The genomic landscape of prostate cancer

Sylvan C. Baca1,2,3 and Levi A. Garraway1,2,3,4*

1 Harvard Medical School, Boston, MA, USA
2 Department of Medical Oncology, Dana-Farber Cancer Institute, Boston, MA, USA
3 The Broad Institute of MIT and Harvard, Cambridge, MA, USA
4 Center for Cancer Genome Discovery, Dana-Farber Cancer Institute, Boston, MA, USA

Prostate cancer is a common malignancy in men, with a markedly variable clinical course. Somatic alterations in DNA drive the growth of prostate cancers and may underlie the behavior of aggressive versus indolent tumors. The accelerating application of genomic technologies over the last two decades has identified mutations that drive prostate cancer formation, progression, and therapeutic resistance. Here, we discuss exemplary somatic mutations in prostate cancer, and highlight mutated cellular pathways with biological and possible therapeutic importance. Examples include mutated genes involved in androgen signaling, cell cycle regulation, signal transduction, and development. Some genetic alterations may also predict the clinical course of disease or response to therapy, although the molecular heterogeneity of prostate tumors poses challenges to genomic biomarker identification. The widespread application of massively parallel sequencing technology to the analysis of prostate cancer genomes should continue to advance both discovery-oriented and diagnostic avenues.

Keywords: prostate cancer, genomic, genome sequencing

Prostate cancer is the second most common cancer in men worldwide and causes over 250,000 deaths each year (Jemal et al., 2011). However, many men with prostate cancer do not develop symptomatic disease. Overtreatment of indolent tumors may result in significant morbidity. A deeper understanding of the genomic differences between lethal and indolent prostate cancer, as well as elucidation of “druggable” effectors dysregulated by genetic alterations, should improve patient stratification and speed the development of targeted therapies.

With the advance of genome characterization technologies over the last two decades, the somatic alterations that may drive prostate tumors have come into sharper focus. In this mini-review, we survey the field of prostate cancer genomics, highlight recent findings, and discuss prospects for future research.

THE MUTATIONAL SPECTRUM OF PROSTATE CANCER

All categories of DNA sequence alterations contribute to prostate tumorigenesis, including point mutations, small insertions or deletions, copy number changes, and chromosomal rearrangements (Figure 1). An overview of each category of alteration, and discussions of its contribution to prostate cancer biology, is presented below.

SOMATIC COPY NUMBER ALTERATION

Most prostate cancers exhibit somatic copy number alterations (SCNAs), with genomic deletions outnumbering amplifications in early stages of disease (Visakorpi et al., 1995). Early studies relied on cytogenetics, fluorescence in situ hybridization and molecular genetic approaches to map candidate cancer genes to regions of SCNAs (Brothman et al., 1999). In recent years, comparative genomic hybridization and high-density single nucleotide polymorphism arrays have allowed high-resolution genome-wide analysis of SCNAs. Statistical analyses of genome-wide copy number data have narrowed the boundaries of recurrent alterations considerably and have pinpointed novel cancer genes in these regions (Beroukhim et al., 2007; Taylor et al., 2010; Robbins et al., 2011).

The extent of SCNA is generally modest in pre-cancerous prostatic intraepithelial neoplasia (PIN), but becomes increasingly prevalent along the spectrum from localized adenocarcinoma to metastatic disease (Zitzelsberger et al., 2001). Particular recurrent SCNAs are enriched in advanced tumors. For example, tumors that fail androgen ablation therapy show frequent amplification of chromosomes 7, 8q and X (Visakorpi et al., 1995; Ales et al., 2006; Holcomb et al., 2009). Animal models of prostate cancer indicate that genes in these regions, such as the androgen receptor gene (X) and the MYC proto-oncogene (8q), contribute to cancer progression (discussed in detail below).

POINT MUTATIONS AND SMALL INSERTIONS–DELETIONS

Relative to structural alterations, recurrent point mutations are less common in primary prostate cancers (Kan et al., 2010). Primary tumors generally harbor one to two somatic variants per million base pairs – far fewer than known carcinogen-driven tumors such as lung cancer or melanoma, but comparable to breast, renal, or ovarian cancers (Greenman et al., 2007; Plesance et al., 2010a,b; Berger et al., 2011). While most of these mutations confer no proliferative advantage, a handful of recurrent oncogenic mutations have been defined.

The reported prevalence of mutations in several known cancer genes varies widely and depends on tumor purity, stage, histological grade, and exposure to treatments. For example, RB1, TP53, and PTEN are preferentially mutated in locally advanced...
Defects in DNA mismatch repair (MMR) machinery have been reported in prostate cancers and may accelerate progression to display more clinically aggressive behavior. Activating mutations in KRAS and BRAF occur in 10% of Asian patients but are rare in Caucasian men, perhaps reflecting different environmental etiology or biological behavior of cancers in these populations (Watanabe et al., 1994; Konishi Cairns et al., 1997) while the androgen receptor is mutated only in metastatic or treatment-resistant disease (Linjaa and Visakorpi, 2004; Taylor et al., 2010). Ethnicity may influence mutation prevalence as well. Activating mutations in KRAS and BRAF occur in ~10% of Asian patients but are rare in Caucasian men, perhaps reflecting different environmental etiology or biological behavior of cancers in these populations (Watanabe et al., 1994; Konishi Cairns et al., 1997; Cho et al., 2006).

Defects in DNA mismatch repair (MMR) machinery have been reported in prostate cancers and may accelerate progression to castration-independence (Dahiya et al., 1997; Chen et al., 2001). Reported in prostate cancers and may accelerate progression to reflect different environmental etiology or biological behavior of cancers in these populations (Watanabe et al., 1994; Konishi Cairns et al., 1997; Cho et al., 2006).

FIGURE 1 | Genomic alterations in four high-risk prostate cancers. Cross-plots depicting genomic rearrangements and copy number alterations in four prostate tumors analyzed by whole-genome sequencing (unpublished data). Green and pink lines designate interchromosomal and intrachromosomal rearrangements, respectively. Somatic copy number alterations are indicated in red (amplification) and blue (deletion) in the inner rings. Gleason scores indicate the two most prevalent histologic grades in each tumor. Pathological stage is noted as well, where pT3 indicates locally invasive disease.

GENOMIC ALTERATIONS

Genomic alterations in prostate cancer. The discovery of ETS family gene fusions in roughly half of prostate cancers heralded a novel class of alterations in epithelial malignancies as a whole (Tomlins et al., 2005). The most common and prototypical ETS fusion places the oncogenic ERG transcription factor under control of the androgen-regulated TMPRSS2 gene, leading to high expression in the prostate epithelium. Subsequent research has identified a host of similar oncogenic fusions, where a proto-oncogene is adjoined to a highly active promoter (Tomlins et al., 2007; Kumar-Sinha et al., 2008; Palanisamy et al., 2010). Since mutation or amplification of oncogenes is less common in early-stage prostate cancer, genomic rearrangements may comprise an important means of cancer gene dysregulation in nascent tumors.

Complete sequencing of prostate cancer genomes has provided further insight into chromosomal rearrangements in prostate cancer. Primary tumors may harbor an average of approximately 100 rearrangements, including translocations, deletions, insertions, and inversions (Figure 1, Berger et al., 2011). Some tumors display “closed chains” of balanced rearrangements, in which multiple DNA breaks occur throughout the genome and the resulting fragments are shuffled and rejoined to one another. These rearrangements may arise when the affected genetic loci are physically proximal to each other, possibly due to co-regulation by transcriptional machinery or nuclear co-localization in open- or closed-chromatin compartments (Osborne et al., 2004; Berger et al., 2011). Consistent with this hypothesis, androgen stimulation can induce physical co-localization of TMPRSS2 and ERG and permit fusion of these genes de novo via a topoisomerase 2B-mediated mechanism (Halffner et al., 2010).

The diverse categories of genomic alterations underscore the need for comprehensive genomic analyses both to understand tumor biology and to direct targeted therapies on a genotype-specific basis (Roychowdhury et al., 2011).

CELLULAR PATHWAYS DYSREGULATED BY RECURRENT PROSTATE CANCER GENOMIC ALTERATIONS

Genomic alterations in prostate cancer can increasingly be conceptualized in terms of the molecular processes and pathways on which they impinge (Taylor et al., 2010). Mutations in prostate cancer may affect signal transduction pathways that regulate growth and proliferation, as well as genes involved in the normal development of the prostate. Below, we highlight several themes and pathways that provide a framework for understanding genomic alterations in prostate cancer.

PI3K AND MAPK SIGNALING

The phosphoinositide 3-kinase (PI3K) pathway is a central mediator of cellular proliferation and growth that is aberrantly activated in prostate cancer. In response to pro-proliferative signals, PI3K catalyzes the formation of phosphatidylinositol (3,4,5)-triphosphate (PIP3), which recruits Akt to the plasma membrane. Upon phospho-activation at the plasma membrane, Akt phosphorylates a wide array of substrates that promote proliferation and cell survival. Prostate tumors achieve activation of PI3K signaling most frequently via inactivation of the tumor-suppressor gene PTEN (Figure 2). PTEN encodes a lipid-protein phosphatase that counteracts signaling by PI3K via dephosphorylation of PIP3. Loss of heterozygosity at the PTEN locus is found in up to 70% of primary prostate cancers and inactivating mutations occur in 5–10%...
FIGURE 2 | Somatic alterations in the PI3K pathway in prostate cancer. Selected genes in the PI3K pathway are depicted, alongside the mechanisms by which they are altered in prostate cancer. Putative proto-oncogenes are boxed in red and tumor-suppressor genes in blue. PI3K signaling is frequently activated by deletion of PTEN. PHLPP1 encodes a phosphatase that dephosphorylates activated Akt, and is frequently co-deleted with PTEN in metastatic tumors (Chen et al., 2011). Genomic rearrangements disrupt MAGI2, which encodes a scaffolding protein that stabilizes PTEN (Ely et al., 2000; Berger et al., 2011). Recurrent deletions inactivate the FONDH1A gene, which encodes a transcription factor substrate of Akt that mediates PI3K signaling. Although rare, oncogenic mutations in the receptor tyrosine kinase EGFR or AKT1 may activate the pathway upstream or downstream of PI3K (Cai et al., 2006; Boermans et al., 2008). The expression of most pathway members is dysregulated at the transcript level as well.

Amplification of PIK3CA, which encodes the catalytic subunit of PI3K, occurs in 13–39% of primary tumors and 50% of castration-resistant tumors (Edwards et al., 2003; Sun et al., 2009; Agell et al., 2011). Activating mutations have been observed in ~5% of primary tumors (Sun et al., 2009; Barbieri et al., 2011). PIK3CA activation and PTEN loss tend to be mutually exclusive, which suggests functional redundancy — although larger sample sizes are needed to assess this relationship robustly (Sun et al., 2009). Interestingly, PTEN loss and PIK3CA activation co-occur in endometrial cancer, suggesting that multiple lesions are required to activate the pathway, or that these events engage disparate oncogenic mechanisms (Ma et al., 2005). In support of the latter possibility, oncogenic Akt-independent signaling downstream of mutant PIK3CA has been observed in both primary tumors and cancer cell lines (Nusse et al., 2009).

The PI3K pathway may be activated by genomic alterations at additional pathway nodes and dysregulated expression of constituent genes (Figure 2; Dong et al., 2006; Cai et al., 2008; Taylor et al., 2010). Determining whether these lesions predict sensitivity or resistance to PI3K pathway inhibitors has become an active area of translational research.

The mitogen-activated protein kinase (MAPK) pathway also plays a role in prostate cancer pathogenesis, especially in advanced and castration-resistant tumors. MAPK pathway activation is associated with higher tumor stage and grade and recurrent disease (Guzo et al., 1999). In the setting of castration resistance, PI3K and MAPK signaling are often coordinately dysregulated (Gao et al., 2006; Kinkade et al., 2008). Evidence for collaboration between

(Cairns et al., 1997; Gray et al., 1998; Barbieri et al., 2012). Inactivation of PTEN is enriched in advanced tumors and correlates with decreased cancer-specific survival (McMenamin et al., 1999; Sirsat et al., 2009). PTEN loss in the mouse prostate collaborates with other tumor-promoting events such as loss of TPS3 and over-expression of c-Myc or ERG (Chen et al., 2005; King et al., 2009; Kim et al., 2012).

Amplification of PIK3CA, which encodes the catalytic subunit of PI3K, occurs in 13–39% of primary tumors and 50% of castration-resistant tumors (Edwards et al., 2003; Sun et al., 2009; Agell et al., 2011). Activating mutations have been observed in ~5% of primary tumors (Sun et al., 2009; Barbieri et al., 2011). PIK3CA activation and PTEN loss tend to be mutually exclusive, which suggests functional redundancy — although larger sample sizes are needed to assess this relationship robustly (Sun et al., 2009). Interestingly, PTEN loss and PIK3CA activation co-occur in endometrial cancer, suggesting that multiple lesions are required to activate the pathway, or that these events engage disparate oncogenic mechanisms (Ma et al., 2005). In support of the latter possibility, oncogenic Akt-independent signaling downstream of mutant PIK3CA has been observed in both primary tumors and cancer cell lines (Nusse et al., 2009).

The PI3K pathway may be activated by genomic alterations at additional pathway nodes and dysregulated expression of constituent genes (Figure 2; Dong et al., 2006; Cai et al., 2008; Taylor et al., 2010). Determining whether these lesions predict sensitivity or resistance to PI3K pathway inhibitors has become an active area of translational research.

The mitogen-activated protein kinase (MAPK) pathway also plays a role in prostate cancer pathogenesis, especially in advanced and castration-resistant tumors. MAPK pathway activation is associated with higher tumor stage and grade and recurrent disease (Guzo et al., 1999). In the setting of castration resistance, PI3K and MAPK signaling are often coordinately dysregulated (Gao et al., 2006; Kinkade et al., 2008). Evidence for collaboration between
these pathways continues to emerge. For instance, PTEN-induced senescence may be overcome by up-regulation of MAPK signaling induced by overexpression of HER2 (Ahmad et al., 2011). Up-regulation of RAS family members, RAF1 and BRAF, or down-regulation of SPRY1 or SPRY2 genes, are common and enriched in prostate cancer metastases (Kwabi-Addo et al., 2004; McKie et al., 2005; Taylor et al., 2010). In some cases, expression of RAS, RAF1, and BRAF is activated by oncogenic fusions with highly expressed promoters (Palaisamy et al., 2011; Würg et al., 2011). Repression of the RAS-GAP gene DARCIP by EZH2 may activate MAPK signaling and drive progression and metastasis (Mån et al., 2010). Defining the relevant mechanisms of pathway activation in greater detail will likely inform strategies for targeting castration-resistant tumors.

**CELL CYCLE REGULATORY GENES**

Several cell cycle regulatory genes are disrupted in prostate cancer. Inactivation of cell cycle inhibitors appears to be required to avoid senescence induced by oncogenic signaling and possibly to bypass androgen-regulation of growth in metastatic or castration-resistant tumors.

Two critical cell cycle regulatory genes, TP53 and RB1, are commonly deleted or mutated in metastatic tumors (Bookstein et al., 1993; Heidenberg et al., 1995; Tricoli et al., 1996; Hyytininen et al., 1999). p53 activates expression of the p21WAF1 cyclin-dependent kinase inhibitor, and the Rb protein regulates transition from the G1 to S cell cycle phase. Rb1 inactivation is common in castration-resistant tumors (Holcomb et al., 2009; Sharma et al., 2011). Likewise, inactivation of p53 is necessary to bypass cellular senescence mechanisms that are activated upon loss of PTEN (Chen et al., 2005).

Another key cell cycle regulator, CDKN1B, encodes the p27Kip1 cyclin-dependent kinase inhibitor, and resides within the 12p13 chromosomal region that is frequently deleted. Low p27Kip1 expression correlates with poor pathological prognostic markers (Vis et al., 2000; Dreher et al., 2004). Amplification of SKP2, which encodes a ubiquitin ligase that targets p27Kip1 for proteosomal degradation, may also serve to inactivate p27Kip1 (Taylor et al., 2010; Robbins et al., 2011). Disruption of CDKN1B promotes prostate cancer coordinately with hemizygous deletion of PTEN, suggesting an interaction between p27Kip1 and the PDK pathway (Di Cristofano et al., 2001). Likewise, p27Kip1 induces senescence in PIN lesions driven by Akt1 in mice (Maumader et al., 2008).

**DEVELOPMENTAL AND ANDROGEN-REGULATED GENES**

Normal developmental and androgen-regulated processes appear to be co-opted during oncogenesis in the prostate. Several genes that participate in the development and differentiation of the prostate epithelium are dysregulated in prostate cancer (Prins and Putz, 2008).

The androgen receptor regulates cellular proliferation and differentiation in response to hormonal signals in the prostate epithelium. While androgen receptor is not mutated in primary tumors, the AR gene is frequently mutated or amplified in metastatic and castration-resistant disease (Visakorpi et al., 1995; Koivisto et al., 1997; Linja and Visakorpi, 2004). AR point mutations allow promiscuous activation by steroid hormones such as estrogens, progestins, glucocorticoids, and androgen antagonists in 10–30% of refractory cases (Gaddipati et al., 1994; Linja and Visakorpi, 2004). Alteration of androgen signaling may participate in localized disease as well: several AR-interacting genes are mutated or dysregulated in primary tumors, including NCOA2, NRIP1, TFK2, and EP300 (Taylor et al., 2010).

**GENOMIC HETEROGENEITY OF PROSTATE CANCER**

Prostate cancer may arise in multiple foci from independent precursor cells that are driven to neoplastic transformation by carcinogenic exposures or genetic predisposition (Androulidakis and Cheng, 2010). The presence of genomic lesions can vary between foci, including TMPRSS-ERG fusion, MYC amplification, and TP53 mutation (Mirandani et al., 1995; Jenkins et al., 1997; Melera et al., 2007). Multiple distinct clones can be identified in a single biopsy (Ruiz et al., 2011), but most metastatic prostate cancers appear to originate from a single clone within a primary
for discovery of novel cancer genes and biomarkers as well, since genomic characterization of large cohorts of aggressive tumors has only recently become feasible.

Indeed, whole-exome sequencing of over 100 primary prostate tumor–normal pairs revealed that the ubiquitin ligase complex subunit gene SPOP is among the most frequently mutated genes in primary tumors, though its role in cancer was heretofore unrecognized (Barbieri et al., 2012). This study also identified novel recurrent mutations in the fork-head transcription factor gene FOXA1 and mediator complex gene MED12. Experimental study will be required to determine whether these mutations engage known molecular pathways relevant to prostate cancer or reflect novel mechanisms of oncogenesis.

Several hurdles must be overcome for prostate cancer genomics to impact the clinical management of this disease. For instance, biopsies produce scarce material for clinical genotyping and may not fully capture the relevant molecular heterogeneity of a given tumor. Expression signatures have not yet demonstrated sufficient prognostic value to merit widespread use. In addition, recurrent genomic lesions identified thus far are largely not considered “druggable.”

These challenges can likely be surmounted by new approaches. For example, genomic characterization may identify opportunities to leverage synthetic lethality by inhibiting targets that are essential in the setting of a particular mutation, such as poly(ADP-ribose) polymerase in ETS-fusion positive prostate cancer (Brenner et al., 2011). The analysis of multiple samples from a primary tumor and perhaps from circulating tumor cells may allow aggressive tumor subclones to be identified. Ultimately, new paradigms for clinical trials may be required that incorporate cancer genomic information. In spite of these challenges, genomic profiling is likely to play a critical role in the clinical management of this malignancy.


Conflict of Interest Statement: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.