

Stem Cells and Prostate Cancer

Scott D. Cramer
Editor

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Preface

Prostate cancer is common and kills people every day. Recently, understanding of the biology of adult tissue stem cells and their cognate cancers has identified striking similarities in normal stem cells and tumor-initiating cells, or the so-called cancer stem cells. The defining properties of a stem cell are self-renewal and multilineage differentiation. Many cancers possess tumor-initiating cells with these properties. Several groups have been investigating these principles in the prostate from multiple perspectives. *Stem Cells and Prostate Cancer* is meant to synthesize current directions in research on prostate stem cells and prostate cancer tumor-initiating cells.

Similarities between normal prostate stem cells and prostate tumor-initiating cells, for instance the ability for self-renewal and multilineage differentiation, have focused attention on normal stem cell biology. There are now very good data, summarized in this book, which demonstrate self-renewal and multilineage differentiation of populations of adult prostate cells from both mouse and humans. Although few studies have taken these experiments to clonal resolution, the mounting evidence is for one or more stem cell populations in the adult prostate. There is controversy regarding multiple aspects of prostate stem cell biology: Is it the cell of origin of prostate cancer or is it a more differentiated prostate cell that “gains” more stem-like properties, is there one prostate stem cell or multiple stem cells in different compartments, and what is the role of stem cells in castrate-resistant disease? These concepts and more are addressed by leaders in the field of *Stem Cells and Prostate Cancer*. The potential significance of the prostate stem cell in prostate cancer development and in the etiology of castrate-resistant disease makes this area of high clinical and translational significance for basic, translational, and clinical scientists interested in disease models.

The topics covered in *Stem Cells and Prostate Cancer* range from hormonal control of the prostate stem cell, methods of identification and characterization of prostate stem cells and prostate tumor-initiating cells, the role of the stem cell niche in differentiation, the tumor microenvironment, targeting the stem cell for prevention, and the use of stem cell models for validating prostate cancer genetics. The authors and topics were chosen to represent the spectrum of research in prostate stem cells from some of the best in the field. Each chapter represents a unique view on prostate

stem cells. In general, I have had a very light hand in editing these chapters so that the intent, tone, and perspective remain those of the contributing authors.

One underlying technique that is described in virtually all chapters is tissue recombination developed and refined by Jerry Cunha over several decades of pioneering research. In tissue recombination, fetal urogenital sinus mesenchyme, dissected from rodent embryos, is recombined with prostate epithelium and regrafted into a mouse host. This technique is described in multiple places in *Stem Cells and Prostate Cancer*. Originally these studies were used to demonstrate the instructive power of the mesenchyme in prostate epithelial development. Through multiple iterations of the model, this technique has guided our understanding of hormonal control of prostate development, endocrine targets in cancer, the contribution of tumor-associated fibroblasts to prostate cancer development and, most recently as described in this book, the use in evaluating prostate stem cells. The reader will find it clear that no definitive description of work on prostate stem cells is without discussion of the valuable contributions of tissue recombination to the field. My hat goes off to Jerry for his pioneering work that has facilitated our progress in the prostate stem cell field in uncountable ways.

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Chapter 1

Prostate Stem Cells, Hormones, and Development

Gail S. Prins and Wen-Yang Hu

Abstract While it is established that prostate cancer is a hormone-dependent disease, the cell(s) of origin of prostate cancer, i.e., the tumor-initiating cells, is still in debate. Strong evidence has emerged which indicates that prostate cancer can originate from both basal and luminal epithelial cell populations. In addition, prostate epithelial stem cells are candidates for the tumor-initiating cell based on work in hematopoietic and breast cancers and because of the growing acceptance of the cancer stem cell paradigm. To appreciate the interrelationships between the multiple cells of origin of prostate cancer, it may be necessary to first fully understand the prostate stem cell differentiation lineage during normal development and adult tissue maintenance as well as the factors that regulate stem cell self-renewal and lineage commitment. Recent advances in stem cell research have permitted isolation of prostate stem cells and shed light on the hierarchical relationship between the epithelial stem cells and their differentiated lineage. Furthermore, prostate cancer stem cells have been isolated and characterized from several prostate tumors which may provide an explanation for the known clinical and molecular heterogeneity of human prostate cancers. Although prostate stem cells and prostate cancer stem cells appear to be androgen receptor negative, new findings have established key roles for several other hormones in regulating prostate stem cells and their niche. Together, this new knowledge should allow for greater insight into the details of prostate development and to increased understanding of prostate cancer initiation and progression. In this chapter we will highlight recent advances in hormone modulation of prostate stem cells and their early progeny in development, normal tissue homeostasis, and cancer.

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1.1 Prostate Gland Development

The prostate gland develops embryologically from the endodermal urogenital sinus (UGS) under the influence of androgens produced by fetal Leydig cells upon chorionic gonadotropin stimulation. In humans, prostate development occurs during the second and third trimester and is complete at the time of birth (Lowsley 1912; Prins 1993). The prostatic portion of the urethra develops from the *pelvic* (middle) part of the UGS, and prostate development initiates when UGS epithelium in this region penetrates into the surrounding mesenchyme to form the primordial prostate buds. The glandular epithelium of the prostate differentiates from these endodermal UGS cells and the associated mesenchyme differentiates into the prostate stroma, which primarily contains fibroblasts and smooth muscle cells (Prins 1993; Donjacour and Cunha 1993, 1995; Prins and Putz 2008; Moore and Persaud 2008). While the human prostate does not consist of separate lobes, four morphologically distinct prostatic zones have been identified by McNeal. The prostatic urethra divides the prostate into an anterior fibromuscular zone and a posterior glandular portion that contains the peripheral, central, and transition zones (McNeal 1983).

A significant amount of information about prostate gland development at the morphologic, cellular, and molecular levels has been derived from studies using rodent models. In contrast to humans, the rodent prostate gland is rudimentary at birth and undergoes the majority of its development during the first 15 days of life. Although the developmental process is continuous, the development of the rodent prostate can be categorized into five distinct stages involving determination, initiation or budding, branching morphogenesis, differentiation, and pubertal maturation (Prins and Putz 2008). Determination of the prostate occurs before there is clear morphological evidence of a developing structure and involves expression of molecular signals that commit a specific field of UGS epithelial cells to a prostatic cell fate. Development of the prostate phenotype commences as UGS epithelial stem and progenitor cells form outgrowths or buds that penetrate into the surrounding UGS mesenchyme (UGM) in the ventral, dorsal, and lateral directions caudal to the bladder (Cunha et al. 1983; Cunha 1973, 1976, 1984). At birth, the ventral, dorsal, and lateral rodent prostate lobes primarily consist of unbranched, solid, elongating buds or ducts, and subsequent outgrowth and patterning occur postnatally (Fig. 1.1a). During this time, proliferation of epithelial cells occurs primarily at the leading edge of the ducts (i.e., distal tips) (Prins et al. 1992). Branching morphogenesis begins when the elongating UGS epithelial buds contact the prostate mesenchymal pads that are peripheral to the periurethral smooth muscle. At that point, secondary, tertiary, and further branch points are established with continued outgrowth in the proximal-to-distal direction and with increased complexity (Hayashi et al. 1991; Timms et al. 1994). Epithelial and mesenchymal cell differentiation is temporally coordinated with branching morphogenesis. Lumenization of the solid epithelial cords begins in the proximal ducts and spreads to the distal tips, occurring concomitantly with epithelial differentiation into separate basal and luminal cell layers to form a simple columnar epithelium (Fig. 1.1b).

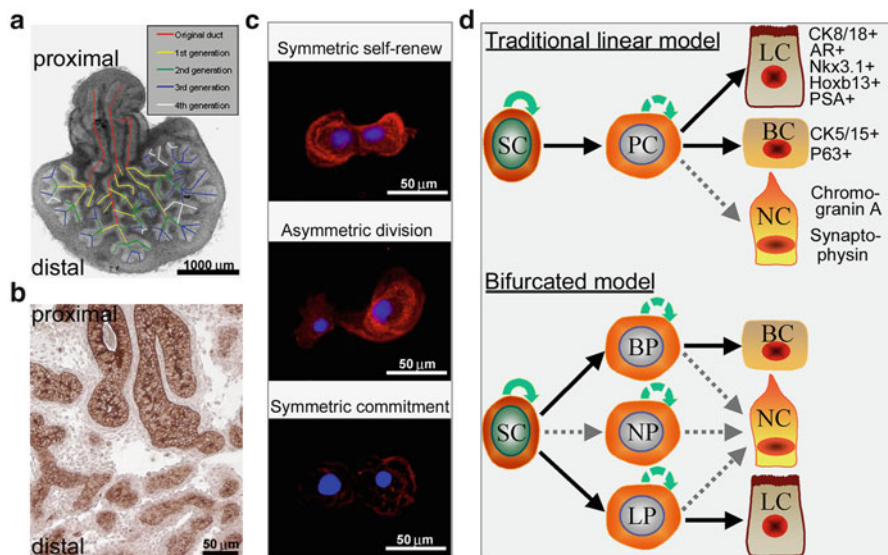


Fig. 1.1 Prostate development and stem cells hierarchy. **(a)** Branching morphogenesis of rat ventral prostate lobe. The gland was removed at birth and cultured for 90 h as described (Huang et al. 2009). Images were taken every 30 min to track the branching events and a color-coded skeleton is used to indicate the generation of branches according to the following convention: The three primary buds that emerged from the UGS are considered the original ducts (red), branches that formed off the primary ducts are considered the first generation (yellow), and branches that formed off the first generation and elongate are considered the second generation (green), third generation (blue), and fourth generation (white). **(b)** Day 4 rat ventral prostate immunostained for CK8/18 reveals the proximal-to-distal spread of epithelial differentiation and lumen formation. Ducts in the proximal region of the gland have initiated lumenization concomitant with differentiation of luminal cells positive for CK8/18. In contrast, distal regions contain solid epithelial ducts with minimal luminal cell differentiation. **(c)** Immunolabeling of human prostate stem cells (isolated from day 4 prostaspheres) with stem cell marker CD49f identifies three types of stem cell divisions: (1) symmetric renewal, one stem cell gives rise to two identical daughter stem cells (CD49f^{high}); (2) asymmetric division, one stem cell gives rise to one daughter stem cell (CD49f^{high}) and one daughter progenitor cell (CD49f^{low}); and (3) symmetric commitment, one stem cell gives rise to two differentiated daughter cells (CD49f^{low}). **(d)** Prostate stem cell hierarchical models: in the traditional linear hierarchy model (top), self-renewing prostate stem cells (SC) give rise to intermediate, transit-amplifying progenitor cells (PC). These cells have high proliferative capacity and enter differentiation pathways to give rise to terminally differentiated luminal cells (LC), basal cells (BC), and neuroendocrine cells (NC). In the bifurcated model (bottom), a common SC with self-renewal capacity undergoes asynchronous cell division to give rise to lineage-restricted basal progenitor cells (BP) and luminal progenitor cells (LP). These PCs possess transient self-renewal capacity and terminally differentiate into basal and luminal epithelial cells. The lineage of neuroendocrine cells (NC) is unclear and may arise from the hierarchical intermediate BP and LP that produce BC and LC, or it may have a separate neuroendocrine progenitor (NP) origin

Mature prostate ducts contain three phenotypically and functionally distinct epithelial cell types (basal, luminal, and neuroendocrine cells) embedded in a fibromuscular stroma (Cunha et al. 1983, 1987; Cunha 1973; Long et al. 2005; Prins 1993; Prins and Putz 2008). Prostate basal epithelial cells are located adjacent to the

basal lamina and express p63, cytokeratin (CK) 5, and CK 14. They are largely androgen receptor (AR) negative and are independent of direct androgen action for survival (Prins and Birch 1995). Luminal epithelial cells, which comprise the majority of the prostate epithelium, are cuboidal and short columnar exocrine cells with an apical surface towards the ductal lumen. They are characterized by the expression of CK8/18, NKX3.1, and AR (Bhatia-Gaur et al. 1999; Hayward et al. 1996; Isaacs et al. 1981; Robinson et al. 1998; Wang et al. 2001a). Luminal cells are dependent on androgens for viability and function, producing prostatic secretory proteins such as prostate-specific antigen (PSA), prostatic acid phosphatase (PAP) in humans, and prostate-binding protein (PBP) in rodents. Neuroendocrine cells are dendritic-like intraepithelial regulatory cells with a hybrid phenotype having both neural and epithelial characteristics. They are a minor population scattered throughout the basal layer and are identified by the expression of neuroendocrine markers chromogranin A and synaptophysin (Rumpold et al. 2002).

1.2 Prostate Epithelial Stem Cells and Lineage Hierarchy

Adult prostate stem cells have been identified in human and rodent prostate glands where they play an essential role in tissue replenishment throughout life (Bhatt et al. 2003; Garraway et al. 2010; Goldstein et al. 2008; Isaacs 2008; Kasper 2007; Lawson et al. 2010; Leong et al. 2008; Liu et al. 2011; Xin et al. 2007). This rare cell type self-renews and has potential to differentiate into the three distinct epithelial cell types, essential characteristics of bona fide stem cells. Prostate stem cells are relatively growth quiescent, occasionally dividing to self-renew and generate daughter progenitor cells. Studies across multiple systems as well as the prostate epithelium have characterized three types of stem cell divisions (Fig. 1.1c): (1) symmetric division, aka symmetric self-renewal, which generates two identical stem cells; (2) asymmetric division which generates a single self-renewing stem cell and a daughter cell that has entered the earliest stage of differentiation (progenitor cell); and (3) symmetric commitment division whereby a stem cell produces two daughter progenitor cells (Morrison and Kimble 2006; Scaffidi and Misteli 2011; Tomasetti and Levy 2010; Wu et al. 2007). Unlike the stem cell, the daughter progenitor cell has transit-amplifying capacity through rapid cell divisions. As the progenitor cell proliferative potential is exhausted, it undergoes terminal differentiation.

While prostate stem cells are present in several regions of rodent prostatic ducts, accumulated prostate stem cells with considerable growth potential have been found in the proximal region of ducts close to the UGS, and the survival of these cells does not require the presence of androgens (Tsujimura et al. 2002; Goto et al. 2006). Primitive proximal prostate stem cells that are able to regenerate functional prostatic tissue *in vivo* are also programmed to reestablish a proximal-distal ductal axis. In contrast, prostate stem cells in the distal region of the prostate duct have more limited growth potential and require androgens for survival (Goto et al. 2006). See Chapter 6 for a more complete discussion of the prostate stem cell niche.

Although the lineage hierarchy for the prostate epithelium has not been settled, epithelial differentiation of stem cells into differentiated basal, luminal, and neuroendocrine cells has been documented in the rodent prostate and in isolated human prostate cancer stem cells (Hudson 2004; Isaacs 2008; Kasper 2007; Long et al. 2005; Robinson et al. 1998; Wang et al. 2001a, b). These studies on stem cell differentiation have been observed with changing patterns of cytokeratins, cell-specific markers, and alterations in AR expression, an early marker of luminal epithelial cell differentiation. Two models have been proposed for the prostate epithelial stem cell lineage into differentiated basal, luminal, and neuroendocrine cell types (Fig. 1.1d). In the traditional linear hierarchy model, self-renewing prostate stem cells residing in the basal cell layer undergo asymmetric cell division giving rise to daughter progenitor cells with high proliferative potential, aka the transit-amplifying cells. In response to signals from the stem cell niche, these cells enter early differentiation pathways to eventually form separate basal, luminal, and neuroendocrine cells (Hudson 2004; Hudson et al. 2000; Isaacs and Coffey 1989). Phenotypic intermediate-type cells that co-express basal and luminal markers have been observed both *in vitro* and *in vivo* (Garraway et al. 2003; Long et al. 2005; Prins et al. 1995; Robinson et al. 1998). This suggests that basal and luminal cells are hierarchically related through common progenitor cells that give rise to differentiated basal cells and luminal cells. In the bifurcated model, basal cells and luminal cells represent separate epithelial cell lineages that originate from a common stem cell. These lineages may be sustained by intermediate transit-amplifying cells and/or lineage-restricted basal and luminal cell progenitors (Hudson 2004; Long et al. 2005; Wang et al. 2001a). The lineage of neuroendocrine cells is unclear. Neuroendocrine cells may arise from the hierarchical prostate epithelial stem and progenitor cells that produce basal and luminal cells, or they may have a separate progenitor cell origin as shown in the bifurcated model.

1.3 Prostate Stem Cell Isolation and Characterization

It is widely accepted that adult stem cells are involved in normal tissue maintenance throughout life while cancer stem cells support cancer growth (Presnell et al. 2002; Smith et al. 2007). Although the cell(s) of origin for prostate cancer may include luminal, basal, neuroendocrine, progenitor, and stem cells (Goldstein et al. 2010a, b; Kasper 2008, 2009; Wang and Shen 2011), it is increasingly evident that the resultant prostate cancers contain cancer stem cells that continuously seed and maintain tumor growth (Gu et al. 2007; Maitland et al. 2011). While conventional therapies for prostate cancer eradicate the majority of cells within a tumor, most patients with advanced cancer eventually progress to androgen-independent, metastatic disease that remains essentially incurable by current treatment strategies. Recent evidence has shown that cancer stem cells are a subset of tumor cells that appear to be therapy-resistant and are responsible for maintaining cancer growth which may be the underlying cause of disease relapse (Cocciadiferro et al. 2009;

Maitland and Collins 2008; Miki and Rhim 2008; Oldridge et al. 2012; Wang et al. 2012). Thus understanding the regulation of both normal stem cells and cancer stem cells may provide new insight into the origin and treatment of prostate cancer. Towards this end, identification and characterization of these rare cell populations has been a major research effort during the past decade with marked progress being realized utilizing flow cytometry and prostasphere culture (Garraway et al. 2010; Liu and True 2002; Xin et al. 2005).

Flow cytometry sorts cell populations by their specific cell surface CD markers, and expression profiles of CD markers have been extensively described for both normal and neoplastic prostate cell types (Liu et al. 2004; Liu and True 2002). Importantly, multiple CD molecules are enriched in prostate stem cells including Sca-1 (Xin et al. 2005), $\alpha 2\beta 1$ integrin (Collins et al. 2001), CD133 (Richardson et al. 2003; Vander Griend et al. 2008), CD44 (Liu et al. 2004), CD117 (Leong et al. 2008), CD49f, and Trop2 (Garraway et al. 2010; Goldstein et al. 2008, 2010a). Combinations of antibodies specific for these markers have been used to isolate stem-like cells by FACS from dissociated prostate tissues or epithelial cell cultures, and their stem cell capabilities have been tested using various *in vivo* systems (Goldstein et al. 2008; Guo et al. 2012; Leong et al. 2008). An example of this approach using 2-channel flow cytometry from primary prostate epithelial cell cultures is shown in Fig. 1.2a. It is important to note, however, that there is no current consensus on the antigenic profile required for isolating a pure stem cell population from prostate epithelium by flow cytometry. The disadvantages of FACS include relative low cell yield when using multiple stem cell markers and cell damage following dissociation, labeling, and sorting.

Side-population analysis utilizing flow cytometry in combination with functional properties of stem cells is a convenient tool to characterize stem-like cells within mixed epithelial cell populations. Stem cell side-populations were first identified in hematopoietic stem cells enriched from heterogeneous cell populations based upon their unique ability to actively extrude Hoechst 33342 (Brown et al. 2007; Goodell et al. 1996). ABCG2 is a member of the family of ATP-binding cassette (ABC) transporters, and it pumps several endogenous and exogenous compounds out of cells including Hoechst 33342. Widely expressed in a variety of stem cells, ABCG2 was found to be a molecular determinant of the side-population phenotype and is recognized as a universal marker of stem-like cells (Ding et al. 2010; Zhou et al. 2001). The side-population assay, based on exclusion of Hoechst dyes, has proven to be a valuable method for identifying and sorting stem and early-stage progenitor cells in a variety of tissues and species. Application of this approach to assess putative prostatic stem cell numbers from heterogeneous prostate epithelial cell populations is shown in Fig. 1.2b (Bhatt et al. 2003; Brown et al. 2007; Mathew et al. 2009).

Another approach for enrichment and characterization of prostate stem cell populations is the prostasphere assay which utilizes a three-dimensional (3D) culture system to form spheroid structures (Garraway et al. 2010; Hu et al. 2011, 2012; Lukacs et al. 2010; Xin et al. 2007). First used for the isolation and characterization

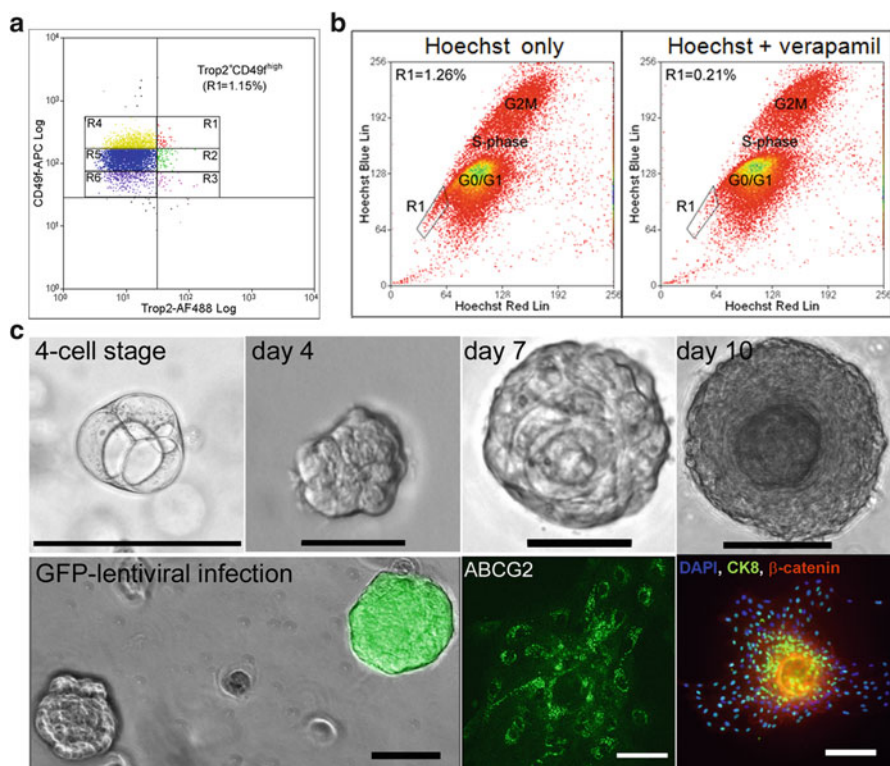


Fig. 1.2 Methodological approaches for prostate stem cell isolation and characterization. (a) Flow cytometry analysis of normal human prostate epithelial cells (PrEC) from primary cell culture following labeling with Trop2-AF488 and CD49f-APC antibodies. A subpopulation of Trop2⁺CD49f^{high} (R1=1.15%, red) represents prostate stem cells. (b) Hoechst 33342 dye efflux fluorescence-activated flow cytometry analysis reveals a side population in human PrEC (gated as R1) that actively excludes the dye. PrEC were stained with 5 μ g/mL of Hoechst 33343 either in the absence or presence of 50 μ M of verapamil hydrochloride, an ABCG2 inhibitor. Windows for the side population are determined by comparison of cells without and with verapamil in each FACS analysis. (c) Prostate stem/progenitor cells isolation using prostasphere assay. Human PrEC from disease-free organ donors were established in primary 2D cultures and transferred to 3D Matrigel-slurry culture as described (Hu et al. 2011). Under these conditions, ~0.2–1% of primary PrEC cells (stem cell population) survive and undergo self-renewal to form spheroid structures termed prostaspheres. By day 4 of culture, prostaspheres 30–40 μ m in diameter are visible, increasing in size through transit amplification to 60–100 μ m by day 7. To confirm clonality of the spheroids, mixed primary PrEC cells with or without lentiviral-GFP were transferred to 3D Matrigel cultures. At day 7, formed prostaspheres were either entirely GFP⁺ or GFP[−] (bottom left), indicating the clonal origin of prostaspheres. Day 7 prostasphere cells express multiple prostate stem cell markers (Hu et al. 2011) including the transporter protein ABCG2 (bottom middle). By day 10 of culture, prostaspheres grow >150 μ m in diameter and form a visible double layer of cells (top right). Immunocytochemistry of a day 10 prostasphere shows central cells as differentiating CK8⁺ (green) luminal cells (lower right) and peripheral cells p63⁺ basal cells (Hu et al. 2011). Bar = 50 μ m

of neural stem cells, it is widely accepted that only stem-like cells have the capacity to survive and proliferate to form spheroids in 3D culture. Using a Matrigel-slurry culture system in our laboratory, 0.2–1% of 2D cultured primary prostate epithelial cells (PrEC) are capable of survival and proliferation to form free-floating prostaspheres that are clonal in origin (Fig. 1.2c). Immunofluorescent labeling with multiple prostate stem cell markers confirms their stemness characteristics (Hu et al. 2011). That these spheroids consist of stem cells is best demonstrated by their ability to form fully differentiated and functional human prostate basal and luminal cells *in vivo* when reconstituted with inductive UGM (Hu et al. 2011). This prostasphere culture system closely mimics the *in vivo* situation as the cells are grown in a suspended semisolid gel, which allows the development of intercellular interactions. Several key variables contribute to the formation of these prostaspheres from PrEC including the age of the prostate donor, cell plating density, culturing techniques, and passage number, all of which influence the homogeneity or heterogeneity of the spheroids. The major advantages of the prostasphere assay are the functional isolation of prostate stem cells, expansion of the stem cell numbers *in vitro*, and the ability to manipulate them *in vitro* which provides research opportunities to identify regulation of stem and progenitor cell proliferation and differentiation.

At early stages of formation, the prostaspheres consist of stem-like cells undergoing synchronous self-renewal and asynchronous cell division to generate daughter early-stage progenitor cells that have not yet differentiated along cell lineages (Fig. 1.1c). By days 3–4 of culture, prostaspheres that are ~30 μm in diameter and consist of 20–40 cells are visible to the naked eye. Through rapid cell proliferation, they continue to grow with diameters reaching ~80–100 μm by day 7 (Fig. 1.2c). At this stage, cell markers indicate that the majority of cells express Nanog, Trop2, CD49^{high}, ABCG2, CD133, CD44, and SSEA4 with no immunostaining for p63, CK8, NKX3.1, and HOXB13 suggesting that the day 7 spheroid cells consist of prostate stem and progenitor cell populations. Gene expression analysis of day 7 spheroids by real-time qRT-PCR supports their stem/progenitor cell status with lack of luminal cell gene expression (Fig. 1.3). Interestingly, although the cells are p63 negative by immunocytochemistry, p63 mRNA levels similar to parental PrEC cells are observed suggesting that early differentiation towards a basal cell lineage has initiated. With continued culture through day 10 to day 30, spheroid cells undergo cytodifferentiation, forming double-layered prostaspheres with sizes of 150–200 μm (Fig. 1.2c). Immunostaining of day 10 prostaspheres reveals that peripheral cells are p63-positive basal-type cells while centrally located cells are positive for CK8/18 and NKX3.1 indicating their differentiation towards a luminal phenotype (Fig. 1.2c). With continued culture under basal conditions through day 30, prostaspheres form branching-type structures and undergo functional differentiation as indicated by PSA gene induction (Hu et al. 2011). Furthermore, their growth and differentiation can be driven by various conditions including coculture with stromal cells and treatment with differentiating factors such as hepatocyte growth factor (HGF) (Schalken 2007) or hormones as described below.

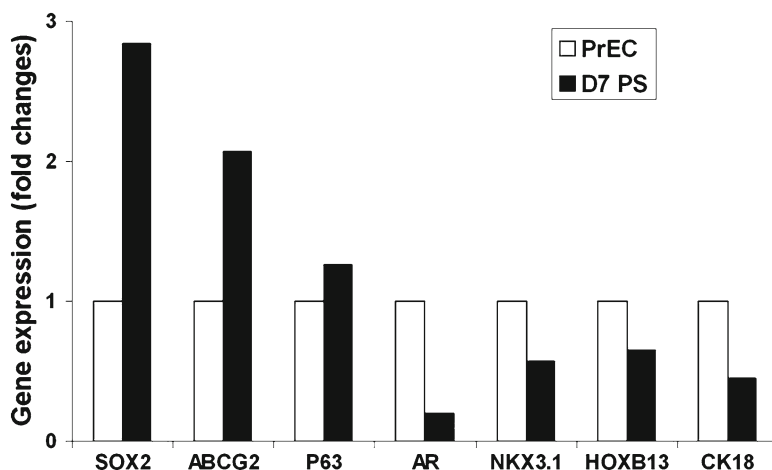


Fig. 1.3 Day 7 Prostate Stem Cell gene expression analyzed by real-time qPCR. Relative to the normal parental PrEC cells in 2D primary culture, day 7 prostate stem cells express increased levels of prostate stem cell markers Sox2, ABCG2, and basal cell marker p63 and low to negligible (<30–35 Ct cycles) levels of luminal cell differentiation markers including AR, NKX3.1, HOXB13, and CK18

1.4 Hormone Receptor Expression and Hormonal Regulation of Prostate Stem and Progenitor Cell Self-Renewal and Differentiation

Androgens are essential for prostate gland development and maintenance throughout life and are believed to play central roles in prostate cancer initiation and progression. Despite this, prostate epithelial stem and early progenitor cells are AR negative (Hu et al. 2011; Kasper 2009; Oldridge et al. 2012) and are thus not directly regulated by androgen action. As a result, any effects of androgens on prostate epithelial stem cell homeostasis and differentiation are most likely mediated through indirect actions on the stem cell niche which includes AR⁺ stromal cells and, in the mature prostate, AR⁺ luminal epithelial cells (Berry et al. 2008). Androgens have been shown to influence the secretion of multiple paracrine-acting factors by these cells during prostate development and in the adult tissue that may influence the stem cell niche including *Fgfs*, *Shh*, and *Wnts* (Prins and Putz 2008). While several studies have shown that prostate cancer stem-like cells are similarly AR negative (Kasper 2009; Oldridge et al. 2012), there are scattered reports on direct androgen action and AR protein in prostate cancer-initiating cells and prostate cancer stem cell subpopulations (Sharifi et al. 2008; Vander Griend et al. 2010). In addition to androgens, a number of other hormones are known to regulate prostate growth and function and to influence growth and progression of prostate cancer including estrogens (Prins and Korach 2008), retinoids (McCormick et al. 1999; Schenk et al. 2009), prolactin (Dagvadorj et al. 2007), growth hormone, and IGF-1 (Chan et al. 1998; Wang et al. 2005). Further, there is

clear evidence that mammary gland stem cells and daughter progenitors are under direct regulation by several of these hormones (Asselin-Labat et al. 2010; Joshi et al. 2010). In this context, we investigated whether prostate stem and progenitor cells express other hormone receptors and respond to the non-androgenic hormones that are known to influence the prostate gland.

Past research on estrogen action in the prostate gland has focused entirely on estrogen receptor (ER) α , ER β , and G protein-coupled receptor 30 (GPR30) within differentiated stromal, basal, and luminal cells. It is noteworthy that the different ERs within these cell types have apparent opposing actions; stromal cell ER α has proliferative and cancer-promoting actions (Ricke et al. 2008; Sissung et al. 2011) while ER β in basal and luminal epithelial cells has antiproliferative and proapoptotic activity (McPherson et al. 2010). GPR30, expressed at the plasma membrane and endoplasmic reticulum and activated by estradiol, initiates growth arrest and induces necrosis in prostate cancer cells (Chan et al. 2010). Recently, our laboratory discovered that human prostate epithelial stem and progenitor cells from disease-free prostates express robust levels of ER α , ER β , and GPR30 mRNA and protein (Hu et al. 2011). Further, prostaspheres cultured from primary PrEC in 1 nM estradiol-17 β (E₂) exhibited a marked increase in spheroid size and number (Hu et al. 2011) with elevated expression of multiple stemness genes at day 7 of culture as compared to vehicle alone (Fig. 1.4a). Using a side-population analysis of primary PrEC, we noted a biphasic effect of estradiol with increased stem cell numbers at 1–10 nM E₂ but limited stimulation at higher doses (Fig. 1.4b). Taken together, these findings implicate prostate stem/progenitor cells as direct estrogen targets and indicate that estrogens support stem cell self-renewal and progenitor amplification and maintain their stemness state within the prostate gland. Moreover, these results raise the intriguing possibility that prostate stem and early progenitor cell populations may be susceptible targets of elevated estrogen levels in aging men (Vermeulen et al. 2002).

To evaluate whether prostate cancer stem-like cells may likewise express ERs and respond to estrogens, we examined ER α , ER β , and GPR30 expression in stem and progenitor cells from prostate cancer specimens (Fig. 1.4c). Prostaspheres were cultured from primary prostate cancer cells (PCa-E) and matched benign prostate epithelial cells (EPZ) from the same patient at prostatectomy (kindly supplied by Dr. L. Nonn, University of Illinois at Chicago). The PCa-E cells were cultured from pathologically confirmed cores containing >80% cancer cells and expressed significantly elevated AMACR and reduced NKX3.1 as compared to the EPZ cells. As shown in Fig. 1.4c, there was a sixfold increase in ER α mRNA and 8–12-fold increase in GPR30 expression in both the patient benign and cancerous prostasphere cells as compared to spheroids grown from normal donor PrEC. For ER β , there was a fourfold increase in the PCa-E-derived stem/progenitor cells but not the benign EPZ cells relative to normal donor PrEC expression. Since the prostaspheres from PCa-E were mixed stem and progenitor cells that are not confirmed as prostate cancer stem-like cells, ERs were also evaluated in two human prostate cancer stem-like cell lines, HPET (Gu et al. 2007) and HuSLC (kindly supplied by Dr. S. Kasper, University of Cincinnati). Each cell line was generated from separate Gleason score 9 tumors, spontaneously immortalized and is capable of fully reestablishing the

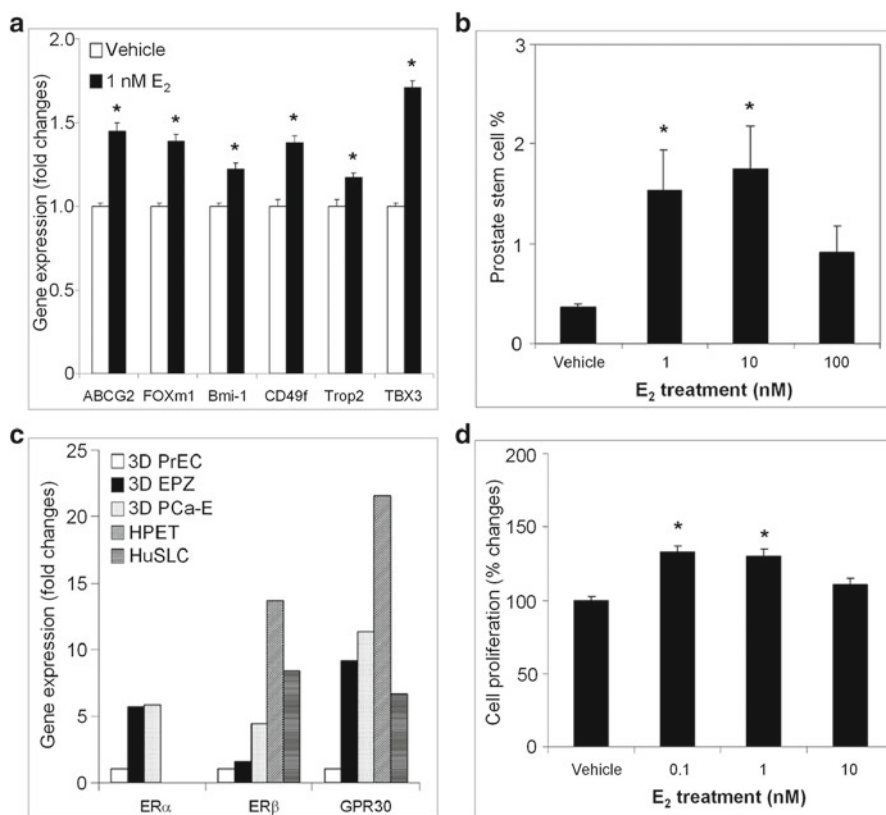


Fig. 1.4 Modulation of prostate stem and progenitor cell populations by estrogen. (a) Prostraspheres were cultured from disease-free primary epithelial cells in the absence or presence of 1 nM of estradiol-17 β (E₂) for 7 days, and gene expression was evaluated by qRT-PCR. E₂ significantly increased mRNA levels of stem cell markers ABCG2, FOXm1, Bmi-1, CD49f, Trop2, and TBX3. * P <0.05 vs. vehicle; n =4. (b) 2D primary prostate epithelial cells from disease-free donors were cultured for 72 h in 1, 10, or 100 nM E₂, and the Hoechst 33342 exclusion based side-population analysis by flow cytometry was used to measure the percentage of stem-like cells. * P <0.05 vs. vehicle by ANOVA; n =6. (c) ER expression by q RT-PCR in normal prostate stem-like cells and prostate cancer stem-like cells. A 3D prostrasphere assay was used to isolate and amplify the stem/early-stage progenitor cell populations from disease-free primary prostate epithelial cultures (PrEC), matched prostate epithelial primary cultures from benign regions (EPZ) and prostate cancer cores with >80% cancer cells from the same patient (PCa-E). HPET and HuSLC are two human prostate cancer stem-like cell lines established from Gleason score 9 human prostate cancer (kindly supplied by Dr. Susan Kasper). Data is normalized to ER expression levels in PrEC-derived prostraspheres which was set as 1. (d) HuSLC cells were cultured in the absence or presence of 0.1–10 nM of E₂ for 72 h. Cell proliferation was evaluated by MTT assay. Treatment of 0.1 and 1 nM of E₂ significantly increased the HuSLC cell proliferation. * P <0.05 vs. vehicle; n =4

original tumors *in vivo*. While both prostate cancer stem-like cell lines were negative for ER α , they expressed 10–15-fold higher ER β and 7–20-fold higher GPR30 levels compared to prostrasphere cells from normal prostate epithelium (Fig. 1.4c).

To determine if these cells are responsive to estrogens, HuSLC cells were cultured for 72 h in increasing concentrations of E_2 (Fig. 1.4d). Similar to the disease-free PrEC primary cultures, a biphasic response was observed on proliferation; however, the stimulatory effects were found at tenfold lower doses (0.1–1 nM E_2) than normal PrEC stem-like cells. Together, these results support heightened ER expression and estrogen action in prostate cancer stem-like cells. Importantly, this may provide a unique therapeutic opportunity to specifically target prostate cancer stem-like cells with selective estrogen receptor modulators (SERMs) or novel small molecules that interfere with ER signaling.

Recent findings from our laboratory demonstrate that retinoic acid can directly drive prostate stem/progenitor cells into differentiation pathways. Retinoids and retinoic acids are derivatives of vitamin A and play a major role in tissue homeostasis and organ development. Their actions are mediated through retinoid receptors $RAR\alpha$, β , and γ and $RXR\alpha$, β , and γ which form RAR/RXR dimers that directly regulate target gene expression (Metallo et al. 2008; Vezina et al. 2009). Retinoic acid and its synthetic analogs have great potential as anticarcinogenic agents since they trigger antiproliferative effects and augment differentiation in tumor cells. Because it has been suggested that stem cells are potential targets of cancer initiation and disease management, retinoids may influence the development and progression of prostate cancer by regulating stem cell differentiation and proliferation (Metallo et al. 2008). In a screen for steroid receptor expression in human prostaspheres derived from disease-free primary PrEC, we observed high expression levels of $RAR\gamma$, $RXR\alpha$, and $RXR\beta$ with lower expression of $RAR\alpha$ and $RAR\beta$ suggesting that stem/progenitor cells are potential retinoid targets (Fig. 1.5a). To test this directly, prostaspheres were established from PrEC in 10 nM all-trans retinoic acid (ATRA) and at day 4, spheroids were dispersed, stained with CD49f antibodies and dividing stem cells classified for division type (Fig. 1.1c). In vehicle cultures, 50% of stem cell divisions were symmetric self-renewal, and 18% were asymmetric cell divisions to generate a daughter progenitor cell (Fig. 1.5b). Exposure to ATRA shifted this to 28% symmetric stem cell self-renewal and 40% asymmetric cell division indicating that retinoic acid was driving the stem cells to enter a differentiation pathway. Continued culture of prostaspheres in ATRA resulted in advanced differentiation by day 7 as compared to vehicle cultures with increased size, bilayer formation, lumen initiation (Fig. 1.5c), and induction of AR, NKX3.1, and HOXB13 expression, markers of luminal epithelial cell differentiation (Fig. 1.5d). These findings support the multiple studies on the usefulness of retinoids in chemoprevention and treatment for prostate cancer (Huss et al. 2004; Schenk et al. 2009) and suggest that their actions may, in part, be mediated through direct actions on prostate stem cells, driving differentiation and limiting self-renewal. Thus, we predict that chemicals which either augment or interfere with retinoid signaling will have the capacity to directly alter human prostate stem cell differentiation with potentially beneficial or detrimental outcomes with regards to prostate health.

Several other members of the steroid receptor gene superfamily are highly expressed in the day 7 prostaspheres from disease-free PrEC including glucocorticoid receptor (GR), estrogen-related receptor- α ($ERR\alpha$), aryl hydrocarbon receptor (AhR), peroxisome proliferator-activated receptor (PPAR)- γ , vitamin D receptor

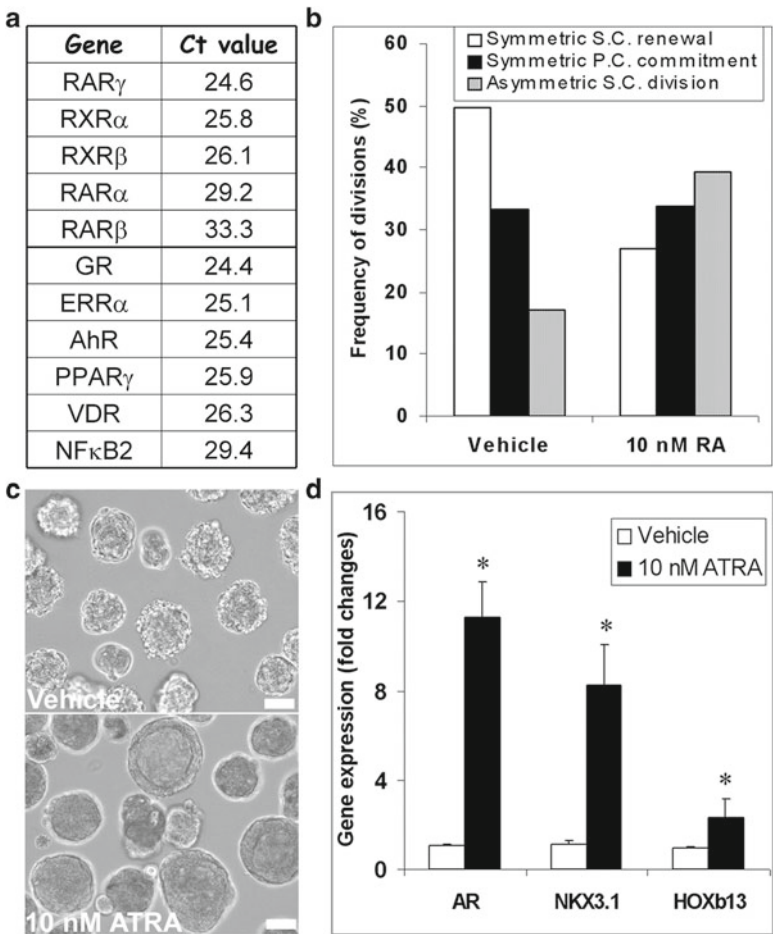


Fig. 1.5 Prostate stem/progenitor cells differentiation by retinoic acid. **(a)** PCR Array analysis (SA Biosciences) of nuclear receptor superfamily gene expression in day 7 prostaspheres cultured from primary PrEC. Ct <35 cycles considered detectable expression. **(b)** Stem cell division types observed in day 4 prostasphere cells as determined by CD49^{high} staining (see Fig. 1.1c). Division frequency in vehicle-treated spheroids was ~50% symmetric stem cell renewal, ~32% symmetric division of committed progenitor cells, and ~18% cells asymmetric division to one stem cell and one daughter progenitor cell. Culture in 10 nM ATRA shifted this cell division pattern to 28% symmetric stem cell self-renewal and 40% asymmetric stem cell division. Total 100~150 pairs of daughter cells/group were counted. **(c)** Culture of prostaspheres to 7 days in basal media (*top*) or 10 nM ATRA (*bottom*). ATRA stimulated spheroid growth and formation of double-layered epithelial cells compared to vehicle. Bar=50 μ m. **(d)** Culture of prostaspheres in 10 nM ATRA significantly increased AR, NKX3.1, and HOXB13 mRNA levels (qRT-PCR) compared to vehicle. * P <0.05. n =4

(VDR), and nuclear factor kappa beta (NF κ B2) (Fig. 1.5a). These receptors and their cognate ligands may thus have potential roles in regulating either stem cells or progenitor cell populations in the prostate gland. In support of this, a recent study documented that 1,25-dihydroxyvitamin D₃ induced cell cycle arrest in mouse

prostate epithelial stem/progenitor cell populations and drove them into differentiation pathways towards a luminal epithelial cell fate (Maund et al. 2011). Similar to retinoid treatment, these findings suggest a possible chemopreventive role for vitamin D₃ by targeting stem and progenitor cells to limit their proliferation and maintain epithelial differentiation phenotypes. Another recent study demonstrated that human prostate tumor-initiating cells with sphere-forming potential and multipotency exhibit increased NFκB signaling (Rajasekhar et al. 2011). Further, specific inhibitors of NFκB activation blocked their secondary sphere formation capacity and *in vivo* tumor initiation in animals suggesting that targeting NFκB in prostate cancer stem-like cells may have therapeutic efficacy.

In addition to steroid receptors, there is emerging evidence that prostate stem-like cells and progenitor populations may also be targets for protein hormones. Studies with transgenic mouse models determined that local prostate-specific prolactin (PRL) production resulted in a marked increase in the Sca-1 stem-like cells in prostate ducts which was associated with PRL-induced tumorigenesis (Rouet et al. 2010). Recent findings from our laboratory have also found significant expression of growth hormone (GH) receptor and insulin-like growth factor (IGF)-1 receptor in second passage prostaspheres cultured from Sprague–Dawley rat ventral, dorsal, and lateral lobes (unpublished studies with Dr. S. Swanson, University of Illinois at Chicago). Interestingly, these spheroids exhibited significant growth responses to exogenous GH (10–100 nM) suggesting that the stem/progenitors are direct targets of GH action in controlling prostate size and growth. These early findings indicate potential for regulation of normal and pathologic prostate growth via targeting this cell population with available pharmaceuticals that interfere with PRL and GH/IGF-1 signaling pathways.

1.5 Conclusions

In summary, although prostate epithelial stem cells and early-stage progenitor cells are AR negative and not considered direct androgen targets, there is emerging evidence to indicate that they are direct targets of multiple other steroid and protein hormones that can regulate their proliferative as well as differentiation status. This is schematized in Fig. 1.6 which proposes a hierarchical stem cell model (although this could equally apply to a bifurcated system) where some hormones including estrogens, GH, PRL, and others such as NFκB maintain stem/progenitor cell self-renewal and homeostasis whereas others including retinoids and vitamin D₃ stimulate the stem and progenitor populations to differentiate towards lineage cells. We propose that this tight balance of signals is involved in maintaining the stem cell niche and homeostasis within the prostate epithelium during normal development and through adulthood, responding to conditions as needed. It is possible that dysregulation of this balanced homeostasis contributes to prostate carcinogenesis and progression. A detailed insight into this regulatory system within the epithelial stem/progenitor cell populations may provide novel opportunities for chemoprevention and therapeutics for prostate cancer in the future.

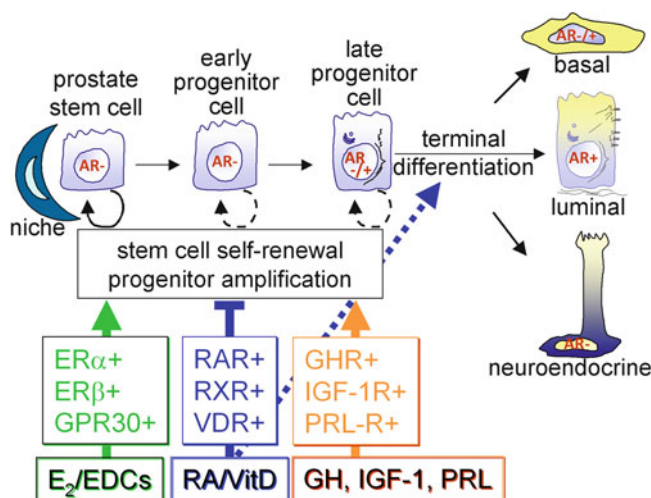


Fig. 1.6 Hormones directly target prostate stem/progenitor cells. Prostate stem cell hierarchy shows self-renewing prostate stem cells give rise to transit-amplifying progenitor cells. These cells possess transient self-renewal activity and produce large numbers of terminally differentiated basal cells and secretory luminal cells as well as a small number of neuroendocrine cells. While androgen receptor is not detectable, prostate stem/early-stage progenitor cells do express robust levels of steroid receptors including ERs and GPR30, RARs/RXRs, VDR, PRL, and GHR/IGF-1R. When activated by their cognate ligands, these receptors mediate diverse effects including stem cell self-renewal, progenitor cell amplification, and entry into differentiated lineage pathways. Together, these hormones influence development and homeostasis of the normal prostate gland and may play important roles in prostate cancer initiation and progression

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Chapter 2

Isolation and Characterization of Prostate Stem Cells

Andrew S. Goldstein and Owen N. Witte

Abstract Based on the unique capacity of the rodent prostate to undergo seemingly endless rounds of androgen cycling in response to castration and androgen add-back, the prostate has been proposed to contain long-term self-renewing stem cells. However the prospective isolation and characterization of stem-like cells from rodent and human prostate tissue has only been described over the last 2 decades. Several models of epithelial homeostasis in the adult prostate have been proposed based on either the presence of a multipotent tissue stem cell that differentiates through a series of intermediate developmental stages or the coexistence of

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multiple unipotent lineage-restricted stem cells. The isolation of cells with stem and progenitor activity is an important first step to delineate the epithelial hierarchy of the prostate. In addition, isolation of stem cells allows characterization of their functional capacities and the molecular programs regulating their activity. These studies will enable detection or targeting of stem and progenitor cells during various stages of neoplastic transformation and tumor progression, including the lethal phase of the disease, castration-resistant prostate cancer.

2.1 Introduction

While the existence of stem cells in the prostate has long been postulated, their isolation or purification for functional testing has only been described in the last decade. Pioneering androgen cycling experiments by Isaacs and colleagues (Isaacs 1985), later repeated by Wilson and colleagues (Tsujimura et al. 2002), show that long-term castration-resistant stem cells in the rodent prostate are capable of almost indefinitely regenerating the gland after castration-mediated prostate involution and androgen add-back. The adult prostate gland predominantly comprises basal cells and luminal secretory cells with a very minor component of neuroendocrine cells (Abate-Shen and Shen 2000; Shen and Abate-Shen 2010). While basal cells in the rodent prostate predominantly remain after castration, a subset of luminal cells also survive and may participate in gland regeneration upon administration of androgen (English et al. 1987). Divergent models have been proposed to describe prostate homeostasis, from a bipotent prostate stem cell capable of regenerating all mature cell types in the gland to the coexistence of multiple unipotent or lineage-restricted stem cells (Lawson and Witte 2007; Shen et al. 2008). Based on differential keratin stains in both the mouse and human prostate, some have proposed a developmental model starting from a primitive stem cell that undergoes maturation and differentiation through several intermediate cell stages (Okada et al. 1992; Xue et al. 1998; van Leenders et al. 2000, 2003; Hudson 2004). However, functional evidence of such a hierarchical structure has been lacking until recently.

In order to accurately define the prostate epithelial hierarchy based on functional studies, isolation of prostate stem and progenitor cells is an essential first step. In addition to delineating hierarchical relationships, stem cell isolation enables both molecular and functional characterization to determine the capacity of isolated stem cells and define the pathways regulating stem-like behavior. A comprehensive analysis of stem cell properties may lead to targeted therapies of stem-like cells in various stages of disease including the lethal castration-resistant prostate cancer (Feldman and Feldman 2001; Shen and Abate-Shen 2010).

2.2 Methods of Stem Cell Isolation

A number of indirect approaches have been taken to investigate stem cells in the prostate, including the use of BrdU labeling to identify slow-cycling label-retaining cells (Tsujimura et al. 2002). While label retention is a property that some believe

to be associated with stem cells (Cotsarelis et al. 1989; Berardi et al. 1995; Thorgeirsson 1996; Beauchamp et al. 2000; Lavker and Sun 2000; Slack 2000), this method alone does not provide functional evidence for stem cell activity. Importantly, intestinal tissue stem cells and hair follicle stem cells marked by the Wnt target gene *Lgr5* are rapidly dividing (Barker et al. 2007; Jaks et al. 2008), indicating that quiescence is not a universal property of adult stem cells. In this chapter, we will describe the two general approaches that have been described to functionally define stem cell populations in the prostate: isolation of enriched cell preparations from dissociated mouse and human prostate tissues and lineage tracing in genetically engineered mouse models.

In the first approach, cells are purified and isolated from preparations of dissociated prostate tissue. Isolated cells, separated or fractionated into populations enriched for stem cells and those depleted for stem cells, are placed into various *in vitro* and *in vivo* functional assays to determine their inherent proliferative, clonogenic, and regenerative capacities. This strategy enables parallel identification of cell populations from naïve rodent (primarily mouse) and human tissues taken from surgical specimens (Lukacs et al. 2010a; Goldstein et al. 2011). Importantly, cell preparations are easily collected for analysis of DNA, RNA, or protein to determine what molecular characteristics distinguish stem cells from their non-stem cell counterparts. An alternative strategy described to define prostate stem cells is lineage tracing in genetically engineered mice. In this approach, genetic marking is performed in a stem cell leading to expression of a reporter protein in the stem cell and all of its progeny (Wang et al. 2009; Choi et al. 2012). This strategy (described in greater detail in Sect. 2.2.2.2) allows for demonstration of hierarchical relationships within the intact gland, maintaining important interactions with neighboring epithelial cells, non-epithelial stromal and immune cell populations, and other components of the local microenvironment.

2.2.1 *In Vitro* Assays to Measure Function of Isolated Stem/Progenitor Cells

When taken out of their native site and grown in tissue culture, primitive cells should possess the capacity to extensively proliferate and self-renew under the appropriate conditions including growth factors and adhesive substratum (Barrandon and Green 1987; Ogawa 1993; Hudson et al. 2000; Uzgare et al. 2004; Lukacs et al. 2008). In contrast, more mature or differentiated cell populations, particularly those that are postmitotic, would be less likely to grow or persist long term. For this reason, clonogenic assays have been particularly useful in identifying cell subsets enriched for long-term immature cell activity (Ploemacher and Brons 1989; Reynolds and Weiss 1996; Dontu et al. 2003; Shackleton et al. 2006; Lim et al. 2009; Rock et al. 2009). Isolated cell populations can be tested using clonogenic *in vitro* assays that provide a quantitative measure of their proliferative and self-renewal activity. The two most commonly used assays are the colony-forming assay, measuring clonogenic and proliferative potential, and the sphere-forming assay, measuring both clonogenicity and self-renewal *in vitro* in a quantitative fashion (Fig. 2.1).

In vitro clonogenic assays

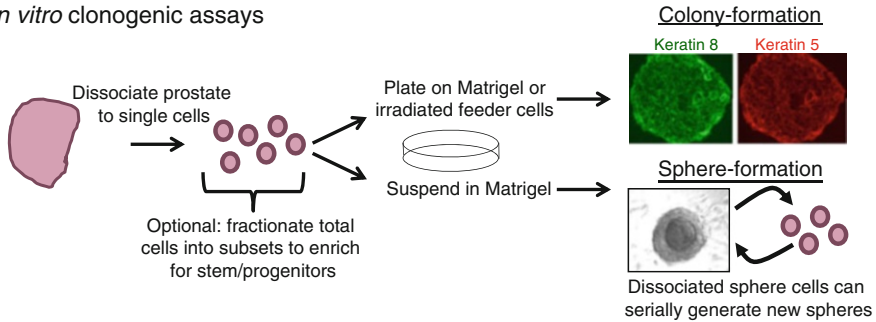


Fig. 2.1 *In vitro* clonogenic assays. Mouse or human prostate tissues are dissociated to single cells. Subsets of epithelium can be fractionated from dissociated preparations to compare functional activity of enriched or depleted cell populations. Cells that are plated in a two-dimensional environment on irradiated feeder cells or Matrigel will form colonies, the majority of which express both luminal (keratin 8) and basal (keratin 5) epithelial keratins. Alternatively, cells that are suspended in a three-dimensional environment of Matrigel will form spheres that can be dissociated to single cells and serially replated to measure self-renewal activity

2.2.1.1 Colony-Forming Assay

In the colony-forming assay, isolated cells are plated either directly onto a tissue culture dish, cocultured with irradiated feeder cells (such as adult fibroblasts, 3T3 fibroblasts, mouse embryonic fibroblasts), or on a matrix substratum (collagen or Matrigel) (Collins et al. 2001; Lawson et al. 2007; Lukacs et al. 2010a). Interestingly, colonies from mouse prostate co-express both basal (K5) and luminal (K8) keratins, representing an intermediate or putative transit-amplifying phenotype rarely observed in normal glands. When dissociated to single cells and serially replated, colonies exhibit limited self-renewal activity which is at least partially due to a Rho-kinase (ROCK)-mediated response, as inhibition of ROCK promotes colony self-renewal *in vitro* (Zhang et al. 2011). Alternatively, cultures of human prostate epithelial cells (PrECs) grown in low-calcium conditions demonstrate stem cell-like colony-forming activity (Litvinov et al. 2006).

While primary cells that form colonies maintain expression of some markers of cells in the gland, such as epithelial keratin expression, these cells lose the glandular structure characteristic of their native environment. Tsujimura et al. (2002) described a clonogenic assay where primary mouse prostate cells are suspended in collagen and grown *in vitro* to form ductal structures (Tsujimura et al. 2002). Cells from the proximal region are enriched for this activity and can generate glands containing distinct keratin 14+ basal and keratin 8+ luminal cells. Although a range of conditions can be used to measure colony-forming activity of naïve primary mouse and human prostate cells, each assay has been effectively utilized to compare the growth of distinct epithelial subpopulations (described further in Sect. 2.3). Recently, methods have been developed for long-term culture of mouse prostate stem cells that retain multi-lineage differentiation and self-renewal *in vitro* and *in vivo* (Barclay et al. 2008). These methods are discussed in more detail elsewhere in this book (Chaps. 9 and 10).

2.2.1.2 Sphere-Forming Assay

To quantitatively measure self-renewal activity, primary cells grown within a three-dimensional matrix of Matrigel can be expanded in vitro (Lawson et al. 2007; Shi et al. 2007; Xin et al. 2007). Matrigel is rich in extracellular matrix proteins including laminin, collagen, and fibronectin (Emonard et al. 1987a, b) which are found in the basement membrane structures surrounding benign prostate glands in their native microenvironment (Bonkhoff et al. 1991; Fong et al. 1991). Dissociated single cells can be isolated from primary spheres and replated in Matrigel to generate secondary spheres, demonstrating self-renewal activity (Lawson et al. 2007; Xin et al. 2007). This activity can be repeated numerous times during serial replating or passaging to demonstrate the presence of long-term self-renewing cells (Lawson et al. 2007; Shi et al. 2007; Xin et al. 2007; Goldstein et al. 2008; Garraway et al. 2010).

The outer layer of cells in mouse prostate spheres comprises p63+ cells, analogous to the outer layer of p63+ basal cells in the gland, that are proliferating based on positive stains for Ki67. Proliferating p63+ cells appear to spontaneously differentiate toward the center or luminal space, which is filled with p63- cells undergoing apoptosis as marked by TUNEL staining (Xin et al. 2007). Sphere cells of both mouse and human origin retain in vivo stem-like activity to reconstitute glandular structures containing both basal and luminal epithelial cells when transplanted into mice (Shi et al. 2007; Xin et al. 2007; Garraway et al. 2009). Both spheres and colonies are clonally derived indicating that they arise from a single stem or progenitor cell (Lawson et al. 2007; Garraway et al. 2010). These assays allow for identification of markers to enrich for functional stem/progenitor cell subsets that can grow in vitro. They also provide quantitative measures of progenitor function that can be used to determine pathways and factors regulating stem and progenitor cell activity (Mulholland et al. 2009; Lukacs et al. 2010b; Shahi et al. 2011).

2.2.2 *In Vivo Assays to Measure Prostate Stem Cells*

While in vitro assays have been utilized to quantify the functional activity of isolated cells from adult epithelial tissues, colony and sphere-forming assays are believed to measure progenitor activity rather than true stem cell function. For example, far greater numbers of mammary stem cell-enriched Lin⁻CD24⁺CD29^{hi} cells can generate clonogenic colonies in vitro than can repopulate mammary gland structures in vivo (Asselin-Labat et al. 2010). Therefore, in vivo assays are the most stringent tests of stem cell activity (Fig. 2.2), three of which will be described in the following section.

2.2.2.1 *In Vivo Tissue-Regeneration Assays to Measure Prospectively Isolated Stem Cell Populations*

Cunha and colleagues first described a tissue fragment recombination assay where mid-gestation urogenital sinus, the region destined to develop into the prostate, can

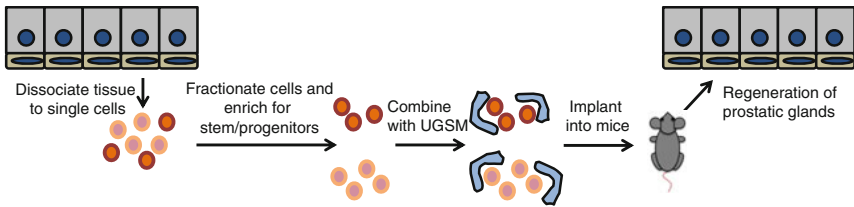
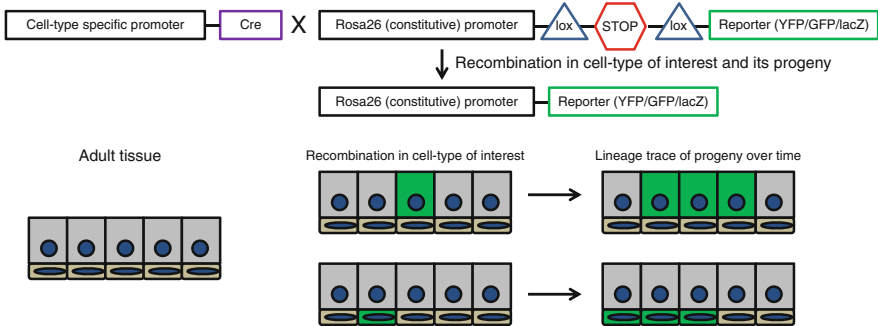
a *In vivo* tissue-regeneration**b** *In vivo* lineage tracing

Fig. 2.2 *In vivo* stem cell assays. **(a)** In the *in vivo* tissue-regeneration assay, prostate glands are dissociated to single cells and enriched/depleted subsets of cells are fractionated, combined with Urogenital Sinus Mesenchyme (UGSM), and implanted back into immune-deficient mice, either under the renal capsule or skin. Over 6–12 weeks, dissociated cells will regenerate prostatic glands. **(b)** An alternative approach is *in vivo* lineage tracing. The Cre recombinase, expressed in a cell-type-specific manner, will remove a STOP codon leading to constitutive expression of a reporter protein in the cell type of interest and all of its progeny

be physically separated into urogenital sinus mesenchyme (UGSM) and urogenital sinus epithelium (UGSE) and put back together under the renal capsule of immune-deficient mice (Cunha and Lung 1978). After a period of weeks to months, the recombined tissue will develop into prostatic glands. Our laboratory has made two important adaptations to utilize this assay with dissociated adult cells (Xin et al. 2003). First, we found that UGSM could support the regeneration of dissociated adult mouse prostate cells. The adult prostate could regenerate glands that resembled the native prostate gland (Xin et al. 2003). Since the epithelium was coming from the adult prostate, a second important adaptation was made to allow greater experimental control and perform transplantations without carefully timed matings. Xin et al. (2003) showed that UGSM could be dissociated to single cells, expanded in culture, frozen and thawed, and maintain its inductive activity on adult epithelium (Xin et al. 2003).

Since total dissociated adult mouse prostate cells could regenerate glands, the pool must contain stem-like tissue-regenerating cells, which could then be isolated using various approaches. Mouse prostate glandular regeneration is an extremely robust assay, used by many labs (Xin et al. 2003; Burger et al. 2005; Shi et al. 2007; Leong et al. 2008; Wang et al. 2009). A parallel dissociated cell tissue-regeneration assay using freshly isolated naïve benign primary human epithelial cells is more

difficult for two reasons. First, obtaining fresh human tissue requires a considerable degree of effort and coordination between surgeons, pathologists, and researchers in a timely manner (Goldstein et al. 2011). Secondly, human prostate tissue is most commonly isolated from aged men who suffer from a disorder either in the prostate or in a neighboring tissue, such as the bladder. In contrast, studies with mouse tissue are generally performed on young, healthy tissue. Despite these difficulties, we demonstrated the use of an analogous tissue-regeneration assay where naïve human epithelial cells could regenerate human prostate glands *in vivo* (Goldstein et al. 2010, 2011).

It is important to note that while the tissue-recombination assay can be easily adapted based on cell type and species of origin, the approach requires taking adult cells out of their niche in the prostate gland. The process of gland dissociation could disrupt critical cell–cell interactions, remove signals from supportive cell populations, and preferentially select for one cell type over another in transplanted preparations. As mentioned in the introduction, an alternative approach to retain the native structure is genetic lineage tracing.

2.2.2.2 In Vivo Lineage Tracing of Prostate Stem/Progenitor Cells and Their Progeny

The most common lineage tracing experiments utilize a cell-type or lineage-specific promoter to drive expression of the Cre recombinase either in a constitutive or regulated manner, reviewed by Fuchs and Horsley (2011). The Cre enzyme is a bacteriophage topoisomerase that specifically recognizes a short 34-base-pair stretch of DNA called a lox sequence, made up of two inverted repeats and a spacer region (Lakso et al. 1992). Mice engineered to express Cre from a lineage-specific promoter are most commonly bred with a reporter strain where lox sites flanking a STOP codon are placed between the ubiquitously expressed Rosa26 promoter and a reporter protein, such as green fluorescent protein (GFP) or lacZ (which can be detected upon the addition of the β -galactosidase substrate) (Soriano 1999; Barker et al. 2007; Fuchs and Horsley 2011). Using this strategy, the lox sites are excised allowing reporter expression only in the presence of the Cre recombinase. Since the recombination event occurs at the DNA level in the stem cell, all cells derived from that stem cell will retain the recombined allele and exhibit reporter expression. This strategy allows for robust tracing of the progeny from the original cells engineered to express the Cre protein. Therefore, the specificity and sensitivity of Cre expression in the cell type of interest are of vital importance for interpreting results.

2.2.2.3 In Vivo Castration and Androgen-Mediated Regeneration to Demonstrate Stem Cell Activity

The most impressive display of prostate stem cell activity is in its capacity to survive androgen ablation or castration and promote regeneration of the gland upon

administration of androgen (Tsuji-mura et al. 2002). The involution following castration and regeneration upon androgen add-back can be repeated almost indefinitely. Lukacs et al. (2008) utilized the tissue-recombination approach to demonstrate that adult prostate cells contain long-term self-renewing stem-like cells that can survive androgen deprivation and mediate regeneration following androgen add-back (Lukacs et al. 2008). Adult dissociated cells were combined with UGSM and implanted under the renal capsule of intact mice. Recipient mice were then subjected to rounds of castration-induced involution and androgen-mediated regeneration (Lukacs et al. 2008). In a manner analogous to the native prostate, regenerated tissue under the renal capsule was also capable of castration resistance and self-renewal. The lineage tracing approach has been combined with castration/regeneration to mark cells in the castrated or involuted state, using an inducible Cre recombinase to label cells with a fluorescent reporter protein, and then demonstrate the labeled progeny of those cells after androgen-mediated regeneration (Wang et al. 2009). These experiments prove that castration-resistant cells contribute to local tissue regeneration after addition of androgen.

2.3 Identification of Stem Cell Populations

2.3.1 *Isolated Stem Cells in Dissociated Mouse Tissues*

Having developed assays to measure stem-like activity, numerous groups have now defined methods to purify cell populations enriched for stem/progenitor cells. Purification methods have been primarily based on cell-surface markers combined with Fluorescence-Activated Cell Sorting (FACS) although methods to enrich for functional or enzymatic activity have also been used for stem/progenitor purification. While the majority of studies from numerous laboratories implicate basal-like cells from the mouse prostate as stem/progenitor cells (Lawson et al. 2007, 2010; Goldstein et al. 2008; Burger et al. 2009; Choi et al. 2012), recent studies have also proven that the luminal epithelial layer contains stem cells (Wang et al. 2009; Choi et al. 2012).

2.3.1.1 Evidence for Stem Cells with a Basal Localization

The stem cell antigen-1 (Sca-1), a marker of primitive stem/progenitor cells in many adult tissues (Spangrude et al. 1988; Welm et al. 2002; Kim et al. 2005), was used by two different groups to enrich for cells from the mouse prostate capable of tissue regeneration in vivo (Burger et al. 2005; Xin et al. 2005). While Sca-1+ cells, isolated from dissociated adult mouse prostate by FACS, can efficiently regenerate prostatic glands under the renal capsule, Sca-1- cells are devoid of this activity (Xin et al. 2005; Burger et al. 2009). A subset of Sca-1+ cells concentrated in the region

most proximal to the urethra also express the Wnt target gene *Axin2*, indicating a potential role for Wnt signaling in maintaining these progenitor cells in their niche (Ontiveros et al. 2008). *Sca-1* is expressed both in stromal and epithelial cells, indicating that additional markers are necessary to isolate epithelial stem cells (Lawson et al. 2010). Lawson et al. (2007) found that integrin alpha 6 (CD49f), which is a stem cell marker in several adult tissues (Stingl et al. 2006; Rock et al. 2009; Notta et al. 2011), could further enrich for cells in the mouse prostate capable of tissue regeneration in vivo (Lawson et al. 2007, 2010). Up to 1 in every 44 cells in this population exhibited colony formation in vitro on either irradiated 3T3 mouse fibroblast feeder cells (Lawson et al. 2007) or on Matrigel (Lawson et al. 2010). These stem cells were identified by depleting for lineage (Lin) antibodies against hematopoietic (CD45+), endothelial (CD31+), and red blood cells (Ter119) to generate a Lin⁻Sca-1⁺CD49f^{hi} (LSC) profile. LSC cells identified a basally located stem cell population in the mouse prostate (Lawson et al. 2010).

The type I transmembrane protein Trop2, which is overexpressed in numerous cancers and associated with poor prognosis (Ohmachi et al. 2006; Fong et al. 2008a, b; Muhlmann et al. 2009; Kobayashi et al. 2010), was found to be highly expressed on a subset of mouse prostate LSC cells enriched for in vitro and in vivo stem-like activity (Goldstein et al. 2008). By gating on high levels of Trop2, up to 1/11 LSC Trop2^{hi} cells from the mouse prostate could generate spheres in vitro (Goldstein et al. 2008). In vivo, DsRed labeled LSC Trop2^{hi} cells could regenerate glands containing basal, luminal, and neuroendocrine cells. Importantly, neuroendocrine cells in regenerate glands were labeled with the DsRed protein, indicating that they were derived from donor stem cells capable of tri-lineage differentiation upon transplantation (Goldstein et al. 2008).

A single study implicates expression of the hematopoietic stem cell and germ cell marker *ckit*/CD117 (Manova et al. 1990; Ikuta and Weissman 1992) on putative mouse prostate epithelial stem cells and human prostate basal cells (Leong et al. 2008). However, numerous groups have found *ckit* expression in the adult human prostate to localize exclusively to the non-epithelial compartment on immune-infiltrating mast cells and specialized stromal cells termed interstitial cells of Cajal (ICC) (Van der Aa et al. 2003; Shafik et al. 2005; Nguyen et al. 2011). Other groups have reported an absence of *ckit* expression in mouse prostate luminal cells (Wang et al. 2009) or on adult mouse prostate epithelium (Blum et al. 2009).

While several surface markers can be combined to isolate basal stem cells from the mouse prostate, other approaches have also been utilized for mouse prostate stem cell purification. Cells with high levels of aldehyde dehydrogenase (ALDH) enzymatic activity can be labeled with a substrate that gets trapped inside of target cells and fluoresces at a detectable wavelength for FACS isolation. Burger et al. (2009) showed that Aldefluor^{bright} cells are enriched for stem cell activity and that these cells predominantly localize to the basal cell layer (Burger et al. 2009). Finally, using a cyan fluorescent protein (CFP) reporter expressed from the basal cell-specific keratin 5 promoter, K5-CFP+ cells show stem cell properties when isolated and grown in vitro or in vivo (Peng et al. 2011).

2.3.2 Identification of Stem Cells Using a Lineage Tracing Approach

2.3.2.1 Luminal Stem Cells in the Castrated/Regressed Prostate

Using a genetic lineage tracing approach, Wang et al. (2009) identified a luminal stem cell population in the castrated/regressed mouse prostate (Wang et al. 2009). Although the androgen target gene and homeobox transcription factor Nkx3.1 is dramatically downregulated following castration, rare luminal cells in the regressed/involuting mouse prostate gland remain in Nkx3.1+. By engineering an inducible Nkx3.1 promoter to drive expression of the Cre allele, Shen and colleagues were able to label *CAstration-Resistant* Nkx3.1+ luminal cells (CARNs) and their progeny with YFP (Wang et al. 2009). After androgen add-back and regeneration of the gland, the authors found evidence of basal, luminal, and neuroendocrine cells labeled with YFP, indicating that CARNs represent a stem cell population capable of multi-lineage differentiation. CARNs were isolated in the castrated state and subjected to in vivo tissue regeneration to show that this stem cell population can also regenerate prostatic glands upon transplantation under the kidney capsule (Wang et al. 2009).

2.3.2.2 Parallel Identification of Unipotent Basal and Luminal Stem Cells in the Adult Mouse Prostate

Given the findings that in the normal prostate, basal cells are the predominant cell type capable of tissue regeneration upon transplantation, but rare luminal cells in the castrated prostate can regenerate prostate tissue, Choi et al. (2012) performed lineage tracing on both basal and luminal cells in the normal adult murine prostate (Choi et al. 2012). Using a K14 promoter driving expression of Cre to label basal cells and their progeny and a K8 promoter driving Cre to mark luminal cells and their progeny, Xin and colleagues found that both basal and luminal cells are predominantly self-sustained lineages, presumably due to the coexistence of distinct unipotent lineage-restricted stem cells (Choi et al. 2012). Even after serial castration and regeneration, basal cells only gave rise to new basal cells, while luminal cells only gave rise to new luminal cells. A discussion of seemingly conflicting results (as basal cells and CARN cells are multipotent upon transplantation, but lineage-marked basal and luminal cells are unipotent) is included in Sect. 2.4.

2.3.3 Markers of Isolated Basal Stem Cells in Dissociated Human Prostate Tissues

Using in vitro assays, it was shown that basal cells from the human prostate can give rise to luminal-like cells in vitro, suggesting a linear relationship between stem cells that reside within the basal layer and their luminal progeny (Robinson et al. 1998).

Collins et al. (2001) demonstrated that CD44+ basal cells from human prostate specimens expressing high levels of alpha-2 integrin preferentially adhere to collagen and form colonies on extracellular matrix-coated plates (Collins et al. 2001). Human prostate basal colony-forming cells can be further enriched in the CD133+ subset when grown on ECM proteins and with irradiated mouse embryonic fibroblasts as feeder cells (Richardson et al. 2004). In vivo, alpha2+ and CD133+ basal cells from the human prostate can generate epithelial structures at a low efficiency (Collins et al. 2001; Richardson et al. 2004). Human prostate basal cells isolated based on mouse prostate stem cell markers Trop2 and CD49f can form spheres at an average rate of almost 1/3, demonstrating significant progenitor activity within the phenotypic fraction Trop2+ CD49f^{hi} (Goldstein et al. 2008). Trop2 and CD49f isolate basal cells that can generate glands upon transplantation into immune-deficient mice that are indistinguishable from primary human prostate tubules (Goldstein et al. 2010). These collective data show that human prostate basal cells show stem cell activity in both in vitro and in vivo assays.

2.4 Unresolved Questions for Future Research

As described in Sect. 2.3.2.2, lineage tracing in the adult mouse prostate demonstrated that basal cells give rise to basal cells and luminal cells give rise to luminal cells in a unipotent manner (Choi et al. 2012). Using a dissociated cell tissue-regeneration assay, numerous groups have identified cells capable of multi-lineage differentiation capacity (Burger et al. 2005, 2009; Xin et al. 2005, 2007; Lawson et al. 2007, 2010; Goldstein et al. 2008, 2010; Leong et al. 2008; Wang et al. 2009). Do these assays (tissue recombination using embryonic mesenchyme vs. lineage tracing) measure different activities?

Experiments in the mouse skin indicate that hair follicle bulge stem cells are capable of generating all epidermal lineages upon transplantation, which mimics a wound healing type of response, but they only give rise to hair follicles under normal conditions in the intact skin by lineage tracing (Blanpain and Fuchs 2009). Mouse mammary gland stem cells, identified based on expression of basal cell-surface markers such as high levels of integrins CD49f and CD29, can reconstitute an entire mammary gland upon transplantation into a cleared fat pad (Shackleton et al. 2006; Stingl et al. 2006). However this multi-lineage differentiation capacity is not observed in the intact postpubertal adult mouse mammary gland using lineage tracing tools, as unipotent basal stem cells only give rise to basal cells and lineage-restricted luminal cells are limited to generating adult luminal cells (Van Keymeulen et al. 2011). Interestingly, all adult mouse mammary cells derive from a common embryonic precursor cell, marked by keratin 14 (Van Keymeulen et al. 2011). These collective data suggest that in the prostate and other epithelial tissues, a transplantation approach may push unipotent stem cells toward a more primitive multipotent state, most similar to early development. The use of embryonic mesenchyme in the prostate-regeneration assay may aid adult cells in adopting this embryonic-like fate.

Besides the predominant epithelial cell types, basal and luminal, rare neuroendocrine cells are also found in the developing and adult prostate. However the stem cell that gives rise to neuroendocrine cells remains uncertain. Given the presence of neuroendocrine cells outside of the epithelial glands in the developing human urogenital sinus region, Aumuller et al. (1999) proposed that neuroendocrine cells are derived from the neural crest or ectodermal lineage (Aumuller et al. 1999). However studies by our group and others showed that labeled basal stem cells (Goldstein et al. 2008) or labeled CARN cells (Wang et al. 2009) can give rise to labeled neuroendocrine cells, indicating that they can derive from an endodermal origin in the prostate epithelium.

Through the identification of a panel of cell-surface markers including CD49f, Dick and colleagues have recently demonstrated the purification of single human hematopoietic stem cells capable of long-term engraftment and multi-lineage differentiation (Notta et al. 2011). Isolating stem cells to such a high degree of purity allows for the investigation of their unique properties. Future studies will be necessary to determine whether mouse or human prostate stem cells can be purified to such a degree. Given the emerging role of tissue stem cells in the initiation of mouse (Wang et al. 2006, 2009; Lawson et al. 2010; Choi et al. 2012) and human (Goldstein et al. 2010; Taylor et al. 2012) prostate cancer, identification of unique targets and pathways regulating stem cells will be useful for the future detection and elimination of stem cells in malignant transformation.

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Chapter 3

Prostate Cancer Stem Cells: A Brief Review

Xin Chen and Dean G. Tang

Abstract Human cancers have been shown to harbor stem cell-like cells called cancer stem cells (CSCs). These cells are thought to be endowed with indefinite self-renewal ability and believed to be involved in tumor initiation, promotion, progression, metastasis, and therapy resistance. Prostate cancers (PCa) have also been shown to contain CSCs. Here we briefly review the literature reports of CSCs in various tumor systems. We then summarize studies of prostate CSCs (PCSCs) in human cancers and mouse models and discuss their respective limitations. We further discuss the current controversies with respect to identifying the cell of origin for PCa. Elucidating the unique characteristics of PCSCs will enhance our understanding of the mechanisms underlying the emergence of castration-resistant disease and may provide new opportunities for developing therapeutics that target the recurrent PCa.

Abbreviations

ADT	Androgen-deprivation therapy
ALDH	Aldehyde dehydrogenase
AML	Acute myeloid leukemia
AR	Androgen receptor
CSCs	Cancer stem cells
HPCa	Human prostate cancer
miRNAs	MicroRNAs

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PCa	Prostate cancer
PCSCs	Prostate cancer stem cells
SCs	Stem cells
SP	Side population
TICs	Tumor-initiating cells

3.1 Introduction

Prostate cancer (PCa) is one of the most common cancers affecting men in the Western world and the second leading cause for cancer-related death in American males. There are ~241,740 estimated new cases and ~28,170 estimated deaths in the USA in 2012 (Siegel et al. 2012). Radical prostatectomy is commonly utilized for treatment of early-stage PCa, whereas androgen-deprivation therapy (ADT) is the mainstay treatment for advanced PCa. Unfortunately, almost all treated patients eventually fail ADT and develop castration-resistant PCa, at which stage the disease becomes incurable and fatal.

PCa is a multifocal, heterogeneous disease. The exact etiology for PCa development is not clearly understood. Cancer cell heterogeneity in general is explained by two models: (stochastic) clonal evolution model or the cancer stem cell (CSC) model. The classic clonal evolution model has postulated that all cancer cells are tumorigenic, and therapies need to eliminate as many tumor cells as possible to cure the disease. On the other hand, considerable evidence has shown that many cancers may contain a population of stem cell-like cells that is capable of phenotypic diversification and functional maturation, thus generating heterogeneous cancer cell progeny. These CSCs are believed to be responsible for tumor initiation, formation, progression, relapse, metastasis, and therapy resistance. Importantly, these CSCs have the ability to self-renew and generate diverse bulk cells that constitute the tumor (Visvader and Lindeman 2008). In PCa, CSCs are also posited to be cells that mediate PCa recurrence upon androgen deprivation (Feldman and Feldman 2001; Sharifi et al. 2006). It should be noted that the clonal evolution and CSC models may not be mutually exclusive in explaining tumor cell heterogeneity (Tang 2012).

3.2 Cancer Stem Cells: Early Findings, Current Studies, Functional Definition, and Purported Characteristics

In 1937, Furth and Kahn (1937) performed quantitative assays in leukemia cell lines and found that a single murine leukemic cell was able to reinitiate a tumor in a mouse, providing early evidence for CSCs. In 1960, Pierce et al. (1960) observed that undifferentiated teratocarcinoma cells had higher mitotic activity and suggested that these cells might represent teratocarcinoma stem cells. This work was followed

by Bruce and Van Der Gaag (1963), in 1963, to measure clonogenic potential of tumor cells that are capable of initiating tumor development. Several groups in the 1960s and 1970s revealed functional heterogeneity in hematological tumors (Clarkson et al. 1970; Clarkson 1969; Killmann et al. 1963), and the work (together with others') suggested that a fraction of proliferative leukemic cells can replenish the bulk leukemic blasts and result in leukemia *in vivo*. However, identification of a true CSC population was not successful until the 1990s, when Dick and colleagues provided solid evidence that most subtypes of acute myeloid leukemia (AML) are organized as a hierarchy and only the CD34⁺CD38⁻ leukemic stem cells have the ability to serially reconstitute AML in immunodeficient mice (Lapidot et al. 1994; Bonnet and Dick 1997). Clarke and colleagues were the first to report stem cell-like cells in a solid tumor, i.e., CD44⁺CD24^{-/lo} breast cancer cells (Al-Hajj et al. 2003). They found that as few as 100 of CD44⁺CD24^{-/lo} breast cancer cells were highly tumorigenic, whereas cells from the other subsets could not regenerate tumors. Since then, putative CSCs have been reported in a variety of human cancers.

CSCs are frequently identified (and characterized) by marker-dependent strategies via flow cytometry sorting for cells positive for specific markers (e.g., CD44) or marker-independent methods, e.g., Aldefluor assay, side population (SP) analysis, and sphere formation assays, combined with limiting-dilution xenotransplantation in immunodeficient mice. For example, in addition to the CD44⁺CD24^{-/lo} phenotype mentioned above, breast CSCs have also been reported to be enriched in ALDH⁺ (Ginestier et al. 2007), SP (Hirschmann-Jax et al. 2004), or PHK26^{pos} (Pece et al. 2010) cell populations. Brain CSCs have been identified by using the cell-surface marker, i.e., CD133 (Singh et al. 2004) combined with functional analysis such as SP (Bleau et al. 2009) and neurosphere assays (Pastrana et al. 2011). Similarly, colon CSCs have been enriched by using markers such as CD133 (O'Brien et al. 2007; Ricci-Vitiani et al. 2007; Todaro et al. 2007) and CD44 (Dalerba et al. 2007) as well as functional strategies including Aldefluor (Huang et al. 2009) and SP analysis (Inoda et al. 2011). Putative CSCs have now been reported in most other human cancers including those in the lung (Ho et al. 2007; Curtis et al. 2010), pancreas (Li et al. 2007; Lonardo et al. 2011), liver (Yang et al. 2008a; Cairo et al. 2008), head and neck (Prince et al. 2007), stomach (Matsumoto et al. 2009), kidney (Nishizawa et al. 2012; Grange et al. 2011), and ovary (Silva et al. 2011; Meirelles et al. 2011), as well as in melanomas (Schatton et al. 2008; Quintana et al. 2008; Boiko et al. 2010).

How should CSCs be defined? In the strictest sense, a CSC is the *only* cell within the tumor that has the ability to self-renew and generate the heterogeneous lineages of bulk cancer cells (Clarke et al. 2006). None of the reported CSCs would fit this stringent definition. In reality, CSCs are tested in functional assays, in which CSCs are defined as a population of tumor cells that can initiate serially transplantable tumors and can, at least partially, reconstitute the heterogeneity of the original tumors at the histopathological level. The "gold" standard to functionally define CSCs is to show their ability to initiate tumor development in immunodeficient mice and to self-renew by performing serial transplantation assays (Li et al. 2009).

At present, there exist some confusion, controversies, and misunderstandings with respect to characteristics ascribed to CSCs. *First*, the abundance of CSCs may depend on the models studied. It has been mistakenly believed that CSCs represent a small percentage of all tumor cells, which may not always be the case. For example, it was initially estimated that only one in a million human melanoma cells possesses the tumor-initiating ability (Schatten et al. 2008). But it was later reported that frequency of human melanoma CSCs could be as high as one in four melanoma cells when more immunocompromised mice were used (Quintana et al. 2008), suggesting that the frequency of melanoma CSCs varies in different xenograft models. *Second*, normal adult stem cells are characterized by long-term quiescence. Based on this property, CSCs are also assumed to remain at dormancy and retain DNA labels much longer than the non-CSCs, which might help explain why CSCs in some reports are resistant to chemotherapeutics and radiation therapies. Nevertheless, whether or not CSCs are dormant in human tumors has not been clarified and needs further investigation with approved assays, in which a single candidate CSC with a defined quiescence status should be xenotransplanted (Clevers 2011). *Third*, CSCs may or may not originate from normal stem cells. For example, most CSCs are identified via the corresponding normal stem cell marker(s) (Lapidot et al. 1994; Bonnet and Dick 1997), suggesting that CSCs may derive from their normal counterparts. However, CSCs can also derive from restricted progenitors or even differentiated cells. For example, medulloblastoma, the most malignant brain tumor in children, can be initiated in either restricted neuronal progenitors or stem cells (Yang et al. 2008b), suggesting that progenitor/differentiated cells can function as the targets of tumorigenic transformation. *Fourth*, CSCs may or may not always be resistant to therapy. On the one hand, CD133⁺ glioma stem cells, but not the CD133⁻ bulk tumor cells, survive after ionizing radiation by preferentially activating the DNA damage checkpoint (Bao et al. 2006). On the other, recent evidence suggests that some CSCs can be targeted by conventional treatments, not all CSCs are therapy resistant, and, vice versa, not all drug-resistant cancer cells are CSCs. For example, we have shown that drug-tolerant (i.e., drug-resistant) residual Du145 PCa cells lacked the expression of the progenitor marker CD44 and actually exhibited reduced tumorigenicity (Yan et al. 2011).

3.3 Human Prostate Cancer Stem Cells: Identification, Characterization, Implication, and Challenges

Many studies have reported stem-like PCa cells in long-term cultured PCa cell lines, xenograft models, and primary tumor samples. These reported PCSCs populations seem to be phenotypically divergent, and some have not been rigorously tested in vivo.

Collins et al. (2005) have shown that a small percentage of primary human prostate tumor cells bears the phenotype of CD44⁺α2β1^{hi}CD133⁺ and is highly clonogenic and proliferative, although it remains unclear whether the CD44⁺α2β1^{hi}CD133⁺ PCa cells can initiate serially transplantable tumors, because such an in vivo experiment

was lacking in this study. Using similar flow cytometry-based cell-surface marker strategies, we have reported that in xenograft models (Du145, LAPC4, LAPC9), the CD44⁺ PCa cells are enriched in tumorigenic and metastatic stem/progenitor cells (Patrawala et al. 2006). We have shown, in subsequent studies, that CD44⁺ α 2 β 1⁺ PCa cells further enrich CSCs compared to the CD44⁺ PCa cells (Patrawala et al. 2007). Isaacs's group reported that a small population of CD133⁺ cells is enriched in several human PCa cell lines (i.e., LNCaP, CWR22Rv1, LAPC4), which can self-renew and produce heterogeneous progeny (Vander Griend et al. 2008). Recently, Rajasekhar et al. (2011) reported a minor subset of human prostate CWR22 xenograft cells expressing TRA-1-60, CD151 and CD166, is capable of reconstituting serially transplantable tumors.

Stem-like PCa cells have also been enriched using functional assays. For example, the LAPC9 SP cells, although rare, are more tumorigenic than non-SP cells (Patrawala et al. 2005). Similarly, aldehyde dehydrogenase (ALDH) 1A1⁺ PCa cells (PC3 and LNCaP), isolated by Aldefluor assay, were shown to be highly clonogenic and tumorigenic, and ALDH1A1 expression can be used to predict patient outcome (Li et al. 2010). Intriguingly, ALDH-positive PCa cells were shown to be enriched in tumor-initiating and metastasis-initiating cells (van den Hoogen et al. 2010). Stem-like PCa cells have also been uncovered using several marker-independent methods. For instance, we have demonstrated that holoclones from cultured PC3 cells are more clonogenic and express higher stem cell-associated molecules than meroclones and paraclones (Li et al. 2008). Importantly, the holoclone cells are able to initiate serially transplantable tumors. Prostatospheres derived from primary human PCa cells harbor cells with self-renewal and clonogenic potential (Guzmán-Ramírez et al. 2009). Recently, we employed a lentiviral reporter system to provide convincing evidence in PCa cell lines, xenografts, and primary PCa that the PSA^{-lo} PCa cell population harbors CSCs (Qin et al. 2012). The PSA^{-lo} PCa cells are quiescent and resistant to stresses (e.g., androgen deprivation, chemotherapeutics, and prooxidants). Furthermore, using time-lapse video microscopy, we are the very first to show that a fraction of PSA^{-lo} cells can undergo asymmetric cell division generating PSA⁺ cells that constitute the bulk in the tumor. Moreover, PSA^{-lo} cells can maintain long-term clonogenicity and tumor propagation and mediate castration resistance. As the PSA^{-lo} cell population is still heterogeneous, we can further enrich tumorigenic and castration-resistant PCa cells using the ALDH⁺CD44⁺ α 2 β 1^{hi} phenotype (Qin et al. 2012). This recent study (Qin et al. 2012) provides concrete evidence that human PCa contains CSCs.

What are the mechanisms that regulate human PCSCs? Some evidence suggests that PTEN/PI3K/AKT pathway may play a vital role in maintaining PCSCs, and as a result PI3K signaling is a potential target for PCa treatment (Dubrovskaya et al. 2009). Combination of PI3K/mTOR inhibitor NVP-BEZ235 and chemotherapeutic drug Taxotere, which target PCSCs and bulk cells, respectively, shows synergistic effects in inhibiting PCa xenograft tumors (Dubrovskaya et al. 2010). The TRA-1-60⁺ CSCs showed increased level of NF- κ B signaling, and NF- κ B inhibitors (i.e., 481407 compound, parthenolide, and celastrol) abrogated sphere formation in a dose-dependent manner (Rajasekhar et al. 2011), suggesting that NF- κ B signaling

might be involved in PCSC maintenance and functions. By using loss- and gain-of-function studies, our lab has shown that Nanog plays a role in regulating CSC activities and castration resistance and may represent another therapeutic target, especially for CRPC (Jeter et al. 2009, 2011). Finally, we have uncovered that miR-34a is a key negative regulator of PCSCs and PCa metastasis by directly targeting CD44 (Liu et al. 2011). Administration of miR-34a significantly inhibits metastasis and extends the survival of tumor-bearing mice (Liu et al. 2011), indicating that tumor-suppressive microRNAs such as miR-34a could represent potent therapeutic agents for PCa.

Although providing critical information on PCSCs, the above-discussed studies do suffer some limitations. For example, although primary prostate tumors clearly contain highly clonogenic cells (Collins et al. 2005; Guzmán-Ramírez et al. 2009), it remains to be shown whether such cells, freshly purified from patient tumors truly possess enhanced tumorigenic potential and whether primary PCa cells are organized as a hierarchy. These uncertainties are related to the well-known fact that we have yet to find reliable approaches to reconstitute human PCa in immunodeficient mice using freshly purified single tumor cells (Pienta et al. 2008), which is why the majority of the aforementioned studies have been conducted mainly using long-term cultured cell lines and/or long-term xenograft models. In addition, our current CSC assays need improvement and optimization. For instance, many tumor experiments have been performed subcutaneously, which will certainly be different from the authentic PCSC niche in vivo. On the other hand, although orthotopic transplantation may partially ameliorate this problem, these assays will have difficulties in estimating the accurate CSC frequency owing to species incompatibilities. Finally, PCSCs seem to be very heterogeneous, and the interrelationship among the above-mentioned PCSC subpopulations needs to be investigated.

3.4 Murine PCSCs: Identification, Characterization, and Implications

Mouse PCa models can overcome the species incompatibility issues that the transplanted human PCa cells may experience in immune compromised hosts. As in the case of human PCSCs, the reported murine PCSCs are also phenotypically divergent. Xin et al. (2005) have demonstrated that the Sca-1⁺ mouse prostate epithelial cells, but not the isogenic Sca-1⁻ cells, are capable of regenerating prostate intraepithelial neoplasia (PIN) lesions after AKT1 lentivirus infection, suggesting that Sca-1⁺/AKT^{hi} cells could become tumor-initiating cells. Mulholland et al. reported a tumor-initiating subpopulation from *Pten*-null PCa model, which bears the phenotype of Lin-Sca-1⁺CD49^{high} (or LSC) and can regenerate tumors in vivo (Mulholland et al. 2009). To date, the LSC subpopulation is one of the few mouse PCSC populations more thoroughly studied.

Molecular mechanisms regulating the maintenance and functions of murine PCSCs remain largely unknown, although some recent exiting evidence starts to emerge. For example, prostaspheres from *Pten*/*TP53*-null cells possess CSC

properties and display increased levels of AKT/mTORC1 and AR pathways, thus implicating such pathways in regulating murine PCSCs (Abou-Kheir et al. 2010). More recently, it has been demonstrated that cooperation of *Pten* loss and *Ras* activation significantly enhances the activity of LSC stem/progenitor cells, leading to their increased EMT (epithelial-mesenchymal transition) and distant metastatic capabilities (Mulholland et al. 2012). In addition to the signaling pathways discussed above, the polycomb group transcriptional repressor Bmi-1 seems to be required for the self-renewal activity in adult murine prostate stem cells (Lukacs et al. 2010). This work may provide another layer of mechanisms, i.e., at the chromatin level, in that Bmi-1 may also regulate PCSCs characteristics such as self-renewal.

Although mouse models have their own advantages for studying CSCs, there also exist apparent limitations. It is unclear to what extent studies in the mouse models can be generalized to human PCa as the mouse and human prostates are quite different. Moreover, considering the heterogeneous nature of CSCs (Tang 2012), it is highly likely that LSCs only represent one population of murine PCSCs, dictated by *Pten* mutation/loss. Future work should determine whether the LSC population also exists in other mouse PCa models, how different genetic mutations may generate distinct CSC types, and the interrelationship among different murine PCSC populations.

3.5 Cell of Origin for PCa and CSCs

The potential cell of origin for PCa has attracted much attention and is still under debate. Normal prostatic glands are composed of three distinct types of cells: basal, luminal, and neuroendocrine cells. Basal cells form the basal layer that lines along the basement membrane, and luminal cells constitute the luminal layer that sits above the basal layer and secrete prostatic proteins into the lumen, whereas neuroendocrine cells are dispersed throughout the basal layer and generate neuropeptides and biogenic amines (Abate-Shen and Shen 2000).

It is well known that the untreated clinical prostate tumors contain mostly luminal-like cells expressing AR and cytokeratin 8 with basal-like cells very rare. As such, luminal cells have been presumed to be the cells of origin for PCa. Recent studies (Ma et al. 2005; Korsten et al. 2009) have provided some support to this view. Additionally, using genetic lineage tracing, Wang et al. (2009) have reported that a luminal stem cell population, manifested upon castration and called castration-resistant Nkx3.1-expressing cells (CARNs), can function as the cell of origin for PCa after *Pten* deletion. Using similar strategies, Choi et al. (2012) have shown recently that murine prostatic luminal cells are more susceptible to *Pten* loss-induced PCa, whereas basal cells appear to first need to differentiate into transformation-competent luminal cells in order for *Pten* loss-induced PCa to occur. These two studies (Wang et al. 2009; Choi et al. 2012) were conducted in mouse models, and it is presently unclear whether human prostatic luminal cells can also function as the cells of origin for human PCa. The answer to this latter question awaits the development of culture medium that can propagate AR⁺ and PSA⁺

differentiated luminal cells. Interestingly, stem-like cells in BM18 human PCa xenograft express both stem cell markers (i.e., ALDH1A1, Nanog) as well as luminal markers (e.g., NKX3.1 and CK18), but not basal markers, and these cells are selected by castration and are able to regenerate tumors after androgen replacement (Germann et al. 2012), suggesting that stem-like cells with luminal progenitor phenotype in human PCa might represent the cell of origin for CRPC.

In contrast to the above lineage tracing studies (Wang et al. 2009; Choi et al. 2012), tissue recombination/regeneration assays using FACS-purified cells have shown that prostatic basal cells are targets for malignant transformation (Wang et al. 2006; Lawson et al. 2010). When combinations of genetic alterations such as ERG1, constitutively active AKT, and AR are introduced into either purified basal or luminal cells from the mouse prostate, only basal cells seem to be competent for tumorigenic transformation (Lawson et al. 2010). When the same combination of ERG, AKT, and AR is introduced into the isolated human prostatic luminal (CD49^{lo}Trop2^{hi}) or basal (CD49^{hi}Trop2^{hi}) cells, tissue recombination assays in NOD-SCID-IL2R γ ^{null} (NSG) mice reveal that only basal cells can be transformed, leading to adenocarcinoma that, remarkably, resembles the clinical PCa histology (Goldstein et al. 2010). A recent study also shows that the α 2 β 1 integrin^{hi}, basal-like cells from nontumorigenic BPH-1 cells, when combined with either human cancer-associated fibroblasts or embryonic stroma, can lead to tumor grafts using tissue recombination assays (Taylor et al. 2012).

There are several potential explanations for the seemingly contradictory results from the lineage tracing versus transplantation-based studies. The obvious one is that both luminal and basal epithelial cells can function as the cells of origin for PCa, depending on specific genetic hits and context. The second is technical. Although lineage tracing studies are performed in intact animals, the Cre-mediated tagging efficiency frequently is low and varies with the promoter used, which can confound interpretation of data. On the other hand, there are also several caveats associated with the transplantation-based studies. Transplantation per se may elicit a wound healing response, which could lead to heightened activity of the transplanted cells and skewed results. More important, as of yet we still fail to maintain and propagate fully differentiated luminal prostatic epithelial cells expressing AR and PSA (in human), as all currently used culture media favor only basal cells. Therefore, it remains officially possible that differentiated human prostate luminal cells also can become the targets of tumorigenic transformation. Finally, the different results obtained with the lineage tracing and transplantation studies might also be related to differences between human and mouse cells. It is well established that terminally differentiated human epithelial cells such as PSA-expressing luminal cells generally lack telomerase expression, and in the human prostate most proliferating cells lie in the basal layer (Bonkhoff et al. 1994). In contrast, “differentiated” murine cells have long telomeres and retain high telomerase activity, and in the mouse prostate most proliferative cells reside in the luminal layer (Choi et al. 2012). These species-specific differences could help account for the different results obtained with respect to the cell of origin for PCa.

It should be noted that whether it is lineage tracing or transplantation studies, just because one population of cells can be transformed by specific genetic hit(s) does

not necessarily mean that they are the actual cells of origin for human PCa. Also, the potential cells of origin are not to be confused with CSCs, which refer to stem-like cancer cells in the established prostate tumors.

3.6 Conclusions and Perspectives

Using different approaches, many studies have demonstrated PCSCs in both mouse models and cultured human PCa cells, xenografts as well as primary patient samples. For example, recent study has shown convincingly that the PSA^{-lo} PCa cell population harbors stem-like cells that preferentially express stem cell-associated genes, can undergo authentic asymmetric cell division, possess long-term tumor-propagating activity, and can mediate castration resistance (Qin et al. 2012). In mouse PCa models, the best characterized CSC population is the LSCs in *Pten*-less prostate tumors (Mulholland et al. 2009). Both human and mouse PCSCs seem to be phenotypically divergent and future efforts should be directed towards characterizing the interrelationship among various reported CSC populations. Another important breakthrough is urgently needed to develop the assays that allow reliable tumor reconstitutions in mice from purified single primary PCa cells.

Moreover, some recent evidence has implicated certain signaling molecules and pathways such as PTEN/PI3K/AKT, NF- κ B, Nanog, and miRNAs in regulating PCSC properties. Better understanding of these and other potential mechanisms is likely to help us develop novel therapeutics to target PCSCs, and eventually benefit PCa patients by preventing recurrence.

Finally, lineage tracing and tissue recombination assays seem to suggest that both luminal and basal cells can function as the targets of tumorigenic transformation. Interpretation of these results should take into account of the experimental system used. Future studies with improved techniques are needed to further elucidate the cells of origin for human PCa, the success of which will be instrumental to stratifying PCa patients and developing personalized and targeted therapeutics.

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Chapter 4

Cancer Stem Cells Provide New Insights into the Therapeutic Responses of Human Prostate Cancer

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Abstract Whilst there has been a dramatic improvement in the survival of men with prostate cancer in the last few decades, we find ourselves at a crossroads, where another significant therapeutic advance is required. Current treatments for prostate cancer including hormone therapy, radiotherapy and chemotherapy all have their place, but result in almost inevitable treatment failure. In this chapter, we describe the role of cancer stem cells in tumour relapse as well as the potential they provide to develop novel treatment strategies. We examine the clinical implications of cancer stem cells as a therapy-resistant pool within prostate tumours and propose three strategies to target both cancer stem cells and bulk tumour cells, namely, combination therapy, differentiation therapy and targeted therapy. This chapter summarises the challenge of designing future therapies taking into account both the heterogeneity of prostate cancers and the resistant cancer stem cells at their core.

4.1 Introduction

The existence of the presence of a primitive underlying epithelial tissue stem cell (SC) in prostate has provided the impetus for a new generation of cell and molecular studies on the origins and the very nature of human prostate cancers. Whilst current thinking about the cellular origins, composition and phenotype of prostate tumours is treated elsewhere in this volume, the existence of primitive epithelial cell populations within tumours contributes to intratumoral heterogeneity and its therapeutic consequences, i.e. the development of treatment-resistant tumour clones. Indeed,

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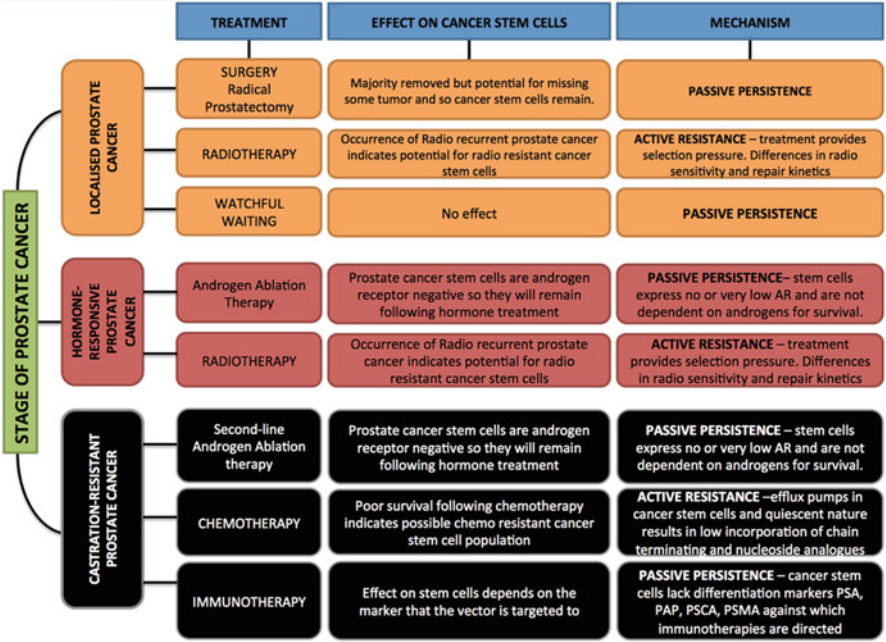


Fig. 4.1 Therapy resistance in the context of cancer stem cells. The different stages of prostate cancer are represented, ranging in their severity from localised to hormone responsive to castration resistant. Each stage has a range of treatments available and the effect of the treatment on cancer stem cells is listed alongside the mechanism of cancer stem cell maintenance including passive persistence and active resistance

human prostate cancer has justified its reputation as a tumour that is difficult to treat by conventional therapeutic strategies (as summarised in Fig. 4.1).

In the context of organ confined disease, external beam radiotherapy and brachytherapy techniques offer a high degree of disease control, even cure, but with an acknowledged relapse rate of 30% (Ishkanian et al. 2010; Jones 2011; Xiao et al. 2012). In many cases, this is attributable to the pre-existence of metastatic clones, outside the irradiated zone, but recurrence within the prostate is also found. Responses to manipulation of hormone levels, either directly by blocking the androgen receptor or indirectly by (1) stemming the supply of adrenal androgens, (2) preventing activation of testosterone to the more bioactive dihydrotestosterone or (3) the recent introduction of inhibitors of the salvage synthetic pathway for testosterone biosynthesis, are all effective but are clearly time limited in their efficacy (Rehman and Rosenberg 2012; Schroder et al. 2012). However, it is particularly after the failure of such hormone manipulation strategies that the chemoresistance of prostate tumours is most manifest, where survival times for castration-resistant prostate cancer (CRPC) patients rarely exceed 2 years (Kirby et al. 2011).

To justify such rapid failure of potent anti-proliferative treatments, several explanations have been proposed. The emergence of new tumour clones, either spontaneously due to more rapid growth or in a new environment after therapy, can be viewed as a form of adaption and selection. Induction of mutations can be far from random, but the overwhelming pressure comes from the selection process. It is clear that there is considerable clonal evolution of prostate cancers (Ruiz et al. 2011; Kallioniemi and Visakorpi 1996; Cheng et al. 1999). In addition, next-generation DNA/RNA sequencing has indicated that the degree of overall genetic changes in a prostate cancer is somewhat less than in other solid tumours. However, prostate cancer appears to differ from several other common cancer types (e.g. colon), in that the incidences of DNA repair defects and genetic instabilities are frequently lower than expected. The ability to resist the apoptotic consequences of genetic instability does appear to be greater in CRPC, where inactivating mutations in p53 have most recently been confirmed in around 21.4% of cases (Eastham et al. 1995; Navone et al. 1999; Mirchandani et al. 1995). Whilst prostate cancer cells express classical markers of apoptosis resistance, they nevertheless turn over rather rapidly, dividing more frequently than epithelial cells in the normal prostate, and certainly much more frequently than normal luminal epithelial cells, which the bulk of a tumour most closely resembles phenotypically (Limas and Frizelle 1994; Hudson et al. 2001). There are also the common arguments about life span of tumour cells versus the time required to generate the desired mutation, which imply that the tumour originates in relatively long-lived stem/progenitor cells, in contrast to luminal cells, which turn over more rapidly (De Marzo et al. 1998).

Therapy resistance resulting from adaptive mutagenesis in a replicating luminal cell population of prostate tumours is not only appealing but also has some circumstantial evidence in its favour (Germann et al. 2012; Kumar et al. 2011) as shown in Fig. 4.2a. The latter experiments in cell lines and established xenografts, which at least in vitro, seem spectacularly vulnerable to the effects of chemotherapy, did pose the question of just how easy it is to select for the appropriate changes. Recent studies to generate a TMPRSS2-ERG fusion designed under ideal conditions of cell replication, hormone treatment and selection in culture took many months with many millions of starting cells (Bastus et al. 2010; Haffner et al. 2010; Mani et al. 2009). This is at best equivalent to several years' selection in patients. However, chemotherapy-resistant cell clones arise in vivo within several months of treatment instigation (Marin-Aguilera et al. 2012; Mezynski et al. 2012; Seruga et al. 2011) in the clinic. The other consideration must be the phenotype of the most aggressive CRPCs, which is frequently neuroendocrine (Matei et al. 2012; Marcu et al. 2010). How simple is a 'transdifferentiation' from a replicating luminal cancer cell into such a NE phenotype? Clearly, it can be achieved in established cell lines such as LNCaP (Zelivianski et al. 2001), but are such changes so likely in vivo? Direct DNA sequencing has now indicated that patient tumours have many fewer genetic changes than established cell lines and retain some heterogeneity. The most common mechanism of castration resistance is not, as previously proposed, specificity-changing mutations in the androgen receptor sequence (Hay and McEwan 2012) (made easier by the single copy of AR on the X chromosome in human male cells) but rather an

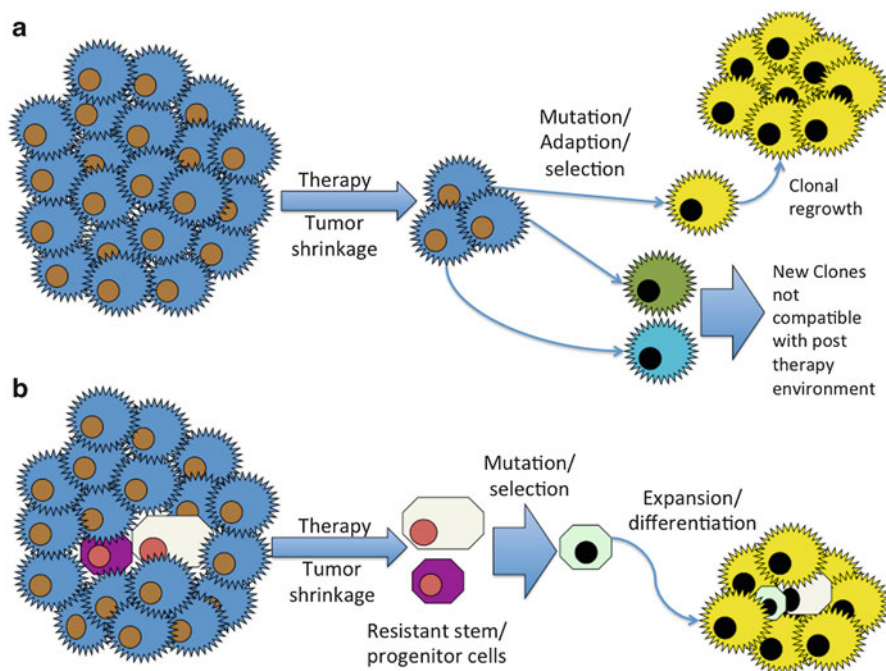


Fig. 4.2 Adaptive mutagenesis versus stem cell mutation and selection in therapy resistance. **(a)** Adaptive mutagenesis: changes are induced in many tumour cells in response to therapy leading to emergence of a successful relapse originating in a single clone. **(b)** Stem cell mutation and expansion arises from stem/progenitor cells which can expand and differentiate to reconstitute the relapsed tumour mass

amplification of AR gene, resulting in an overexpression of the AR protein under castrate conditions (Koivisto et al. 1997). This has also been considered surprising, but perhaps should not be so, since on consideration of another common chemotherapeutic resistance mechanism, against methotrexate, it was shown as long ago as the 1980s (Stark and Wahl 1984) that resistant tumours had also amplified the substrate binding/metabolising (dihydrofolate reductase) gene (Sharifi et al. 2006).

An alternative mechanism for the development of treatment-resistant clones can be derived from the existence of an underlying stem/progenitor population within the heterogeneous tumour mass (Fig. 4.2b). This is also not a novel or recent idea, both in leukaemia (Lapidot et al. 1994), solid tumours (Visvader and Lindeman 2008) and indeed in prostate cancer (Collins et al. 2005), where Isaacs and Coffey proposed just such an hypothesis almost 30 years ago (Isaacs and Coffey 1981, 1989; Kyprianou and Isaacs 1988). However, these historical hypotheses were generated in scientific times when the ability to purify discrete cell populations was limited by the available technology. With an increasing use of cell sorting techniques, more homogeneous populations resulting from fractionation of cell cultures and tissues resulted in a rediscovery of the cancer stem cell hypothesis. Better

knowledge of the cancer stem cell phenotype suggested the molecular mechanisms whereby cancer stem cells could indeed provide the therapy-resistant fraction, from which a new recurrent clone could arise. In 2005, we proposed that a rare cell with cancer stem cell-like properties could provide the reservoir for therapy resistance in prostate cancer (Maitland and Collins 2005). A number of subsequent publications have endorsed this idea, mainly with studies of stem-like cells from prostate cell lines, but also from our own studies on fractionated cells and primary cultures from human subjects (Frame et al. 2010; Goldstein et al. 2010a, b; Maitland et al. 2011; Patrawala et al. 2006, 2007; Trerotola et al. 2010; Lawson et al. 2010).

4.2 Success and Failure with Current Prostate Cancer Treatment

There has been great progress in recent decades in terms of detection and diagnosis of prostate cancer. The 5-year survival rate has risen in the last 20 years, taking into account all stages, with mortality declining by about 40% (Siegel et al. 2012; Etzioni et al. 2012). This relates to early diagnosis resulting from PSA testing, refined surgical techniques, successful radiotherapy, improved awareness and evolving imaging techniques. Men are cured of prostate cancer by radical prostatectomy and/or successful radiotherapy, either external beam or brachytherapy. In addition, there is the acknowledgement that the PSA test is less than perfect and judicious use of the watchful waiting/active surveillance approach has prevented unnecessary surgery for a subset of patients, typically older patients with low-grade cancers (Drachenberg 2000). However, there is still an unacceptably high rate of failure of radiotherapy, which consists of either nonresponsive tumours or recurrent tumours. In addition, although androgen ablation therapy is initially very effective and is typically initiated once the tumour has escaped the prostate capsule, hormone resistance almost inevitably emerges. This is followed by the more rapid failure of chemotherapy used to treat castration-resistant tumours. Indeed, the real therapeutic challenge at the moment is with patients harbouring metastatic castration-resistant disease, for whom untreated survival is typically 9–13 months (Kirby et al. 2011).

4.3 Therapy Resistance in the Context of Cancer Stem Cells

Illustrated in Fig. 4.1 are the stages of prostate cancer, together with the typical current treatments used against each stage. Considering the prostate cancer(s) as a heterogeneous tumour with a core of cancer stem cells, the figure also describes the potential effect of each of these treatments on the cancer stem cell population. Essentially, the effects are divided into *active resistance* and *passive persistence*. In all cases, the stem cells are maintained, and in some cases they may even be stimulated to replenish the lost cells of the tumour following treatment, similar to a wound

healing response in normal tissues (Maitland and Collins 2010). Indeed, there are numerous examples in the literature demonstrating that treatment of tumours (colon, breast, glioblastoma) can result in enrichment of the cancer stem cell population and a resultant secondary, more aggressive therapy-resistant tumour (Calcagno et al. 2010; Creighton et al. 2009; Dylla et al. 2008; Phillips et al. 2006). There is therefore the necessity to include a strategy to eliminate cancer stem cells as part of any novel therapeutic aim.

4.4 Therapy Resistance Mechanisms and Opportunities for Novel Targets

A variety of proven and potential therapy resistance mechanisms have been described in prostate cancer. Some relate to the tumour as a whole, whilst others are specific to the presence, activity and unique characteristics of cancer stem cells. In addition, the identification of several possible mechanisms of resistance allows us to characterise the failure of a treatment whilst providing indications of novel therapeutic targets. This strategy should have the potential to inhibit the resistance mechanisms and thus sensitise the cancer stem cells to traditional treatments. Examples of these mechanisms and how they might be overcome are described below.

4.4.1 *Hormone Resistance*

Once advanced prostate cancer becomes hormone resistant, the therapeutic arsenal is diminished. There are several mechanisms of hormone resistance, which primarily relate to an alternative regulation of the androgen/androgen receptor axis (Bluemn and Nelson 2012; Waltering et al. 2012). These include androgen receptor gene amplification, which results in overexpression of the androgen receptor. There is also mutation of the androgen receptor gene, which results in an increased sensitivity to lower levels of androgen or a diversification of the receptor (increased promiscuity) that allows the androgen receptor to respond to and be activated by other hormones such as oestrogen and progesterone. Mutations can also result in constitutive expression of androgen, which then allows crosstalk between pathways. Activation by non-hormone growth factors in a ligand-independent fashion also occurs. Here, the androgen receptor is stimulated by either EGFR (epidermal growth factor receptor) or HER2 (human epidermal growth factor receptor 2), known as the outlaw pathway (Bonkhoff 2012). In addition, androgen receptor isoforms resulting from splice variants and gene rearrangements have been identified that result in expression of receptor variants that lack the ligand binding domain which are constitutively active in the absence of androgens (Dehm et al. 2008; Dehm and Tindall 2011).

Recent work has demonstrated intracrine de novo steroidogenesis following androgen ablation therapy and the onset of castration resistance (Locke et al. 2008; Montgomery et al. 2008). This occurs in the presence of low or negligible levels of

circulating (exogenous) androgen and androgens produced *within* tumours at a level that can activate AR-target genes. The bulk of experimental evidence has shown that prostate cancer stem cells are androgen receptor negative and therefore do not respond directly to hormonal stimuli (Collins et al. 2005). However, it is conceivable that the cancer stem cells may respond to signals from androgen-responsive progenitor and stromal cells. It has been shown in cell lines that cells can be androgen responsive without being androgen dependent, so depletion of androgens does not signal the death knell for these cells (Marques et al. 2005).

4.4.2 Radioresistance

Radioresistance is a consideration in all cancers where radiotherapy is a treatment modality. Resistance can arise through a variety of mechanisms, for example, gross mechanisms related to tumour mass and location and more refined molecular mechanisms related to activation of radiation-responsive signalling pathways and also specific mutations that affect the radiation response.

4.4.2.1 Role of Tumour Size, Location and Genetic Characteristics

When discussing failure of radiotherapy, there is an initial distinction between non-responsive tumours and radio recurrent tumours. In some patients, radiotherapy simply does not provide a cure, despite extensive optimisation with the aim of administering carefully controlled doses to maximise impact on tumour and minimise side effects (Brawer 2002). Nonresponsive tumours can arise from inherent radioresistance of the tumour due to their genetic landscape, inaccurate external beam therapy so the whole tumour(s) is not irradiated and the presence of hypoxic regions within the tumour (Bonkhoff 2012). Refinements in imaging techniques are improving the accuracy of both external beam radiotherapy and brachytherapy (e.g. ultrasound-guided brachytherapy) to ensure that the whole tumour is targeted. Hypoxia is a marker for biochemical failure of radiotherapy in prostate cancer, and studies have shown that cells in hypoxic regions undergo a cell cycle arrest and hence reduced apoptosis (Milosevic et al. 2012). Tumours preferentially develop hypoxic regions due to disorganised angiogenesis, anaemia associated with a large tumour burden and increased interstitial pressure (Seiwert et al. 2007).

Hypoxia is thought to contribute to radioresistance because radiation exerts its DNA-damaging effect (at least partly) through free radicals including oxygen radicals (reactive oxygen species (ROS)) (Cook et al. 2004). In addition, breast cancer stem cells have been shown to have increased production of ROS-quenching enzymes, leading to neutralisation of free radicals and reduced DNA damage (Diehn et al. 2009). In a prostate cancer in a cell line model, it was shown that hypoxia treatment resulted in increased colony-forming ability and increased expression of HIF-1 α and HIF-2 α as well as Nanog and Oct3/4. The cells with higher colony-forming ability had induced CD44 and ABCG2 expression. Therefore, hypoxia treatment resulted in

an increase of stem cell-like properties in this study (Ma et al. 2011). The level of hypoxia, be it chronic or acute, affected disease outcome, with acute hypoxia increasing clonogenic activity and chronic hypoxia inducing cell death (Dai et al. 2011).

4.4.2.2 Anti-apoptotic Factors and Radioresistance

Another mechanism employed by cancer stem cells is evasion of apoptosis (Fulda and Pervaiz 2010). Upregulation of Inhibitor of Apoptosis (IAP) family members has been observed in cancer stem cells (Liu et al. 2006). One family member, Survivin, is involved in regulation of normal stem cells and is a known radiation-resistance factor due to interaction with DNA repair factors (Reichert et al. 2011). Survivin is a potential therapeutic target since knockdown or inhibition of Survivin leads to decreased survival. Indeed, Survivin antagonists have been used in clinical trials to target prostate cancer, and so it remains a strategy with potential (Altieri 2012). In addition the Bcl-2 family can have anti-apoptotic properties that lead to radioresistance, and Bcl-2 overexpression is observed and associated with both stem cells and with aggressive prostate cancer (An et al. 2007).

4.4.2.3 Signalling Pathways

Radiation induces activation of a variety of signalling pathways that govern cell survival, growth, proliferation, senescence, invasion, motility and DNA repair (Skvortsova et al. 2008). Understanding these pathways allows us to determine the signalling required for cell death and successful treatment, and which pathways contribute most to radioresistance and therapy failure. This information has been used by the Radiation Therapy Oncology Group to identify biomarkers that can be used to predict treatment failure. The most significant markers are p16 (proliferation), Ki67 (proliferation), MDM2 (degradation of p53 and reduced apoptosis/increased proliferation), COX-2 (pro-inflammatory) and Protein Kinase A (Bonkhoff 2012). In addition, radioresistance can be generated by radiation-induced activation of EGFR through the PI3K/Akt/mTOR pathway, which leads to increased HIF-1 α and increased VEGF, which in turn promotes angiogenesis (Shi et al. 2007). Alternatively, loss of PTEN leads to activation of the PI3K/Akt/mTOR pathway, phosphorylation of androgen receptor making it hypersensitive and downregulation of p27, which together result in increased cell proliferation, and is implicated as a further radioresistance mechanism (Heinlein and Chang 2004).

4.4.3 Chemoresistance

The main chemotherapeutic agent used in prostate cancer is docetaxel, and there have been few advances in chemotherapy for prostate cancer since its introduction. In order to design novel chemotherapies for prostate cancer, one has to consider the potential resistance mechanisms and unintended consequences of new agents.

4.4.3.1 Adaptive Mutations and Selection

Decisions about the optimum doses of various chemotherapies to shrink prostate tumours are made on the basis of maximal tolerated dose (to the patient). Little is known about the effective dose distribution of chemotherapeutics within a tumour mass. Existing evidence from other cancer stem cell systems, and data accumulating about the expression of various drug efflux pump proteins, suggests that the dosages required to achieve toxicity in hypoxic and cancer stem cell-enriched regions of a tumour will be considerably higher when compared to those for a small spheroid grown in normoxic conditions or indeed two-dimensional cultures of cells on plastic substrates (as is most commonly used in preclinical high-throughput screening). Without a treatment combination to prevent drug efflux and to increase tumour permeability, all attempts to achieve toxic doses for cancer stem cells might be fruitless. In addition, the sublethal doses may have a similar effect to persistent treatment with low levels of specific toxins resulting in a resistant phenotype. In which cell therefore do such adaptive mutations arise? Short-term survival could be achieved by mutation in the replicating fraction of the tumour (where mutations most easily arise and can be established). It has been proposed that such changes arise, for example, after hormone therapies, in luminal tumour cells expressing extremely low levels of AR, with no need for a cancer stem cell. If the stem cells and cancer stem cells are AR-, as we propose, then such adaptation is more likely to be achieved in the replicating bulk population. In this case, we do currently have a potential genotypic marker of the phenotype, namely, the amplification of AR seen in about 30% tumour populations after emergence of castration resistance (Haapala et al. 2007). Such amplification is a classical cellular reaction to low substrate concentrations. One would predict that the mutation would not be required in the persisting stem cells, although CRPC is an extremely heterogeneous disease, and there remains the possibility that a stem-like cell can be regenerated (Fig. 4.3a, b(i)) from a mutated progenitor. Intriguing questions remain to be answered, and the definitive proof can only come from human tumours, rather than cell lines, where selective pressure (to grow) has already been applied for many years.

4.4.3.2 Anti-angiogenic Factors Lead to Hypoxia that Stimulates Cancer Stem Cell Enrichment

VEGF-neutralising antibodies have been used in the clinic for a variety of cancers including colorectal cancer and breast carcinoma (bevacizumab) (Kubota 2012; Koutras et al. 2012). However, some serious consequences of using this anti-angiogenic factor to treat tumours have now been realised. The anti-angiogenic activity can lead to hypoxia in the tumours following the reduction in blood vessel formation, and hypoxia can have the unintended effect of enriching for cancer stem cells and unleashing a recurrent, more aggressive tumour (Conley et al. 2012). This highlights the need to take into account the heterogeneity of the tumours and in this case, ignoring the cancer stem cell population means that therapies have the potential to do more harm than good (Wicha 2008).

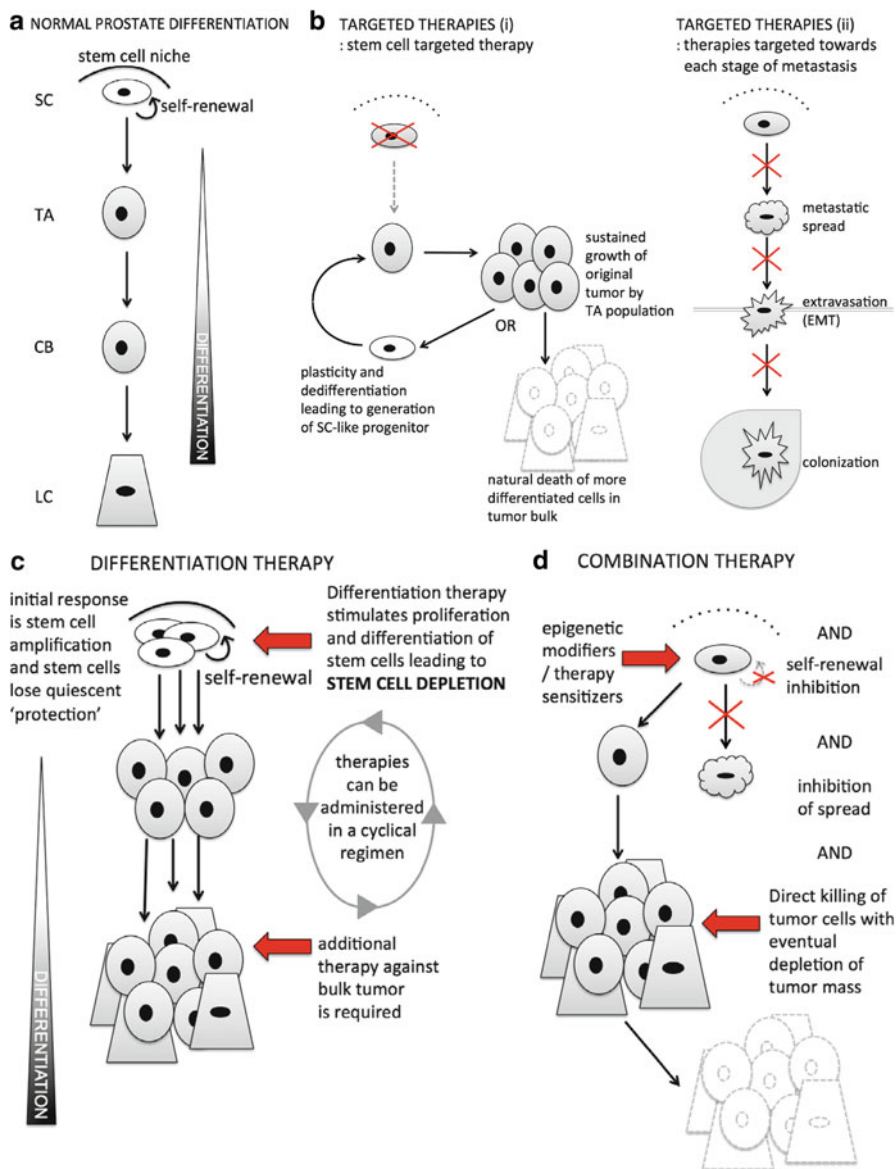


Fig. 4.3 Clinical applications of cancer stem cell therapies in prostate cancer. **(a)** Normal prostate epithelial cell differentiation initiates from a normal stem cell (SC), which gives rise to a hierarchical cascade of transit-amplifying (TA), committed basal (CB) and terminally differentiated luminal cells (LC). **(b)** Targeted therapies could be used to target cancer stem cell-specific markers (i) resulting in reduction of the ability of the tumour to regenerate tumour progenitor cells, and the differentiated cells would gradually die, or there may be dedifferentiation of the progenitor cells to gain stem cell-like features, and the tumour would continue to be propagated. Alternatively, targeted therapies could be designed against each step of metastasis with the intention to inhibit spread of the disease (ii). **(c)** Differentiation therapy would have the aim of depleting the cancer stem cell fraction such that more differentiated cells would be produced that are susceptible to traditional therapies. Stimulating the cancer stem cells to proliferate would reduce the protection of their niche. This therapy could be administered cyclically to ensure elimination of all cancer stem cells and all bulk tumours. **(d)** Considering the heterogeneity of prostate tumours, combination therapy is likely to yield greater success. Targeting the stem cells as well as the bulk population and preventing spread of the tumour would be an optimum multipronged approach.

4.4.3.3 Signalling Pathways

The growth of bulk tumours in the prostate is known to be dependent on androgenic stimuli. Salvage pathways can provide some alternative sources of hormone, but the tumours can still develop resistance to new generation treatments such as abiraterone (Li et al. 2012a). There are two explanations for such resistance: either the cancer cells have found yet another alternative source of hormone, or they have become truly androgen independent as a means of achieving the same growth-related signalling to that stimulated by the hormones. One commonly explored pathway, which has been shown to intersect with AR signalling, is the response to pro-inflammatory cytokines such as IL-1, IL-4 (Lee et al. 2003, 2008, 2009) and IL-6 (Azevedo et al. 2011). Since cancer stem cells in prostate already display such an inflammation-related phenotype, for example, expressing high levels of IL-6 and IL-6R, as well as phosphorylated STAT3, and NF κ B, they already have the potential to respond in this way (Birnie et al. 2008). IL-4 contributes to survival of colon cancer stem cells conferring resistance to chemotherapy, partly through induction of the anti-apoptotic regulator, Survivin (Di Stefano et al. 2010). It is feasible that the cytokines regulate prostate cancer stem cells in a similar manner. Indeed, NF κ B is highly expressed in prostate cancer stem cells and progenitor cells and when inhibited by parthenolide resulted in apoptosis of the cancer stem cells (Birnie et al. 2008). However, generalised NF κ B inhibition can result in host toxicity (Aggarwal and Sung 2011). We, and others, have proposed the link between persistent inflammation, previously established on epidemiological grounds and with animal models, and prostate cancer induction in vivo (Maitland and Collins 2008; De Marzo et al. 2007).

Other growth factor-linked pathways such as those for Notch, Wnt and Hedgehog signalling have also been shown to be active in cancer stem cells from prostate and other human tumours (Takebe et al. 2011). The components of the pathways have therefore been considered to be therapeutic targets. Wnt signalling has been associated with self-renewal in normal stem cells, but it has also been linked to cancer and cancer stem cells. In terms of stem cell control, along with self-renewal, there is also controlled proliferation, inhibition of differentiation, maintenance and survival (Reya and Clevers 2005). It is likely that these pathways, whilst acting to give cancer stem cells similar characteristics as normal stem cells, e.g. self-renewal, in the cancer phenotype, the signalling is dysregulated. Activation of the Hedgehog pathway induces cell proliferation, and inhibition of the pathway inhibits growth (Sanchez et al. 2004). Hedgehog is active in prostate cancer and continuous activation allows a progression both from normal to tumorigenic cells and from tumorigenic to invasive cells (Karhadkar et al. 2004). Similarly, Notch signalling has a broad spectrum of activities including survival, differentiation and proliferation, and Notch-1 is overexpressed in metastatic prostate cancer (Wang et al. 2010). Inhibition of Notch signalling is therefore another valid therapeutic approach, and indeed there is evidence that Notch inhibition leads to reduced growth, migration and invasion and increased apoptosis (Wang et al. 2010). However, tests on all these pathways are often extensively characterised in cell lines, where the response can be neat and unambiguous. There is still the need for the progression to patient samples

before embarking on clinical trials. Since such ‘embryonal’ signalling pathways are essential for cell survival, there is the potential for crosstalk and redundancy between pathways or even bypass pathways that will cancel out the effect of inhibitors. However, some agents are now being tested in clinical trials, and there is an expectation that they will succeed in targeting cancer stem cells (Takebe et al. 2011).

All such pathways present very real barriers to therapeutic development, as they are essential for maintenance of normal tissue architecture and in some cases are necessary for stem cell survival. In addition, there is extensive crosstalk between pathways and unpredictable side effects. Unless a particular signalling intermediate is uniquely expressed in the cancer stem cells, the potential for short- and more seriously long-term side effects, following inhibition of these pathways, in normal tissues and normal stem cells is very real.

4.4.3.4 Flexibility of Metabolic Status

There is now evidence that cancer cells have a different metabolism compared to normal cells, in particular relating to glucose metabolism and oxidative metabolism. Perhaps more significantly, glioma stem cells have also been shown to switch their primary metabolism pathways (Vlashi et al. 2011). This chameleon property of these cells contributes to the complexity of developing novel therapies. Interestingly, one recent study showed a relationship between CD44 expression and glucose metabolism (Tamada et al. 2012). CD44 is a marker of basal/progenitor prostate epithelial cells, and expression is associated with tumour-initiating properties to many cell types including prostate (Maitland et al. 2011). Cancer cells typically produce energy using glycolysis in preference to mitochondrial respiration, which results in reduced reactive oxygen species (ROS) and therefore resistance to ROS-inducing therapies, e.g. radiation and some chemotherapeutic drugs. CD44 interacts with a component of the glycolysis pathway such that it is favoured over respiration in p53-deficient and hypoxic cancer cells. Furthermore, when CD44 was inhibited using siRNA, this resulted in a shift of metabolism and also sensitised the cells to cisplatin, thus linking a progenitor phenotype and stem cell marker with a known cancer phenotype (the Warburg effect). However, this study was carried out only in cell lines under normoxic conditions. It would be most intriguing to characterise these relationships in primary cultures and real patient samples.

4.5 Immune Evasion of Stem Cells

The gold standard for cancer stem cell phenotype analysis remains their ability to reinitiate tumour growth in immunocompromised mice (Brunner et al. 2012). The power of the immune system to eliminate even the cancer stem cell population is demonstrated by the increasing tumour take rates (A. Collins, manuscript in preparation) when the degree of immunodeficiency is increased from nude (athymic so deficient in CD4+ and CD8+ T cells), NOD-SCID (impaired ability to make T or B

lymphocytes or activate some components of the complement system), to the RAG2^{-/-}, gamma c^{-/-} mouse which totally lacks B and T cells, but also an essential natural killer (NK) cell response. The expression of NK targets on cancer stem cells has already been noted in other cell systems (Jewett and Tseng 2012; Jewett et al. 2012), most notably in melanoma (Pietra et al. 2009). This therefore poses the question about how cancer stem cells can function in the immunocompetent environment in a human patient, an issue which has been summarised by Qi et al. (2012). It is likely that the cancer stem cells can induce an immune tolerance, in addition to the interaction and cooperation by the stem cell niche and the tumour microenvironment. Such immune evasion could conceivably be overcome, perhaps even allowing a vaccination strategy, but again necessarily as part of a combination therapy.

4.6 Tumour Dormancy and Stem Cell Quiescence

Relapse of a cancer after treatment can take months or sometimes years. The period where there is no apparent tumour growth is termed dormancy (Aguirre-Ghiso 2007). Dormancy can occur due to internal factors such as a block in proliferation and a cell cycle arrest related to cell signalling, external pressures within the microenvironment (Bragado et al. 2012; Sottocornola and Lo Celso 2012) such as a lack of angiogenesis or activation of the host immune system, or induction of apoptosis. It is thought that cellular quiescence is one of the internal mechanisms by which the cells are arrested. Quiescence is considered likely to contribute to tumour dormancy because it has the potential to be reversed as a result of a change in external signals and the microenvironment. For this reason, the more permanent and less reversible senescence is less likely to be involved in dormancy but has been acknowledged as a tumour-suppressive mechanism (Aguirre-Ghiso 2007).

In terms of the therapeutic opportunity with dormancy, if we were able to *maintain* a dormant tumour or dormant metastases, then the patient could live with asymptomatic minimal residual disease. Maintenance, rather than elimination, in this case could be an acceptable outcome. Indeed, maintenance therapy is in routine use for myeloma and lymphoma, albeit with continual room for improvement (Maiolino et al. 2012; Badros 2010), but not yet for prostate cancer. Of course in terms of therapy, this would require more understanding of the trigger that activates cells to exit dormancy. This could be due to different growth-promoting signals or else an adaptation of the cells, which allows them to respond differently to growth-promoting signals. Significantly, once relapse has occurred and primary tumour or metastatic growth has been initiated, the cancer presents a difficult therapeutic challenge.

It is also possible to marry tumour dormancy with cancer stem cells (Kusumbe and Bapat 2009). There is now evidence that cancer stem cells are predominantly, though not entirely, quiescent. Therefore, it has been postulated that quiescent cancer stem cells are responsible for preserving the potential for recurrent primary and metastatic tumours (Moore et al. 2012; Moore and Lyle 2011). Naturally, quiescent cells are not sensitive to chemotherapy and radiotherapy that predominantly target proliferating cells, and so alternative therapies are required for this subpopulation. Evidence

of quiescent cancer stem cells has been presented for melanoma, pancreatic, breast, ovarian and haematopoietic malignancies (Buczacki et al. 2011). One study in mouse prostate cites TGF- β as a key factor in maintaining normal prostate stem cell dormancy (Salm et al. 2005). Assays used to identify quiescent cells include staining with the Ki67 proliferation marker where Ki67-negative cells being indicative of the G0 stage of the cell cycle. Also, label-retaining experiments have been used with the principle that a label which inserts into the cell membrane (e.g. PKH26) is diluted as cells divide and proliferate whilst being retained in nondividing or quiescent cells (Moore and Lyle 2011). This has been shown in a variety of tumour types (Chen et al. 2012; Munoz et al. 2012; Li et al. 2012b), and indeed it has even been suggested that these quiescent cells are more invasive and more aggressive, at least in breast cancer (Pece et al. 2010). If this is the case in prostate cancer, then quiescent cancer stem cells can be thought of as ‘the sleeping assassin’.

4.7 Functional Assays for Cancer Stem Cell Therapeutics

4.7.1 Transplantation

Although the gold standard for identifying cancer stem cells has been tumour initiation in immunodeficient mice (Brunner et al. 2012), this has been brought into question. In a melanoma model, it was shown that tumour initiation was not a feature of a *rare* population of cells and in fact almost 33% of cells had the ability to form tumours. However, efficiency of tumour formation depended greatly on the genetic background and therefore the permissiveness of the mouse model (Quintana et al. 2008). This brought into question the core of the cancer stem cell hypothesis, i.e. that not all cells are equal. However, on testing in pancreatic, head and neck and lung models, Ishizawa et al. (2010) showed that whilst there was variation between mouse models, in these tumours, there remained a rare subpopulation of tumour-initiating cells. Currently, there is nothing to replace the use of *in vivo* models to test novel therapeutics and to assess the enrichment of stem cells as well as testing serial passaging of human tumours. This latter assay can distinguish between cells that can initiate primary tumours but are unable to initiate secondary tumours, from true cancer stem cells which can initiate tumours potentially indefinitely over multiple *in vivo* passages (Brunner et al. 2012).

4.7.2 Lineage Tracking

A recent article by Wright (2012) has argued against the use of mouse models and indeed against the selection of subpopulations of cells *in vitro* to identify stem cells and cancer stem cells. In contrast, the use of lineage tracking *in vitro* and *in vivo* to determine the *fate* of cells rather than their surface marker expression at a single

point in time is proposed. The most elegant studies of lineage tracking have been demonstrated in the small intestine from Hans Clevers' group, and these indeed have allowed identification of stem cells as well as elucidation of their life cycle (Snippert and Clevers 2011). Whilst not disagreeing with this viewpoint, it is not entirely practical to do *in vivo* lineage tracking for all tissues. However, within the prostate, lineage tracking in culture has been attempted, and indeed infection of primary prostate epithelial cells with lentivirus encoding fluorescent marker genes under the control of differentiation-specific promoters has been undertaken. This showed proof-of-principle results to indicate a method of tracking differentiation (Frame et al. 2010). Any such lineage tracking firstly has to overcome limitations of the vector as well as optimising the strategy for the specific cell types. Other methods of lineage tracking can include mapping genetic changes in human cancers and evolution of tumours through clonal selection, most elegantly done in leukaemia (Ding et al. 2012). Alternatively, in prostate there has been a lineage tracking study of prostate stem cells within benign tissue (Blackwood et al. 2011), which used laser capture microdissection to assess respiratory chain defects that resulted from mitochondrial DNA mutations. This allowed analysis of individual acini within the prostate gland and identification of a single progenitor cell.

4.7.3 Stem Cell Markers

Markers of stem cells include surface markers that define a rare subpopulation of cells with the characteristics of stem cells including self-renewal and differentiation. Cells can be selected using specific antibodies to these markers and FACs sorting or MACs sorting (Visvader and Lindeman 2008; Miki and Rhim 2008). In addition, isolation of side populations has been used as another method to identify and extract stem cell populations. This approach is based on the principle that stem cells have increased drug efflux proteins including aldehyde dehydrogenase (ALDH) (Ginestier et al. 2007; Ma and Allan 2011) and ABC transporters (Dean et al. 2005; Ding et al. 2010; Elliott et al. 2010; Scotto 2003; Tanei et al. 2009).

4.7.4 In Vitro Assays

There are a variety of *in vitro* assays to test for stem cells and cancer stem cells. Typically, these assays are focussed on examining the *potential* of the cells. Clonogenic assays assess the ability of the cell to give rise to new progenitor cells, and importantly secondary colony-forming assays can distinguish between highly proliferating progenitor cells and cells with stem cell properties. Also, cells with stem cell-like features are more able to form 3D spheres in sphere-forming assays. Other assays *in vitro* include proliferation assays to determine when the cells reach exhaustion as well as differentiation assays by adding different media and growth

factors, or in the case of prostate adding serum, stroma and DHT can differentiate the cells (Swift et al. 2010). Differentiation can be detected using immuno-staining for basal and luminal cytokeratins, as well as differentiation markers, such as androgen receptor, prostatic acid phosphatase (PAP) and PSA. Another in vitro assay is the label-retaining assay that has been described above (Moore and Lyle 2011).

4.8 Clinical Applications of Cancer Stem Cell Therapies in Prostate Cancer

4.8.1 The Role of Stem Cells in Multifocal Prostate Cancer

We have established that design of novel therapeutics for prostate cancer must take into account the cancer stem cell population. Alongside this consideration, we have to evaluate the heterogeneous tumour as a whole, which has resulted from a series of mutations resulting in clonal selection, evolution and expansion (Marusyk et al. 2012). The consequences of these events and the potential for more than one cell of origin with an ability to initiate tumours can be multifocal disease, typically in two thirds of patients. Multifocal disease is associated with more aggressive, higher-grade prostate tumours than unifocal disease (Djavan et al. 1999). In therapeutic terms, there is also the consideration of adaptation of the tumour to promote invasion and metastasis (Fig. 4.3b(ii)). Heterogeneity may also exist at this stage within the cancer stem cell population, as there is likely to be considerable plasticity of the stem cell phenotype, given the different properties of the tumours resulting from different selection pressures due to external signalling, tumour microenvironment and stem cell niche (van der Pluijm 2011; Risbridger and Taylor 2008; Kelly and Yin 2008).

4.8.2 Combination Therapies

Monotherapies can be successful depending on the tumour type and the mode of action. However, with the huge variety of cancers and the potential adaptation and mutation in response to environmental selection pressures and indeed treatment itself, along with increased understanding of the mechanisms of therapy resistance, combination therapies are likely to be effective and longer lasting (Fig. 4.3d). Recent proposals to combine next-generation anti-androgen response modifiers, such as MDV3100 and abiraterone, may fail to exploit the biggest advantage of combination therapies, i.e. the ability to block different or complementary pathways.

In prostate cancer, radiation alone can lead to recurrence, hormone therapy leads to resistance, and responsiveness to chemotherapy is short-lived. Along with these observations and known heterogeneity of tumours, combination therapies are

predicted to be a more successful strategy in the future of prostate cancer treatment, and indeed it has already been embraced. As described above, radiotherapy is not 100% effective due to inherent tumour resistance and to dose limits to reduce toxicity. Therefore, combining radiotherapy with other treatment modalities could greatly enhance therapeutic effect. This is currently already carried out in terms of using radiotherapy alongside surgery or radiotherapy with androgen ablation treatments. However, more targeted approaches are being investigated that could enhance radiosensitivity of prostate tumour cells.

Inhibitors of poly (ADP ribose) polymerase (PARP) are under consideration as a treatment for prostate cancer and are being used in current clinical trials. This enzyme is essential for the repair of single-strand DNA breaks and can complement radiotherapy. PARP inhibitor use for prostate tumours has some promise because a proportion of prostate cancer cells are mutated in the BRCA1 and BRCA2 genes and also in PTEN; these mutations indicate a defect in homologous recombination, and inhibition of other repair pathways with PARP inhibitors acts as a double hit to the cancer cell (de Bono et al. 2011). There is also evidence that PARP inhibitors inhibit ETS gene-driven prostate cancer models (Brenner et al. 2011).

Finally, several other therapeutics are being considered as partners for radiotherapy, reviewed in (Verheij et al. 2010), such as EGFR inhibitors, anti-angiogenic drugs and apoptosis-modulating agents.

4.8.3 Differentiation Therapies

The principle of differentiation therapy is to first stimulate stem cells out of quiescence or stress-induced growth arrest, thereby inducing proliferation and producing differentiated cycling progeny (Sell 2004). Such ‘pre’-treatment should result in the cells being susceptible to radiation and anti-proliferative drugs as well as drugs that target more differentiated cells. Ultimately, the aim will be to deplete the cancer stem cell stores to reduce the regeneration and recurrence potential of the tumour (Fig. 4.3c). One note of caution when considering differentiation therapy is that normal stem cells should not be affected; otherwise, they too could be depleted with catastrophic consequences for the patient as a whole (Moore and Lyle 2011). One example of a therapy which has had the desired effect of reducing cancer stem cell frequency is use of a DLL4 inhibitor (Hoey et al. 2009). DLL4 is a potent ligand for the Notch pathway and when inhibited, there was a concomitant reduction in tumour recurrence and angiogenesis, as demonstrated in a colon cancer xenograft model. However, similar untargeted DLL4 inhibition/knockout in a mouse model had serious longer-term consequences on vascular functions, resulting in multiple liver haemangiomas (Yan et al. 2010). The observation that the haemangiomas arose as a long-term (8 week) consequence of chronic DLL4 block implies that side effects of cancer stem cell therapies may only emerge in human patients after proportionately

long time scales and could be managed in advanced cancer patients for whom the short-term prognosis is poor.

In terms of clinical rather than experimental success, retinoids as the differentiation stimulator in acute promyelocytic leukaemia have improved patient survival, with the application of ATRA (all-trans-retinoic acid) leading to release of the differentiation block that occurs as a result of the PML-RAR α fusion (Cruz and Matushansky 2012). There has been less success in solid tumours due to a poorer understanding of differentiation pathways and perhaps the inability of the cancer cells to differentiate, depending on their defining mutations and the likelihood that many pathways are affected (Rane et al. 2012).

Epigenetic modifiers including histone deacetylase (HDAC) inhibitors and DNA methyltransferase (DNMT) inhibitors were initially studied due to their ability to promote differentiation, which was associated with reduced cell proliferation (Piekarz and Bates 2009). It is now known that the differentiation observed was due to perturbations of DNA methylation and histone acetylation. This feature was clearly of interest for treatment of cancer cells, and indeed monotherapies of DNMT inhibitors and HDAC inhibitors have been used against AML (acute myelogenous leukaemia) and T cell lymphomas. However, in solid tumours, it is thought that they will be most effective as part of a combination therapy (Pili et al. 2012). Proposed therapies would combine the differentiation-inducing ability of the epigenetic modifiers with toxic drugs or radiation. In addition, they have the effect of decondensing the chromatin, such that the DNA is more susceptible to damage by the latter agents.

4.8.4 Targeted Therapies

In order to design therapies that target cancer stem cells specifically, it is possible to design immunotherapies or small molecule inhibitors that target stem cell-specific surface markers (Fig. 4.3b(i)) (Qi et al. 2012). The ability to select stem cells from tumours has allowed extensive microarray and proteomic studies to identify cancer stem cell-specific markers. The most crucial criteria when choosing such a target are that it should be tissue specific and should not be expressed on normal stem cells. The successful targeting molecule should necessarily be required for cancer stem cell survival, to reduce the chances of gene expression silencing as an immediate resistance mechanism. Along with targeting stem cells, targeted therapy should be designed against the other steps of tumour progression including invasion and metastasis (Fig. 4.3b(ii)).

4.9 Conclusions

We have provided here an overview of the complexity of prostate cancer treatment, taking into account the progression of the disease, current treatments and the problem of therapy resistance, as seen from a cancer stem cell perspective. However, the mechanisms of therapy resistance are many and varied. In order to improve prostate cancer treatment, an understanding of the molecular mechanisms of resistance as well as the biology of the disease is required. Despite many billions of dollars expended on 'new' treatments, and thousands of publications in the scientific literature, we still measure advances in months rather than genuinely increased survival for advanced prostate cancer. Adoption of a stem cell-based approach to new therapy targets to complement the improved tolerability of the new therapies could provide the paradigm shift in therapeutic outcome which researchers seek.

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Chapter 5

Genetic and Signaling Pathway Regulations of Tumor-Initiating Cells of the Prostate

David J. Mulholland and Hong Wu

Abstract Here we review current literature on genetic and signaling pathway regulators of tumor initiating cells in prostate cancer. While we emphasize the consequence of PTEN loss and PI3K/AKT activation in prostate cancer initiating cells, we also assess the importance of other signaling regulators, including RAS/MAPK, WNT/ β -catenin, MYC, NKX3.1 and p53 on these cells. Importantly, we stress how these factors alone, or in collaboration, alter tumor initiating cell/cancer stem cell function and consequently, phenotypes in in vivo prostate cancer models. Our review also highlights the understanding of how genetic pathway alteration influences cancer initiation by way of lineage tracing or cell type specific disruption. Functional similarities and differences of how tumor suppressor loss impacts human prostate cancer are also addressed, where appropriate. Finally, we touch on outstanding questions that future experimentation will hopefully address.

5.1 Introduction

A significant portion of men with prostate cancer will experience recurrent disease after successfully responding to front-line therapies (Grubb et al. 2007). Of those that receive androgen-deprivation therapy (ADT), many will progress to

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castration-resistant prostate cancer (CRPC) (Kasper and Cookson 2006). At clinical presentation, recurrent primary and metastatic prostate cancer is composed mostly of well-differentiated epithelium. This observation suggests the existence of unique populations of prostate cancer cells with the ability to survive therapy, remain quiescent for an extended period of time, and eventually differentiate to clinically detectable disease. Given this, the “holy grail” of prostate cancer treatment may depend on the identification of those genetic and pathway alterations responsible for the formation, or the maintenance, of these unique populations of cancer cells and ultimately leading to their elimination.

Though many terms have been used to describe these unique populations, for clarity we adapt the terminology defined by Dr. Visvader (Visvader and Lindeman 2008) and term those cells within the normal epithelium that acquire initial genetic or pathway alterations as tumor-initiating cells (TICs). Cells within the tumor mass that are capable of escaping therapies and responsible for repopulating tumor cells are referred to as cancer stem cells (CSCs) (Visvader and Lindeman 2008). Although a large body of published works based on prostate cancer cell lines, xenografts, in vitro spheroids cultures, genetically engineered mouse models (GEMs), and human cancer samples support the presence of prostate TICs and CSCs, few studies have resolved the relationship between TICs and CSCs in prostate cancer. This is partly due to a less well-defined lineage hierarchy of prostate stem cells in comparison to other somatic stem cells such as those of the hematopoietic system or mammary gland, as well as limited information on the major genetic and pathway alterations that are responsible for prostate cancer initiation, progression, and acquisition of therapeutic resistance. Recently developed model systems that allow lineage tracing and lineage-specific manipulation of key pathway alterations found in human prostate cancers have begun to provide clarity to the outline of the prostate stem cell hierarchy (Fig. 5.1).

Prostate cancer is genetically multifocal and frequently presents with aberrations in pathways that could regulate the activity of TICs/CSCs. This is exemplified by recent integrated genomic and mutational landscape studies, which have identified deletion/mutations of the PTEN, RB, p53 tumor suppressors, and heightened activities of PI3K/AKT, RAS/MAPK, RB/p53, AR, and WNT signaling pathways (Taylor et al. 2010; Barbieri et al. 2012; Grasso et al. 2012). Remarkably, PI3K/AKT and RAS pathway alterations are found in over 40% of primary tumors and over 90% in metastatic lesions while RB/p53 signaling is altered in more than 30% and 70% of primary and metastatic sites, respectively (Taylor et al. 2010). Studies have also implicated overexpression of the Polycomb members EZH2 and BMI-1 with late-stage prostate cancer (van Leenders et al. 2007; Ogata et al. 2004). Importantly, many of these mutations and their associated pathways are known to play essential roles in regulating TIC and CSC activities, including self-renewal and multi-lineage differentiation. These deregulated pathways may also represent potential targets for TIC and CSCs. Here we highlight evidence that such pathway alterations, elicited by certain genetic aberrations, can regulate the activity of TIC/CSC function during prostate cancer progression. We will summarize and interpret results from two experimental approaches, namely, in vitro manipulation of prostate cancer cell lines

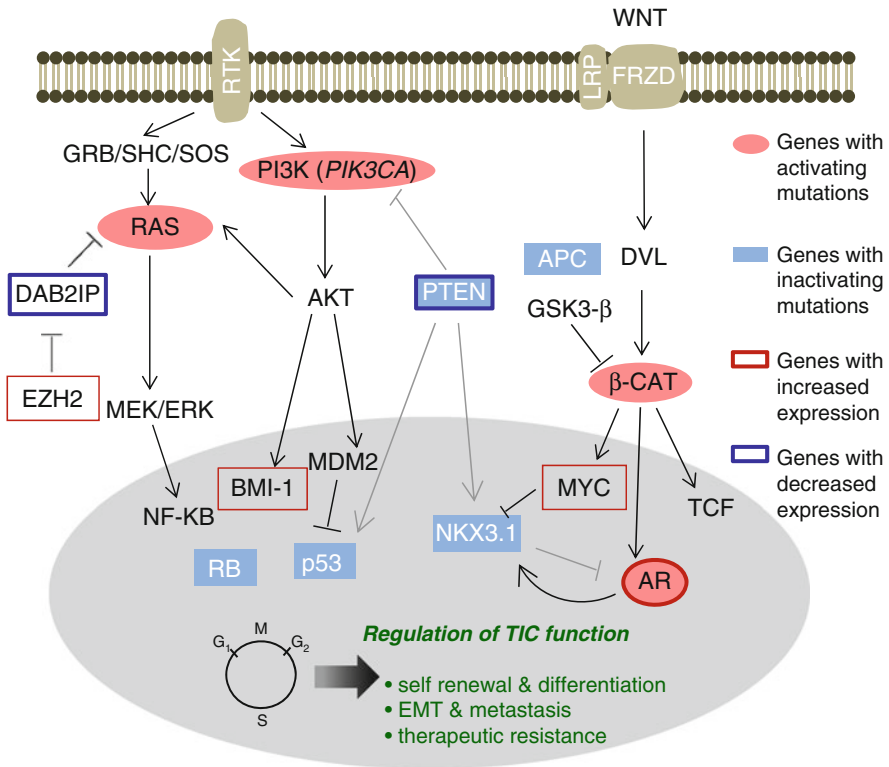


Fig. 5.1 Genetic mutations and pathway alterations found in human prostate cancers that are known to regulate TIC function. Silencing of PTEN results in PI3K/AKT activation and NKX3.1, AR, and p53 suppression, leading to stem/progenitor cell expansion. RAS pathway activation occurs, in part, through increased EZH2 expression and reduced DAB2IP which may then act in concert with PI3K/AKT signaling to facilitate cancer progression, EMT, and metastasis. Cooperativity between loss p53 and RB can promote expansion of TICs through regulation of cell cycle checkpoints and potentially facilitate neuroendocrine differentiation. WNT/β-catenin pathway activation may regulate self-renewal through TCF activation but may also promote differentiation by coactivation of AR

and in vivo genetically engineered mouse models. Results from in vivo tissue recombination of murine and human origins will be reviewed by Drs. Goldstein and Witte (see Chap. 2).

5.1.1 Genetic Regulation of TIC/CSC In Vitro

Increasing evidence indicates that many human prostate cancer cell lines and xenografts contain minor populations of cells, identifiable by either cell surface marker expression or enhanced drug efflux (Patrawala et al. 2005), with enhanced CSC

function upon in vivo transplantation (Patrawala et al. 2006). Reports also suggest that genetic and pathway alterations in these cell lines can result in altered CSC number and activity. Knocking down the *PTEN* tumor suppressor by short hairpin RNA interference (sh-RNAi) in *PTEN*-positive DU145 cells leads to an increase in cells positive for CD44⁺;CD133⁺, putative cell surface markers for human prostate stem cells (Richardson et al. 2004; Patrawala et al. 2006), accompanied by enhanced sphere forming ability, clonal outgrowths and tumorigenic potential (Dubrovskaya et al. 2009). Conversely, pharmacological inhibition of PI3K/AKT signaling using NVPBEZ235 (Maira et al. 2008) can reverse the expansion of CD44⁺;CD133⁺ cells potentially mediated by increased nuclear expression of FOXO (Dubrovskaya et al. 2009). These data provide direct evidence that alteration of pathways regulated by the PTEN/PI3K/AKT axis can directly influence CSC activity.

TICs have also been studied in vitro by deleting floxed *Pten* and *p53* alleles and selecting for self-renewing stem/progenitor activity using the prostosphere culture system (Abou-Kheir et al. 2010). Interestingly, these established lines contain a stable minor population of progenitor cells that are capable of self-renewal, multi-lineage differentiation, and initiating both primary and invasive prostate cancers upon orthotopic implantation. Similarly, NANOG, p16, and telomerase are also shown to regulate self-renewal and proliferative lifespan of human prostate epithelial progenitors (Jeter et al. 2009; Bhatia et al. 2008).

5.2 Genetic Regulation of TICs In Vivo

5.2.1 Phenotypes Associated with Genetic and Pathway Manipulations

The development of genetically engineered mouse models (GEMs) that recapitulate major genetic or pathway alterations found in human prostate cancers has facilitated our understanding of the relationship of cell of origin, pathway alteration, and prostate cancer pathology. The first generation of transgenic models include TRAMP (Greenberg et al. 1995; Gingrich and Greenberg 1996) and LADY, which rely on the androgen-responsive probasin promoter to drive SV40 T-antigen expression, leading to the inhibition of both p53 and RB functions (Ahuja et al. 2005). The LADY model progresses to high-grade PIN while the TRAMP model progresses to invasive and metastatic disease accompanied by high content of neuroendocrine marker-positive cells. Using the same promoter, prostate-specific overexpression of the constitutively activated AKT (Majumder et al. 2003 PNAS 100:7841-6) and the MYC oncogene (Ellwood-Yen et al. 2003) leads to the development of PIN and invasive adenocarcinoma, respectively. They are potentially facilitated by the coinciding reduction of NKX3.1 expression (Iwata et al. 2010). However, no published studies have investigated the presence of either TICs or CSCs in these models. Moreover, it is unclear as to whether the different pathologies observed in these models are due to (1) a cell of origin, (2) specific genetic or pathway alterations, or (3) both.

The *Pten* conditional knockout prostate cancer model, driven by Cre4-Cre transgene (Wu et al. 2001), progresses to invasive adenocarcinoma and micrometastasis with well-defined kinetics (Wang et al. 2003) and has been used to study the effects of *Pten* deletion in both basal and luminal cells (Wang et al. 2006). *Pten* deletion leads to increased basal cell density, altered basal cell morphology, and localization (Wang et al. 2006), as supported by the expansion of Cre⁺ and basal cell marker-positive cells along the basement membrane and migration of basal marker-positive cells to the lumen. *Pten* deletion also leads to increased cell proliferation and decreased cell death in the CK5⁺;CK8⁺;P63⁺;Ki67⁺;AR⁺;BCL-2⁺ population that is immediately adjacent to the basal compartment, which may be similar to the transit-amplifying (TA) cell population found in the human prostate (Wang et al. 2006; Vander Griend et al. 2008). Such observations are in parallel with the finding that PSCA, a marker associated with TA cells in human prostate cancer (Tran et al. 2002), is increased in *Pten*-deleted prostates (Dubey et al. 2001; Wang et al. 2003). Collectively, these data indicate that PTEN loss in the prostate epithelium can lead to the expansion of cells that function as TICs for prostate cancer development.

Greater understanding of the effects of pathway alterations on TIC has also been facilitated by the use of surface antigens to enrich for specific cell populations. LSC^{high} cells (lineage marker negative [CD31^{neg}CD45^{neg}Ter119^{neg}]) and Sca-1⁺;CD49^{fhigh} (Lawson et al. 2007), and more recently LSC^{high}CD166^{high} cells (Jiao et al. 2012), are minor basal/TA cell populations within the wild-type prostate epithelium that harbor a high content of stem/progenitor activity and are enriched in the proximal region of the murine prostatic lobes (Fig. 5.2). In *Pten*-null prostates, Sca-1⁺ cells are expanded by tenfold (Wang et al. 2006) and LSC^{high} content increases by 2.5-fold during disease progression and further enhanced after castration (Mulholland et al. 2009; Liao et al. 2010). Interestingly, upregulation of the PI3K pathway and increased AR expression in human basal LTC^{high} cells (Lin⁺;Trop2⁺;CD49^{fhigh}), which are the human equivalent of murine LSC^{high} cells, are also necessary and sufficient for the initiation of human prostate cancer (Goldstein et al. 2010). Studies using in vivo transplants have demonstrated that the predominant tumor-regenerating cell population within the *Pten*-null model is also enriched in the LSC^{high} but not LSC^{low} subpopulations. This is true whether cells are prospectively isolated by flow cytometry (Goldstein et al. 2010; Lawson et al. 2010; Xin et al. 2005) and manipulated ex vivo or isolated directly from GEMs (Mulholland et al. 2009, 2012; Liao et al. 2010). LSC^{high} cells also have the capacity to generate differentiated luminal cells upon transplantation (Mulholland et al. 2009, 2012; Goldstein et al. 2008, 2010).

At least four *Pten* conditional deletion lines (Backman et al. 2004; Wang et al. 2003; Chen et al. 2005; Ma et al. 2005) and two other prostate Cre lines (Ma et al. 2005; Maddison et al. 2000) have been generated by various laboratories. Of these models, not all conditional *Pten* prostate deletion models elicit the same phenotype. For instance, unlike the *Probasin-Cre4⁺;Pten^{loxP/loxP}* model (Wang et al. 2003), *PSA-Cre⁺;Pten^{loxP/loxP}* mutants (Ma et al. 2005) do not exhibit pathology in the proximal regions of the prostate but display accumulation of cells positive for the luminal markers CK8 and P-AKT. In this model, rare Clu⁺;Tacstd2⁺;Sca-1⁺ cells may

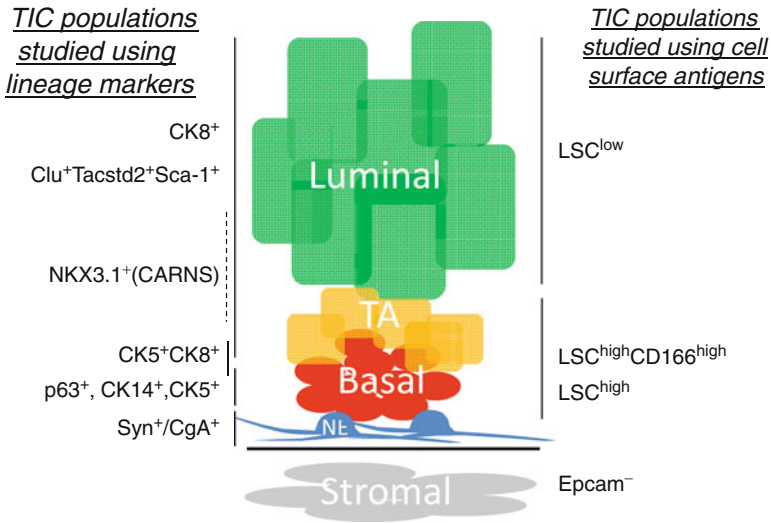


Fig. 5.2 Lineage and cell surface markers used for identifying TICs in *Pten*-null murine prostate epithelium. The prostate epithelium consists of basal, transient-amplifying, luminal, and neuroendocrine cells. Basal cells are p63⁺;CK5⁺;CK14⁺ while luminal cells are CK8⁺. Intermediate or transient-amplifying (TA) cells include CK5⁺;CK8⁺ cells and may putatively include (*dashed line*) rare NKX3.1⁺ (CARN) cells. Various cell surface markers have been used for isolating subpopulations with the epithelium, including LSC^{high} (Lin⁺Sca-1⁺CD49^{high}), LSC^{high}CD166^{high} (Lin⁺Sca-1⁺CD49^{high}CD166^{high}), and LSC^{low} (Lin⁺Sca-1⁺CD49^{low}) subpopulations. Although these subpopulations correspond to the basal/TA and luminal cells in the WT epithelium, respectively, their localizations are altered in the *Pten*-null epithelium, especially after castration

constitute luminal TICs (Korsten et al. 2009) (Fig. 5.2). These data suggest that multiple stem/progenitor cells can serve as the cell of origin of prostate cancer initiated by PTEN loss and more defined systems, *via* lineage tracing and cell type-specific deletion, are necessary to characterize their role(s) in prostate cancer initiation and progression.

5.2.2 Lineage Tracing for Identifying TICs

Two general approaches have been used for identifying specific cell types associated to TICs, including lineage tracing and using cell type-specific promoters to drive pathway alterations. By crossing an *NKX3.1-Cre^{ER}* inducible line with the *Rosa26-floxed-LacZ* line, a rare population of cells called CARNs, or Castration-Resistant Nkx3.1-expressing cells (Fig. 5.2), have been identified to have self-renewal capacity *in vivo* and can give rise to both basal and luminal cells. Targeted deletion of *Pten* driven by the *NKX3.1-Cre^{ER}* leads to the formation of invasive carcinoma and suggests

that these bipotential CARN cells may be TICs (Wang et al. 2009). Using a similar lineage-tracing strategy but with more cell type-specific *Cre^{ER}* lines, recent studies have provided more definitive proof that both basal and luminal prostate epithelial cells are self-sustainable lineages and can serve as a cell of origin for prostate cancer initiation and progression upon *Pten* deletion (Choi et al. 2012).

However, precautions need to be made when interpreting the current data concerning TICs in the prostate. Although CK5⁺;CK8⁺ double-positive TA cells represent a minor and almost undetectable population in the normal prostate epithelium, they may expand upon oncogenic insult, such as with *Pten* deletion (Wang et al. 2006). Interestingly, *Pten*-null lesions derived from the *CK5-Cre^{ER}* promoter also yield CK5⁺;CK8⁺ double-positive TA cells and potentially to the expansion of CK8⁺ luminal cells. Since TA cells share both basal and luminal cell features, induced genetic or pathway alterations by cell type-specific Cre expression including, those driven by the *Nkx3.1*, *Ck5*, or *Ck8* promoters, may have differential effects on the currently poorly defined TA population. Second, the timing of genetic manipulation may influence TIC formation. While early deletion of *Pten* leads to micrometastatic disease, postpubescent deletion of *Pten* yields considerably more latent disease (Luchman et al. 2008), suggesting that the increased proliferation observed during normal prostate development may compound with oncogenic insults to affect cancer initiation, progression along with TIC content and activity. Nevertheless, the consensus is that multiple cell types or progenitor cells can serve as the cells of origin for prostate cancer development and become TICs upon PTEN loss. Future work should investigate whether such multi-TIC models apply to other genetic and pathway alterations and whether TIC cells from different cells of origin have similar or different capacity in cancer metastasis and CRPC development.

5.2.3 Cooperative Effects of Pathway Alteration on TIC Function

Multi-genetic events are known to collaboratively contribute to human cancer initiation, progression, metastasis, and therapeutic resistance. Recent studies suggest that the genetic events involved in “multiple-hit” tumorigenesis likely take place at the level of TICs (Guo et al. 2008). Similarly, second hits or multi-pathway alterations are frequently associated with enhanced progression in genetically defined prostate cancer GEMs. In some cases, this accelerated progression is associated with increased and sustained self-renewal activity of TICs (Martin et al. 2011). For example, advanced human prostate cancer frequently presents with PTEN and TP53 loss (Schlomm et al. 2008; Sircar et al. 2009). Mice with PTEN and TP53 loss (*Pb-Cre4⁺;Pten^{loxP/loxP};TP53^{loxP/loxP}*) recapitulate this collaborative effect with accelerated locally invasive disease (Chen et al. 2005; Abou-Kheir et al. 2010; Martin et al. 2011), which may be explained both by the reduced senescence observed in *Pten*-null *P53* null prostate cells (Chen et al. 2005) and the higher content of TICs observed in more aggressive cancers (Savona and Talpaz 2008; Pece et al. 2010). *Pten*-null;*TP53*-null prostate spheres and colonies displayed increased self-renewal

capacity compared to spheres derived from *Pten*-null or WT prostates (Martin et al. 2011), observations that are consistent with findings that p53 loss leads to increased asymmetrical cell division in mammary stem cells (Cicalese et al. 2009). More recent studies also demonstrate the collaboration of JNK and the PI3K/AKT pathway in prostate cancer development. Downregulation of the JNK signaling pathway by way of conditional deletion of both *Jnk1/2* and upstream kinases *Mkk4/Mkk7* in *Pten*-null prostate epithelium leads to the expansion of p63⁺ and CD44⁺ cells and enhanced disease progression (Hubner et al. 2012).

Epithelial to mesenchymal transition, or EMT, is a phenotype associated both with increased cellular migration and stem cell function (Mani et al. 2008). Enhanced EMT-like qualities have been implicated in human prostate cancer recurrence (Zhang et al. 2009) and may also have potential as therapeutic targets (Tanaka et al. 2010). Activation of the RAS/MAPK signaling axis has been demonstrated to cooperate with PTEN loss in promoting EMT and macrometastasis in distant organs, accompanied by enhanced TIC function (Mulholland et al. 2012). In contrast to LSC^{high} TIC of the *Pten*-null model (Mulholland et al. 2009), a new EpCam^{low}/CD24^{low} EMT-like cells from mice with coordinate homozygous *Pten* loss and *K-ras* activation (*Pb-Cre4⁺;Pten^{loxP/loxP};K-ras^{G12D/WT}*) were revealed to have considerable TIC activity as compared to cells with only PTEN loss (Mulholland et al. 2012). Importantly, the ability of these EMT-like cells to initiate prostate carcinogenesis (Mulholland et al. 2012) and distant metastasis is correlated with their increased stem cell signature (Mulholland et al. 2012; Kong et al. 2010), suggesting that EpCam^{low}/CD24^{low} EMT-like cells may represent a unique TIC population with metastatic potential, similar to what has been reported in breast (Mani et al. 2008) and pancreatic cancers (Hermann et al. 2007).

The correlation between cancer aggressiveness and TIC content has prompted the examination of how molecules known to enhance cancer progression may regulate stem cell functions. Besides its key function in antagonizing the PI3K/AKT pathway, PTEN is known for its function in negatively regulating stem cell self-renewal, proliferation, and survival (Groszer et al. 2001; Stiles et al. 2006). PTEN loss promotes G₀-G1 cell cycle transition of neural and hematopoietic stem cells (Groszer et al. 2006; Yilmaz et al. 2006; Zhang et al. 2006), which leads to expansion of stem cell pools. With increased expression during human prostate cancer progression, the Polycomb member EZH2 (Varambally et al. 2002) has been linked to the regulation of EMT (Cao et al. 2008) and stem cell function (Kamminga et al. 2006; Suva et al. 2009). Loss of the microRNA let-7 is not only inversely correlated with EZH2 expression in clinical prostate cancer specimens but can directly regulate EZH2 activity in culture with potential to inhibit clonal growths in prostate epithelial cell lines (Kong et al. 2012). BMI-1 is another Polycomb family member whose elevated expression in low-grade prostate cancer samples has been correlated with biochemical recurrence (van Leenders et al. 2007) and poor clinical outcome (Glinsky et al. 2005). BMI-1 overexpression leads to expansion of p63⁺ cells in p53-null prostate sphere cells (Lukacs et al. 2010) while its knock-down led to impaired carcinogenesis driven by either FGF overexpression or *Pten* deletion in tissue regeneration assays (Lukacs et al. 2010). By extension, it is feasible that over expression of BMI-1

in the murine prostate could lead to invasive carcinoma when combined with *Pten* haploinsufficiency. In vitro observations show that AKT phosphorylates and activates BMI-1, which parallels the observations of increased BMI expression human prostate cancers (Nacerddine et al. 2012). These findings indicate that PTEN negatively regulates BMI-1 function (Fan et al. 2009) and provides an additional link between PTEN function and stem cell self-renewal.

Activation of WNT signaling has been associated with maintenance of stem cell function in many cancers (Clevers and Nusse 2012). Exogenous WNT3a can increase prostate sphere size and self-renewal activity both in the LNCaP and C4-2B human prostate cancer cell lines (Bisson and Prowse 2009) and in primary murine prostate epithelium while in turn be inhibited by Notch signaling (Shahi et al. 2011). While activating point mutations in β -catenin occur at a low frequency in human prostate cancer (Gerstein et al. 2002), murine GEMs with either activated β -catenin (*Pb-Cre⁺;Ctnnb ^{Δ ex3}*) or deletion of *Apc*, a component of the β -catenin destruction complex, results in localized expansion of p63⁺ cells. When K-ras and β -catenin signaling are coactivated (*Pb-Cre⁺;Ctnnb ^{Δ ex3};K-rasV12*), the resulting mutant mice have increased CD44⁺ cells and a paralleled increase in progression (Pearson et al. 2009). Collectively, these data suggest that Polycomb and WNT signaling maintain a critical balance in cells thought to be necessary for tumor initiation that occur upon genetic aberration.

Pathway-specific alterations occurring as a consequence of two genetic hits may also have an impact on lineage differentiation. For example, while *p53* or *Rb* loss alone is not sufficient in cancer development (Zhou et al. 2006), their coordinate deletion yields locally invasive disease as well as the expansion of neuroendocrine marker-positive cells in the proximal region deemed the stem cell niche of the murine prostate (Tsujimura et al. 2002).

5.3 Summary and Future Directions

The development of more sophisticated models, especially those from GEMs, has allowed control over pathway alterations in a cell type and temporally controlled manner. Such systems demonstrate the ability of basal, transit-amplifying, and luminal cells to serve as TIC populations. These exciting findings now pave the way for investigators to dissect which cell populations may belong to the “holy grail” of cancer progression and to determine whether such cells may be targetable with currently available therapeutics.

Among many urgent issues need to be addressed, we suggest three:

1. To study how complimentary genetic and pathway alterations collaborate in regulating TICs and CSCs. Integrated genomic and mutation landscape studies will provide rich genetic and pathway information related to prostate cancer development, as exemplified by the presence of TMPRSS2-ERG fusion events coinciding with PTEN loss in human prostate cancer (Squire 2009) and their

cooperability in promoting progression (King et al. 2009). Future studies should consider whether such interactions may take place in stem/progenitor cells and in TIC formation. Additional molecular subtypes of human prostate, such as those characterized by *CHD1*, *SPOP*, *FOXA1*, and *MED12* mutations (Barbieri et al. 2012), should also be evaluated for their functional impact on TIC activity and disease progression.

2. To investigate both cell-intrinsic and cell-extrinsic mechanisms of TIC regulation. Studies of normal stem cells indicate that stem cell properties, including self-renewal and multi-lineage differentiation and homeostasis, are influenced by their local microenvironment or “niche.” Alterations of the microenvironment can drive normal stem cells to become TICs or CSCs. Although most of the current studies focus on the cell-intrinsic regulation of TICs and CSCs, future studies should consider TIC and CSC activities with a “system” approach, especially in an immune-competent setting and within tumor’s native environment or niche.
3. To determine whether, subsequent to initiation, CSCs are functionally important for progression, metastasis, and therapeutic resistance. Despite the multifocal and heterogeneous nature of human primary prostate cancers, where distinct molecular and genetic alterations are associated with various “clones,” most metastatic prostate cancers and CRPC is monoclonal in origin, suggesting that metastatic lesions in different anatomical sites of the same patient may arise from a single precursor cell within the primary lesions (Grasso et al. 2012; Liu et al. 2009; Holcomb et al. 2009). Determining which genetic and pathway alterations lead to the formation of CSCs within the primary tumors and are responsible for metastasis and CRPC will be critical for the understanding and treatment of lethal prostate cancers.

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Chapter 6

The Prostate Stem Cell Niche

David Moscatelli and E. Lynette Wilson

Abstract Stem cells reside in a localized region called a niche where interactions with surrounding cells, especially stromal cells, maintain stem cell quiescence and multipotency and guide their transition to proliferation and differentiation. The mouse prostate stem cell niche has been localized to the proximal region of the gland, while the human niche is more diffuse. Stromal cells that may contribute signals to the niche include smooth muscle cells, fibroblasts, vascular endothelial cells, Schwann cells, and adipocytes. Signaling molecules that the stromal cells and stem cells use to communicate with each other include members of the BMP/TGF- β , Wnt/ β -catenin, FGF, notch, hedgehog, and ephrin signaling pathways. Imbalances in signaling between the stroma and stem cells in the niche can lead to excessive proliferation of both epithelial and stromal components. Knowledge of the specific signals used and their source and targets may help decipher the complex interactions that keep prostate stem cells functioning normally and result in targeted therapies for treating benign and malignant prostatic proliferation.

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6.1 Introduction

Organ-specific stem cells are cells that are able to generate all of the differentiated cell lineages of that organ. Under normal conditions, these cells are deeply quiescent, rarely replicating. In response to a loss of tissue, homeostatic signals activate a subset of these cells to divide. Cell division will result in two alternate fates: some daughter cells give rise to new stem cells to replenish the stem cell pool, while others differentiate into transit amplifying cells that proliferate further and differentiate to regenerate the lost cells. Once activated, stem cells are highly proliferative. Thus, their proliferation must be tightly regulated to prevent overgrowth of the tissue and to prevent exhaustion of the stem cell pool. A niche is a localized region of an organ that nurtures stem cells keeping them in an undifferentiated state and regulating their differentiation into more mature cells. It is the role of the niche to maintain stem cell quiescence and regulate their differentiation.

The concept of a niche arose from studies of hematopoietic stem cells. The niche for hematopoietic stem cells is located in the bone marrow and requires interactions between the stem cells and osteoblasts and/or vascular endothelial cells for the proper balance between stem cell renewal and differentiation (Orford and Scadden 2008). Localized niches have also been identified in the bulge region of the hair follicle, the base of intestinal glands, and the neck of stomach glands. Now restricted niches have been identified for a variety of tissue-specific stem cells, including corneal, skin, intestinal, neuronal, and prostate stem cells (Lavker et al. 2004; Fuchs and Horsley 2008; Clevers 2009; Miller and Gauthier-Fisher 2009; Tsujimura et al. 2002).

Stem cell niches keep cells with high proliferative potential quiescent. In tumors, cells with high proliferative potential proliferate without constraint. As tumor-initiating cells are thought to have properties in common with their organ-specific stem cell counterparts, knowledge of the mechanisms by which the niche controls stem cell renewal and differentiation may provide insights into targets that may be utilized to control tumor proliferation. Therefore, there has been much interest in defining the stem cell niche and the molecular signals between the niche cells and stem cells that regulate stem cell activity.

6.2 Evidence for a Prostatic Niche

The first evidence for a niche that supports stem cell function in the prostate came from the transplant experiments of Cunha and his coworkers. They observed that when the tips of prostate ducts were transplanted under the renal capsule of recipient mice, growth of prostate-like tissue occurred only when urogenital sinus mesenchyme (UGM) was co-implanted (Norman et al. 1986). Indeed, the amount of growth of the epithelial tissue depended on the amount of UGM added (Chung and Cunha 1983; Goto et al. 2006). Implantation of the tips alone or co-implantation of mesenchyme from the bladder in place of the UGM did not

result in growth of prostate-like tissues (Norman et al. 1986). These experiments suggested that important signals for prostate development came from the stroma and that prostate stroma alone contained the signals to guide prostate development. Co-implantation of human prostate epithelial cells with rat UGM under the renal capsule also resulted in formation of prostate duct-like structures, suggesting that human and mouse stem cells respond to similar signals from the stroma (Hayward et al. 1998).

Further experiments showed that UGM was not only supportive of prostate development but was also instructive. When bladder epithelium was co-implanted with UGM under the renal capsule, prostate-like growths were produced. These growths synthesized prostatic proteins, demonstrating that full transdifferentiation into prostatic epithelium had occurred (Cunha et al. 1980, 1983; Neubauer et al. 1983). Similarly, when vaginal epithelium from female embryos was co-implanted with male UGM, the female epithelium formed prostate-like structures (Boutin et al. 1991). Thus, signals from the stroma directed undifferentiated epithelial cells in the bladder or female urogenital sinus to differentiate into functional prostatic epithelium.

6.3 Localization of the Adult Niche

In the mouse, two different niches can be defined. The first is the embryonic niche, in the urogenital sinus, which consists of the UGM and undifferentiated urogenital sinus epithelial cells that signal to each other to guide differentiation into adult prostatic tissue containing the proper balance of basal and luminal epithelial and neuroendocrine cells. The UGM is quite potent in guiding prostate development and can even direct the development of adult prostate stem cells (Xin et al. 2003; Goto et al. 2006). There have been no attempts to determine if the stem cell-supporting activity of the UGM can be further localized, but given the small size of the tissue, it is likely that the entire UGM has stem cell-supporting activity. The second niche is the adult stem cell niche. This niche is responsible for maintaining multipotent adult stem cells and regulating their differentiation in response to fluctuations in androgen levels.

Although the unfractionated UGM could act as a niche during development and in transplant experiments, the stem cell niche in adult prostate was expected to be more restricted. To map the adult niche in the mouse, advantage was taken of one characteristic of stem cells, their slow turnover. In this approach, the cells of prostates of young mice were uniformly labeled with bromodeoxyuridine, and the mice were subjected to multiple rounds of prostate involution and regeneration (Tsujimura et al. 2002). The cells that retained the bromodeoxyuridine label after this cycling of the prostates were presumed to be slowly turning over stem cells. These label-retaining cells were found predominately in the proximal region of the prostatic ducts. Later experiments found that prostate cells expressing high levels the cell-surface antigen Sca-1 (Sca-1^{high}) had two other properties of stem cells: a high

growth potential and the ability to regenerate prostate-like organs when implanted under the renal capsule of recipient mice. The Sca-1^{high} cells with high growth and regenerative capacity were preponderantly located in the proximal region (Burger et al. 2005; Xin et al. 2005). Interestingly, the proximal region of the regenerated prostate-like organs also contains cells with high growth capacity and greater ability to regenerate prostate-like organs when implanted under the renal capsule, suggesting that the stem cells are able to regenerate their niche (Goto et al. 2006).

Thus, the proximal region of the prostate gland contains cells with three attributes of stem cells, slow cycling, high growth potential, and prostate regenerating ability. Recent studies have suggested that stem cells may reside in both the basal cell and luminal cell compartments of the prostate epithelium (Wang et al. 2009; Goldstein et al. 2010; Lawson et al. 2010). As the slow cycling cells were localized in both the luminal and basal compartments of the proximal region with approximately equal frequency (Tsujimura et al. 2002), the proximal region may be the niche for both types of stem cells.

In humans, the niche appears not to be localized. Cells expressing CD133 and high levels of $\alpha_2\beta_1$ integrin have high proliferative potential and can regenerate prostate duct-like structures when implanted into immunocompromized mice, two attributes of stem cells. These rare $\alpha_2\beta_1$ integrin^{high}/CD133⁺ cells are found scattered throughout the prostatic ducts often at the base of budding or branching regions (Richardson et al. 2004). While the human niche is not restricted in a particular region of the organ, it seems to be limited to highly characteristic microdomains of the organ.

6.4 Cells That Contribute to the Niche

The characteristics of the proximal region that specify it as the prostate stem cell niche must consist of the peculiar mix of signals from stromal cells found there (Fig. 6.1). There have been several attempts to identify the stromal cells that contribute to the support of stem cells. As the proximal ducts have a thicker investment with smooth muscle cells than other regions of the ducts (Nemeth and Lee 1996), smooth muscle cells may make an important contribution to the niche. In experiments co-implanting smooth muscle cells with prostate epithelial cells under the renal capsule, the smooth muscle cells supported the growth of the epithelial cells and their organization into duct-like structures, whereas no growth was observed in the absence of smooth muscle cells (Takao et al. 2003). In addition, when prostate epithelial cells were implanted with UGM cells the epithelial cells induced abundant differentiation of smooth muscle from the UGM, suggesting reciprocal signals between these compartments (Cunha et al. 1996). Although the smooth muscle cells can support limited duct formation, they are not able to support the formation of full prostate-like organs as UGM does.

The stem cells in many organs are closely associated with the vasculature. Slow cycling, label-retaining cells in the endometrium were found in close association

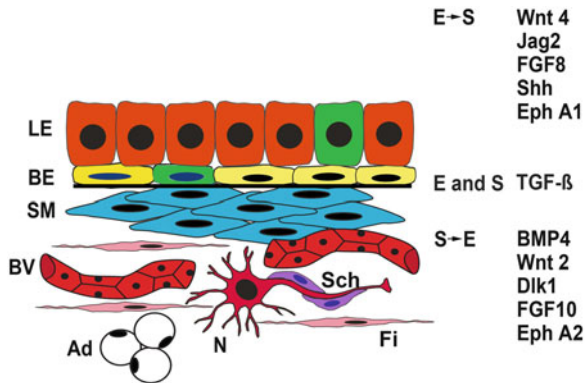


Fig. 6.1 Epithelial–stromal interactions in the prostate stem cell niche. In the stem cell niche, luminal (LE, orange) and basal (BE, yellow) epithelial cells send signals that support the maintenance of a specialized stroma. Stem cells (green) that have been identified in both epithelial layers contribute to these signals. In turn, stromal cells, including smooth muscle cells (SM, blue), fibroblasts (Fi, pink), cells of the blood vessels (BV, red), neurons (N, magenta) with their associated Schwann cells (Sch, purple), and adipocytes (Ad, white), send signals that regulate the balance between quiescence, proliferation, and differentiation in the epithelial stem cells. Some epithelial-derived molecules that signal to the stroma or stroma-derived molecules that signal to the epithelium are listed on the right. Some signaling molecules, such as TGF- β , are produced by both epithelium and stroma and act on both layers

with blood vessels (Chan and Gargett 2006), and cells with molecular markers of mesenchymal stem cells were identified in vascular walls (Shi and Gronthos 2003). In the adult hippocampus, proliferating neuronal progenitor cells were found to be preferentially associated with remodeling vasculature with proliferating endothelial cells (Palmer et al. 2000; Ohab et al. 2006). Similarly, cells with the molecular markers of hematopoietic stem cells have been observed in close association with vascular sinuses in the bone marrow and spleen (Yin and Li 2006; Kiel et al. 2005). In addition, knockout of stem cell factor expression in vascular endothelium inhibited hematopoiesis, suggesting that the endothelial cells are an important source of signals to stem cells in the bone marrow hematopoietic niche (Ding et al. 2012). Finally, in the testes, spermatogonia were also found associated with blood vessels, and alteration of the course of the vessels caused a redistribution of the spermatogonia so that they realigned with the new position of the vessels (Yoshida et al. 2007). These observations suggest that vascular endothelial cells impart signals that are important for the organization and function of stem cells. The proximal region of the prostate is also highly vascularized with twice the vessel density of the intermediate region and eight times the density of the distal region (Wang et al. 2007b). Prostatic epithelial growth and regression are tightly correlated with the growth or regression of the prostatic vasculature (Folkman 1998; Franck-Lissbrant et al. 1998; Shabisgh et al. 1999; English et al. 1985; Lissbrant et al. 2004; Wang et al. 2007a), suggesting that there may be important signals between prostate stem cells and the vasculature. Further, co-implanting vascular endothelial cells with prostate epithelial cells under

the renal capsule also supported the formation of duct-like structures (Bates et al. 2008), suggesting that endothelial cells also contribute signals that can support the growth of prostate epithelial cells *in vivo*.

Other stromal cell types have also been proposed as sources of signals to expanding prostate epithelium. Fibroblasts may have a role in signaling to the stem cells, as expression of a dominant-negative TGF- β type II receptor under control of a fibroblast-specific promoter led to increased proliferation in the epithelial compartment, suggesting that TGF- β signaling to fibroblasts modifies their production of molecules that regulate prostate stem cells (Bhowmick et al. 2004). However, fibroblasts derived from the whole embryo co-implanted with prostate epithelial cells under the renal capsule supported the formation of small tissue growths but did not support duct formation (Hayward et al. 1999). This result may indicate that fibroblasts alone do not produce an appropriate range of regulatory molecules to support prostate differentiation or a more specific subset of fibroblasts from the proximal prostate are needed. In addition, even adipocytes have been reported to support the growth of prostatic tissue *in vitro*, suggesting that these cells may also contribute to prostate stem cell proliferation and differentiation (Tokuda et al. 1999). Finally, as nonmyelinating Schwann cells wrapping sympathetic neurons help regulate the stem cell niche of hematopoietic cells (Yamazaki et al. 2011; Kunisaki and Frenette 2012), they may play a similar role in the prostate niche. The relative importance of signals from smooth muscle cells, vascular endothelial cells, fibroblasts, adipocytes, and Schwann cells in prostate stem cell function (Fig. 6.1) is difficult to ascertain, as these cells have never been directly compared in the same assay. Moreover, none of these cell types seems to be as efficient as UGM in supporting stem cell growth *in vivo*, suggesting that the niche requires a concert of signals contributed by multiple cell types, and fractionating the cells may disrupt important interactions that are necessary for a functioning niche. Perhaps a more sophisticated analysis is needed in which specific signaling molecules are knocked out or overexpressed in each of the stromal cell types in order to judge the contribution of a specific cell type to stem cell quiescence, proliferation, and differentiation.

6.5 Niche Signaling Molecules

There is much interest in the molecules used by stem cells and the specific stroma in their niche to signal to each other. These signaling molecules may provide a point of entry to the manipulation of stem cell quiescence and proliferation. Initial experiments have focused on the murine stem cell niche. However, as experiments with more purified human prostatic stem cells have confirmed that rat UGM will support the growth of human cells in transplant experiments (Goldstein et al. 2008), the signals used in rodents are likely to be applicable to manipulation of the human stem cell niche.

To obtain information on the signaling molecules used in the stem cell niche, molecules expressed by the urogenital sinus of the embryonic developing prostate

were examined. Urogenital sinus epithelial cells (UGE), containing primitive prostate stem cells, and UGM cells were isolated from 16-day-old embryos, just prior to the invasion of the primitive prostatic buds into the surrounding mesenchyme (Blum et al. 2010). RNA isolated from these cells was examined by microarray analysis to identify mRNAs that were uniquely overexpressed in either the embryonic prostate stem cells or their niche. Two thousand four hundred eight transcripts were expressed with at least twofold higher levels in UGE than UGM, and 3,129 transcripts were expressed with at least twofold higher levels in UGM than UGE. From these differentially regulated genes, transcripts were selected that were expressed selectively in UGE cells that encode proteins that have cognate receptors or ligands expressed in UGM cells. In addition to pairs in which the ligand was expressed in one compartment and the receptor expressed in the other, indicating paracrine signaling, some ligand–receptor pairs were expressed in the same compartment, indicating autocrine signaling. Multiple ligand–receptor pairs were identified that may have roles in regulatory signaling between the stem cells and their niche (Blum et al. 2010). Prominent among the ligand–receptor pairs indicating paracrine or autocrine signaling were members of the BMP/TGF- β /inhibin pathways. Other paracrine signaling pathways identified included the Wnt/ β -catenin, FGF, notch, hedgehog, PDGF, ephrin, and neurotrophic factor pathways. In a separate study examining molecules overexpressed in mouse adult prostate stem cells compared to differentiated cells, many of these same pathways were active in the adult stem cells, suggesting that these signaling molecules may also function in maintaining the adult niche (Blum et al. 2009). There is evidence that many of these pathways contribute to cell communication during prostate development.

6.5.1 TGF- β

Members of the BMP/TGF- β family are important regulators of stem cell quiescence and differentiation in embryonic, intestinal, mesenchymal, and skin stem cells (Watabe and Miyazono 2009). The TGF- β signaling pathway also has an essential role in regulating prostate stem cell quiescence. The proximal region of the prostate responds differently to TGF- β than the remainder of the gland (Tomlinson et al. 2004). High levels of TGF- β signaling are found in the proximal region of normal adult prostate, and this signaling in combination with the high levels of Bcl-2 found in the proximal region presumably keeps the stem cells quiescent (Salm et al. 2005). This correlates with a signature of TGF- β -induced genes that was observed in RNA expression analysis of adult prostatic stem cells (Blum et al. 2009). Androgen ablation increases TGF- β signaling in the remainder of the prostate, where Bcl-2 levels are low, leading to apoptosis of cells in these regions. In contrast, androgen ablation decreases TGF- β signaling in the proximal region, priming the stem cells to respond to growth factors when androgens are restored (Salm et al. 2005). Indeed, isolated prostatic stem cells produce abundant active

TGF- β that inhibits their proliferation, differentiation into luminal cells, and ability to form ducts (Salm et al. 2012).

In addition to its importance in maintaining quiescence in the epithelium, TGF- β signaling is also critical to the ability of the stroma to guide differentiation of stem cells. When UGM that was unresponsive to TGF- β because of a fibroblast-specific knockout of TGF- β receptor type II was co-inoculated with wild-type bladder epithelial cells under the renal capsule, the UGM was unable to transdifferentiate the bladder cells into prostate cells (Placencio et al. 2008; Li et al. 2009). Decreased TGF- β signaling in the UGM affects stem cell function through alterations in Wnt/ β -catenin signals to the stem cells (Placencio et al. 2008; Li et al. 2009).

6.5.2 *BMP*

Other members of the BMP/TGF- β family that may alter stem cell function are BMP4 and BMP7. Although TGF- β and the BMPs are structurally related, they interact with different receptors and activate a different set of signaling molecules. Both BMP4 and BMP7 are expressed in the prostatic mesenchyme during prostate development (Lamm et al. 2001; Grishina et al. 2005). Addition of BMP4 or BMP7 to urogenital sinuses cultured in vitro inhibited epithelial cell proliferation and decreased ductal branching (Lamm et al. 2001; Grishina et al. 2005). In contrast, adult BMP4 haploinsufficient mice and BMP7 knockout mice had increased ductal tips (Lamm et al. 2001; Grishina et al. 2005).

6.5.3 *Wnt/ β -Catenin*

The Wnt/ β -catenin pathway may also play a role in modulating prostate stem cell functions. The Wnt pathway regulates other stem cells, including keratinocyte, embryonal, colon, intestinal, and follicular stem cells (Reya and Clevers 2005; Wray and Hartmann 2012) and is critical in maintaining quiescence in hematopoietic stem cells (Fleming et al. 2008). The Wnt/ β -catenin pathway may be utilized by adult prostate stem cells, as a fraction of the Sca-1-positive cells (the population that contains stem cells) expressed a marker of activation of this pathway, axin2 (Ontiveros et al. 2008). The relevance of the Wnt/ β -catenin pathway to prostate stem cells is further indicated by the finding that knockout of secreted frizzled-related protein 1 (SFRP1), a homolog of the frizzled receptor for Wnt proteins that is expressed in prostatic stroma, inhibited epithelial proliferation in developing prostates, reduced branching, and increased expression of secretory proteins. Overexpression of SFRP1 had the opposite results, with increased epithelial proliferation and decreased expression of secretory proteins (Joesting et al. 2005, 2008). These results suggest that the stromal-derived SFRP1 regulates prostatic stem cell proliferation and differentiation.

6.5.4 *FGF*

The FGF family of growth factors has been implicated in the regulation of self-renewal in stem cells from a variety of organs (Coutu and Galipeau 2011; Eiseleova et al. 2009) and is essential for the maintenance of the embryonic stem cell niche (Bendall et al. 2007). The FGF ligands and receptors were also identified as potential niche signaling molecules in RNA array analysis of the stem cell niche (Blum et al. 2010). FGF10 is expressed in the prostatic mesenchyme and is required for the development of the prostate (Donjacour et al. 2003; Thomson and Cunha 1999). In FGF10 knockout mice, only rudimentary prostatic buds were occasionally observed in the urogenital sinus (Donjacour et al. 2003). Administration of FGF10 and testosterone to the rudimentary buds in culture partially restored prostate duct formation (Donjacour et al. 2003). Conditional knockout of FGF receptor-2, a receptor for FGF10, in prostatic epithelium ablated the development of the ventral and anterior lobes of the prostate and resulted in reduced growth of the dorsolateral lobes (Lin et al. 2007). Similarly, conditional knockout of FRS2 α , an intracellular signaling molecule in the FGF pathway, in prostate epithelial cells resulted in reduced growth of the gland, although all lobes were present (Zhang et al. 2008). The discrepancy in results from knockout of the growth factor, its receptor, and their signaling intermediate may be due to the promiscuity of these molecules, in which the ligands can interact with multiple receptors and the receptors can signal through several intermediates. Nevertheless, the importance of FGF signaling in communication between prostate stem cells and their niche was emphasized by the observation that when UGM cells overexpressing FGF10 were co-inoculated under the renal capsule with prostatic stem cells, there was hyperproliferation in the epithelial compartment of the prostate-like organs formed (Memarzadeh et al. 2007).

6.5.5 *Notch*

The notch signaling pathway is also critical for a variety of tissue-specific stem cells (Bolos et al. 2007; Lai 2004). In prostates, this pathway is involved in both epithelial and stromal development. Administration of a γ -secretase inhibitor, which inhibits notch signaling, to explants of developing prostate increased epithelial cell proliferation and led to an accumulation of undifferentiated cells that expressed both luminal and basal cell markers (Wang et al. 2006b). Induced knockout of notch-1 in prostate epithelial cells had similar effects on prostates in situ (Wang et al. 2004, 2006b). In agreement with these results, expression of a constitutively active notch-1 receptor increased cell proliferation in the basal cell compartment of the epithelium and in smooth muscle (Wu et al. 2011). Knockout of a notch signaling molecule, Cbfl/Rbp-J, decreased cell proliferation in both compartments (Wu et al. 2011). The effects of notch on smooth muscle may be an example of cross signaling between cells in the stromal compartment. Notch-2 and a potential notch ligand,

delta-like-1, are expressed in nonoverlapping regions of developing prostatic smooth muscle (Orr et al. 2009). Inhibition of notch signaling with γ -secretase inhibitor inhibits smooth muscle differentiation (Orr et al. 2009).

6.5.6 *Hedgehog*

Hedgehog signaling is important in regulating neural and hematopoietic stem cell proliferation, survival, and differentiation (Komada 2012; Vue et al. 2009; Bhardwaj et al. 2001). Hedgehog signaling may have a similar role in modulating prostate stem cells. Sonic hedgehog is expressed in the urogenital sinus epithelium during prostate development but becomes restricted to the proximal (stem cell containing) region of the developing ducts as prostate differentiation progresses (Podlasek et al. 1999). Patched, a hedgehog receptor that is induced in response to hedgehog signaling, is expressed in the UGM, suggesting epithelial to mesenchyme signaling (Podlasek et al. 1999; Lamm et al. 2002). Antibodies to sonic hedgehog blocked prostate development in embryonic prostates transplanted under the renal capsule of recipient mice and prostate regeneration in castrated mice administered testosterone (Podlasek et al. 1999; Karhadkar et al. 2004). However, others have found that addition of sonic hedgehog or activation of hedgehog signaling in prostate explants inhibits prostate ductal development (Pu et al. 2004; Freestone et al. 2003; Wang et al. 2003). These discrepancies may be due to the complex interaction of sonic hedgehog, its homolog Indian hedgehog, and the multiple signaling pathways they control (Doles et al. 2006). Nevertheless, it is clear that hedgehog signaling between the stroma and epithelium plays a critical role in prostate development.

6.5.7 *Ephrins*

There is evidence that ephrins and their receptors, the Eph proteins, play a role in the regulation of stem cells in a variety of organs. Ephrins and Eph receptors support early thymocyte survival and maturation (Alfaro et al. 2007; Stimamiglio et al. 2010; Wu and Luo 2005). Bidirectional signaling between ephrin B2 on osteoclasts and Eph B4 on osteoblasts regulates osteoclast maturation (Zhao et al. 2006). Knockdown of Eph A4 in neural stem cells caused premature differentiation, suggesting that this receptor maintains the stem cells in an undifferentiated state (Khodosevich et al. 2011). EphB2 expression identifies colonic stem cells (Jung et al. 2012), and administration of soluble forms of ephrin B2 or Eph B2 extracellular domain decreased cell proliferation in the intestinal crypts, suggesting that ephrin signaling regulates intestinal progenitor cell turnover (Holmberg et al. 2006). Disruption of either ephrin A or B interactions with Ephs in mouse skin doubled the rate of proliferation in hair follicles and epidermis, suggesting that these molecules

are negative regulators of proliferation (Genander et al. 2010). Thus, ephrin–Eph interactions can modify the proliferation or differentiation of progenitor cells from a variety of organs, but their role in regulating prostate stem cells has not been addressed. The fact that four ephrins and eight Eph receptor homologs were identified as differentially expressed between embryonic prostate stem cells and the UGM may indicate that these molecules are also important in signaling in the prostate niche (Blum et al. 2010).

6.6 Aberrant Signaling from the Stroma Can Lead to Tumorigenesis

Disruption of the normal communication between stem cells and their niche can alter prostate homeostasis. It is obvious that decreased stimulatory signals or increased inhibitory signals may lead to atrophy of the gland as occurs after castration. However, there is evidence that increased stimulatory signals or decreased inhibitory signals can lead to tumor formation. Conditional knockout of the TGF- β type II receptor in fibroblasts removed their growth inhibition by TGF- β , caused an expansion of the stromal compartment, and induced PIN-type lesions in mouse prostate epithelium (Bhowmick et al. 2004). Presumably, the decreased TGF- β regulation resulted in increased stromal growth stimulatory signaling to the stem cell compartment. Similarly, directly increasing growth stimulatory signals from the stroma by overexpression of FGF10, a stroma-derived epithelial growth factor, in UGM cells caused formation of well-differentiated prostate adenocarcinomas when these cells were co-transplanted with normal prostatic stem cells under the renal capsule of recipient mice (Memarzadeh et al. 2007). Tumor formation was abrogated if the stem cells were transfected with a dominant-negative FGF receptor-1 (Memarzadeh et al. 2007), showing that the stem cells were responding to the increased growth factor (Memarzadeh et al. 2007). Conversely, increased growth stimulatory signals from the stem cells to the stroma may also result in tumor formation. FGF8 is an epithelial-derived growth factor that normally signals to the stroma. Overexpression of FGF8 in prostate epithelium resulted in an atypical hypercellular stroma with an increased proportion of fibroblastic cells, rich vasculature, and inflammation (Song et al. 2002; Elo et al. 2012). Hyperplasia of the epithelium was also observed, leading to PIN lesions and sometimes progressing to adenocarcinoma in older animals (Song et al. 2002; Elo et al. 2012).

The formation of tumors as a result of imbalances in signaling between the niche and stem cells resembles the interaction of prostate tumor cells with their reactive stroma. It has been recognized that tumor stroma is fundamentally different from normal stroma and plays an important role in the aggressiveness of the tumor (Schor et al. 1987). In cell transplant experiments, initiated prostate epithelial cells from benign prostatic hyperplasia form tumors when co-inoculated with prostate tumor stromal cells but not when co-inoculated with stromal cells from benign prostatic

hypertrophy or normal stromal cells, suggesting that tumor reactive stroma sends abnormal growth stimulatory signals to initiated epithelial stem cells (Olumi et al. 1999; Barclay et al. 2005). However, in contrast to the aberrant signaling between normal stem cells and stroma described above, combinations of tumor reactive stroma with normal epithelial cells did not lead to tumor formation (Olumi et al. 1999). This may be due to lower levels of these signaling molecules in the tumor reactive stroma. Thus, as tumors are thought to arise from transformation of normal organ stem cells, the reactive stroma may represent a niche for tumor stem cells or tumor-initiating cells. Some of the pathways used in tumor reactive stroma signaling to the tumor epithelium are the same as those identified for interactions of the embryonic niche with normal stem cells, including TGF- β , Wnt/ β -catenin, and hedgehog pathways (Basanta et al. 2009; Franco et al. 2011; Ao et al. 2007; Li et al. 2008; Shaw et al. 2009).

6.7 Stem Cell Niche and Tumorigenesis

Normal stem cells have been proposed to be the source of tumor-initiating cells (Visvader and Lindeman 2012; Tang 2012). In this view, oncogenic transformation of a normal stem cell leads to the generation of tumor-initiating cells that undergo uncontrolled proliferation. Some tumor-initiating cells differentiate, forming the mixture of cells normally found in a tumor, while others maintain stemlike properties, including a high proliferative potential. Prostate tumors seem to follow this model. Prostate tumors in mice were shown to arise from the stem cell-containing proximal region of the ducts (Zhou et al. 2007). Transformation of both mouse and human prostate stem cells led to formation of adenocarcinomas, whereas transformation of non-stem cell populations did not result in tumors (Lawson et al. 2010; Goldstein et al. 2010, 2011). As noted before, stem cells have been identified in both the basal and luminal epithelial compartments (Goldstein et al. 2010; Lawson et al. 2010; Wang et al. 2009). Transformation of either basal or luminal stem cells has been shown to form tumors (Wang et al. 2009; Goldstein et al. 2010; Lawson et al. 2010; Choi et al. 2012; Moscatelli and Wilson 2010). Transformation leads to an expansion of cells with stem cell markers (Wang et al. 2006a). Once tumors arise, the stroma appears to be altered along with the tumor, suggesting that the niche is expanded to support the growth of the tumor-initiating cells (Sung and Chung 2002; Jossion et al. 2010). Even prostate tumor metastases are dependent on the support of a niche. Metastases to bone co-opt the hematopoietic stem cell niche in the bone marrow, where they take on some of the properties of hematopoietic stem cells, including the ability to be mobilized into the circulation by administration of GM-CSF (Shiozawa et al. 2011). Thus, formation of tumors, their expansion, and their metastatic spread are modulated by interactions with the niche.

6.8 Summary

The prostate stem cell niche consists of a localized area of the proximal region of the ducts that contains a high concentration of epithelial stem cells. The stem cells interact with other epithelial cells and underlying stromal cells to modulate their quiescence, proliferation, and differentiation (Fig. 6.1). Several signaling molecules involved in these interactions have been identified, and others have been proposed. Some of these signals are paracrine, with molecules produced by the epithelium acting on the stroma and molecules produced by the stroma acting on the epithelium (Fig. 6.1). Other signals are autocrine, with the signaling molecule produced by and affecting the same cell type, or paracrine within a compartment, for example, one stromal cell type signaling to another. However, the specific signals and their cellular sources and targets have only begun to be elucidated. Additional investigations with cell-specific knockout or overexpression of the signaling molecules and their receptors are necessary to map out the complex interactions. Knowledge of these interactions will provide insights into the etiology of proliferative diseases of the prostate, both benign and malignant.

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Chapter 7

Tumour Stroma Control of Human Prostate Cancer Stem Cells

Gail P. Risbridger and Renea A. Taylor

Abstract Prostate cancer is an epithelial malignancy and stem cells are a major focus of current research efforts. This is a warranted approach, since the processes of self-renewal and differentiation underpin the fundamental biology of malignancy and cancer recurrence due to therapeutic resistance. In this chapter, we review the regulation of stem cells through reciprocal interaction with the surrounding micro-environment. In both normal tissues and in prostate cancer, stem cells are controlled by both intrinsic and extrinsic mechanisms, the latter involving stromal directed stem cell differentiation. Herein, we discuss the current experimental models to study stromal-stem cell interaction and present the current knowledge on how the two cellular compartments should be considered in unison to design more effective therapies for clinical management of prostate cancer.

7.1 Introduction

The focus of this book is on stem cells in prostate cancer. As in many systems, regulation of prostatic stem cells requires intrinsic and extrinsic mechanisms. This chapter will focus specifically on the extrinsic regulation, which has proven to be as important as intrinsic mechanisms of modulating stem cells. The multiple cell types in the prostate are located in epithelial or stromal compartments, each with their own role in maintaining structural architecture, secretory activity or differentiation. These cells work together in an orchestrated fashion to maintain glandular homeostasis. The stroma surrounding the epithelium regulates secretory function, as well

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as differentiation of stem cells involved in initiation and progression of cells of origin of prostate cancer.

The identification of prostatic stem cells in normal and cancerous tissues is an obvious research priority, and significant advances have been made by several groups in the last 5 years. Yet the function and differentiation of stem cells by their stromal niche has also emerged as being important to understanding the extrinsic regulation of stem cells. In this chapter, we will review the literature on stromal requirement for prostate stem cell viability in normal tissues and in cancer, particularly focussing on *in vivo* models, and the use of stroma to direct differentiation and malignant transformation of stem cells in prostate cancer. Although the stroma is often peripheral to the discussion and perceptions about cancer stem cells or cells of origin of prostate cancer, it is a matter of fact that all of the assays used to detect stem cells *in vivo* required stroma. The necessity of stroma indicates it is essential and should be prominent in consideration of stem cell biology and regulatory mechanisms: the stem cells do not function in a vacuum and therefore cannot be considered in isolation. The goal of this chapter is to provide provocative opinion on the major role played by stroma in regulating prostate cancer stem cell function and stimulate this debate.

7.2 Defining Prostatic Stem Cells

There have been multiple seminal studies published in the field that identified and/or characterised prostatic stem cells in normal and tumour tissues. Most of these studies were in mice, but more recently included the use of human tissues. The discovery of cells in normal tissue, that have properties of long-term self-renewal and multi-lineage differentiation, underpins our fundamental understanding of the prostatic lineage and hierarchical arrangements, and more recently, their role in tumour initiation and progression (Taylor et al. 2012).

For clarity, in this chapter, we define the terms we use to describe different types of stem cells. Normal tissue stem cells are those that undergo self-renewal and repopulate the normal epithelial cells. Secondly, cells of origin are the cells in normal tissue (*can be stem cells or non-stem cells*) that have malignant potential and can give rise to tumours. Thirdly, cancer-repopulating (or stem) cells are the cells within a cancer that are hypothesised to self-renew and repopulate the bulk of a tumour. These definitions are stated in order to avoid the confusion of the term ‘cancer- or tumour-initiating cells’ which is not specific to either disease initiation or progression (Taylor et al. 2010).

7.2.1 Role of Stroma in Identifying Normal Prostatic Stem Cells

In general, the approach to identifying prostate stem cells has been to use cell surface markers to isolate populations of cells that have stem cell properties, and in mouse, these have included Lin⁻CD49^{hi}Sca-1^{hi} or Lin⁻Sca-1⁺CD133⁺CD44⁺CD117⁺

and in human can include stem-enriched $\alpha 2\beta 1$ integrin^{hi}/CD44⁺/CD133⁺ and basal Lin⁻,CD49f^{hi},Trop2^{hi} cells (Goldstein et al. 2008, 2010; Lawson et al. 2007; Leong et al. 2008; Richardson et al. 2004; Xin et al. 2005; Burger et al. 2005), *discussed in more detail in other chapters of this book*. All of these cell fractions were defined by basal cell phenotypes, confirming the original prediction-based castration and testosterone replacement studies (English et al. 1987) that basal cells harbour prostatic stem cells. More recently, additional populations of stem cells were identified in the luminal compartment, initiated by the discovery of rare cells, visualised as castrate-resistant Nkx3.1-expressing cells (CARNs) that have multi-lineage and malignant potential (Wang et al. 2009). An alternate approach included in vivo tracing of lineage commitment and differentiation in normal prostate epithelia to determine the source of basal and luminal epithelia (Choi et al. 2012; Liu et al. 2011; Blackwood et al. 2011). In normal tissues, PSA-expressing luminal cells resist castration and regenerate luminal epithelium (Liu et al. 2011), and the same is true in cancer, although the PSA^{lo}-expressing cells harbour highly tumourigenic castration-resistant cancer cells (Qin et al. 2012).

This collection of high-profile publications significantly advanced the field, but compared to progress in other solid tissues such as breast and colon, our understanding in this area is comparably slow. For example, the study by Leong et al., showing CD117 was a unique prostatic stem cell surface marker, was the only study to use single cell transfer of fractionated murine epithelia (Leong et al. 2008); these cells have not yet been identified in human prostate. Secondly, the two cell fractions isolated by the Witte laboratory (LSC in mice and CD49^{hi}/Trop2^{hi} in human) select for basal cells with enriched stem cell activity in vitro and in vivo. However, these are heterogeneous enriched populations of cells, and the full complement of prostatic epithelia cannot be derived from a single cell (Lukacs et al. 2010). The identification of luminal stem cells by the Shen Laboratory presents technical difficulties as CARNs can only be visualised in tissue following castration, using intracellular antibodies that limit their utility in sorting procedures (Wang et al. 2009). Nonetheless, enriched stem cell populations exist in the adult prostate, and they can have multiple phenotypes, being either basal or luminal cells, and their contribution to tissue repair and regeneration is vital.

Of all of these studies, the three main assays used to define stem cell potential have been (1) colony and sphere forming assays, (2) in vivo regeneration of prostatic epithelium and (3) castration and testosterone replacement. Whilst these have been adapted from other tissue types, their use in prostate biology is complex and warrants discussion.

The sphere forming assay involves aggregation of fractionated prostatic cells in a Matrigel mixture to which growth factors are added. This is an in vitro assay that has been widely used to retrospectively or prospectively identify stem cells based on the self-renewal and differentiation capabilities of single cells in normal and tumour tissues (Xin et al. 2007; Miki et al. 2007; Hu et al. 2011a, b; Goodyear et al. 2009). Whilst it provides a 3D model system that is supported by an enriched matrix of structural proteins, limitations include the ability of progenitor cells to generate spheres for short periods of time, lack of stromal cell interaction and failure to undergo full differentiation into a mature pseudostratified glandular epithelium.

Therefore, the proof of stem cell identity relies heavily on the use of *in vivo* transplantation studies.

In vivo confirmation of stem cell activity for multiple cell fractions, including all of those mentioned above, involves transplantation of single or enriched populations of cells, often co-grafted with stromal cells, into immune-deficient host mice to determine the potential to differentiate and generate the pseudostratified prostatic epithelium (Xin et al. 2003). In similar studies to identify mammary stem cells, the cleared mammary fat pad model was used where single cells were implanted and full outgrowths generated (Shackleton et al. 2006), but an equivalent bioassay in prostate is not used. More typically, prostatic epithelia is recombined with embryonic or neonatal mesenchyme from the urogenital area (either urogenital mesenchyme, UGM or seminal vesicle mesenchyme, SVM) and then implanted underneath the kidney capsule of nude or SCID mice. Pioneered by Cunha in the 1970s, this has proven to be a reliable and reproducible approach, although it has several limitations. Firstly, the site of xenografting is not within the prostate, but under the kidney capsule, because it is more easily accessible and has high vascularity. Secondly, the selected stroma is not matched for age, anatomical origin or even strain or species of the origin of epithelial cells; in fact some recombinants are heterospecific (being rat and mouse or mouse and human). Yet, the embryonic/neonatal stroma induces proliferation and instructs differentiation of prostatic epithelia and thus provides an effective experimental model to test the potential of putative stem cell populations. But is it the most appropriate niche to test stem cell potential? (Fig. 7.1).

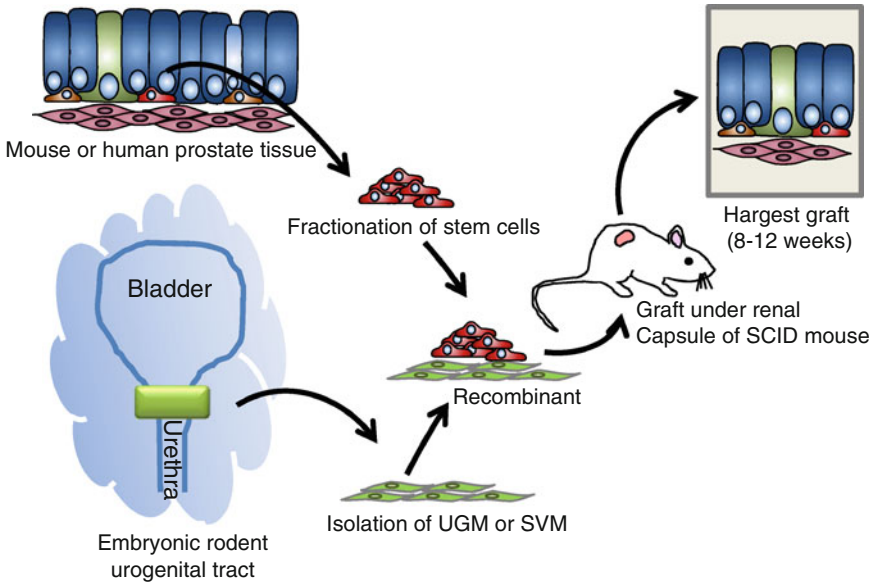
Whilst human CD49f^{hi}/Trop2^{hi} basal cells repopulated normal prostatic epithelium using this mouse-human recombinant approach with embryonic stroma (Goldstein et al. 2010), luminal cell fractions failed to produce viable epithelial structures. One interpretation of this result is that the luminal population does not have stem cells, but it is equally plausible that the stroma recombination bioassay was inadequate. This latter explanation is supported by the parallel study, using stem-cell enriched fractions of CARNs, where Wang et al. showed these rare luminal cells can give rise to prostatic epithelium using the mouse-mouse tissue recombination approach (Wang et al. 2009). Therefore, there is a need to be cautious when interpreting negative results and to be certain that failure to repopulate epithelial progeny is due to a lack of stem cell activity, rather than due to limitations of a bioassay.

Proof of the power of embryonic stroma lies in its ability to direct epithelial cell differentiation and even change lineage status as shown using human or mouse embryonic stem cells, to generate mature prostatic or bladder epithelium by tissue recombination (Taylor et al. 2006; Oottamasathien et al. 2007). These inductive and instructive stromal-stem cell signals are absent in adult stroma, or otherwise tissue homeostasis could not be achieved and tissue overgrowth would continue, underscoring the difference between embryonic and adult stroma signalling.

7.2.2 Assays to Identify Cells of Origin of Prostate Cancer

With these caveats in mind, we now discuss the role of stroma in determining the cells of origin of prostate cancer. These cells are currently of great interest because

a Tissue Recombination Assay



b Lineage-marked mouse prostate glands

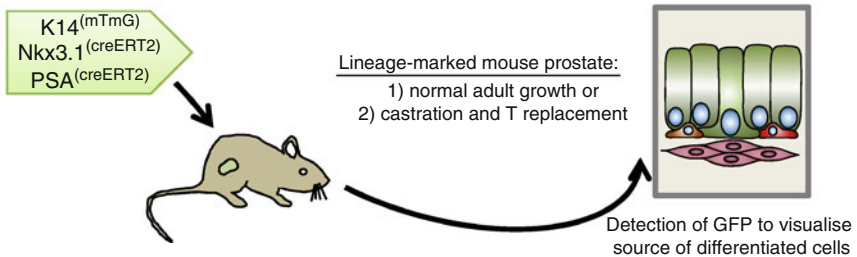


Fig. 7.1 Different approaches used to identify prostatic epithelial stem cells and their progeny. **(a)** Tissue recombination utilises the inductive and instructive properties of rodent developmental (urogenital, UGM, or seminal vesicle, SVM) mesenchyme to induce differentiation in prospectively isolated sub-fractions of epithelium using cell surface markers (including CD133, CD44, Trop2, CD49f among others). **(b)** A complementary approach is genetic lineage marking/tracing in mice to determine the source of epithelial progeny using promoters such as PSA, cytokeratin 14 and/or Nkx3.1. This latter method relies on stromal and epithelial of the adult mouse prostate, which are significantly different to developmental mesenchyme, or castration and testosterone replacement to identify regenerating cells. Collectively, these approaches identified multiple stem cells in normal and tumour prostate tissues

they directly influence tumour phenotype and genotype. Two main questions in the field are as follows: (1) do both basal and luminal stem cells give rise to tumours and (2) are cells of origin restricted to stem cells in normal tissue, or are more differentiated (non-stem) cell types also susceptible to malignancy? Firstly, there is consistent evidence that basal and luminal stem cells from normal and non-malignant tissues can *both* act as cells of origin for prostate cancer if genetically modified

(Lawson and Witte 2007; Goldstein et al. 2010; Wang et al. 2009; Choi et al. 2012; Blackwood et al. 2011; Liu et al. 2011). The second question of whether or not tumours arise exclusively from stem cells (rather than from more differentiated cell types such as transit amplifying or luminal cells) is more difficult to answer and less often considered. To investigate the tumourigenic potential of different subpopulations of basal cells, CD133⁺ stem cells were compared to CD133⁻ progenitor/transient amplifying cells. Although the data showed that basal CD133⁺ cells are a cell of origin of prostate cancer, the transient amplifying CD133⁻ cells also had significant tumourigenic potential (Taylor et al. 2012), and therefore, tumourigenicity is a feature not limited to stem cells.

A variety of approaches and techniques were used to generate these findings. Most commonly, direct oncogenic activation in selected stem cell populations using activation of AKT, ERG, AR or loss of PTEN (refs) was used (Lawson and Witte 2007; Goldstein et al. 2010; Wang et al. 2009; Choi et al. 2012). Since these studies do not consider the role of stroma, we applied stromal-based assays to test malignant potential and complement previous studies including (a) tissue recombination with carcinoma-associated fibroblasts (CAFs) (*detailed in Sect. 7.3*) that induce malignant transformation when co-grafted with BPH-1 cells (Olumi et al. 1999) and (b) the administration of high doses of testosterone and 17 β -estradiol to drive malignancy in tissue xenografts (Ricke et al. 2006). The tumour-forming potential of the latter assay requires signalling via ER α in the stromal cells, closely mimicking the steroidogenic environment observed in prostate cancer (Ricke et al. 2006, 2008). Using these approaches, we confirmed that basal cells are a cell of origin of prostate cancer. Within the basal cell fraction, CD133⁻ transient amplifying cells were more susceptible to malignancy compared to CD133⁺ stem cells.

Using a different approach, Prins and colleagues studied how steroid hormones regulated stem cell proliferation and malignant transformation using prostaspheres (that are notably devoid of stromal cells). The clonogenic stem/early progenitor cells expressed oestrogen receptors α , β and the G protein-coupled receptor 30, and in response to 17 β -estradiol, the prostaspheres increased in number and size, showing them to be direct oestrogen cell targets (Hu et al. 2011b). Most importantly, in tissue recombination grafts human prostate progenitor cells were tumourigenic when stimulated with high-dose testosterone and 17 β -estradiol, similar to our previous observations (Hu et al. 2011b; Taylor et al. 2012). Hormone action via stromal steroid receptors in stroma, rather than epithelia, remains to be fully elucidated, but it is clear that prostate stem/progenitor cells are highly susceptible to hormone-induced malignant transformation.

In combination, these data indicate that multiple cell types (i.e. basal and luminal/stem and progenitor) give rise to prostate cancer and show similarity to breast cancer, where multiple cell types give rise to distinct tumour types (Lim et al. 2009; Shackleton et al. 2006). In breast cancer, the differentiation hierarchy is better defined, and there are robust molecular profiles that can be correlated with the potential cells of origin, which are associated with a predicted outcome, and applicable therapeutic strategy (Visvader and Lindeman 2008). None of this type of information is available in prostate cancer, and the clinical relevance of the cellular

origin of prostate cancer is not evident, because most tumours are adenocarcinomas and only rarely are neuroendocrine tumours. The main clinical need in prostate cancer is a predictor of tumour aggressiveness (Freedland 2011). A biological tool to predict tumour progression would significantly enhance the efficiency of our current treatments and limit overtreatment with complicated surgical interventions for indolent or nonaggressive disease. Whether the cellular origin of prostate cancer correlates to or is associated with clinical outcome is yet to be determined.

7.2.3 Role of Stromal in Identifying Prostate Cancer-Repopulating Cells

The concept that minor tumour cell fractions with greater self-renewal and multi-lineage differentiation potential initiated debate in the cancer biology field (Reya et al. 2001). The suggestion that these cells were also resistant to chemotherapy and radiotherapy was an added reason to pursue their identity. Targeting of these cells would ensure effective long term cure from cancer by preventing any possible tumour regrowth or recurrence, as most therapies are directed at the fast growing tumour mass but not the slow-dividing cancer stem cells (Visvader and Lindeman 2012). It is plausible that these ‘cancer-repopulating cells’ are likely to be the root of tumour metastasis, even though they constitute a minority of the tumour itself, although this is unproven. Most recently, new evidence emerged that cells with metastatic potential undergo epithelial-to-mesenchymal transition and exhibit stem-like features as they prepare to exit the primary tumour site (Creighton et al. 2010; Zhang et al. 2012), supporting this concept of a major role for cancer-repopulating or stem cells in metastasis.

In prostate cancer, the identity of cancer stem (or repopulating) cells has not been fully elucidated. If we consider the three main properties of cancer stem cells, (1) self-renewal, (2) multi-lineage differentiation and (3) therapy resistance, some but not all of these parameters have been identified in various systems, but the presence of a single tumour cell that meets all three criteria has not been reported. Most of the work on prostate cancer-repopulating cells has been done using cell lines or xenograft lines that bear limited resemblance to the parental tumour. Common stem cells markers (i.e. CD133 and CD44) are easily detected in prostate cancer cell lines, LNCaP, DU145 and PC3, which typically display enriched tumour-forming potential compared to their negative fraction counterparts (Patrawala et al. 2007). These cells consistently show increased self-renewal and proliferative potential, although recent data suggests that not all drug-tolerant (or therapy-resistant) cells reside within these cell populations (Yan et al. 2011). Using primary specimens, prostate cancer-repopulating cells have been artificially generated using human prostate epithelial TERT, and their differentiation potential has been investigated in vitro and in vivo (Gu et al. 2007; Kasper 2007). The most relevant studies have been on prospectively isolated fresh cell fractions from primary prostate cancer specimens, showing that tumour cells with stem cell characteristics and repopulating potential are located in human tissues

(Collins et al. 2005; Toivanen et al. 2011); these tumour cells are highly dependent on surrounding stromal cues, unlike cell lines that have adapted to cell-autonomous growth. Subsequently, elegant lentivector tracing of human prostate cancer cells demonstrated populations of stem cells that robustly support tumour development and resist androgen ablation (Qin et al. 2012; Gaisa et al. 2011).

Maitland and colleagues demonstrated stem cell activity in primary specimens within the CD44⁺integrin α 2 β 1⁺CD133⁺ fraction using assays for self-renewal and differentiation potential, although the transplantation assays *in vivo* have not yet been conducted (Collins et al. 2005), whilst Tang and colleagues showed PSA^{lo}-expressing cells to show repopulating activity (Qin et al. 2012). We recently enhanced the assay to test cancer stem cell activity using tissue recombination to enable dissociated cancer cells to be co-grafted with embryonic mouse mesenchyme, similar to that reported for normal stem cells (Toivanen et al. 2011). Using this assay, we tested the tumour repopulating potential of α 2 β 1 integrin^{hi} cells and showed that selection for this single cell surface marker did not influence the repopulating potential of primary cancer cells, confirming data obtained from xenograft cell lines (Patrawala et al. 2007). This assay, based on the inclusion of embryonic stroma, is now available to test the repopulating potential of isolated cell fractions of cancer cells derived from fresh primary specimens. However, as a note of caution, it is important to restate that this model relies on using stroma that is different to that which the cancer cells are exposed *in vivo* and further improvements using human stromal cells could advance the field.

Given there is lack of consensus on markers to identify cancer stem cells in human tissues, it has not been possible to fully determine the role of tumour stroma on directing their differentiation. This deficiency hampered studies to determine the importance of stromal stem cell signalling in tumour tissue. In fact, the cell surface markers used to identify cancer cells with stem cell-like features have proven to be dynamic, and isolation using prospective sorting strategies will produce varying cell populations at any given time (Vander Griend et al. 2008).

Using the broad definition of cancer-repopulating cells being immune positive for AR, PSA and PSCA whilst not expressing the basal cell marker DNp63, Vander Griend and colleagues showed that AR promotes malignant growth of prostate cancer-repopulating cells via cell-autonomous signalling pathways, whereby AR acquires gain of function oncogenic ability to stimulate malignant growth (Vander Griend et al. 2010). This was postulated based on the finding that stromal AR expression was not required for prostate cancer growth, since tumour stroma surrounding AR-positive human prostate cancer metastases is characteristically AR negative (Wikstrom et al. 2009) and human AR-positive prostate cancer cells grew equally well when xenografted in wild-type vs. AR-null nude mice (Vander Griend et al. 2010). The mechanistic differences between stromal vs. cancer cell AR are poorly defined, and a greater understanding is essential to define the role of androgen actions in prostate cancer-repopulating or stem cells in hormone-naïve disease.

One of the confounding issues with isolating cancer-repopulating cells from prostate cancer specimens is that unlike colon, breast or lung cancer, the pathological specimen is rarely all (100%) tumour. Prostate cancer is notoriously heterogeneous in its cellular composition, and tumour foci and benign glands sit adjacent to each

other throughout the structure. The probability of obtaining a pure tumour sample is improbable (Priolo et al. 2010), and even with confirmation by examining frozen section at the time of removal, it is impossible to prove no benign tissue is present (Toivanen et al. 2011) and may compromise the quality of the data if this is not understood. At present, there is no single cell surface marker that can reliably distinguish benign from tumour epithelium, and so the cells derived from any primary specimen should be considered as mixed phenotypes. Likewise, the cell surface markers used to identify stem cells (especially $\alpha 2\beta 1$ integrin^{hi}/CD44⁺/CD133⁺) are the same for normal and cancerous cells, so the situation is even more complex. This is also true for studies on tumour stroma that are derived from mixed pathologies, complicating studies on stroma-cancer stem cell interactions in human primary tissues that are required to advancing the field.

7.2.4 Stem Cells in Castration-Resistant Prostate Cancer

Perhaps the most clinically relevant stem cells in prostate cancer are the castrate-resistant cells. These are the tumour cells that evade androgen deprivation therapy and are responsible for tumour regrowth and recurrence in those with advanced disease. Whilst there is speculation about the origins and/or evolution of these cells, there is little evidence to support any argument. These cells have simply not been identified in clinical specimens. A recent study using an established xenograft BM18 cell line showed that stem cell-like prostate cancer cells are selected by castration and survive as totally quiescent cells (Germann et al. 2012). Upon androgen replacement, the stem cell-like cells reinitiate BM18 tumour growth, confirming their repopulating potential. Since these were subcutaneous tumours, the contribution of stroma was not considered. It is unclear where castrate-resistant stem cells emerge under the pressure of androgen withdrawal, by an adaptation mechanism, or whether these repopulating cells are pre-existing and facilitate disease progression. Whatever is correct, the stroma should be considered as an active participant in their extrinsic regulation, particularly in response to androgen withdrawal, as it does in development. The paucity of knowledge about the genotype or phenotype of tumour stroma in castrate-resistant disease is an important area of need, as it will likely contribute significantly to novel therapeutic design for advanced disease.

7.3 Stromal Directed Differentiation and Malignant Transformation of Stem Cells

It is widely recognised that stroma-epithelial interactions underpin the differentiation and function of the prostate gland. As such, many groups intentionally use in vivo assays for stem cell studies in order to maintain these cell-cell interactions. However, as mentioned, there are technical limitations of the experimental stem cell assays used to assess prostate-regenerating potential. One important issue is that

tissue recombination approaches fail to provide a naturally occurring stromal or niche environment to test stem cell regeneration potential. Most laboratories, ours included, use mismatched stroma, which represent an artificial situation and may stimulate stem cells differently, or inefficiently estimate the capability of stroma to elicit a stem cell response. It will be important to develop better models that more accurately mimic the stem cell-stromal interactions that occur *in vivo*, particularly in human, but this is currently a significant technical limitation.

Tumour stroma is part of the natural niche for cancer-repopulating cells. The normal stromal compartment has evolved with an inherent plasticity to respond rapidly to aberrant situations, including cancer, and act in concert with the adjacent epithelium leading to the emergence of 'reactive stroma'. Reactive stroma in prostate cancer is composed of CAFs and myofibroblasts which include remodelled matrix and altered expression of repair-associated growth factors and cytokines (Desmouliere et al. 2004; Gabbiani 2003). Prostatic CAFs can be isolated and cultured as primary cell lines, retaining their tumour promoting potential for a moderate but limited time span. These cells have been extensively characterised by multiple laboratories, in terms of phenotype and genotype, and are biologically distinct to their adjacent counterparts, normal prostatic fibroblasts obtained from the same patient specimen (Tuxhorn et al. 2002; Ayala et al. 2003; Ao et al. 2007; Joesting et al. 2005; Rowley and Barron 2012).

Tumour fibroblasts exhibit multiple similarities to developmental mesenchyme, reflecting a reawakening or reactivation of the growth regulatory systems and signalling pathways present in embryonic life, but quiescent in adulthood. However, tissue recombination studies using BPH-1 cells challenge this hypothesis; whilst human CAFs induce malignancy, UGM induces organised ductal structures of benign pathology (Wang et al. 2001; Taylor et al. 2012; Olumi et al. 1999). Defining the differences between developmental mesenchyme that stimulates proliferation and normal differentiation and CAFs that stimulate proliferation and carcinogenesis will reveal tumour-specific therapeutic targets.

It is important to consider that tumour stroma consists of more than CAFs, even though they are one of the predominant and functionally important cell types. It is widely accepted that progression of organ-confined tumours is influenced by angiogenesis and inflammatory cells, which contribute to the stem cell niche, providing a complex signalling environment. Interestingly, both the CAFs and prostate cancer stem cells mediate key regulatory pathways. For example, CAFs show elevated expression of key cytokines and chemokines, SDF-1, CXCL12 and CCL2, which contribute to an immune-rich microenvironment (Ao et al. 2007; Joesting et al. 2005). Likewise, prostate cancer stem cells are also highly responsive to immune modulation, and an immune signature was expressed in human CD133⁺ cancer stem cells, including interleukin 6 (*IL6*) and interferon- γ receptor 1 (*IFGRI*) (Birnie et al. 2008). Studies defining the complex role of immune cell regulation of stem cells are required, but are reliant on new *in vivo* and *in vitro* approaches that allow these multicell interactions to be maintained.

Whilst the major focus of this chapter has been on human models, mouse models of prostate cancer where only stroma is genetically modified provide convincing

proof of the biological importance of stroma. Single or multiple gene mutations in stromal fibroblasts result in abnormal pathologies in the adjacent glandular epithelium of the mice. This was demonstrated with overexpression of FGF10 in a tissue recombination model (Memarzadeh et al. 2007) and TGF β RII in transgenic mice (Bhowmick et al. 2004). The latter has developed into a reliable model of prostate intra-epithelia neoplasia which progresses to adenocarcinoma (Cheng et al. 2005; Bhowmick et al. 2004). This severe pathology resulted from the deletion of a single growth factor signalling pathway, in stromal cells alone. The finding that tumours were resistant to castration broadens the biological implications of this model and provides a system to study the effects of stromal signalling on stem cell differentiation and their role in malignant transformation and castrate-resistant disease.

7.4 Summary/Conclusions/Future Directions

The purpose of this review has been to highlight cells with significant therapeutic potential, as they hold the key to improved clinical treatments for men with prostate cancer. We propose that the regulation of stem cells in prostate cancer is a combination of intrinsic or extrinsic signalling. Further understanding of the cellular biology and mechanistic approaches to arrest tumour growth will be essential to improving clinical outcomes for patients. We have presented a case to suggest both stem cells in cancer (either cells of origin or cancer stem cells) and their surrounding stromal cells are active contributors to tumourigenesis and are thus valid therapeutic targets. This is not unique to prostate cancer, but is typical of many solid tumours, including hormone-dependent cancers of the breast, endometrium and ovary.

We propose that the way forward will include better model systems, which allow alignment of stroma and stem cells. Whilst this is a simple concept, it is technically challenging since the identity of human stem cells is not clearly defined. Additionally, whilst the effects of CAFs are significant, there are other stromal components that comprise the stem cell niche, which should also be examined. Doing this *in vivo* is even more complicated because the host endogenous stromal contribution also contributes to the phenotype.

It is probable that the development of improved *in vitro* coculture or 3D model systems to directly test the stromal-stem cell interactions will be as useful and informative. Such approaches are under development in collaborations between biologists and bioengineers that generate smart bio-scaffolds to replicate the *in vivo* situation (Hutmacher 2010; Sieh et al. 2010). These base models can then be built upon to include the individual tumour components including subtypes of immune cells, endothelial cells or lymphatics or vasculature that contribute to stem cell behaviour in cancer.

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Chapter 8

Targeting the Prostate Stem Cell for Chemoprevention

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Abstract Prostate cancer is the most common cancer diagnosis and the second deadliest non-cutaneous cancer in men in the western world. Despite the advancement of new therapies, survival rates remain tightly correlated to the stage in which a patient is diagnosed. The heterogeneous nature of tumor and their variable response to therapies is now being attributed to tumor-initiating cells or cancer stem cells. The cancer stem cell hypothesis suggests that cancer initiates from a specific subset of tumor cells that possess “stemlike” properties. Over the past several decades, the use of natural or synthetic agents such as vitamins, foods, or spices has been shown to correlate with lower incidences of cancer. Many of these chemopreventive agents have now been reported to cause differentiation of cancer stem cells and suppress their proliferation, thereby making them more amenable to conventional therapies. This chapter will discuss the use of chemoprevention to target cancer stem cells and how these approaches can be applied to prostate cancer.

8.1 Introduction

Despite the advances in screening and early diagnosis, prostate cancer (PCa) remains a leading cause of cancer-related deaths in the western world. One in six men in the USA will be diagnosed with prostate cancer in his lifetime, and one in eight diagnosed will die from this disease. In 2010 alone, over 33,000 men died of prostate cancer in the USA (Siegel 2012). Early diagnosis can often lead to disease-free survival; however, survival rates decrease drastically in advanced disease. In addition, even survivors of early stage prostate cancer face a lifetime of

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complications from treatment such as urinary incontinence and erectile dysfunction. As PCa is a slow-growing tumor that affects men late in life, delaying its initiation and progression by 5–10 years, by use of chemoprevention, could save thousands of lives each year.

The factors leading to prostate cancer development and progression are poorly understood; cellular mechanisms that drive prostate cancer initiation and progression continue to be investigated in an effort to find new ways of better fighting this disease. Tumor-targeted therapies have been met with many challenges, and the existence of cancer stem cells (CSCs) in tumors offers an attractive reason for failed therapies. The CSC hypothesis (reviewed in Ito et al. 2012; Li and Tang 2011) suggests that cancer initiates from a mutated stem cell in the tissue or from dedifferentiation of mature (cancer) cell. Like normal stem cells, CSC or tumor-initiating cells (TICs) have the potential to self-renew and differentiate, giving rise to tumors (Dick 2008; Donnenberg and Donnenberg 2005; Ito et al. 2012; Maitland and Collins 2008; Visvader and Lindeman 2008). Additionally, they possess innate resistance to chemotherapeutic and radiation treatment and comprise a limited targetable population of TICs in tumors.

Epidemiological studies have suggested age, race, family history, and hormone status as risk factors for developing PCa (Strope and Andriole 2010). There is also a correlation between diet/dietary supplementation and prostate cancer risk (Klein 2005; Syed et al. 2008; Venkateswaran and Klotz 2010). Various natural and synthetic compounds have demonstrated the ability to induce differentiation of CSCs, thereby making them more targetable. Due to these issues, as well as an interest in developing less toxic and more effective therapies, cancer research has turned to chemoprevention with reasonable success.

8.2 Cancer Stem Cell Hypothesis

Tumors are comprised of functionally and phenotypically heterogeneous cells. At least two models have been put forward to account for the manifestation of these differences. Although a detailed description of these models is beyond the scope of this chapter, they are widely reviewed (Li and Tang 2011; Subramaniam et al. 2010; Tu and Lin 2012; Visvader and Lindeman 2008), discussed in Chap. 1, and summarized in Fig. 8.1. A normal cellular hierarchy comprises of stem cell (at the apex), which has the potential to self-renew as well as progressively generate common and restricted progenitors, and mature cells (Fig. 8.1a). In contrast, tumor heterogeneity is attributed to either (1) clonal evolution (stochastic model) or (2) CSC (hierarchical model). According to the clonal evolution model, tumors are biologically homogeneous, and all undifferentiated cells have similar tumorigenic capacity. Any functional variations are thought to arise due to intrinsic (genetic, epigenetic) and extrinsic (environmental) influences (Fig. 8.1b). In contrast, the CSC model proposes hierarchical organization of cells in tumors (similar to normal tissue), in which a subpopulation of cells has the ability to initiate tumor growth. These CSC possess the ability to self-renew and give rise to non-tumorigenic progeny that

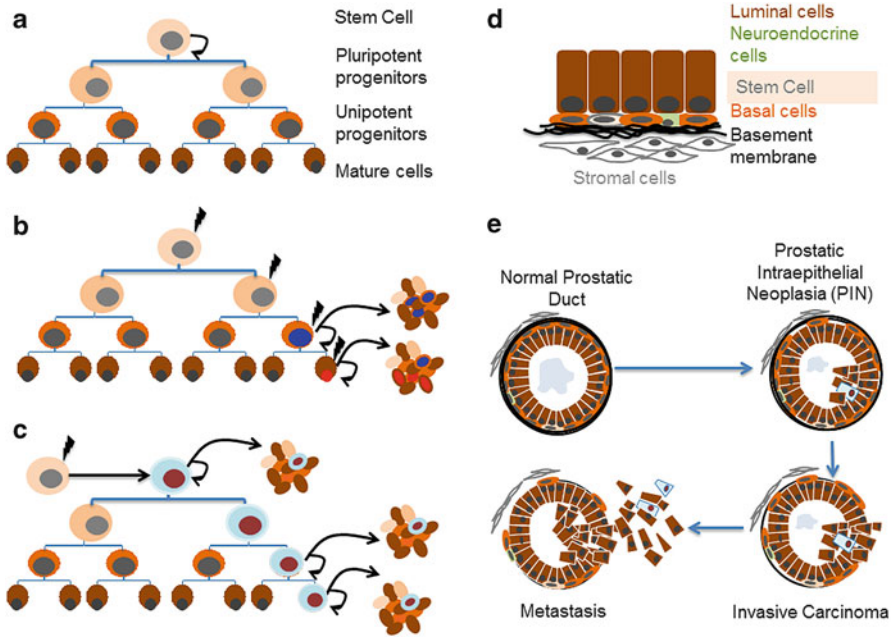


Fig. 8.1 Models for normal and cancer stem cell propagation and its effect on tissue architecture. (a) Normal stem cells (at apex) maintain their population by self-renewal and also replenish mature cell population by generating progenitors with variable potency. In prostate, the transit amplifying cells represent the pluripotent subset. (b) Clonal evolution or stochastic model proposes that all undifferentiated cells in the tumor have the potential to initiate tumor growth. Additionally it is thought that mature cells could acquire mutations that revive their self-renewal capabilities and hence endow on them tumorigenic capacity. (c) Cancer stem cell hypothesizes that only a subset of cells, i.e., CSC, can generate tumors. (d, e) Schematic representation of stem and mature cells in prostate ducts. (e) Hyperplasia of epithelial cells in prostatic duct progressively leads to PIN, invasive carcinoma, and eventually metastasis. This process usually takes place over a long period and offers an excellent opportunity for chemoprevention (figure adapted from Abate-Shen and Shen 2000; Visvader and Lindeman 2008)

make up the bulk of tumor (Fig. 8.1c and Chap. 1). When normal stem cells mutate into a CSC, they continue to possess the inherent properties to self-renew and differentiate. Whereas if mature (or progenitor) cells transform into a CSC, they most likely acquire “stemlike” properties. It is possible that both models fuel tumor maintenance. Irrespective of the mechanism that gives rise to CSC, they possess genetic and epigenetic alterations leading to modifications in cell-surface and metabolic markers, gene expression, signaling pathways, and cellular fate (proliferation, senescence, apoptosis, autophagy, etc.) (Fig. 8.2). In prostate tissue, differentiation of normal stem cells leads to appropriate organization of mature cells (Fig. 8.1d) into functional ductal structure (Fig. 8.1e). This tissue organization is lost over time due to aberrant cell proliferation (Fig. 8.1e). In light of the current evidence, it is reasonable to postulate that this aberrant cellular behavior is most likely initiated and maintained by CSCs.

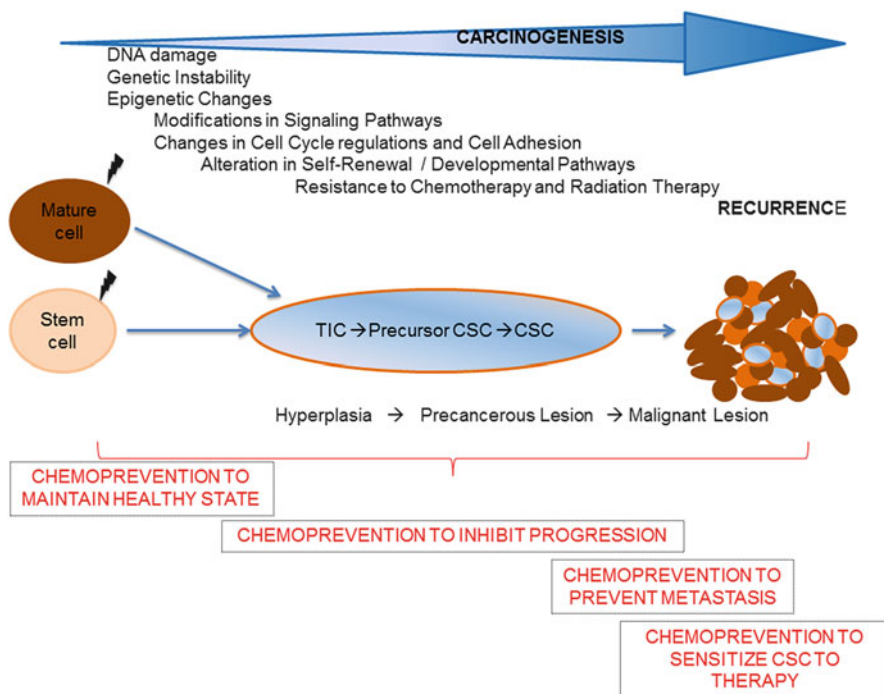


Fig. 8.2 Schematic diagram summarizes the cellular processes involved in transformation of a normal stem cell to a CSC via stages of tumor-initiating cell (TIC) and precursor CSC. These cellular stages are most likely associated with the pathological cancer stages. Chemopreventive intervention has demonstrated the potential to inhibit carcinogenesis by altering key pathway that prevents self-renewal of CSCs and stimulates their differentiation, thereby making them sensitive to conventional therapy

8.3 Chemoprevention Targets for Cancer Stem Cells

The study of carcinogenesis has led to the current dogma that human carcinogenesis is a multiyear process involving multiple hits. This slow process provides the opportunity to intervene prior to accumulation of mutations and/or phenotypic changes, and chemoprevention can be the tool to accomplish this. The term “chemoprevention” was first coined in 1976 by Sporn et al. (1976) to define “the specific use of agents to reverse, suppress or prevent the carcinogenic process to invasive cancer” (Fig. 8.2). Thus, chemoprevention is a means to slow the process of carcinogenesis by the use of natural or synthetic agents such as vitamins, foods, or spices. Many ancient cultures believed that certain natural substances contained medicinal properties. Current scientific research has been focused on understanding how these compounds function and how these might be used in modern medicine. It is the hope that by targeting prostate cancer-associated stem cells or TICs with chemopreventive methods, fewer cases of prostate cancer will be clinically

diagnosed and tumors will become more treatable or less aggressive. CSC-targeted chemoprevention studies and their overall findings are summarized in Table 8.1. Significant advances have been made in targeting stem cells in many systems such as breast, colon, blood, liver, brain, and lungs (Izrailit and Reedijk 2012; Kavalierchik et al. 2008; Ricci-Vitiani et al. 2009; Yi and Nan 2008); however, studies in the prostate have lagged behind. Applying concepts discovered in other systems to prostate cancer may assist in advancing this field. Additionally, no clinical trials for any cancer have shown efficacy for chemopreventive agents. This is likely due to multiple factors, including inappropriate design and lack of statistical power.

8.3.1 Preventing Cancer Initiation by Maintaining Normal Stemness

Stem cells survive in a tissue for much longer than typical differentiated cells. During this time, stem cells must respond to environmental and physical challenges in order to maintain homeostasis of a tissue. Any alterations to their tightly regulated signaling made by mutations or epigenetic modifications could potentially stimulate tumor initiation. The ability of a chemopreventive agent to obstruct transformation of normal stem cells could theoretically prevent the beginnings of tumor formation.

Chemopreventive agents may help repair DNA damage and assist in maintaining cellular genomic integrity when challenged by mutations and epigenetic modifications. Resveratrol, found in red grapes and red wine, prevented DNA damage from radiation in mouse embryonic stem cells. In these cells, repair was accelerated, generation of reactive oxygen species was minimal, and genomic integrity was not compromised (Denissova et al. 2012). Resveratrol also promoted survival of primary endothelial stem cells in culture. In a dose-dependent manner, these cells were able to evade culture-induced senescence by maintaining their stem cell characteristics, possibly from increased telomerase activity (Wang et al. 2011). These data demonstrate that a naturally occurring chemopreventive agent has the potential to impede transformation of NSC into TIC or CSC, thereby preventing initiation of tumorigenesis.

8.3.2 Preventing Cancer Progression by Targeting Cancer Stem Cells

CSCs are involved in all stages of cancer development, and chemopreventive agents have been shown to inhibit progression of already developing lesions by targeting the self-renewing capacity of CSC and by stimulating their differentiation. CSCs have the ability to self-propagate, and chemoprevention has exhibited the ability to

Table 8.1 Chemopreventive agents and their response in cancer stem cells

Chemopreventive agent	Food origin	Cancer/CSC	Target/mechanism of action	Reference
Auraptene	Fruits and edible plants	Colon (CD116 ⁺ CD44 ⁺ HT-29 and HCT-116 cell lines)	Down regulation of EGFR	Epifano et al. (2012)
Curcumin	Turmeric	Breast (ALDH ⁺ MCF7 and SUM159 cell lines) Leukemia Glioma (SP C6 cell line) Brain (CD133 ⁺ DAOY cell line)	Inhibition of Wnt signaling Inhibition of drug resistance transporter	Kakarala et al. (2010) Anuchapreeda et al. (2006)
Epigallocatechin-3-gallate (EGCG)	Green tea	Ovaries (KB-V-1) and Breast (MCF7)	Down regulation of STAT3 or IGF	Fong et al. (2010) Lim et al. (2011)
		Colon (CD116 ⁺ CD44 ⁺ HT-29 and HCT-116 cell lines)	Inhibition of STAT3	Yu et al. (2009)
		Pancreas (CD133 ⁺ CD44 ⁺ CD24 ⁺ ESA ⁺ cells)	Inhibition of drug resistance transporter	Limtrakul et al. (2007)
		Endothelium	Apoptosis, inhibition of sonic hedgehog, inhibition of EMT	Tang et al. (2012)
		Prostate (CD44 ⁺ CD133 ⁺ α2β1 ⁺ cells, PC3 and LNCaP cell lines)	Down regulation of MMP-9	Ohga et al. (2009)
		Breast (CD44 ⁺ MDA-MB-231 cell line)	Apoptosis, inhibition of EMT	Tang et al. (2010)
Genistein	Soy	Prostate (CD44 ⁺ DU145 and 22RV1 cell lines)	Activation of AMPK	Chen et al. (2012)
		Prostate (LNCaP)	Inhibition of hedgehog/Gli	Zhang et al. (2012)
Piperine	Black pepper	Breast (MCF7, MDA-MB-231)	Inhibition of EMT	Zhang et al. (2008)
		Breast (ALDH ⁺ MCF7 and SUM159)	Inhibition of Wnt signaling	Montales et al. (2012) Kakarala et al. (2010)
PSP	Turkey tail	Prostate (CD133 ⁺ CD44 ⁺ PC3 cell line)	Inhibition of in vivo tumor growth	Luk et al. (2011)

Quercetin	Plant flavonoid	Pancreas (ALDH+)	Apoptosis, inhibition of EMT, inhibition of in vivo tumor growth	Zhou et al. (2010)
Resveratrol	Grapes, berries, plum	Pancreas (CD133+ CD44+ CD24+ ESA+ human pancreatic cells)	Inhibition of pluripotency genes, inhibition of drug resistance gene, inhibition of EMT	Shankar et al. (2011)
Sulforaphane	Cruciferous vegetable	Breast (CD24CD44+ ESA+ cells)	Apoptosis, inhibition of lipid synthesis	Pandey et al. (2011)
		Bone (RAW 264.7)	Apoptosis	He et al. (2010)
		Endothelium (EPC)		Wang et al. (2011)
		Breast (ALDH+ MCF7 and SUM159 cell lines)	Down regulation of Wnt/ β -catenin	Li et al. (2010b)
		Pancreases Blood Endothelium Prostate (DU145) Prostate (CD133+ CD44+ PC3 and DU145 cell lines)	Down regulation of NF κ B Apoptosis Apoptosis Promotes drug sensitivity Apoptosis	Kallifatidis et al. (2011) Fimognari et al. (2008) Nishikawa et al. (2009) Kallifatidis et al. (2011) Luk et al. (2011); Zhou et al. (2010)
γ -Tocotrienol (T3)	Vitamin E	Prostate (mouse prostate progenitor)	Inhibition of proliferation, cell cycle arrest, differentiation	Maund et al. (2011)
Vitamin D3	Fish, eggs, etc.	Bone	Differentiation	D'Ippolito et al. (2002); Piek et al. (2010)
NSAID (Sulindac)	–	Breast (CD44+ MCF10DCIS)	Apoptosis, inhibition of tumor growth in vivo	So et al. (2011)
		Intestine (Lgr5+ <i>APCMin</i> + crypt cells)	Apoptosis, down regulation of Wnt/ β -catenin	Qiu et al. (2010)

apply the brakes on this process by enhancing multi-lineage differentiation. To be able to better target or enhance these cellular processes, it is important to identify the molecular signaling responsible for these pathways. The Wnt, Hedgehog, Notch, and transforming growth factor-beta (TGF- β) pathways have been implicated in the process of self-renewal (Maund and Cramer 2010). Chemoprevention can alter the expression of stem cell markers, expressed by TICs or CSCs, used as a measure of cellular differentiation. Although no universal CSC markers have been defined, several cell-surface markers such as CD44, CD133, CD116, aldehyde dehydrogenases (ALDH), and Lrg5 have been reported to be overexpressed in various solid organ tumors and used to identify CSCs (Subramaniam et al. 2010).

8.3.2.1 Targeting Self-Renewal

Chemoprevention has demonstrated the ability to directly block tumor growth in vivo. Chemopreventive agents aim to target tumor-initiating traits such as spheroid and colony formation, by altering key signaling pathways that inhibit proliferation and cell viability, induce cell cycle arrest, apoptosis, and senescence in stem cells (as well as differentiated cells). As a result, tumors may be more easily targeted by standard therapies.

The spheroid and colony formation assays measure the potential of cells to self-renew in an anchorage-independent and anchorage-dependent environment, respectively. A number of chemopreventive agents including polysaccharopeptide (PSP, extracted from Turkey tail mushroom *Coriolus versicolor* or Yun-zhi), bone morphogenetic protein (BMP7, a member of the TGF- β superfamily), gamma-tocotrienols (γ -T3, component of vitamin E), genistein (from soy), and epigallocatechin gallate (EGCG, from green tea) have exhibited the ability to inhibit spheroid and colony formation in prostate stem cells (Kobayashi et al. 2011; Luk et al. 2011; Tang et al. 2012; Zhang et al. 2012). EGCG also suppressed the spheroid- and colony-forming ability of human breast CSCs. This was mediated by activation of adenosine monophosphate-activated protein kinase (AMPK α) (Chen et al. 2012). AMPK α serves as an energy sensor in eukaryotic cells and its activation suppresses cell proliferation in malignant cells (Motoshima et al. 2006). Similarly, blueberry polyphenolic acid and genistein inhibited the formation of anchorage-independent spheroid in mammary stem cell cultures. The effects of genistein were mediated by increased expression of phosphatase and tensin homolog (PTEN) in these cells (Montales et al. 2012). Loss of PTEN and overactivation of the PI3K/Akt-mediated proliferative pathway strongly correlate with progression of prostate cancer (Sarkar et al. 2010). Other studies using breast TICs indicated that curcumin and piperine, from turmeric and black pepper, respectively, inhibited spheroid formation by down-regulating Wnt signaling (Kakarala et al. 2010). The Wnt/ β -catenin pathways are associated with self-renewal (Li et al. 2011). Studies on brain and colon CSC demonstrate that in the presence of curcumin, signal transducer and activator of transcription 3 (STAT3), a transcription factor, was a major regulator of spheroid and colony formation in vitro and that combination treatment with 5-fluorouracil and

oxaliplatin (FOLFOX) enhanced these effects (Lim et al. 2011; Lin et al. 2011; Yu et al. 2009). Sulforaphane, an organosulfur compound from cruciferous vegetables, blocked colony and spheroid formation in human breast and pancreatic TICs. Nuclear factor kappa-light-chain enhancer of activated B cells (NF- κ B), a protein complex that regulates DNA transcription, was downregulated in these studies (Kallifatidis et al. 2011; Li et al. 2010b; Rausch et al. 2010). Recent studies have also begun to focus on the role of fatty acid synthesis, which is downregulated by resveratrol and altered stem properties such as spheroid formation (Pandey et al. 2011).

Using stem cells from a pancreatic tumor, sulforaphane was found to block expression of Nanog, a transcription factor important in self-renewal and differentiation (Srivastava et al. 2011). Similarly, resveratrol prevented expression of genes essential for pluripotency: Sox2, c-Myc, and Oct4 (Shankar et al. 2011). Treatment with curcumin downregulated stem cell markers including Notch1 and Hes-1, and pro-survival gene Bcl-XL, in addition to inhibiting NF- κ B in pancreatic CSC (Wang et al. 2006). EGCG along with quercetin (a flavonoid found in fruits, vegetables, leaves, and grains) synergized to attenuate TCF/LEF and Gli activities (Tang et al. 2012). TCF/LEF and Gli are involved in Wnt and Sonic Hedgehog signaling; these pathways are essential to supporting a stem cell's self-renewal capacity. Thus, chemopreventive agents present a powerful tool in managing self-renewal of CSCs by modulating various molecular pathways.

8.3.2.2 Differentiation of Cancer Stem Cells

Selective targeting of CSCs in order to avoid normal healthy cells has been challenging; therefore, efforts in chemoprevention have focused on methods of driving CSC into differentiated lineages. The concept of "differentiation therapy" was first proposed in 1961 with the hypothesis that CSCs, upon differentiation, would give rise to progenitors and subsequently differentiated cancer cells that would gradually deplete, resulting in tumor regression (Rane et al. 2012). The proof for this premise came from the clinical trial for promyelocytic leukemia using all-trans retinoic acid (ATRA), where the majority of patients underwent remission and blast cell differentiation was demonstrated (Huang et al. 1988). Based on the success achieved in treating leukemia, there has been a substantial effort in screening chemoprevention compounds that induce differentiation of normal and solid organ tumor-derived stem cells.

Chemoprevention-mediated differentiation of various normal stem cell populations is well documented. Sulforaphane induced human promyelocytic cells to differentiate into granulocytes and macrophages via activity of PI3K and PKC (Fimognari et al. 2008). Our lab has shown that vitamin D stimulates murine prostate progenitor/stem cells (PrP/SCs) in an IL-1 α -dependent manner toward a luminal cell fate (Maund et al. 2011). Other labs have also found vitamin D to stimulate differentiation of human mesenchymal stem cells (hMSC) into osteoblasts through signaling pathways involving regulation of c-Myc by BMP2, or HGF by upregulation of the vitamin D receptor (D'Ippolito et al. 2002; Kuske et al. 2011; Piek et al. 2010).

Vitamin D, with the help of retinoic acid, also increased the differentiation of adipose-derived stem cells (Malladi et al. 2006). Resveratrol had similar effects on hMSC (Dai et al. 2007), as well as inducing pluripotent stem cells to differentiate into functional osteoclasts (Kao et al. 2010). Similarly, fatty alcohol derivatives of resveratrol were able to stimulate the maturation of neuronal stem cells (Hauss et al. 2007), indicating that many methods of differentiation are possible with chemoprevention. These studies highlight the role of chemoprevention in driving cells toward a more differentiated fate.

Chemopreventive intervention has also been explored as a method to drive CSCs down the path of differentiation. Stem cell antigen (Sca-1) is a cell-surface marker that has been used to enrich the stem/progenitor-like subpopulation. Expression of the Sca-1 surface marker was significantly reduced on prostate CSCs by treatment with a prolactin inhibitor (Rouet et al. 2010). Similarly, an $\alpha(v)$ -integrin antagonist, GLPG0187, reduced the percentage of ALDH-positive stem cells isolated from a population of PC-3 human prostate cancer cell line (van der Horst et al. 2011). Furthermore, treatment of prostate stem cells with γ -T3, PSP, and genistein prevented expression of the stemness markers, CD133 and CD44 (Ling et al. 2011; Luk et al. 2011). These results indicate that cells may have been stimulated to leave their stemlike state in favor of a terminal mature fate.

Differentiation of CSCs caused by treatment with chemopreventive agents has the potential to bring the heterogeneous tumor population to a more consistent differentiated phenotype. The ability to treat a more homogeneously differentiated tumor has led to greater success in eliminating cancer cells with standard treatment. However, recurrence is still common for tumors in which cells remain heterogeneous. In an effort to halt progression of prostatic tumor growth, stem cells continue to be a target of chemoprevention research.

8.3.2.3 Growth Arrest of Cancer Stem Cells

Studies from other systems have shed light on pathways that may affect apoptosis as well as proliferation and senescence. Viability of human prostate stem cells was compromised by exposure to γ -T3 (Luk et al. 2011), and senescence was induced by BMP7 to activate the p38 MAP kinase pathway (Kobayashi et al. 2011). EGCG reduced cell viability and inhibited proliferation of prostate and pancreatic CSCs (Tang et al. 2010, 2012). Vitamin D has been shown not only to inhibit proliferation but also to target stem cells of both prostate and bone by arresting cells in the G_0/G_1 phase or by inducing cellular senescence (Artaza et al. 2010; Li et al. 2009). Synergism between vitamin D and genistein has also been reported to cause these effects in prostate cancer cell lines (Rao et al. 2002, 2004); however, this synergism has not been tested in CSCs. Additionally, vitamin D-mediated growth arrest, differentiation, and G_0/G_1 arrest are shown to be mediated by IL-1 α in mouse prostate progenitor cells (Maund and Cramer 2010).

Curcumin treatment of multiple brain tumor cell cultures resulted in decreased viability, cell cycle arrest in G_2/M phase along with reduction of CD133⁺ stem cells;

attenuation of STAT3 and suppression of Notch signaling were shown to mediate these effects (Lim et al. 2011). Cucurbitacins, tetracycline triterpenoids initially identified in cucumbers, are inhibitors of the Jak/STAT pathway. It was reported to reduce CD133⁺ medulloblastoma CSC by reducing phosphorylation of STAT3 (Chang et al. 2012). Similarly, plant derivatives parthenolide and andrographolide were selectively toxic to multiple myeloma CSC compared to non-tumorigenic cells (Gunn et al. 2011). Resveratrol and sulforaphane also induced apoptosis in leukemia stem cells (Fimognari et al. 2008; Hu et al. 2012) and had similar effects in breast, bone, and pancreas by altering expression of apoptosis markers like BNIP3, DAPK2, RANKL, XIAP, caspase 3/7, and Bcl-2 (He et al. 2010; Nishikawa et al. 2009; Pandey et al. 2011; Shankar et al. 2011; Srivastava et al. 2011). In both human and mouse colon stem cells, nonsteroidal anti-inflammatory drugs (NSAIDs) like sulindac and the curcumin analog GO-Y030 have inhibited proliferation by inducing apoptosis and reducing cell viability, either by inhibiting the β -catenin and Wnt signaling pathway (Qiu et al. 2010) or by reducing expression of STAT3 (Lin et al. 2011) in colon CSCs. These pathways could potentially be active targets in prostate cancer and warrant further investigation.

8.3.2.4 Altering Genetic, Epigenetic, and Signaling Pathways

Chemopreventive agents such as sulforaphane, curcumin, genistein, EGCG, quercetin, and lycopene have been shown to regulate cellular epigenetics and various signaling pathways (Vanden Berghe 2012). Epigenetic regulation by DNA methylation, histone modifications, and microRNA can contribute to the process of carcinogenesis by modifying proteins and signaling networks. The reversible nature of epigenetic modifications makes them good targets for chemoprevention. There is substantial literature available on the epigenetic impact of dietary polyphenols in cancer chemoprevention (Izzotti et al. 2012; Li et al. 2010a; Vanden Berghe 2012; Vira et al. 2012). However, there are few studies evaluating these mechanisms in CSC. Yu et al. demonstrated the elimination of colon CSC by the combination of curcumin and FOLFOX. These results were attributed to hypomethylation of the EGFR promoter and alterations in the levels of DNA methyltransferase 1 (Yu et al. 2009) indicating a possible role for epigenetic changes stimulated by chemoprevention. Similar to oncogenes and tumor suppressor genes, microRNAs (miRNAs) have been shown to have cancer promoting and suppressive functions. As many as 145 miRNAs involved in carcinogenesis mechanisms have been reported to be modulated by natural and synthetic agents, either individually or in combination (Izzotti et al. 2012). Kanwar et al. reported that fluorinated curcumin (CDF) decreases the expression of EZH2 (histone H3K27m3 trimethyl transferase) and overexpression of miRNAs let-7a, b, c; miR-26a; miR-101; miR-146a; and miR-200b, c in colon CSC population (Kanwar et al. 2011). Similarly, in pancreatic CSC, CDF decreased EZH2, CD44, and Nanog and upregulated miR-7, miR-26a, and miR-200b (Bao et al. 2012). These studies highlight the role of chemoprevention-mediated epigenetic modulation in restricting the CSC population. Various natural and synthetic chemopreventive agents have demonstrated regulation of

miRNAs in prostate cancer cells, but their role in prostate CSCs remains to be elucidated (reviewed in Maugeri-Sacca et al. 2012).

8.3.2.5 Sensitizing Cancer Stem Cells to Traditional Therapies

A major hurdle in targeting stem cells is their innate resistance to toxic chemotherapies. Upregulation of multidrug resistance transporters (MDRT), specifically multidrug resistance protein 1 (MDR1), responsible for effluxing toxins, is common in stem cell populations making them a very challenging target. Stem cells that are not cleared by treatment go on to repopulate a tumor following remission (Fig. 8.3). Remarkably, curcumin treatment reduced MDRT/MDR1 expression in stem cells in the brain (Fong et al. 2010), ovaries, breast (Limtrakul et al. 2007), and blood (Anuchapreeda et al. 2006), making them more susceptible to therapy. Natural curcumin and a curcumin analog, difluorinated-curcumin (CDF), were also able to downregulate CD44 and CD166 in human colon stem cells. This effect was enhanced when combined with FOLFOX (Kanwar et al. 2011; Yu et al. 2009), both of which are strong DNA-damaging agents that may also hinder kinase activity involved in genomic repair. Sulforaphane was also identified to promote sensitivity to gemcitabine, doxorubicin, and 5-FU in stem cells enriched from prostate and pancreatic cancer cell lines (Kallifatidis et al. 2011). Sulforaphane reduced ALDH activity in human pancreatic CSC when co-treated with quercetin (Zhou et al. 2010). Similarly, sulforaphane augmented the elimination of pancreatic CSC when combined with sorafenib; this was demonstrated to be due to increased DNA fragmentation and apoptosis and decreased cell proliferation and angiogenesis and by downregulation of NF- κ B activity. Additionally, these treatments were selectively toxic to the CSC but not the nonmalignant cells (Rausch et al. 2010). These reports suggest that chemopreventive agents can be an excellent choice for adjuvant therapy.

8.3.3 Preventing Tumor Growth In Vivo

CSC form a rare cell population in tumors, though they have the ability to give rise to tumors, even when as few as one cell is xenografted in vivo (Quintana et al. 2008). Most in vivo chemoprevention studies have not utilized such a limiting dilution model; nonetheless, they provide an insight into the long-term antitumorigenic effects of these agents. Gamma-tocotrienol and PSP inhibited in vivo tumor initiation of human prostate cancer cell lines enriched for stem cells (Luk et al. 2011). Genistein prevented in vivo prostate tumor growth in mice when stem cells were pretreated prior to transplantation (Zhang et al. 2012). Colon and breast stem cells from both human and mouse similarly responded to nonsteroidal anti-inflammatory drugs (NSAIDs) and sulforaphane, respectively (Li et al. 2010b; Qiu et al. 2010). Sulforaphane also abrogated tumor growth of ALDH⁺ breast CSCs in vivo by downregulating the Wnt/ β -catenin pathway (Li et al. 2010b). APC^{Min/+} mice develop

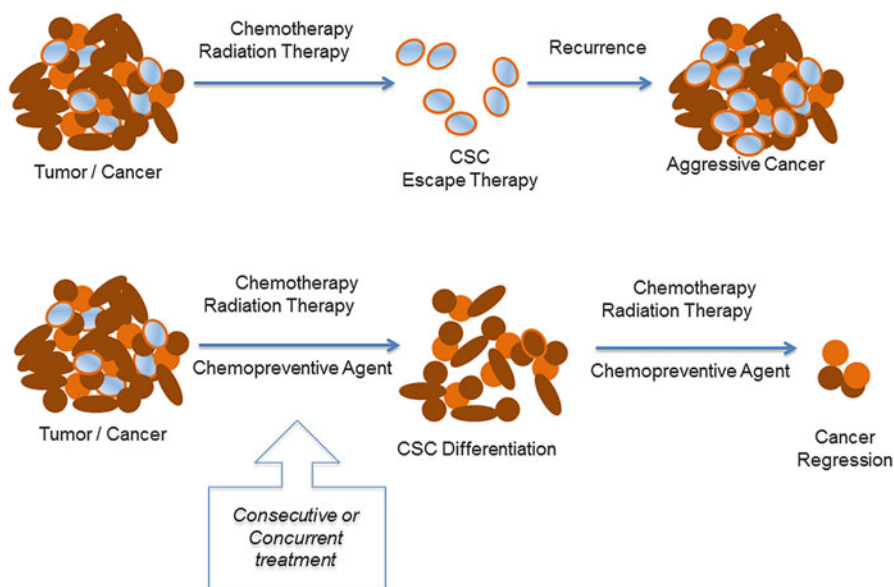


Fig. 8.3 Conventional chemo- and radiation therapy target rapidly growing mature cells, leaving behind the quiescent CSC. These residual CSCs are thought to be the cause of cancer recurrence. Chemopreventive agents can cause differentiation of CSC, thereby making tumors more targetable

spontaneous intestinal adenomas and are a good *in vivo* model for studying colon cancer. Sulindac effectively prevented formation of polyps and colon cancer by inducing apoptosis in Lrg5⁺ colon stem cells (Qiu et al. 2010). All of these functions, stimulated by a naturally occurring chemopreventive agent, impede tumor initiation by targeting CSC.

8.3.4 Preventing Metastasis

Metastasis leads to a dramatically reduced survival rate of patients. Chemoprevention provides the opportunity to target prostate cancer at any stage of development, including the prevention of metastasis. The epithelial to mesenchymal transition (EMT) is a process by which tumor cells change their phenotype from a stationary epithelial cell to a more motile mesenchymal cell and is believed to be the initial transition to a metastatic phenotype. Protein markers and motility studies, for invasion and migration, help in identifying this transition. Chemopreventive agents have been shown to prevent such transformations.

Expression of EMT markers was reduced in human prostate stem cells by genistein (Zhang et al. 2008). The fibroblastic morphology of hMSCs was transformed to a more epithelial-like phenotype *in vitro* by treatment of vitamin D (Klotz et al. 2012). In human prostate and pancreatic cancer cell lines enriched for stemness, EMT markers such as vimentin, slug, snail, ZEB1, twist-1, β -catenin, and LEF1/TCF activity were reduced by exposure to EGCG, resveratrol, and sulforaphane (Shankar et al. 2011; Srivastava et al. 2011; Tang et al. 2010). Additionally, sulforaphane was also reported to synergize with sorafenib or quercetin to reduce the EMT marker twist-2 and upregulate E-cadherin expression (Rausch et al. 2010; Zhou et al. 2010). Genistein and EGCG blocked the invasion and migration of prostatic and pancreatic TICs (Tang et al. 2010, 2012; Zhang et al. 2008). EGCG also prevented migration and angiogenesis of endothelial stem cells by downregulating MMP-9, a secreted metalloproteinase instrumental in migration and invasion (Ohga et al. 2009). Resveratrol was also able to prevent migration and invasion of pancreatic stem cells (Shankar et al. 2011). Furthermore, treatment of human prostate stem cells with GLPG0187, an $\alpha(v)$ -integrin antagonist, not only resulted in increased expression of E-cadherin and reduction of vimentin but also led to reduction in bone metastasis (van der Horst et al. 2011). The remarkable ability of these chemopreventive agents to deter the process of metastasis proves to be one of the many promising directions of the field. Further understanding of these chemopreventive agents and their role in preventing metastasis may lead to the development of new therapeutics for prostate cancer.

8.4 Issues and Limitations of Chemoprevention

Currently there are over 2,000 interventional clinical trials that are focused on either evaluating the prevalence of CSCs in various cancers or measuring them as an outcome of chemotherapy or radiation therapy. On the other hand, there are currently about 200 clinical trials evaluating dietary compounds for cancer chemoprevention, but none seems to be assessing the effects on CSCs (<http://www.clinicaltrials.gov/>). Despite data from various research laboratories demonstrating that chemopreventive agents make stem cells more susceptible to standard therapies, thereby suggesting their promising role for prophylactic or adjuvant therapy, there is significant skepticism in clinics.

CSCs are being increasingly recognized as the cause of recurrence and metastasis, but there is a lack of knowledge about “what defines CSC.” Additionally, the concept of tissue-specific stem cells and the role of tissue microenvironment in modulating functional and phenotypic nature of CSCs prevent generalization of concepts formulated in one cancer to other cancer types. In addition to the chemopreventive agents discussed in this chapter, several other compounds like lycopene, silibinin, 3,3'-diindolylmethane (DIM), pomegranate, fisetin, lupeol (Khan et al. 2010; Sarkar et al. 2010; Venkateswaran and Klotz 2010), and mangostin (Johnson et al. 2011) have been characterized in a variety of cancers (including prostate cancer), but remain unevaluated for their CSC-specific response. This incomplete understanding of tissue-specific cancers, CSC regulation, and possible

tissue-specific role of natural chemopreventive agents could potentially lead to unsuccessful outcome of chemoprevention trials.

8.4.1 Limitations of In Vitro and In Vivo Model

The in vitro colony and serial spheroid formation and 3D cultures are excellent surrogate assays for measuring the self-renewal potential of NSCs and CSCs/TICs. Additionally, evaluating these properties in the context of treatment with various natural and synthetic agents helps identify promising compounds for therapeutics and chemoprevention, as well as understanding their mode of action (Table 8.1). However, these are isolated systems and results might not always extend to a whole body system. Thus, it is imperative to conduct in vivo studies. As discussed earlier, a reduced or delayed tumor growth was reported when human prostate CSCs were pretreated with vitamin E, PSP, or genistein prior to implanting in mice. These studies hint at the prophylactic potential of chemopreventive agents. On the other hand, Rausch et al. reported the effectiveness of addition of sulforaphane to sorafenib in eliminating pancreatic CSCs and restricting tumor growth in vivo, which shows the potential of a natural compound to be used in adjuvant therapy (Rausch et al. 2010). But one must cautiously interpret these results for two reasons: (1) In in vivo models animals are inoculated with a substantial number of CSCs, and (2) these in vivo experiments are almost always conducted in immunocompromised animals. As previously discussed, CSCs or TICs likely form a very small proportion of tumors. Accordingly, it would be more informative to conduct “limiting dilution” experiments in conjunction with pretreatment or combinational therapeutic intervention to eliminate CSCs by using chemopreventive agents. Alternatively, a mixture of CSC and non-CSCs (in combination with tumor-associated mesenchymal cells, Chap. 7) should be inoculated to more accurately mimic the native tumor environment. The immune system is an important aspect of clinical cancer. The in vivo experiments in immunocompromised murine cancer models provide an insight into the effectiveness of chemopreventive agents in a whole body system and allow for the use of human/clinical samples, but they ignore the immunological manifestations that could potentially alter the response to these chemopreventive compounds.

A number of chemoprevention studies have been conducted in murine models that spontaneously develop prostate cancer (reviewed in Lamb and Zhang 2005). However, most of these systems do not accurately mimic the sequence of events in prostate cancer progression. Additionally, conventional in vivo studies involve heterotopic implantation (i.e., subcutaneous, intravenous, intracardiac) of CSCs in immunocompromised murine models. These models address the question of whether CSCs can proliferate and/or metastasize in vivo, but the lack of their histological similarity with human pathology makes it difficult to interpret these results in terms of clinical cancer. Chemoprevention is a very promising method to inhibit cancer progression, but the skepticism in the field could be a manifestation of the current scarcity of accurate models to conduct these studies.

There is a significant impetus in identifying CSC (see Chaps. 1, 2 and 3) and developing rodent models that mimic human cancer (see Chap. 9). Isolating the TICs/CSCs from these animals and evaluating chemoprevention in syngeneic models will result in a better comprehension of the effectiveness of these compounds in blocking carcinogenesis. Our lab has developed an elegant model that addresses these issues where we have shown complete multi-lineage differentiation of a single cell clonal population, derived from murine prostate, in tissue recombinant experiments in vivo (Barclay et al. 2005). Using various gene expression and deletion constructs, the role of specific genes in formation of neoplastic lesions compared to normal prostate architecture can be evaluated. We demonstrated that loss of TGF β -1 activating kinase (Tak1) in murine prostate progenitor cells led to formation of PIN and even carcinoma (Wu et al. 2012). Integration of chemoprevention in these models will help us evaluate the usefulness of specific agents in different phases of carcinogenesis. It would also be most interesting to develop mice in which certain genes, under the control of tissue-specific stem cell promoter, could be exclusively altered in the stem cells of adult animals. This would address the limitations of many transgenic models, i.e. (1) the lack or overexpression of tumor suppressor or oncogenes from embryonic stage and (2) no concerns of embryonic lethality since it would be an intact animal, unless treated to induce gene alteration. Although no stem-cell-specific promoters in the prostate are known yet, development of such a model would not only help in understanding cancer progression but would be valuable in developing preventive and therapeutic compounds.

8.4.2 Timing and Dosage of Chemopreventive Intervention

Cancer chemoprevention during the early phases of carcinogenesis is a viable approach for controlling most cancers; however, it might become a daunting and unmanageable reality as cancer advances. This is most likely due to the increasing number of genetic mutations with time. It was reported that vitamin D was maximally effective in preventing formation of prostatic intraepithelial neoplasia (PIN) in the *NKx3.1; Pten* mutant mice when administered prior to, rather than subsequent to, the initial occurrence of PIN (Banach-Petrosky et al. 2006). Thus, it is appropriate to suggest that specific recommendation for cancer prevention must be based on how far along a patient is on the scale of cancer progression. The models discussed above and in Chap. 9 can help in teasing out these details and developing efficient methods for cancer prevention.

The use of ATRA was one of the pioneering and promising trials supporting chemoprevention or differentiation therapy. Subsequently, ATRA and retinoic acid analogs have been tested in prostate cancer trials, but with limited to no success (Trump et al. 1997). One of the criticisms for such failed trials is the use of considerable variations in dosage. Most chemopreventive compounds, like retinoic

acid (Fong et al. 1993), exhibit a dose-dependent biphasic effect, and their inappropriate use could result in unexpected toxic outcomes. Hence, it seems probable that chemopreventive agents that are effective in controlling carcinogenesis at lower dosages might be ineffective or even pro-cancerous at elevated levels.

8.5 Discussion

While impressive progress has been made in the fields of cancer diagnosis and treatment, cancer remains a serious public health concern. In addition to the toxic side effects of cancer therapy, one of the many challenges that obstruct eradication of cancer is the development of resistance to traditional therapies by cancer cells that ultimately lead to recurrence and death. This resistance and relapse is now being attributed to the rare cancer-initiating stem cell population in tumors. Studies in the past few decades have revealed that certain natural and synthetic dietary compounds can help in cancer management by regulating self-renewal and differentiation of CSC. Thus, chemoprevention emerges as an important tool in controlling cancer progression.

Cancer chemoprevention is believed to be a viable approach to slow or prevent the process of carcinogenesis for most solid organ malignancies. Drawing inspiration from ancient cultures, rapid progress is being made in identifying new chemopreventive agents. The efficacy of many of these agents has been tested in different cancer types. Recently, their role in modulating the chemotherapy-resistant CSC has gained impetus. In addition to low toxicity, the advantages of using chemopreventive agents is that they have multifaceted impacts on tumor cells and CSCs. It is important that these compounds, individually or in combination, specifically target tumor-initiating or CSC and not compromise healthy stem cells in the body. Nonetheless, there is a growing concern about unexpected toxicities as a result of extended chemopreventive regimes. The use of nanotechnology has been suggested and is currently being explored in order to increase bioavailability, improve sustained delivery and reduce toxicities. Advent of more clinically relevant *in vitro* and *in vivo* models is expected to improve screening of chemopreventive agents that can subsequently be incorporated in prophylactic or adjuvant therapy. While the molecular mechanisms associated with tissue-specific cancers and CSC are still under investigation, we hope that lessons learned from one system can be extended cautiously to another. Moreover, the outcome of chemoprevention could not only be associated with tumor stage and ongoing therapy but may also be altered by race, genetics, geographical location, and diet. Thus, chemoprevention can become a success story by identifying the right patient population, the appropriate time and dose for interventions, and administration of the suitable agent.

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Chapter 9

Stem Cell Models for Functional Validation of Prostate Cancer Genes

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Abstract Prostate cancer is a genomically complex disease in which initiation, progression, and metastasis are regulated by numerous molecular processes including oncogene activation or tumor suppressor inactivation. Understanding the molecular mechanisms that drive prostate tumorigenesis has important clinical implications. Putative oncogenes or tumor suppressors are identified using technologies including SNP arrays, microarrays, and whole genome sequencing, but these targets must then be evaluated in cell and animal models to determine the functional consequences of these genomic alterations. Traditionally, potential prostate cancer genes have been validated with human prostate cancer cell line models (i.e., tissue culture and xenograft systems) or genetically engineered mouse (GEM) models. More recently, stem cell models have been utilized to evaluate candidate cancer genes. Because the normal adult prostate stem cell (PSC) shares many properties with the prostate tumor-initiating cell (TIC) including the capabilities for self-renewal, differentiation, and androgen independence, modeling gene alterations in PSCs may be more appropriate than traditional approaches. PSCs can be maintained in cell culture, genetically manipulated, and characterized using techniques including cell sorting, colony formation assays, and prostasphere assays in vitro and tissue recombination in vivo. A number of prostatic oncogenes and tumor suppressors including MYC, ERG, PTEN, P53, NKX3.1, and TAK1 have been evaluated using stem cell models. Compound genetic alterations have also been studied using

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PSC models. In this chapter we describe current approaches being used to investigate putative oncogenes and tumor suppressors in the context of the PSC and highlight a few examples of recent studies using stem cell models for target validation. We also discuss the limitations of existing models as well as strategies to improve upon these models for future studies.

9.1 Introduction

A major goal of prostate cancer research is to identify the molecular mechanisms that drive the initiation, progression, and metastasis of prostate tumors. Understanding the molecular processes that regulate prostate tumorigenesis can lead to the development of new diagnostic, prognostic, and therapeutic alternatives to improve clinical outcome especially for patients with metastatic disease. However, identification of key regulators of prostate cancer is a challenging task because the prostate cancer genome is extremely complex, and tumor development is driven by a variety of molecular events. Events that can initiate tumorigenesis include amplification, mutation, translocation, or upregulation of an oncogene or deletion, downregulation, or methylation of a tumor suppressor gene. MicroRNAs can also modulate gene expression to promote tumor development (Lei et al. 2006; Lukacs et al. 2010; Shen and Abate-Shen 2010). In a study highlighting the complexity of prostate cancer genetics, Garraway and colleagues observed medians of 3,866 point mutations, 20 non-synonymous coding mutations, and 90 genomic rearrangements per prostate tumor genome analyzed (Berger et al. 2011). With the advent of technologies including high-powered SNP arrays and whole genomic sequencing, the entire landscape of the prostate cancer genome can be studied with high sensitivity and precision. A number of recent studies have utilized these genome-wide approaches to identify novel regions of genetic alterations that harbor putative oncogenes or tumor suppressors (Berger et al. 2011; Grasso et al. 2012; Ishkanian et al. 2009; Liu et al. 2012; Robbins et al. 2011; Solimini et al. 2012; Taylor et al. 2010). To distinguish genes that are true regulators of prostate tumorigenesis (drivers) from those genes whose alteration does not affect cancer development (passengers), candidate genes must be thoroughly screened using both cell- and animal-based models. Stem cell models have been effectively and efficiently used for evaluation of numerous oncogenes and tumor suppressors including MYC, ERG, PTEN, P53, NKX3.1, and TAK1.

9.2 Rationale for Stem Cell Models

Historically, tumorigenesis has been proposed to occur through clonal evolution, a process by which normal cells sporadically mutate and generate progeny that later acquire additional mutations, eventually yielding a heterogeneous population of tumor cells in which individual cells equally possess the ability to proliferate and metastasize (Fig. 9.1a) (Greaves and Maley 2012). More recently, another

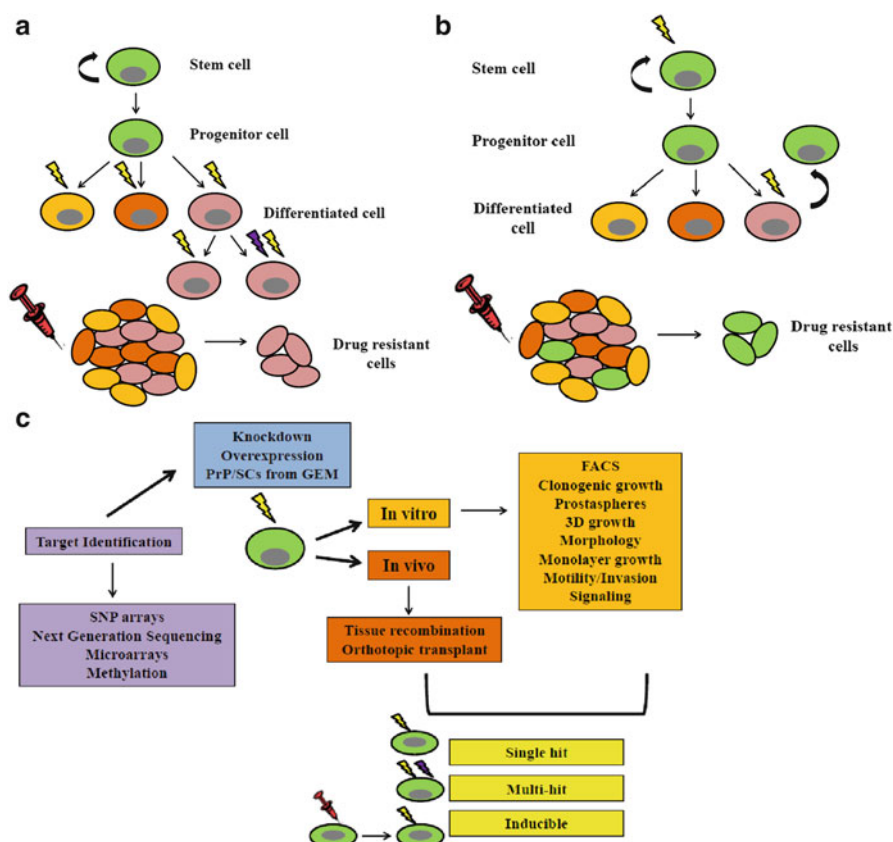


Fig. 9.1 Advantages of stem cell models for validation of candidate cancer genes. **(a)** Clonal evolution model. In this model tumorigenesis is proposed to occur through the accumulation of mutations or alterations in normal cells (not necessarily stem cells). Daughter cells inherit mutations and can acquire additional alterations, eventually resulting in a heterogeneous population of tumor cells in which individual cells equally possess the ability to proliferate and metastasize. Therapeutic intervention may eliminate the bulk of the tumor cell population, but often a small population of drug-resistant tumor cells emerges. These cells may have acquired additional or different mutations than the bulk tumor population. **(b)** Cancer stem cell hypothesis. In this model, tumor development is initiated and sustained by a small population of CSCs or TICs that have properties similar to normal stem cells including the abilities to self-renew, differentiate, and become drug resistant. The CSC may be derived from a normal adult stem cell that has mutated. The CSC may also originate from a more differentiated cell that has mutated and reverted back to a stem-like state. **(c)** Utilization of stem cell models for evaluation of putative oncogenes and tumor suppressors. Candidate cancer genes are identified using technologies including SNP arrays, whole genome sequencing, microarrays, and methylation assays. These targets are then manipulated in PrP/SCs in vitro to suppress or overexpress candidate gene(s). PrP/SCs can also be isolated from GEM mice that already possess a particular genomic alteration (e.g., *Pten* deletion). Manipulated PrP/SCs are assessed for phenotypic changes in vitro by examining various cellular properties including cell morphology, proliferation rate, migration rate, and signaling ability. Growth can be evaluated in standard monolayer growth assays, clonogenic assays, prostasphere assays, or 3D growth assays. PrP/SCs are characterized in vivo using tissue recombination or orthotopic models. PrP/SC models can be adapted to examine the effects of multiple genetic alterations on prostate tumorigenesis (multi-hit/compound models), and this can be done using regulated genetics (drug-inducible models).

hypothesis for tumorigenesis has emerged; the cancer stem cell (CSC) hypothesis proposes a hierarchy for cancer development in which tumors are initiated and propagated by a small population of CSCs or tumor-initiating cells (TIC) which may be more resistant to therapeutic agents than more differentiated cells (Fig. 9.1b) (Wicha et al. 2006). Although it remains unclear whether the TIC originates from a mutated adult stem cell or a more differentiated cell that has reverted to a more stem-like state, the TIC does share many properties of the normal stem cell including the abilities to self-renew and differentiate (Collins et al. 2001, 2005). In the prostate, normal stem cells and TICs may also share the capacity for androgen independence (Collins et al. 2005; English et al. 1987; Evans and Chandler 1987). Therefore, the normal prostate adult stem cell (PSC) is a natural model for studying tumor initiation, progression, and metastasis.

Numerous studies support the existence of both PSCs and prostate TICs. PSCs have been detected in normal mouse and human prostatic tissue, and TICs have been identified in prostate cancer cell lines, xenografts, and mouse and human primary prostate tumors (Collins et al. 2001; Li et al. 2008; Patrawala et al. 2006; Shi et al. 2007; Tran et al. 2002; Xin et al. 2007). The observation that basal and neuroendocrine cells survive following androgen deprivation and subsequent androgen restoration while most luminal cells undergo apoptosis during the regression phase suggests that PSCs may reside in the basal layer (English et al. 1987; Evans and Chandler 1987; Isaacs and Coffey 1989). More recently, Shen and colleagues discovered that a small population of castration-resistant luminal cells expressing Nkx3.1 (CARNs) can self-renew during prostate regeneration, providing evidence for stem cells in the luminal cell population (Wang et al. 2009). Since then, other lineage-tracing experiments have provided evidence that both basal and luminal cells contain populations of PSCs (Choi et al. 2012; Liu et al. 2011). Although the origin of the PSC continues to be debated, it is clear that identification, characterization, and manipulation of the PSC will provide a better understanding of tumor development, resistance to treatment, recurrence, and metastasis.

9.3 Advantages of Stem Cell Models over Traditional Strategies for Validation of Cancer Genes

The many similarities between PSCs and TICs (described in Sect. 9.2) make the PSC a natural model for functional validation of prostate oncogenes and tumor suppressors. With the discovery of PSC and TIC biomarkers and the optimization of assays for characterization of stem cells, utilization of PSCs in functional studies is now possible. Traditionally, the approach to validating putative oncogenes and tumor suppressors has been to manipulate gene expression in human prostate cancer cell lines, determine if there are differences in cellular properties *in vitro*, and then subcutaneously graft cells into nude mice to assess effects on tumor size *in vivo*. Although experiments performed with prostate cancer cell lines are fairly inexpensive, easy, and fast, these cells may not accurately reflect the true genotypic and phenotypic characteristics of prostate tumors. In fact, the three most commonly used

prostate cancer cell lines DU145, PC3, and LNCaP were established from brain, bone, and lymph node metastases, respectively, and harbor numerous and diverse genomic alterations (Liu et al. 2008; van Bokhoven et al. 2003). When a gene is manipulated in a cell population that is already highly altered, the conclusions that can be drawn about that gene's role in tumor promotion or initiation must be tempered by uncontrollable interactions with other genetic alterations. In support of this concept, we have observed that gene suppression can have different or even opposite effects in LNCaP, DU145, and PC3 cells which is likely due to the vast genetic diversity among these cancer cell lines (Ulkus and Cramer, unpublished observations).

If genetic manipulation causes an abnormal phenotype in the human cell line/xenograft system, then there is often rationale for creation of a genetically engineered or transgenic mouse (GEM) model. GEM models introduce genetic alterations into the genomes of embryonic stem (ES) cells allowing for germline incorporation of mutations, deletions, duplications, or other modifications. GEM models are useful for studying tumorigenesis because these mice can develop multifocal prostate cancer that can recapitulate different aspects of the human disease. Types of GEM models that have been used in prostate studies include:

1. First generation transgenic models that utilize prostate tissue-specific promoters such as the rat probasin (PB) gene to drive expression of viral oncogenes (e.g., TRAMP, LADY)
2. Transgenic models that conditionally express nonviral oncogenes (e.g., c-Myc, Akt, FGFR1, Braf)
3. Second generation GEM models that introduce whole body gene knockout by homologous recombination in ES cells (e.g., Pten, Rb)
4. Third generation conditional GEM models that induce genetic alterations in a cell or tissue-specific manner most commonly using Cre-loxP technology (e.g., PB-Cre; Pten^{L/L})
5. Regulated GEM models that utilize drug-inducible promoters to introduce genomic alterations at specific time points in development (e.g., PSA-Cre-ER^{T2}; Pten^{L/L} or K14-CreER^{T2}; Pten^{L/L})
6. Compound GEM models that introduce two or more genomic alterations simultaneously (e.g., PB-Cre; Pten^{L/L}; p53^{L/L} or PB-Cre; Pten^{L/L}; Kras^{G12D/W})

Overall, GEM models have been highly successful for validation of putative oncogenes and tumor suppressors in the prostate, but the major limitation of these models is that they cannot fully recapitulate human tumorigenesis. Advanced stage human prostate cancers commonly metastasize to the bone, but currently no GEM model can consistently form osteoblastic bone metastases. Additionally, some GEM models display phenotypes inconsistent with human pathology. In the TRAMP model, for example, tumors often originate in neuroendocrine cells, a phenotype rarely observed in human prostate cancer (Chiaverotti et al. 2008). In a probasin-cH-RAS-G12V model, mice display low-grade prostatic intraepithelial neoplasia (PIN) as early as 3 months of age but also develop intestinal metaplasia (Scherl et al. 2004). Also, according to the CSC hypothesis, genetic alterations occur in the TIC which is presumably an adult prostate cell with stem cell-like

properties. With the exception of the more recently developed inducible promoter models, which may introduce alterations into the adult prostate cell, all other GEM models target the ES cell. Since alteration of the ES cell impacts embryonic and postnatal development, this strategy may not accurately reflect the initiation and progression of prostate cancer. Even in models that utilize the tamoxifen-regulated inducible Cre-ER^{T2} system, the only tissue-specific promoters available include probasin, PSA, and NKX3.1. These promoters are in reality more cell specific rather than tissue specific because the proteins are predominantly expressed in the (more differentiated) luminal cells of the prostate (Luchman et al. 2008; Ratnacaram et al. 2008; Wang et al. 2009). Other cell-specific promoters utilized in the Cre-ER^{T2} model include K8, a luminal cell-specific cytokeratin and K14, a cytokeratin expressed in the basal cell (Choi et al. 2012). However, a prostate epithelial stem cell-specific promoter has not been identified.

Another issue that can make interpreting results from GEM models difficult is that if the same transgene is introduced into mice originating from different genetic strains, the resulting phenotypes may not be consistent. To study the effects of oncogenic ERG on prostate tumorigenesis, multiple groups have generated transgenic mice that overexpress ERG or TMPRSS2:ERG under the control of the probasin promoter. However, the results from studies using PB-ERG mice have been conflicting. Two reports demonstrate that overexpression of ERG leads to the development of PIN in FVB and 129/SV mice (Klezovitch et al. 2008; Tomlins et al. 2008). However, three studies show that transgenic TMPRSS2:ERG or ERG mice display minor phenotypic changes that do not progress to PIN in FVB and B6J mice (Carver et al. 2009; Casey et al. 2012; King et al. 2009). Contrasting findings may be attributable to minor differences in ERG vector design and integration into the mouse ES cell. However, these findings may also be a result of differences in mouse genetic backgrounds. Finally, GEM models are very time consuming and costly to generate. These models require complex vector design and breeding schemes which can take years to validate and study.

PSC models have many advantages over standard cancer cell line and GEM models. Critically, if the CSC hypothesis holds true, then genetic manipulation of the PSC may better recapitulate tumor development and progression compared to modeling tumorigenesis in a more differentiated cell type. Genetic alteration of an oncogene or tumor suppressor in the PSC is predicted to have visible phenotypic consequences such as altered cellular proliferation, motility, morphology, signaling, and/or abnormal glandular development. Standard biological assays can be used to qualify and quantify these phenotypes. Furthermore, from a practical perspective, stem cell models are less expensive, less time consuming, and less technically challenging to work with compared to GEM models. Isolation, manipulation, and both in vitro and in vivo characterization of PSCs can be completed in a few months. Working with PSCs also affords the researcher a high degree of flexibility at each step in the process of *isolation, culture, manipulation, and characterization*. PSCs can be *isolated* from prostates originating from various mouse backgrounds (Barclay and Cramer 2005) including:

1. Different mouse strains (e.g., C57BL6 or FVB)
2. Mice of varying ages (e.g., embryonic, adolescent, or adult)

3. Mice of varying genetic backgrounds including single and compound GEM
4. Mice with inducible or regulated gene expression

Under optimized tissue culture conditions, PSCs can be *cultured* over many passages while retaining their stem cell properties (Barclay et al. 2008). PSCs can be *manipulated* to alter gene expression using common strategies for gene overexpression or suppression including transient transfection and transduction with lentiviral, adenoviral, or retroviral vectors. PSCs can be infected with drug-inducible vectors to study temporal effects of changes in gene expression or transduced with multiple vectors to easily create compound models of gene alterations. Also, different PSC populations can be purified and studied separately using FACS technology (discussed in Chap. 1). PSCs can be *characterized* using in vitro models including prostasphere/three-dimensional (3D) assays and colony formation assays (described in detail in Chap. 2) as well as in vivo systems including the tissue recombination model and the prostate orthotopic model (Fig. 9.1c). In the next two sections of this chapter, we highlight the importance of PSC culture and tissue recombination systems.

Of course, even PSC models have limitations because none of these systems can exactly recapitulate the adult prostatic stem cell in its natural state. For instance, in vitro assays maintain stem cells in an artificial state in the absence of the prostatic microenvironment. Tissue culture conditions put selective pressure on cells and they can adapt by acquiring genetic mutations or other changes so “stem-like cells” may be sustainable in vitro, but stem cells may not. Likewise, the PSC is not manipulated in its native state in in vivo assays because genetic alterations are introduced into the PSC before normal prostatic glandular development occurs. From this point on, we refer to the cells described in PSC models as prostate progenitor/stem cells (PrP/SCs) to reflect the fact that these cells are not native PSCs but do maintain stem cell characteristics. Because no one stem cell model can simulate the true nature of the prostate stem cell, it is important to evaluate candidate prostate cancer genes using multiple assays. The in vitro and in vivo stem cell models mentioned above can be used in combination to provide a more complete assessment of prostate cancer genes and their roles in tumorigenesis.

9.4 PSC Culture Models

In the 1980s, numerous research groups began to experiment with various culture conditions and mitogens required for sustained growth of normal and malignant human and rodent epithelial cells from various tissues including the breast and prostate (Imagawa et al. 1982; Kubota et al. 1981; McKeethan et al. 1982; Peehl and Stamey 1984, 1986). Nandi and colleagues first utilized a collagen gel matrix system to improve in vitro propagation of mouse mammary epithelial cells, and this method has since been adapted to culture of mouse prostate epithelial cells (MPECs) (Kusama et al. 1989; Yang et al. 1980). We have developed a modified culture method in which epithelial organoids are plated on collagen-coated dishes and remain on collagen until MPEC outgrowths survive crisis at which

time they are transferred to plastic dishes and serially passaged (Barclay and Cramer 2005). We have isolated MPECs from various genotypes including wild-type B1/6;129/SVEV, Rb^{L/L} FVB129-Rb1tm2Bm, Ink4a^{-/-} B6;129-Cdkn2atm1Rdp, VDR^{-/-} B6;CD-1; Pten^{L/L} C57BL/6, and Map3k7(Tak1)^{L/L} C57BL/6 mice. During in vitro characterization of wildtype B1/6;129/SVEV MPECs, hereafter called WFU3 cells, we first observed that these cells possess PrP/SCs properties. When WFU3 cells were weaned from serum (1% to 0% fetal bovine serum (FBS)) in monolayer cultures, they formed patches of tightly clumped cells resembling spheroids. Spheres collected from monolayer cultures and replated in 3D collagen matrices formed large, branched ductal-like structures (Barclay and Cramer 2005). To confirm the existence of PrP/SCs within the WFU3 cell population, we tested the differentiation capability of WFU3 cells using the tissue recombination system (see Sect. 9.5 for a detailed description of this model). WFU3 tissue recombinants regenerated normal prostatic ductal structures with a p63+ basal layer and an AR+ lumen that produced prostatic secretory products. WFU3 PrP/SCs also express high levels of Sca1 and Cd49f and possess the ability to self-renew upon serial transplantation of tissue recombinants in vivo (Barclay et al. 2008). Because WFU3 cells maintain their PrP/SC characteristics over long-term culture, they are an invaluable PSC model and can be genetically manipulated to determine effects of genomic alteration(s) on numerous biological processes including normal development and tumorigenesis. To date, WFU3 cells have been manipulated to alter expression of numerous genes including Pten, IL1- α , Chd1, and Map3k7/Tak1 (Axanova et al. 2010; Liu et al. 2012; Maund et al. 2011; Wu et al. 2012).

Interestingly, mixed populations of MPECs isolated by our culture technique from various genetic backgrounds differ in their proportions of PrP/SCs and thus their ability to generate prostatic ductal structures in tissue recombinants. We found that tissue recombinants from bulk populations of Rb^{L/L} and Pten^{L/L} MPECs generated prostatic ductal structures while Tak1^{L/L} MPECs did not (Barclay et al. 2008 and unpublished observations). Flow cytometry of these populations of MPECs stained with Sca1 and Cd49f antibodies revealed that 30.6% of Rb^{L/L}, 12.5% of Pten^{L/L}, and 2.8% of Tak1^{L/L} MPECs cells had a Sca1⁺Cd49f^{hi} phenotype. The low percentage of PrP/SCs within the total Tak1^{L/L} population likely explains the inability of Tak1^{L/L} cells to form ductal structures in vivo. Single cells were plated from sorted Sca1⁺Cd49f^{hi} Tak1^{L/L} cells and clonal populations of PrP/SCs were established. Unlike the bulk Tak1^{L/L} cells which grew in a single layer on plastic dishes, numerous Sca1⁺Cd49f^{hi} Tak1^{L/L} clones formed spheroids under monolayer culture conditions even in the presence of serum and after serial passaging (Fig. 9.2b). The same clones generated large, branched structures in 3D collagen matrices (Fig. 9.2c). Although the majority of 3D structures were branched, we observed the presence of some rounded structures mixed in among the branched structures (Fig. 9.2c, *left*) (Romero and Cramer, unpublished). Variation in 3D structure may be indicative of PrP/SCs at different stages of differentiation. Further characterization by staining individual structures with markers of prostatic stemness and differentiation can provide more insight into

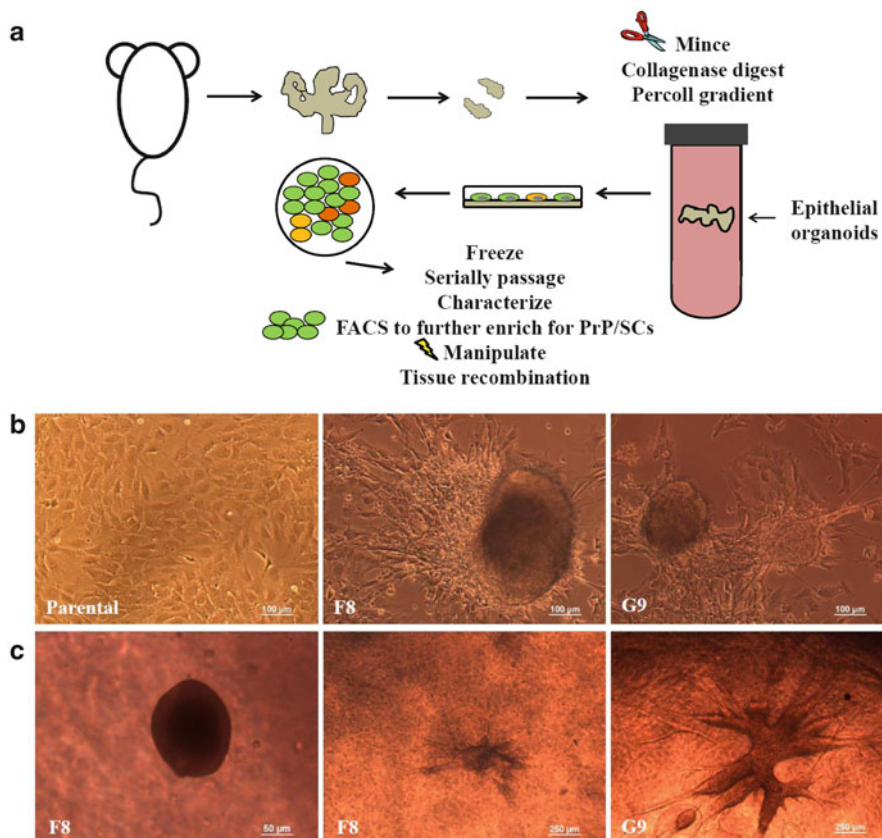


Fig. 9.2 PrP/SC culture model. **(a)** Strategy for isolation and culture of PrP/SCs. Prostates are removed from 6- to 8-week-old mice and the different prostatic lobes (anterior, dorsal, lateral, and ventral) are isolated. Lobes from age and genetically matched mice can be pooled. Prostatic tissues are then minced, collagenase digested, and transferred to a Percoll gradient to separate epithelial cells from stromal cells and debris using gradient centrifugation. Epithelial organoids are collected and plated on collagen-coated plastic dishes in DMEM/F12 medium supplemented with FBS, bovine serum albumin (BSA), cholera toxin, epidermal growth factor (EGF), bovine pituitary extract (BPE), insulin, transferrin, Vitamin E, trace elements, and gentamicin (Barclay and Cramer 2005). Once cells survive crisis, they can be cultured on regular tissue culture plates. Cells can then be frozen, serially passaged, characterized in vitro, genetically manipulated, and used in tissue recombination experiments in vivo. FACS can also be used to enrich for PrP/SCs before characterization, manipulation, or tissue recombination. **(b)** Enrichment for Tak1^{L/L} PrP/SCs and growth in monolayer culture. Tak1^{L/L} MPECs were isolated from the anterior lobes of 7-week-old mice and cultured as illustrated in Fig. 9.2a. Parental (unsorted) Tak1^{L/L} MPECs display a typical cobblestone-like pattern when grown in monolayer culture conditions (left). Tak1^{L/L} MPECs can be enriched for PrP/SCs using FACS. Tak1^{L/L} MPECs were co-stained with anti-Sca1-APC and anti-Cd49f-FITC antibodies and FACS sorted. Single Sca1⁺Cd49f^{hi} PrP/SCs were sorted directly into individual wells of a 96-well plate. Clonal populations were established, expanded, and serially passaged. Tak1^{L/L} PrP/SC clonal cell lines F8 and G9 form spheroid-like structures in monolayer culture even in the presence of serum (middle and right). **(c)** Characterization of Tak1^{L/L} PrP/SCs in 3D culture. 1 × 10⁴ cells in a collagen matrix mixture were plated in wells of a 24-well collagen-coated plate and maintained in culture for 21 days. Media was refreshed every other day. Tak1^{L/L} PrP/SC clones F8 and G9 generated large, branched structures in 3D culture (middle and right). Clone F8 also formed some small, rounded structures when grown in collagen suggesting that not all cells within this population have retained their PrP/SC characteristics (left)

this phenomenon. Based on their *in vitro* characteristics, Sca1⁺Cd49^{hi} Tak1^{L/L} cells likely have regenerative capability in tissue recombination and this prediction is currently being tested. We have demonstrated that PrP/SCs can be enriched and sustained even in mixed epithelial populations with low numbers of stem cells. Therefore, the PrP/SC model can be adapted to MPECs isolated from any genetic background.

9.5 Tissue Recombination Model

The mouse prostate tissue recombination model, also called the prostate regeneration model or the prostate reconstitution model, was originally developed by Gerald Cunha in the 1970s (Cunha 1972a, b) and has since been modified by others (see Fig. 9.3a, model adapted by Cramer lab). Cunha's initial experiments were designed to study the interaction between the mesenchyme and epithelium during embryonic development of the mouse prostate, and he demonstrated that a reciprocal interaction between the urogenital sinus mesenchyme (UGM) and the urogenital sinus epithelium (UGE) is critical for (1) development and differentiation of the prostate epithelium and (2) differentiation of the mesenchyme into stromal components. In classical recombination experiments, the urogenital sinus (UGS) is removed from a mouse or rat during embryogenesis prior to prostatic bud development (so that UGM and UGE can be separated cleanly). Following enzymatic digestion, the UGM and UGE can be separated and manipulated individually. UGM can then be recombined with UGE *ex vivo* and grafted under the renal capsule of a host mouse. After several weeks or months, grafts are harvested and the histology is evaluated (see Fig. 9.3b, macroscopic view of grafts after kidney removal). Cunha discovered that grafts containing both UGM and UGE generate fully differentiated prostatic structures demonstrating that the UGS possesses all cell types including stem/progenitor cells required for normal prostate development (Cunha 1972a).

Since these pioneering experiments, the tissue recombination model has been applied to study prostatic tissues from normal adult mice, GEM, prostate cancer cell lines, and primary human prostate samples to evaluate the tumorigenic potential of the prostate epithelium. Additionally, gene expression has been manipulated in MPECs, PrP/SCs, and stromal cells *in vitro* using retroviruses or lentiviruses, and the effects of various genetic alterations on normal prostatic development and differentiation have been assessed using the tissue recombination system *in vivo*. Key experiments by Thompson and colleagues in the late 1980s first demonstrated the utility of tissue recombination models for investigating the functional significance of genetic alterations in prostate tumorigenesis. In the model used by Thompson and colleagues, the intact UGS was retrovirally infected with activated Ras and/or Myc, two oncogenes commonly overexpressed in numerous cancer types. Briefly, UGS cells were isolated from E16- to E17-day-old embryos, dissociated to form single-cell suspensions, and inoculated with retrovirus for 2 h. Retrovirally infected UGS was then implanted under the renal capsule. In grafts of UGS infected with

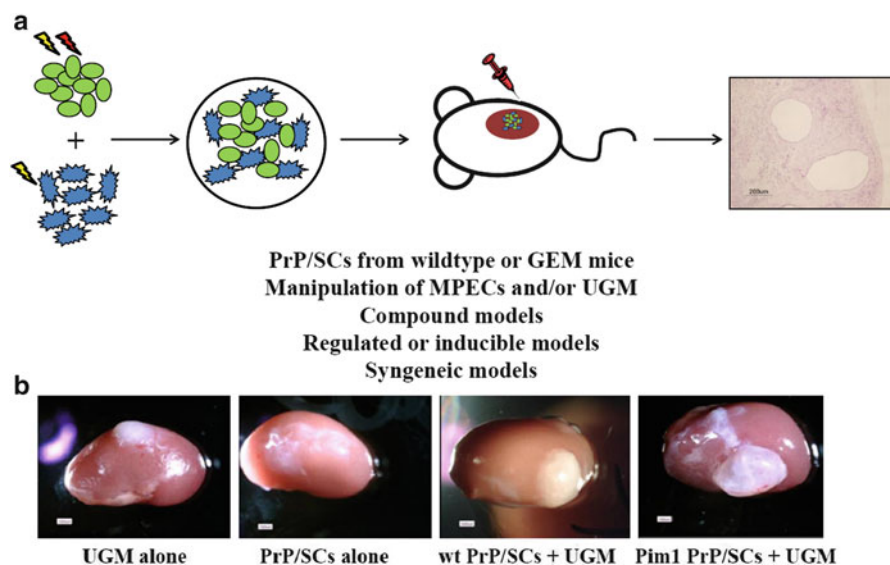


Fig. 9.3 Tissue recombination model. **(a)** Strategy for tissue recombination and renal grafting. 1×10^5 cells PrP/SCs are combined with 2.5×10^5 embryonic day 18 rat UGM cells and resuspended in collagen. Recombinants are plated as collagen buttons and incubated overnight at 37°C before implantation under the renal capsule of male mice. After 6–12 weeks, kidneys are removed, grafts are formalin fixed, and histology is assessed using immunohistochemistry methods. Histology of a normal ductal structure from a wildtype PrP/SC recombinant is shown here. The tissue recombination model can be adapted to evaluate alterations in epithelial and/or mesenchymal cells (indicated by *yellow bolts*) or multiple alterations (*red bolt*). Alterations can also be introduced into PrP/SCs post-grafting using drug-inducible models. **(b)** Renal grafts of Pim1-overexpressing PrP/SCs are larger than PrP/SC wt grafts. PrP/SC wt or PrP/SC Pim1 recombinants were grown under the renal capsules of immunocompromised mice for 12 weeks. Mice were then sacrificed and kidneys were removed. Grafts of UGM alone or PrP/SCs alone form very small grafts while grafts from wt PrP/SCs + UGM and Pim1-overexpressing PrP/SCs + UGM tissue recombinants form large, macroscopic grafts. Although Pim1-overexpressing PrP/SCs + UGM tissue recombinants appear to form the largest grafts, histological analysis is the only conclusive way to determine if Pim1 overexpression effects prostatic development in this model (not shown)

low-titer Ras retrovirus, normal prostatic structures formed, while in high-titer Ras-infected grafts, focal dysplasia, hyperproliferative stroma, and increased angiogenesis were observed relative to grafts with control retrovirus. Myc-infected UGS grafts demonstrated a mild hyperplasia mostly confined to epithelial regions. UGS co-infected with Ras and Myc formed rapidly growing carcinomas even at low viral titers suggesting that co-activation of Ras and Myc is sufficient to induce prostate tumorigenesis (Thompson et al. 1989). Subsequently, GEM Ras models have supported these findings (Scherl et al. 2004). Later, UGS from $p53^{+/-}$ or $p53^{-/-}$ mice was isolated and infected with the Ras-Myc retrovirus. One hundred percent of Ras-Myc retrovirally infected $p53^{+/-}$ and $p53^{-/-}$ UGS grafts formed carcinomas and 95% of mice had metastases (Thompson et al. 1995). These experiments provided the first

evidence that multiple genetic alterations can be modeled using the tissue recombination system. However, because activated Ras and Myc were introduced into cells isolated from the complete UGS, it was impossible to determine the effects of these alterations in the individual epithelial and stromal components. Overexpression of Ras and Myc in total UGS may actually lead to a more dramatic phenotype than what would be observed if these were overactive in either epithelium or stroma alone. Since adult MPECs contain PrP/SC populations that possess the ability to form ductal structures when recombined with UGM (as described in Sect. 9.4), it is now possible to genetically alter stromal and epithelial compartments separately before recombination and renal grafting.

A useful variation of the tissue recombination model is the tissue rescue system which was developed after the construction of whole body GEM models but prior to the advent of tissue-specific GEM models. Whole body GEM models have rapidly advanced our understanding of normal development and tumorigenesis but have limited use in cases where complete gene loss leads to embryonic lethality. However, using the tissue rescue approach, UGS can be isolated from embryos before they reach embryonic lethality. UGS is then grafted renally enabling investigation of the effects of gene deletion on normal prostatic ductal development and tumor initiation. Tissue rescue has been used to characterize UGS from $Rb^{-/-}$ and $p57^{-/-}$ mice. RB and P57 are often lost or downregulated in prostate cancer and nullizygous mice of either genetic background display early lethality (Clarke et al. 1992; Jacks et al. 1992; Jin et al. 2008; Lee et al. 1992). Cunha and colleagues utilized the tissue rescue approach to test the functional significance of complete Rb loss in prostate cancer development. Pelvic visceral rudiments were isolated from day E12 embryos and grafted under the renal capsule of athymic male mice for 4 weeks to generate $Rb^{+/+}$ or $Rb^{-/-}$ prostatic tissue containing characteristic ductal structures. Prostatic epithelial ducts were then removed from the renal capsule, recombined with rat UGM, sub-renally grafted into new athymic hosts along with implantation of an empty capsule or a capsule containing estradiol and testosterone (a drug combination known to induce carcinogenesis in rats) for 5–8 weeks. $Rb^{+/+}$ and $Rb^{-/-}$ grafts without hormonal stimulation (empty capsule) formed mostly normal structures with some hyperplastic foci observed. $Rb^{+/+}$ grafts with hormone treatment generated normal and hyperplastic structures. $Rb^{-/-}$ grafts plus hormone formed normal, hyperplastic, atypical hyperplastic, and carcinomatous structures suggesting that loss of Rb makes the prostate more susceptible to prostate cancer development (Wang et al. 2000). The development of a prostate-specific conditional Rb knockout mouse (Pb-Cre) not only supported the findings of Cunha and colleagues but also demonstrated a direct association between Rb loss and prostate carcinogenesis. Loss of one or both copies of Rb resulted in prostatic hyperplasia in 18-week-old mice but never progressed to carcinoma, suggesting that Rb may be a haploinsufficient prostate tumor suppressor that can initiate prostate cancer but that additional genetic events are required for progression to carcinoma (Maddison et al. 2004). The tumor suppressive ability of p57 was also verified in tissue rescue experiments using UGS isolated from day E15.5 to E18.5 $p57^{-/-}$ mouse embryos. By 2 and 4 months after grafting, $p57^{-/-}$ UGS cells displayed hyperplasia and increased proliferation relative to wildtype UGS grafts. After 6 months, $p57^{-/-}$ grafts displayed

PIN and carcinoma (Jin et al. 2008). With the advent of the tissue-specific knockout mouse, the tissue rescue approach became outdated, but it served as an initial proof of principle that nullizygous genotypes can be studied using PrP/SCs.

A major advantage to using the tissue recombination model is its versatility. Not only can stromal and epithelial cells from various mouse, rat, and human origins be studied in this system, but the grafts can be placed into hosts of various backgrounds including syngeneic mice (Fig. 9.3a). Unlike with GEM models, complex breeding schemes are not necessary. A number of studies have utilized tissue recombination to validate putative oncogenes and tumor suppressors including Ras, Myc, Pten, Tak1, and Erg by manipulating gene expression in MPECs or PrP/SCs in vitro and studying the phenotype in vivo (see Table 9.1). Furthermore, specific stem cell populations can be purified using markers like Cd49f and Sca1 (described in detail elsewhere in this book) before being grafted renally. Also, tissue recombination can be performed using MPECs or PrP/SCs isolated from single or compound GEM mutants. Although most studies have focused on altering gene expression in epithelial cells, UGM or normal stroma can also be manipulated. Overexpression of FGF10 in UGM causes formation of carcinomas when recombined with normal MPECs or PrP/SCs in renal grafts (Lawson et al. 2010; Memarzadeh et al. 2007).

Although the tissue recombination model is used successfully by many researchers, technical expertise in microdissection and microsurgery is required for separation of UGE from UGM and implantation of grafts under the renal capsule. The procedure typically requires consecutive days of intensive preparation to isolate UGM, recombine with epithelial cells, and perform the grafting surgery. However, recent advances that have improved this process include optimization of culture conditions for expanding UGM (Goldstein et al. 2011) and establishment of UGM cell lines (Shaw et al. 2006). These techniques allow UGM to be grown in cell culture, passaged, and frozen before recombination with epithelial cells. Another limitation of the tissue recombination model is that genetic alterations are typically introduced into UGM or PrP/SCs prior to prostatic development under the renal capsule when in actuality genomic lesions form in the fully developed adult prostate. To better recapitulate tumor development, PrP/SCs with regulatable genetics can be introduced into the tissue recombination system to allow prostate structures to form in vivo before genomic alterations are induced (discussed in Sect. 9.7).

9.6 Utilization of Stem Cell Models to Validate Candidate Cancer Genes

A growing number of studies have used stem cell models to evaluate oncogenes and tumor suppressors. Table 9.1 contains a summary of genes that have been investigated using PSC models, the methods used, and conclusions made. In this section, we highlight two examples of how stem cell models have provided valuable insights into the roles of tumor suppressors and oncogenes in promotion of tumorigenesis.

TAK1, TGF- β activated kinase-1, encoded by the *MAP3K7* gene on chromosome 6q15 is a serine/threonine kinase that regulates numerous cellular processes

Table 9.1 Summary of stem cell models used to validate candidate oncogenes and tumor suppressors

Gene(s)	Method(s)	Outcome(s)	Reference
Rb	Tissue rescue of Rb ^{-/-} UGS, Tissue recombination	↓Rb→hyperplasia and carcinoma	Wang et al. (2000)
p57	Tissue rescue of p57 ^{-/-} UGS	↓p57→PIN and carcinoma	Jin et al. (2008)
TGFβ1	Overexpression in UGS, Tissue recombination	↑TGFβ1→basal cell hyperplasia, stromal abnormalities	Timme et al. (1996)
FGF10	Overexpression in UGM, Tissue recombination with FACS-enriched PrP/SCs	↑FGF10→carcinoma in Lin ⁻ Scal ⁺ Cd49 ^{hi} PrP/SC population; Lin ⁻ Scal ⁺ Cd49 ^{lo} cells do not generate ductal structures	Lawson et al. (2010)
Pten	MPECs isolated from wildtype and Pten null mice; FACS sorting for Scal	↓Pten→↑percentage of Scal ⁺ cells	Wang et al. (2006)
Pten	MPECs isolated from control and Pten null mice; FACS-enriched Lin ⁻ Scal ⁺ Cd49 ^{hi} PrP/SCs, Prostatespheres, Tissue recombination	↓Pten→adenocarcinoma in Lin ⁻ Scal ⁺ Cd49 ^{hi} PrP/SC grafts	Mulholland et al. (2009)
PTEN	Knockdown of PTEN in DU145 cells, Prostatespheres	↓PTEN→↑self-renewal ability	Dubrovskaya et al. (2009)
AKT	Overexpress Akt in PrP/SCs sorted for Scal, Tissue recombination	↑Akt→PIN in Scal ⁺ grafts, mostly normal structures in Scal ⁻ grafts	Xin et al. (2005)
TMPRSS2:ERG	MPECs isolated from wildtype and TMPRSS2:ERG transgenic mice, FACS enrichment for PrP/SCs, Prostatespheres	↑TMPRSS2:ERG→↑ self-renewal ability in Scal ⁺ Epcam ⁺ population	Casey et al. (2012)
ETV1	Overexpression in MPECs, Tissue recombination	↑ETV1→hyperplasia	Zong et al. (2009)
Tak1	Knockdown in PrP/SCs, Tissue recombination	↓TAK1→PIN and carcinoma	Wu et al. (2012)
Pim1	Overexpression in PrP/SCs, Tissue recombination	↑PIM1→high grade PIN	Chen and Cramer, unpublished
Myc	FACS-enriched CD133 ^{hi} immortalized primary tumor cells treated with antisense c-myc, Prostatespheres, intrathoracic injection in vivo	Antisense c-myc→↓colony-forming ability and growth, ↓ability of CD133 ^{hi} prostaspheres to form tumors in vivo	Goodyear et al. (2009)
Ras + Myc	Overexpression in UGS, Tissue recombination	↑Ras→dysplasia; ↑Myc→mild hyperplasia; ↑Ras+↑Myc→carcinoma	Thompson et al. (1989)

Ras + Myc + p53	Overexpression in p53 ^{+/+} or p53 ^{-/-} UGS, Tissue recombination	↑Ras+↑Myc+↑p53→carcinoma and metastasis	Thompson et al. (1995)
FGF10 + AKT	FGF10 overexpression in UGM, expression of activated AKT in MPECs, Tissue recombination	↑FGF10→carcinoma (well differentiated); ↑AKT→PIN; ↑FGF10+↑AKT→high-grade carcinoma (poorly differentiated)	Memarzadeh et al. (2007)
ERG + AKT	Overexpression of ERG and AKT in MPECs, Tissue recombination	↑ERG→hyperplasia, focal PIN; ↑ERG+↑AKT→carcinoma	Zong et al. (2009)
ERG + Pten	Overexpression of ERG and knockdown of Pten in MPECs, Tissue recombination	↑ERG→hyperplasia, focal PIN; ↑ERG+↓Pten→carcinoma	Zong et al. (2009)
ERG + AR	Overexpression of ERG and AR in MPECs, Tissue recombination	↑ERG→hyperplasia, focal PIN; ↑AR→↓number of prostatic tubules formed ↑ERG+↑AR→invasive carcinoma	Zong et al. (2009)
AKT + AR	Overactivation of Akt and/or AR in sorted basal or luminal MPEC populations, Tissue recombination	↑Akt+↑Erg→PIN in basal cell grafts; ↑AR→occasional PIN in basal cell grafts; ↑Akt+↑AR→high-grade carcinoma in basal cell grafts; luminal cell grafts do not form prostatic structures under any condition	Lawson et al. (2010)
AKT + ERG + AR	Sort primary human prostate epithelial cells into basal and luminal populations, Overexpress Akt and Erg or Akt and Erg and AR in sorted populations, Tissue recombination	↑Akt+↑Erg→PIN in basal cell grafts and no prostatic structure formation in luminal cell grafts; ↑Akt+↑Erg+AR→invasive carcinoma in basal cell grafts	Goldstein et al. (2010)
p53 + Pten	Wildtype and p53 ^{-/-} Pten ^{-/-} MPECs; Prostatespheres, Colony formation assay, Orthotopic transplant	p53 ^{-/-} Pten ^{-/-} MPECs have ↑self-renewal ability and form large, more irregular spheres, form tumors in vivo	Abou-Kheir et al. (2010)
p53 + Pten	Rosa26-Cre ^{ER} p53 ^{L/L} Pten ^{L/L} MPECs; Prostatespheres, Orthotopic transplant	Tamoxifen-induced co-deletion of p53 and Pten in prostaspheres leads to aggressive tumors, metastasis, and castration-resistance in vivo	Abou-Kheir et al. (2011)
Pten + KRAS	PrP/SCs isolated from PB-Cre ⁺ Pten ^{L/L} KRAS ^{G12D/W} mice, Prostatespheres	↑Lin ⁻ Seal ⁺ Cd49 ^{hi} PrP/SC population, ↑sphere-forming ability in PB-Cre ⁺ Pten ^{L/L} KRAS ^{G12D/W} cells relative to PB-Cre ⁺ Pten ^{L/L} cells	Mulholland et al. (2012)

(continued)

Table 9.1 (continued)

Gene(s)	Method(s)	Outcome(s)	Reference
Pten + Nkx3.1	Forced expression of Nkx3.1 in wildtype and Pten null MPECs; Tissue recombination	↓Pten→hyperplasia/PIN; ↓Pten and ↑Nkx3.1→prevents cancer initiation (normal ductal phenotype maintained)	Lei et al. (2006)
Bmi-1 + Pten	Knockdown of Bmi-1 in wildtype and Pten ^{+/Δ} MPECs, Prostataspheres, Tissue recombination	↓Bmi-1→↓sphere-forming ability, ↓self-renewal, ↓prostatic tubule formation in vivo; ↓Bmi-1 and delete Pten→↓tumor size relative to single-hit Pten null model	Lukaacs et al. (2010)
Bmi-1 + FGF10	Knockdown of Bmi-1 in MPECs and FGF10 overexpression in UGM, Tissue recombination	↓Bmi-1 and ↑FGF10→↓graft size, ↓tumorigenic phenotype relative to FGF10 overexpression alone	Lukaacs et al. (2010)

including proliferation, apoptosis, differentiation, and inflammatory responses. *MAP3K7* is hemizygotously deleted in 30–40% of primary prostate tumors and its loss is correlated with higher-grade cancers (Liu et al. 2007). To validate TAK1 as a prostate tumor suppressor, we suppressed Tak1 expression in mouse PrP/SCs and characterized these cells in vitro and in vivo. Tak1 suppression altered cell morphology and significantly increased proliferation, migration, and invasion of PrP/SCs. In tissue recombination experiments using control or Tak1 shRNA PrP/SCs mixed with rat UGM, the phenotype of Tak1-suppressed grafts was much different than control grafts. After 10 weeks of growth, grafts formed from control cells underwent complete lineage differentiation and generated benign prostatic structures, while Tak1-suppressed grafts formed heterogeneous structures with benign, PIN, and invasive carcinoma phenotypes represented. Furthermore, loss of Tak1 promoted cellular proliferation in vivo as determined by increased expression of Ki67 in Tak1-suppressed grafts relative to control grafts (Wu et al. 2012). Utilization of the PrP/SC and tissue recombination models allowed us to identify a novel and critical prostate tumor suppressor, TAK1, which may serve as a diagnostic biomarker or therapeutic target for treatment of prostate cancer.

PIM1, a serine/threonine kinase involved in cell cycle regulation and inhibition of apoptosis, is overexpressed in high-grade PIN and prostate cancer (Cibull et al. 2006; Dhanasekaran et al. 2001). In unpublished studies in collaboration with Michael Lilly, we evaluated PIM1 as an oncogene in tumor development. We created stable clonal mouse PrP/SC lines that overexpressed Pim1 and assessed the phenotypic consequences. Overexpression of Pim1 did not affect monolayer growth, but did significantly increase 3D growth in collagen. Control or Pim1-overexpressing PrP/SCs were then recombined with rat UGM, grafted under the renal capsules of immunocompromised mice, and removed after 12 weeks. While grafts from control PrP/SC tissue recombinants formed normal ductal structures, Pim1-PrP/SC recombinants displayed a phenotype consistent with high-grade PIN. Pim1-PrP/SC grafts retained intact p63+ basal and AR+ luminal layers but formed abnormal structures characterized by crowded, irregularly spaced micropapillary epithelial cells (Chen, Lilly and Cramer, unpublished). Therefore, Pim1 kinase plays a role in formation of PIN but is insufficient to induce prostate tumorigenesis. Since Pim1-PrP/SCs are in an “initiated” state, further genetic insult may lead to tumor development in this model. In a recent study by Abdulkadir and colleagues, Pim1 was found to cooperate with c-MYC to form highly vascularized carcinomas in tissue recombinants grafted under the renal capsule for 6 weeks (Wang et al. 2010). Collectively, these data demonstrate that Pim1 has an oncogenic role in prostate cancer development.

9.7 Discussion and Future Considerations

The complex mutational landscape of the prostate cancer genome makes identification of critical regulators of prostate tumorigenesis very challenging. Because numerous genomic alterations exist within a primary prostate tumor, the major

goals of prostate cancer research today are to (1) distinguish driver oncogenes/tumor suppressors genes from passenger genes, (2) understand how multiple oncogenes and tumor suppressors cooperate to initiate and progress tumor development, and (3) identify new prognostic indicators and therapeutic targets to improve survival for patients with aggressive disease. The stem cell models described here have been used effectively to identify critical prostate oncogenes and tumor suppressors including PTEN, RAS, P53, and PIM1 as well as others listed in Table 9.1. Some models have begun to explore cooperativity among multiple cancer genes and to test therapeutics, but these types of studies are still in the early stages. Although development of a “perfect” stem cell model may never be achievable, current models can be improved upon to more accurately mimic the genetic events that contribute to tumor initiation, progression, and metastasis. Considerations for future models should include:

1. *Promoter specificity*

Identification of a prostate stem cell-specific promoter would greatly enhance current models. In other tissues, transgenic mice have been developed using tissue-specific stem cell genes to drive target expression. For example, Prx1 and Dermo1 promoters have been used to regulate gene expression in mesenchymal stem cells which are precursors for bone development (Eleftheriou and Yang 2011). To date, the only epithelial prostate-specific promoters utilized in GEM models have been from probasin, PSA, and Nkx3.1, genes known to be highly expressed in more differentiated cells of the prostate (i.e., luminal cells). The FSP1 promoter has been used to drive Cre expression in prostatic fibroblasts (Bhowmick et al. 2004). However, recently, Tang and colleagues used the PSA promoter in a unique way to identify a castration-resistant stem/progenitor population. In this study, LNCaP cells were infected with a lentiviral PSAP-GFP construct in which the PSA promoter drives expression of eGFP. FACS was then used to isolate the brightest 10% of GFP-expressing cells (GFP⁺) and the lowest 2–6% of cells expressing GFP (GFP^{-lo}). GFP level correlated with PSA expression in these cell fractions (i.e., GFP⁺=PSA⁺, GFP^{-lo}=PSA^{-lo}). Gene expression profiling revealed that PSA^{-lo} LNCaP cells overexpress numerous genes involved in antistress signaling and DNA damage repair but have lower expression of antiapoptotic, cell cycle, and mitosis genes. This profile is suggestive of quiescence and stress resistance—characteristics displayed by stem cells. Indeed, PSA^{-lo} LNCaP cells possess high colony and prostasphere-forming abilities, can undergo asymmetric cell division, are resistant to androgen deprivation, and express stem cell-associated genes. Furthermore, PSA^{-lo} LAPC9 xenografts maintain tumorigenicity upon serial transplantation and are resistant to androgen deprivation therapy in vivo (Qin et al. 2012). Future studies could utilize this model to alter gene expression in PSA⁺ and PSA^{-lo} subpopulations in different cell lines and assess tumorigenicity in vivo. Cell-specific models can also be useful for modeling the roles of genomic changes in prostate tumorigenesis. The CK14 and CK8 promoters have been used to drive loss of Pten in basal and luminal cells, respectively (Choi et al. 2012). However, a limitation of this model is that Pten is deleted in all cells expressing CK14 or CK8 not just prostate cells. This model could

be adapted to study gene alterations in a prostate and cell-specific manner by isolation of CK14-Pten and CK8-Pten PrP/SCs and generation of tissue recombinants from these different cell types.

2. *Regulated compound models*

From the numerous models described in this chapter, it is clear that one gene alone cannot drive tumor initiation, progression, and metastasis. Likely, prostate tumorigenesis occurs when multiple alterations occur in critical signaling pathways and override DNA damage and cell cycle checkpoint responses. Future compound models should examine three or more alterations in combination since current two-hit models do not adequately recapitulate metastatic prostate cancer. Since the RB, AKT/PI3K, and RAS/MAPK pathways are most frequently misregulated in prostate tumorigenesis (Taylor et al. 2010), a triple model of Rb loss, Pten loss, and Ras overexpression could result in a more aggressive metastatic phenotype than that observed in the compound Pten^{-/-}/activated Ras model (Mulholland et al. 2012). Combined p53 loss, Ras overexpression, and Myc overexpression may also be a potentially aggressive model since early experiments using UGS demonstrated these three hits together resulted in bone metastasis (Thompson et al. 1995). Another strategy that should be utilized when developing future models is the use of regulated genetics. A weakness of most current models is that genetic alterations take effect before, during, or after prostatic development in GEM and tissue recombinants at specific time points that cannot be altered. If gene activation or deletion could be temporally regulated, then these alterations could be introduced into fully mature adult mice with developed prostates or fully formed prostatic glandular structures of tissue recombinants. Furthermore, a critical question in prostate cancer research continues to be do genetic alterations arise in a particular order during initiation and progression of tumorigenesis? Different systems of regulation could be used in combination to evaluate multiple oncogenes and tumor suppressors in a controlled manner. Current systems that use regulated genetics to control gene expression include the ER-Cre, Tet-ON/OFF, Ecdysone, and FLP-FRT systems (Feil et al. 1996; Galimi et al. 2005; Gossen and Bujard 1992; Sadowski 1995).

3. *Microenvironment*

The tumor microenvironment can significantly impact tumor initiation, progression, and metastasis. Different types of inflammatory and immune cells, for example, can positively or negatively affect tumor growth and invasion through cross talk with tumor cells. Historically, rat UGM is used in tissue recombination models so grafts must be implanted into immunocompromised hosts. In future studies, the use of syngeneic models (e.g., C57BL/6 UGM+C57BL/6 PrP/SCs) in animals with intact immune systems (i.e., C57BL/6) will better recapitulate tumor development in human patients. Additionally, epithelial-stromal interactions play a critical role in both normal prostatic development and tumorigenesis (Cunha et al. 2003). For example, overexpression of FGF10 in the mesenchyme can initiate prostate carcinoma (Lawson et al. 2010; Memarzadeh et al. 2007). As other stromal regulators of tumorigenesis are identified, they can be evaluated using a similar

approach. Eventually, compound models can be developed in which different combinations of genetic alterations are introduced into the stromal and epithelial compartments of the prostate.

4. *Metastasis*

Advanced prostate cancer primarily metastasizes to the bone, yet current models have failed to reliably generate bone lesions. In a recent compound model of Pten loss and Kras activation, cells with the PB-Cre⁺Pten^{L/W}Kras^{G12D/W} and PB-Cre⁺Pten^{L/L}Kras^{G12D/W} genotypes were identified in bone marrow flushes from GEM mice, but due to early lethality, bone metastases were not observed (Mulholland et al. 2012). As we identify more genes involved in prostate cancer progression, castration resistance, and metastasis, stem cell models can be used to assess the ability of these genes to impact development of bone metastases. The utilization of compound genomic models with ≥ 3 alterations will likely produce more aggressive tumors with a greater potential for metastasis.

5. *Human primary cells*

Most current stem cell models utilize mouse cells to evaluate candidate prostate cancer genes. However, two major differences exist between the mouse and human prostates: (1) the anatomies are different and (2) mice do not spontaneously develop prostate cancer without genetic manipulation. Therefore, stem cell models that use normal and tumorigenic human primary prostate cells may be better tools for validating putative oncogenes and tumor suppressors. Currently, epithelial cells can be isolated from primary tumors, stem cell populations can be enriched using FACS, genetics can be manipulated, and cells can be combined with rat UGM in tissue recombinants grafted into immunocompromised mice (Goldstein et al. 2011). This approach has been used successfully to demonstrate cooperativity of oncogenic AKT, ERG, and AR (Goldstein et al. 2010). However, this method has limitations because primary samples are not cultured and expanded so experiments cannot be repeated to verify results. As strategies for human PrP/SC culture improve, primary cell models will become more important for validation of candidate cancer genes.

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