Androgen-regulated metabolism and biosynthesis in prostate cancer

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Abstract

Metabolic changes are a well-described hallmark of cancer and are responses to changes in the activity of diverse oncogenes and tumour suppressors. For example, steroid hormone biosynthesis is intimately associated with changes in lipid metabolism and represents a therapeutic intervention point in the treatment of prostate cancer (PCa). Both prostate gland development and tumorigenesis rely on the activity of a steroid hormone receptor family member, the androgen receptor (AR). Recent studies have sought to define the biological effect of the AR on PCa by defining the whole-genome binding sites and gene networks that are regulated by the AR. These studies have provided the first systematic evidence that the AR influences metabolism and biosynthesis at key regulatory steps within pathways that have also been defined as points of influence for other oncogenes, including c-Myc, p53 and hypoxia-inducible factor 1α, in other cancers. The success of interfering with these pathways in a therapeutic setting will, however, hinge on our ability to manage the concomitant stress and survival responses induced by such treatments and to define appropriate therapeutic windows.

Key Words
- prostate
- androgen receptor
- androgen
- molecular biology
- oncogene

Introduction: the Warburg effect and cancer metabolism

In 1927, Otto Warburg discovered increased lactate production as a common denominator in various cancer cells, naming this the ‘Warburg effect’. He speculated that this was triggered by an unidentified mitochondrial defect and labelled it ‘the cause for cancer’ (Warburg et al. 1927). Increased lactate production is now accepted as a prime example of metabolic reprogramming and an emerging hallmark of cancer cells (Hanahan & Weinberg 2011). In order to understand the significance of this metabolic change in cancer cells, one needs to go back to the basics of biochemistry, to one of the oldest and best conserved metabolic pathways among species – glycolysis, the breakdown of glucose to pyruvate.

Interestingly, proliferating cells (e.g. stem or cancer cells) produce lactate to equalize their electron balance rather than utilizing oxidative phosphorylation, even under aerobic conditions. This is particularly intriguing because the net energy production is significantly lower (2 vs 38 ATP in complete oxidative phosphorylation through the citric acid cycle and electron transport chain). Thus, a lot of potential energy seems to get wasted. However, aerobic glycolysis appears to be advantageous for proliferative active cells – why? It is thought that nutrient availability in proliferative tissue is not a limiting factor, thereby eliminating the selective pressure for an efficient utilization of available energy resources. Instead, the ability to create as much biomass as fast as possible in order to proliferate quickly and efficiently might be the deciding factor while controlling metabolism in those cells.

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A higher metabolic net-rate channels more glucose through glycolysis and yields more intermediates for various anabolic processes, thereby increasing the rate of biomass production and speeding up the cell cycle. In fact, about 10% of the glucose utilized in glycolysis in proliferating cells is being used for anabolic pathways upstream of pyruvate (Vander Heiden et al. 2009). Examples of these pathways include the pentose-phosphate pathway as well as amino acid, lipid and nucleotide synthesis, all processes yielding building blocks required to sustain effective cell proliferation.

A second metabolic hallmark of cancer cells is an elevated uptake and consumption of glutamine, sometimes to a degree where glutamine becomes an essential for maintaining proliferation (Hensley et al. 2013). This increased glutaminolysis provides the cells with carbon backbones, nitrogen and reducing equivalents (NADPH), all necessary building blocks for anabolic processes and therefore proliferation. For example, glutaminolysis feeds into the citric acid cycle via 2-oxoglutarate to keep the cycle up and running. This is crucial as its intermediates are constantly being channelled into anabolic pathways, such as lipid biosynthesis (acetyl-CoA) or the synthesis of non-essential amino acids (e.g. oxaloacetate and 2-oxoglutarate) (DeBerardinis et al. 2008). It is therefore not surprising that metabolic adaptations have been reported in various human cancers (Hsu & Sabatini 2008).

Metabolic status of the prostate gland and cancer predisposition

The prostate gland is principally responsible for secreting factors that enhance sperm viability during reproduction. Both the development of the prostate gland and maintenance of these secretory functions require androgens and the androgen receptor (AR; Pritchard & Nelson 2008). While the AR is now known to be expressed in many other cell types in the body, luminal epithelial cells in the prostate gland express particularly high levels (Bonkhoff & Remberger 1993). These are the specialist secretory cells that release prostate-specific proteins, including kallikreins, such as prostate-specific antigen (Cohen et al. 1998). Furthermore, the prostate gland also has a specialized metabolic role as a secretor of citrate, and citrate secretion falls upon progression to metastasis (Marberger et al. 1962). Apparently, high concentrations of secreted citrate play an important role in maintaining sperm viability through calcium chelation and as an energy source (Ford & Harrison 1984). In order to function as a net secretor of citrate, the normal metabolic activity of luminal epithelial cells is altered so that the tricarboxylic acid (TCA) cycle does not function efficiently and citrate accumulates for secretion (Costello & Franklin 1981). This requires elevated zinc concentrations within prostate cells and concomitant inhibition of cis-aconitase within the TCA cycle (Singh et al. 2006). The impaired efficiency of the TCA cycle in untransformed cells is predicted to mean that basal energy metabolism in the prostate gland is more glycolytic, or Warburg-like, than in other tissues (Fig. 1). Overall, therefore, even in the untransformed prostate, the AR helps to drive the expression of metabolic enzymes and secreted proteins associated with biomass production, although for secretion rather than tumorigenesis (Heemers et al. 2003).

Defining clinically relevant AR target genes and pathways

AR target genes can be classified based on the transcripts and proteins that are hormone responsive. The development of chromatin immunoprecipitation (ChIP) to enrich AR bound to DNA has allowed the presence of AR binding sites within regulatory regions flanking these genes to be used as an additional classifier (Lamont & Tindall 2010, Massie & Mills 2012). However, directly associating a binding site with a given gene and its expression is very challenging because genomic DNA can loop and form higher order structures (Wu et al. 2011). This means that AR binding events can act in cis, i.e. exert proximal regulatory effects on nearby genes, or in trans, i.e. exhibit distal associations with genes many hundreds of kilobases or megabases away from the binding site or indeed on other chromosomes. Consequently, detailed classification criteria for AR target genes vary somewhat from study-to-study but typically associations between AR binding sites and genes are inferred over distances of up to 100 kb. The overall conclusion is that many genes required for glucose consumption, lipid turnover and biomass production/anabolic metabolism are androgen-dependent and regulated by the AR in both untransformed prostate cells and at least in localized prostate cancer (PCa; Massie et al. 2011, Sharma et al. 2013). In untransformed cells, this is an important feature for maintaining high rates of protein synthesis and glycosylation to sustain the secretory function of the prostate gland. Strikingly, meta-analyses of expression array data from localized PCa consistently report significant changes in genes associated with lipid-metabolizing pathways, glycosylation and calcium signalling (Gorlov et al. 2009). Some genes, for
example fatty acid synthase, are both PCa biomarkers overexpressed in early-stage disease but also rather abundantly expressed in untransformed cells, and androgen-regulated in both settings (Swinnen, et al. 1997, Kusakabe et al. 2000, Migita et al. 2009). \(\alpha\)-Methylacyl-CoA racemase, in contrast, is more cancer-specific. While its function remains to be precisely defined, in PCa, it has been implicated in the \(\beta\)-oxidation of fatty acids and associated with peroxisome function in other settings (Rubin et al. 2002, Lloyd et al. 2008). Changes in the expression of lipid-metabolizing enzymes therefore represent a good example of an early hallmark of PCa essentially dysregulating an established feature of AR-dependent gene expression in the prostate gland. At present, we do not know the definitive trigger for dysregulation but family history (genetics), ageing and possibly diet and oxidative stress may play important roles in perturbing AR activity.

Gene silencing is also an important feature of PCa tumorigenesis and contributes to metabolic reprogramming. Silencing of the expression of zinc transporters (hZIP1–3) is an early event in the development of PCa and these proteins are required to maintain high zinc concentrations in prostate tissue and suppress \(\alpha\)-aconitase and presumably mitochondrial activity (Fig. 1; Franklin et al. 2005, Desouki et al. 2007). Other early changes involve promoter hypermethylation and repressed transcription of antioxidant enzymes of the glutathione S-transferase family (Tokumaru et al. 2004).

Although never examined collectively in a single cohort, this implies that, in contrast to the strict definition of the Warburg effect as aerobic glycolysis, both glycolytic and mitochondrial activity may be enhanced in localized PCa. However, exploiting these metabolic changes for the development of cancer biomarkers and therapeutics is not trivial owing to the complex interplay within metabolic pathways.

This complexity is illustrated by an enzyme, calcium/calmodulin-dependent kinase kinase 2 (CAMKK2), which was recently reported to be an AR target gene and highly expressed at the protein and transcript levels in PCa. At the transcript level, CAMKK2 appears to be more significantly expressed in PCa than in cancers at other organ sites based on the data available within Oncomine and other clinical databases (Massie et al. 2011). In untransformed tissues,
CAMKK2 is predominantly expressed in the CNS (Anderson et al. 2008). Inhibitors of CAMKK2 were initially developed to treat obesity and proved effective in mouse models (Tokumitsu et al. 2002, Anderson et al. 2008). Of the small number of CAMKK2 substrates identified, AMP-regulated kinase (AMPK) was the best characterized and has so far provided the predominant reference point to explain the functional effects of CAMKK2 in both the hypothalamus and PCa cells (Hawley et al. 2005, Massie et al. 2011). Interestingly, in the hypothalamus, the CAMKK2–AMPK axis mediates the response to the hunger-stimulating hormone ghrelin, thereby affecting whole-body energy metabolism (Anderson et al. 2008), while in PCa cells, CAMKK2-dependent activation of AMPK leads to increased activity of phosphofructokinase, a rate-limiting enzyme in glycolysis. This promotes glucose consumption and lactate production (Massie et al. 2011). Intriguingly, AMPK is also activated in untransformed cells under conditions of metabolic stress/ATP deprivation. In this context, this enhances glycolysis and catabolic metabolism while inhibiting anabolic metabolism, thus rebalancing metabolic networks towards net energy production (Towler & Hardie 2007). In contrast, in cancer cells, activation of AMPK enhances glycolysis but does not always inhibit anabolic metabolism (Fig. 2). Explaining this paradox is proving a major challenge, but there are indications that certain AMPK substrates that negatively regulate protein synthesis are expressed as inactive androgen-regulated variants, for example tuberous sclerosis 2 (Wu et al. 2010, Rajan et al. 2011).

The availability of other metabolic inhibitors, such as metformin, which is used to treat type 2 diabetes and enhances AMPK activity through various mechanisms including inhibition of complex 1 of the mitochondrial respiratory chain, has increased the interest in defining patient cohorts that will benefit most from these drugs (Margel et al. 2013). However, responses to these drugs may vary and in part reflect differences in metabolic activity in different regions of the same tumour,
particularly in PCa, which is known to be a multifocal, heterogeneous disease. Tackling these issues systematically and in a timely manner will require new partnerships between industry and academia.

**Other oncogenic regulators of metabolism**

Although not the main focus of this review, it is useful to reflect briefly on the fact that PCa is not driven by a single transcription factor despite the heavy focus on the AR. Cell cycle progression and metabolism are convergently regulated by multiple oncogenic signalling events and transcription factors, including c-Myc, which is overexpressed and predictive of poor prognosis in a subset of cases (Hawksworth et al. 2010). Other examples include hypoxia-inducible factor 1α (HIF1A), which is associated with PCa metastasis (Ransinghe et al. 2013). In addition, p53 mutations, PTEN loss and enhanced PI3-kinase signalling are common events in advanced PCa (Elsberger et al. 2010, Grasso et al. 2012). All these are well-characterized regulators of metabolic changes, although so far more extensively studied in other cancers. Metabolic changes should therefore be viewed as central to cancer biology, and as AR-targeted drugs improve, we must be aware that we are applying selection pressures, which in part may enhance the contribution from other pathways to maintenance of cancer metabolism (Fig. 2; Carver et al. 2011, Thompson 2011).

C-MYC contributes to metabolic adaptations, especially the Warburg effect, at many of the same steps in metabolic pathways as the AR. The expression of the glucose transporter GLUT1 and various enzymes of the (oxidative) glycolytic pathway (hexokinase 2, phosphofructokinase, enolase 1 and lactate dehydrogenase A) have been reported to be under direct control of c-MYC in various cancers (Shim et al. 1997, Osthus et al. 2000, Kim et al. 2004). Interestingly, many of these effects are exerted in cooperation with HIF1 (Gordan et al. 2007). Furthermore, recent results have indicated that c-MYC is also responsible for driving enhanced glutaminolysis in cancer cells, thereby maintaining mitochondrial function and oxidative phosphorylation. Glutamine transporters and mitochondrial glutaminase, GLS1, appear to be directly or indirectly (via miRNAs) regulated by c-MYC (Wise et al. 2008, Gao et al. 2009). Intriguingly, many cancers driven by c-MYC amplification or overexpression seem to be highly dependent on glutamine, and glutamine deprivation leads to rapid exhaustion of citric acid cycle intermediates and apoptosis (Yuneva et al. 2007). c-MYC may also play a role in more global metabolic reprogramming, such as redirecting citric acid cycle intermediates into other anabolic pathways like nucleic acid or amino acid synthesis with clear parallels to the reprogramming effects recently attributed to the AR (O’Connell et al. 2003). Potentially, the balance between oncogenic transcription factors might be a crucial factor here as androgen stimulation inhibits the expression of c-MYC in PCa cells (Kokontis et al. 1994).

Loss of WT p53 function is one the most common mutations in virtually all human cancers (Kandoth et al. 2013), leading to loss of cell cycle and apoptotic control as well as chromosomal instability (Hollstein et al. 1991). It is usually a loss of one allele and missense mutation in the second that cause the deficit in p53 WT activity (Kastan & Berkovich 2007). In contrast, gain-of-function mutations in p53 can confer oncogenic properties, promoting resistance to apoptosis upon treatment with chemotherapeutics (Blandino et al. 1999). WT p53 can act as a tumour suppressor and is able to revert many of the metabolic effects on, e.g. glycolytic flux exerted by c-MYC and HIF1α by suppressing the expression of genes associated with glucose uptake and the pentose phosphate shunt pathway (Fig. 2; Jiang et al. 2011, Zawacka-Pankau et al. 2011).

In addition, p53 controls glutamine metabolism through activation of GLS2, a mitochondrial glutaminase (Hu et al. 2010). This seems contradictory at first because c-MYC is also capable of interfering with glutamine metabolism, albeit through controlling the expression of the mitochondrial glutaminase GLS1 (Yuneva et al. 2012). However, while activation of glutaminolysis through GLS1 diverts TCA cycle intermediates into anabolic pathways, p53-mediated activation of GLS2 promotes ATP production through oxidative phosphorylation (Voussen 2010). The crosstalk between the AR and p53 has not been intensively studied but reports indicate that activation of p53 is able to inhibit AR activity (Cronauer et al. 2004), while loss of p53 promotes MYC-dependent PCa (Thompson et al. 1995). It will be important to characterize the effects of mutated p53 on PCa cells, particularly in metastatic disease.

**Metabolic feedback effects and stress responses**

Changes in metabolic flux impose stresses on cells. For example, elevated anabolic metabolism and protein synthesis particularly increase the flux through the endoplasmic reticulum (ER), where newly synthesized proteins are folded and post-translationally modified. ER stress is often associated with increased ribosome
biogenesis and elevated rates of splicing and transcript turnover. As rate-limiting organelles in protein and transcript processing the ER and the nucleolus, are significant sensors and responders to the metabolic stress (Bravo et al. 2013, Grummt 2013). The ER plays a role as a principal site for protein folding and the nucleolus in the processing and assembly of ribonucleoprotein complexes to sustain protein synthesis and splicing. Thus, the genes required for the assembly of these structures and for stress signalling would be expected to be coordinately regulated by the AR and also by other oncogenic transcription factors. Strikingly, the AR has indeed been reported to activate the ER stress response (Segawa et al. 2002). In addition, early studies on rats showed that castration leads to the progressive disorganization of the nucleolus in prostate cells, which can be reversed by testosterone injection (Dahl 1976). Further results indicate that AR can directly enhance the transcription of rRNA (Mainwaring & Derry 1983, Li et al. 2013).

**ER and the unfolded protein response**

The imposition of metabolic stress on cells triggers a series of signalling events in the cell known as the unfolded protein response (UPR). In mammalian cells, there are three arms to this response, each culminating in the processing and activation of a transcription factor (ATF4, ATF6 and XBP1; Gardner et al. 2013). Target genes for these transcription factors include heat-shock proteins with chaperone functions and autophagy genes. During autophagy, misfolded proteins and organelles become enveloped in a membrane structure called the autophagosome and ultimately degraded in the lysosomes (Suh et al. 2012). This process enables cells to maintain quality control and also to produce energy under nutrient-deficient conditions. In addition, the ER-associated degradation pathway can be activated partly by changes in gene expression. This pathway involves active extrusion of misfolded proteins from the ER into the cytoplasm through a pore complex in the ER membrane (Sec61 complex; Brodsky 2012). Once extruded, misfolded proteins can then be polyubiquitinylated prior to proteasomal degradation (Brodsky 2012).

Recently, we employed ChIP and expression profiling on human tumours to identify AR target genes and binding sites associated with castration-resistant PCAs (CRPC; Sharma et al. 2013). We identified around 2500 AR binding sites in CRPC tissue, of which around half were found only in tissue but not in cell lines, indicating context dependency (Sharma et al. 2013). Additionally, gene expression profiling identified a 150-gene signature associated with CRPC, which were defined as genes that were initially androgen-responsive, subsequently repressed by androgen deprivation and ultimately re-expressed/highly expressed in a xenograft model of CRPC and in addition were also highly expressed in human CRPC (Sharma et al. 2013). From this work, it appears that the XBP1 arm of the UPR is androgen-regulated with a key kinase/endonuclease in the pathway, IRE1, being actively induced by androgen treatment in cell lines and XBP1 itself forming part of the 150-gene signature (Sharma et al. 2013). Strikingly, refining this list by linking it tightly to AR binding sites and poor prognosis produced a core signature of 16 genes associated with poor prognosis, which still included ER genes linked to the UPR (Sharma et al. 2013). Interestingly, the gene signature included anterior gradient 2, which is both an XBP1 target gene that represses inflammatory bowel disease and has previously been reported to be a prognostic marker in PCa (Higa et al. 2011, Mimura et al. 2012, Wayner et al. 2012).

More work is needed to determine whether this pathway might be an adaptive response to treatment and/or a necessary adjunct to metabolic stresses imposed by aberrant AR activity in localized disease. Interestingly, a regulator of the UPR, 78 kDa glucose-regulated protein, has been reported to be a biomarker for localized PCa. Hence, it may be that UPR is an important adaptive response in progression to late-stage disease and/or upon the imposition of stresses through treatment (Tan et al. 2011). Evidence has recently emerged from other cancers for the importance of UPR activation in carcinogenesis. In lymphoma, activation of the ATF4 arm of the UPR supports c-Myc-dependent tumorigenesis by driving the expression of genes necessary for the assembly of autophagosomes (Hart et al. 2012).

**Metabolic feedback through changes in metabolite pools**

Changes in metabolic flux may also alter the size of metabolite pools to sustain the post-translational modification of proteins. As discussed earlier, metabolic reprogramming is an important feature of PCa, and furthermore, metabolic pathways are known to provide the adducts to sustain acetylation, methylation and glycosylation. Consequently, it is interesting to consider whether changes in the transcription of metabolic enzymes may in turn affect the stability of transcription factors and/or chromatin accessibility by affecting these
modifications. Recently, the enzymes in the hexosamine biosynthesis pathway were shown to be androgen regulated and overexpressed in PCa patients (Itkonen et al. 2013). Strikingly, this pathway is sustained by metabolites sourced from the major metabolic processes in the cell (glucose from glycolysis, glutamine from amino acid metabolism, acetyl-CoA from lipids and carbohydrate turnover and UTP from nucleotide metabolism; Hanover et al. 2010, Slawson et al. 2010). The end-product is an aminosugar conjugate called UDP-N-acetylglucosamine (UDP-GlcNAc), which serves as a substrate for different protein-modifying enzymes. For example, O-GlcNAc transferase can add a monosaccharide O-GlcNAc modification to serine/threonine residues throughout the cell. Alternatively, UDP-GlcNAc can also be used for more complex N-linked glycosylation in the ER. As an example, O-GlcNAc modification of c-Myc stabilizes the protein by reducing proteasomal degradation rates (Chou et al. 1995a,b). De-convoluting the influence of these changes on cancer cells will require proteomic approaches to map modification sites and further development of glycosylation-site-specific antibodies. In contrast, acetylation and methylation are more established post-translational modifications as global changes in histone acetylation and methylation are hallmarks of cancer cells (Plass et al. 2013). Recently, mutations in iso-citrate dehydrogenases (IDH1 and IDH2) were reported, which result in the production of the ‘oncometabolite’ 2-hydroxyglutarate (Chowdhury et al. 2011). 2-Hydroxyglutarate inhibits 2-oxoglutarate-dependent oxygenases, such as histone lysine demethylases, leading to aberrant histone methylation patterns. Albeit IDH mutations occur at a low frequency in PCa (Ghiam et al. 2012), it is interesting that IDH1 is an androgen-regulated gene and could therefore play a role in a subset of patients. On the other hand, lipid turnover provides a significant source of acetyl groups to a major degree due to the activity of nuclear ATP-citrate lyase (ACLY), an enzyme required for de novo fatty acid synthesis responsible for generating cytosolic acetyl-CoA and oxaloacetate (Zaidi et al. 2012). This enzyme is both an AR target gene and activated by Akt phosphorylation, which is further enhanced by the loss of PTEN in cancer (Berwick et al. 2002, Wellen et al. 2009, Massie et al. 2011). ACLY inhibitors or knockdown of ACLY in turn reduce histone acetylation and tumour growth in xenografts (Hatzivassiliou et al. 2005, Wellen et al. 2009). This raises the intriguing possibility that the transcriptional activity of the AR may be further enhanced by increased histone acetylation and concomitant chromatin opening and enhancer activity.

A further example of regulatory effects on the supply of hydrocarbon adducts in PCa centres on sarcosine, a metabolite in the one-carbon/folate pathway from which methyl groups are generated. Sarcosine is significantly increased in some but not in all PCa cohorts and has been reported to be detectable in urine samples (Sreekumar et al. 2009, Jentzmik et al. 2010, Wagner & Luka 2011). The enzyme required to synthesize this metabolite is glycine N-methyltransferase (GNMT), an AR target gene in PCa cell lines (Ottaviani et al. 2013). Strikingly, both sarcosine and GNMT have been reported to negatively regulate DNA methyltransferase activity (Wang et al. 2011). Collectively, AR may therefore promote histone acetylation at the expense of DNA methylation in PCa. In contrast, c-Myc is known to increase the expression of other genes in the one-carbon/folate pathway as well as targeting DNA methyltransferases to specific loci (Nikiforov et al. 2002, Brenner et al. 2005). Targeted DNA hypermethylation is, in many cancers, a hallmark of reprogramming associated with cancer progression and resulting in the silencing of candidate tumour suppressors including the glutathione S-transferases referred to earlier (Akhavan-Niaki & Samadani 2013). Consequently, like the UPR, chromatin modifications responding to metabolic flux may partly reflect the relative activity of the AR and other oncogenic transcription factors in PCa.

**Future perspectives**

ChIP, sequencing and expression profiling have provided the tools to uncover connections between the AR and metabolic changes in PCa. However, multi-parametric approaches to assess the effects of transcription and signalling on the flux and capacity of metabolic pathways in an integrated manner are still lacking. Arguably, the more progress that is made in affecting the AR using drugs, the more we will select for other oncogenic transcription factors that will sustain cancer metabolism. Consequently, the challenge in targeting cancer metabolism is not to switch it off but rather to tip the balance sufficiently to make a mainstream cytotoxic drug or inhibitor of oncogenic signalling more effective without actively promoting a competing oncogenic process. This is a challenge that can never be entirely met, but if we are able to use glycosylation, acetylation and methylation as surrogate response markers, we may in the future be able to more sensitively assess that balance. As we learn more about the systems biology of cancer metabolism, this will become more achievable and will assist us in repositioning clinically approved drugs developed to treat metabolic diseases to fight PCa.
Declaration of interest
The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of the research reported.

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