infrequent [101,102], raising the question whether this back-door pathway actually plays a role in the acquisition of castration resistance.

### 3.4. Alternative steroid receptors

Glucocorticoids are frequently co-administered with abiraterone in order to counteract the drug-induced reductions in serum cortisol levels [103]. The glucocorticoid receptor (GR) however has been shown to drive a set of certain AR gene targets, including KLK3, in the absence of AR [104]. GR expression is increased in several PCa cell lines treated with the anti-androgens flutamide, bicalutamide and enzalutamide, and GR expression in metastatic tissue specimens isolated from the bone marrow correlates with the patients' response to enzalutamide [104,105]. A recent study demonstrated that GR transcriptional expression is inhibited through AR signalling via a negative androgen response element [106]. Thus, activation of the GR under conditions where AR is inactivated may give PCa cells a survival benefit and drive progression to castration resistance. Furthermore, a role for GR as a negative prognostic factor has already been described in ER-negative breast cancer [107]. This shows that steroid receptors may be able to compensate for the inactivation of another steroid receptor and thereby promote survival of the cell (Fig. 1g).

## 4. Histologic transformation

### 4.1. Neuroendocrine (trans-)differentiation

As stated above, neuroendocrine cells are rare secretory cells in normal prostatic tissue. Variable numbers of neuroendocrine cells can be detected in prostate adenocarcinomas by

immunohistochemical analysis, in part depending on the number of slides and various neuroendocrine antigen markers that are used [108]. The clinical prognostic significance of the presence and percentage of neuroendocrine cells in tumour specimens is unclear, although high grade and stage cancers express higher levels of chromogranin A (CHGA) than low grade or localised disease [109]. In contrast, there is no doubt that growth of malignant neuroendocrine-like cells is favoured by androgen deprivation and associated with acquisition of castration resistance, as well as loss of AR expression in a subset of CRPCa tissues [110,111]. However, due to a lack of a general marker it has been difficult to estimate the frequency of neuroendocrine differentiation in castration-resistant patients. Cancer cells with a neuroendocrine pattern may arise through a trans-differentiation process from luminal cells. *In vitro* evidence for a trans-differentiation process comes largely from studies performed with the androgen-responsive cell line LNCaP. The morphology of these cells changes to a neuroendocrine-like state upon growth in androgen-depleted medium and is accompanied by a secretion of several neuroendocrine markers [112]. The underlying mechanisms of this androgen deprivation-induced trans-differentiation include signalling via cAMP-activated PKA resulting in phosphorylation of RHOA [113,114], human achaete-scute homolog-1 (ASCL1) transcription factor [115], and receptor protein tyrosine phosphatase alpha (PTPRA) [116]. In addition, other factors and mechanisms such as IL6 through suppression of RE-1 silencing transcription factor (REST) [117], inhibition of NOTCH signalling leading to hypoxia [118], and cell-density-induced attenuation of CDK1/2 signalling [119] may induce neuroendocrine trans-differentiation.

Normal and malignant neuroendocrine cells do not express AR, and are unlikely to be affected by AR-targeting therapies [120]. It is therefore possible that while inactivation of AR decreases the number of luminal cells, malignant neuroendocrine cancer cells may repopulate the vacant space in the prostatic tissue and thus drive tumour recurrence. The pressure of AR-targeting therapy could select for a changed differentiation program in a common malignant progenitor cell to a neuroendocrine rather than a luminal phenotype. Most neuroendocrine cells express CD44, which is also a marker for the stem cell-containing, basal layer of the prostatic tissue [121]. Furthermore SOX2, an embryonic stem cell regulator that is repressed through AR signalling [122], is detected in basal cells of benign prostate hyperplasia specimens and in neuroendocrine tumours of murine and human origin, while being absent in primary PCa tissues [123]. CBX2 and EZH2, members of the polycomb group, are involved in epigenetic regulation of neuroendocrine differentiation [124] and are upregulated in metastatic CRPCa samples [125]. The fusion TMPRSS2-ERG can be detected in neuroendocrine cancers with a similar frequency to adenocarcinomas, showing that both cancer phenotypes have the same clonal origin [126]. When taken together neuroendocrine differentiation may be important in response to AR targeting therapies and progression to castration resistance, however due to a lack of adequate *in vitro* models and biomarkers, it remains an under-explored area (Fig. 2a).

#### 4.2. Epithelial-to-mesenchymal transition

Epithelial-to-mesenchymal transition (EMT) as a mechanism of castration resistance has been studied infrequently in the past and clinical evidence for an EMT phenotype induced by AR-targeting therapies is sparse. Despite this, there are several *in vitro* and animal studies which have explored EMT as a resistance mechanism with interesting results. Recently, ADT-induced EMT was demonstrated in normal mouse prostate tissue and in the human LuCaP35 xenograft model [127]. In addition, increased mRNA expression of the mesenchymal markers Vimentin (VIM), ZEB1, Cadherin 11 (CDH11) and Fibronectin 1 (FN1) was detected in human tissue

specimens from patients that underwent ADT. However, another study showed that DHT exposure led to EMT, higher migratory and invasive potential and activation of the EMT-inducing transcription factor Snail [128]. Interestingly, high AR expression can suppress androgen-induced EMT. This conflicting data could be explained by the observation that AR splice variants, that are induced through AR-targeting therapies (see above), have a distinctive transcriptional program compared to the full length receptor [62] and might be responsible for the transition to a mesenchymal phenotype. Overexpression of constitutively active variants AR-V7 and AR Q640X in LNCaP cells resulted in increased expression of mesenchymal markers [129]. Similarly androgen deprivation resulted in an upregulation of AR-V7 and mesenchymal markers, both of which can be reversed by the addition of DHT and reactivation of the full length receptor [130]. In general, EMT seems to be a reasonable explanation for cancers with a mesenchymal phenotype (Fig. 2b). However, to our knowledge there is as of yet no study demonstrating that this mesenchymal phenotype is a consequence of dedifferentiation of the epithelial phenotype or alternatively a clonal expansion from an already existing mesenchymal phenotype.

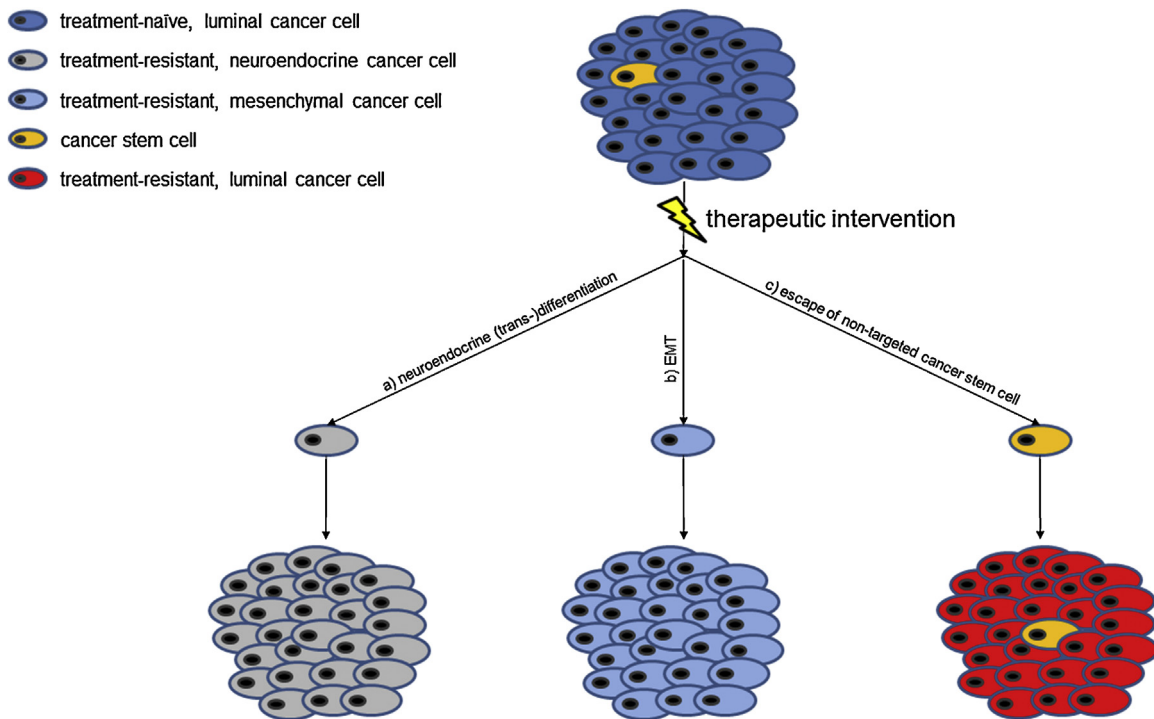
### 5. Cancer stem cells

In the previous sections we have discussed several mechanisms of therapy resistance, which may be well-explained by a stochastic model of cancer progression, i.e. that a random cell acquires a survival benefit in response to the treatment and gives rise to a new, resistant tumour bulk. However, evidence increasingly suggests that cancers are organised in a hierarchical manner, similar to normal tissues, and that resistant tumours arise from cancer stem cells that have adapted to the therapy environment.

#### 5.1. Evidence for CSC in PCa

Since the first report in 1994 of a role for stem cells in human acute myeloid leukaemia subsequent reports have identified so-called cancer stem cells (CSC) in a variety of tumours such as breast, brain, colon, pancreas, lung, melanoma and glioblastoma [131]. CSC represent a small population of cells inside a tumour which share the characteristics of normal stem cells, i.e. self-renewal and the ability to recapitulate the heterogeneous phenotype of the parental cancers by differentiation [132]. However, the capacity to form a parental-like tumour is not sufficient to define a CSC; these tumours must also be serially transplantable. In contrast to initial beliefs, recent studies have suggested that around 25% of cancer cells may have CSC properties [133].

Small CSC populations have also been detected in PCa [134]. Although the main hypothesis is that prostate cancer arises from terminally differentiated luminal cells, there is growing evidence that PCa arises from more undifferentiated cells with a basal phenotype [135–138]. In limiting dilution assays it was demonstrated that androgen-independent tumours arise from AR-negative cells at a frequency of  $1:10^5$ – $10^6$  AR-positive cells [139]. Interestingly, AR-negative cells with very similar properties to stem cells have been found in the PCa cell line LNCaP, which is meant to represent luminal cancer cells [140]. In addition, the laboratory of Collins and Maitland could isolate a population from primary PCa cells with high clonogenic potential and the ability to differentiate into luminal cells (AR<sup>+</sup>, ACP<sup>+</sup>, ITGB2<sup>+</sup>), which were phenotypically identical to normal stem cells (CD44<sup>+</sup>, ITGA2<sup>hi</sup>, PROM1<sup>+</sup>) [141]. PCa CSC have a unique miRNA expression profile overlapping with unfractionated advanced PCa and human embryonic SC [142]. Moreover, these cells express the cancer specific TMPRSS2:ETS fusion genes [143]. In further support of this, CD44<sup>+</sup> PCa xenograft



**Fig. 2.** Altered differentiation as therapy escape mechanisms. Histologic transformations of the treatment-naïve luminal tumour may occur in response to therapeutic intervention due to neuroendocrine (trans-)differentiation (a) and epithelial-to-mesenchymal transition (EMT, b). A small population of cancer stem cells within the treatment-naïve luminal tumour can give rise to a treatment-resistant luminal tumour via aberrant differentiation after/during therapeutic intervention (c).

cells possess enhanced tumour-initiating ability *in vivo* compared to the CD44<sup>-</sup> population and could be successively serially transplanted [144,145]. Lastly, one study demonstrated that tumours containing luminal, basal and neuroendocrine cells could be generated in mice by using AR- and p63-negative cells expressing the stem cell markers CD44, PROM1, nestin (NES) and KIT [146]. However, although there is evidence that supports PCa originating from CSC, until now there is no study to our knowledge that has shown that a single cell could form a tumour which both represents a patient's phenotype and which could be serially transplanted. Also, due to the high heterogeneity of PCa, the possibility that CSC exist in some but not all tumours should be considered.

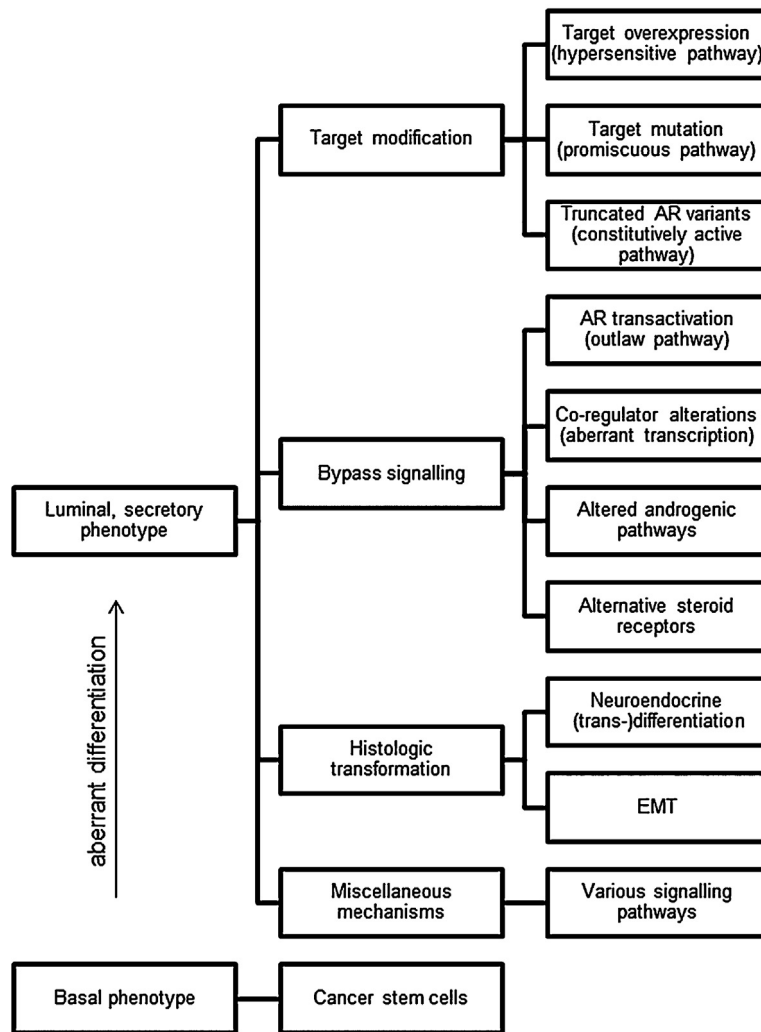
### 5.2. Role of CSC in therapy resistance

ADT, radio- and chemotherapy efficiently target the highly proliferative and AR positive luminal cells representing the bulk (around 99%) of the tumour [138,141,147,148]. However, these therapies fail to target the small population of quiescent and AR-negative CSC, which are able to adapt to their new niche, resulting in the regrowth of a therapy-resistant and more aggressive tumour [149]. Quiescence is generally a challenging problem to target due to the fact that most therapeutics are designed to target highly proliferative cells. In addition, quiescence is not the only reason for prominent therapy resistance of CSC. High DNA repair activity is a property of CSC which protects them from DNA damage-inducing agents (e.g. Cisplatin) and radiotherapy [150]. PCa CSC sustained fewer lethal double-strand breaks than more differentiated cells, suggesting that CSC may have increased DNA repair activity and are therefore better equipped to deal with DNA damage [151]. Several studies reported that CSC as well as normal stem cells have an increased threshold for induction of mitochondrial apoptosis due to elevated expression of anti-apoptotic proteins (e.g. BCL2, BCL2L1 and MCL1) and members of the Inhibitor of Apoptosis family (e.g. BIRC5) and are therefore more resistant to cytotoxic agents

[152–154]. We have recently shown increased MCL1 mRNA expression in PCa CSC [155]. The BCL2 Homology Domain-3 mimetic Obatoclax decreased the clonogenic efficiency of CD44<sup>+</sup> prostate cancer cells derived from a primary tumour supporting a role of the BCL2 family in the tumour forming fraction of PCa. In addition to the increased apoptotic threshold, CSC also have a high ability for drug efflux through proteins such as ATP-binding cassette (ABC) transporter family [156]. By using the Hoechst 33342 dye efflux assay, a stem cell-enriched population was isolated from benign and malignant prostate. This demonstrates that drug efflux transporters are also highly active in prostate CSC and normal SC, and consequently may be able to efflux chemotherapeutic drugs across the plasma membrane [157]. In conclusion, CSC have intrinsically high resistance against various therapies, and they seem a reasonable explanation for the high relapse of PCa after ADT and other therapies (Fig. 2c). However more research is necessary in order to prove the existence of these cells and to determine whether all tumours harbour CSC.

### 6. Miscellaneous mechanisms

A number of signalling pathways have been found to be deregulated in PCa and to contribute to PCa progression. Receptor and non-receptor kinases can circumvent the blocked AR pathway and stimulate the proliferation and survival of the androgen-deprived cells. As discussed above, this may also lead to AR transactivation. A recent quantitative phosphoproteomic study with mCRPCa samples revealed increased activation patterns for SRC, EGFR, RET and ALK kinases compared to treatment-naïve specimens, although with high inter-patient variability [158]. The IGF signalling pathway may also lead to PCa progression in patients undergoing ADT. It was suggested that the hypogonadal state during ADT may lead to insulin resistance and/or obesity and increased IGF-1 expression, driving proliferation and survival of the malignant cells [159]. Insulin resistance, hyperglycemia and metabolic syndrome are



**Fig. 3.** Summary of the reviewed therapy escape mechanisms in PCa. Prostate adenocarcinoma appears as disease of malignant cells with a luminal phenotype, which are essentially dependent on androgenic signalling. Thus, the main therapy target is inactivation of AR. Various mechanisms confer acquired resistance to AR-targeting therapies. These include mechanisms modifying expression and transcriptional activity of AR (target modification), activation of compensatory pathways to circumvent the inhibited target (bypass signalling), phenotypic changes of the epithelial cells (histologic transformation) and miscellaneous pro-survival and pro-proliferative mechanisms. However, there is increasing data that those mechanisms originate in cancer stem cells with a basal phenotype, which give rise to an aberrantly differentiated luminal phenotype under the pressure of the AR-targeting therapy.

known endocrine complications of ADT [160]. Another mechanism leading to increased growth factor signalling is through inactivation of the phosphatase PTEN, which results in aberrant activation of the PI3K–Akt pathway. Loss of PTEN occurs in about 50% of all PCa patients [161] and its inactivation is sufficient to initiate PCa in mice [162]. In that particular mouse model it was shown that castration-resistant growth is an intrinsic property of *Pten*-null PCa cells, as a result of crosstalk between PI3K and AR [163]. Loss of PTEN expression is associated with poor survival and decreased time of patients on abiraterone treatment [164], and it was proposed that PCa patients with PTEN-deficiency might be better treated with PI3K-than AR-targeting therapies [165]. The metal ion-binding metallothionein (MT) superfamily has also been implicated in treatment-resistant prostate cancer. As there are unusually high levels of zinc in the prostate compared to the rest of the body [166], it is possible that this tissue already has high basal MT levels [167]. Carcinogenesis and treatment may further increase MT expression levels by factors such as hypoxia [168], reactive oxygen species [169] and androgen deprivation [170]. The MT protein is thought to play a role in a

number of pathways where it acts to increase proliferation [171], reduce apoptosis [172] and scavenge free radicals [169], and thus increased expression may confer resistance to cells via these pathways [173]. However there are many MT protein isoforms and thus knowing exactly which ones are involved in resistance, and therefore which ones to target, currently proves troublesome. Another side effect of ADT is increased inflammation through infiltration of T-cells into the prostatic tissue [174]. Cytokines and chemokines produced by the infiltrating immune cells, such as Interleukins-1 $\beta$ , -6, and -8 may drive proliferation and survival of prostate cancer cells. In particular, serum IL6 levels are significantly elevated in CRPCa patients [175] and IL6 is known to upregulate expression of MCL1, a member of the BCL2 family, thus promoting PCa cell survival [176]. High expression of MCL1 and PCa cell survival is also a consequence of AR inactivation and subsequent cell cycle arrest [155]. In conclusion, extrinsic and intrinsic mechanisms can lead to increased growth factor production in the tumour environment and increased signalling in the tumour cell resulting in stimulatory effects supporting the cancer cell's survival and proliferation.

## 7. Conclusions

The present review has summarised and classified various PCa therapy escape mechanisms (Fig. 3). While some mechanisms occur more frequently, others are rare or their occurrence statistics are not available, mostly due to a lack of diagnostic detectability. Additionally, due to the heterogeneity of the disease, multiple mechanisms of therapy resistance may co-occur. It is important to note that the same or similar concepts of escape mechanisms as previously identified for ADT and CAB also confer resistance to the second-generation drugs enzalutamide and abiraterone. As a consequence, it remains difficult to select the best treatment option in order to eliminate the risk of *ab initio* resistance. A specific treatment sequence for CRPCa patients after chemotherapy failure is not available at the moment. The occurrence of various treatment resistances also gives a rationale for treating patients as early as possible with combination therapies, where ideally two or more different molecular targets are hit at the same time. For instance, a recent clinical phase III study shows promising results by treating patients with high-risk localised PCa with a combination of ADT and the microtubule-targeting agents docetaxel and estramustine compared to an ADT protocol only [177]. Also, the identification of CSC strongly argues for the use of therapeutic combination regimes. Ideally, this would include a therapy that targets the bulk of more differentiated, but highly proliferative cancer cells while the second aims to eliminate the more undifferentiated, CSC-containing population of the tumour. This concept would recommend for PCa that treatment-naïve tumours should be treated by the approved AR-targeting and/or radiation therapies in synergy with a protocol that targets the CSC-containing, basal layer of the prostate. In conclusion, the development of novel AR-targeting therapies is well-justified in order to better target luminal, androgen-dependent PCa. However, further research should also aim to develop therapeutic options to inactivate the CSC-containing, androgen-independent basal PCa phenotype.

## Conflict of interest statement

The authors declare that there are no conflicts of interest.

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