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Steroid Hormones, Steroid Receptors, and Breast Cancer Stem Cells

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Abstract

The ovarian hormones progesterone and estrogen play important roles in breast cancer etiology, proliferation, and treatment. Androgens may also contribute to breast cancer risk and progression. In recent years, significant advances have been made in defining the roles of these steroid hormones in stem cell homeostasis in the breast. Stem cells are potential origins of breast cancer and may dictate tumor phenotype. At least a portion of breast cancers are proposed to be driven by cancer stem cells (CSCs), cells that mimic the self-renewing and repopulating properties of normal stem cells, and can confer drug resistance. Progesterone has been identified as the critical hormone regulating normal murine mammary stem cell (MaSC) populations and normal human breast stem cells. Synthetic progestins increase human breast cancer risk; one theory speculates that this occurs through increased stem cells. Progesterone treatment also increases breast CSCs in established breast cancer cell lines. This is mediated in part through progesterone regulation of transcription factors, signal transduction pathways, and microRNAs. There is also emerging evidence that estrogens and androgens can regulate breast CSC numbers. The evolving concept that a breast CSC phenotype is dynamic and can be influenced by cell signaling and external cues emphasizes that steroid hormones could be crucial players in controlling CSC number and function. Here we review recent studies on steroid hormone regulation of breast CSCs, and discuss mechanisms by which this occurs.

Keywords

Progesterone; Progesterone receptor; Cancer stem cells; Hormone replacement therapy; Breast cancer; Steroid hormone

Ovarian Steroid Hormones and Breast Cancer

Removal of the ovaries was recognized as an effective treatment for breast cancer in the late 19th century [1, 2]. It is now well established that three quarters of breast cancers are hormone dependent, requiring local or systemic estrogens for growth maintenance. As such, endocrine therapies targeting the estrogen signaling axis have remained the cornerstone of breast cancer treatment since the first use of tamoxifen in the 1970s [3]. In addition to

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perpetuating tumor growth, prolonged exposure to ovarian hormones is an independent risk factor for breast cancer; contributing factors include extended menstrual cycles due to early menarche and/or late menopause, a transient risk tied to pregnancy, the use of oral contraception and/or hormone replacement therapies, and excess hormone production in post-menopausal obesity [4–9]. Although the precise mechanisms of how female hormones increase breast cancer risk remain unknown, most theories have centered on increased proliferation imparted to breast epithelial cells. However, the repopularized concept that normal tissue stem cells may be the origin of many solid tumor malignancies has led to speculation that hormones target a specific population of long-lived cells. The seminal discovery that ovarian hormones, particularly progesterone, expand stem cells in the normal murine mammary gland and human breast $[10-12]$ supports this notion and has led to new implications for hormone involvement in tumorigenesis. Emerging evidence reinforces that hormones influence a stem cell phenotype in established tumors. In this review, we discuss steroid hormone-mediated regulation of breast tumor stem cells, with a particular emphasis on progesterone and progestins.

Breast Cancer Stem Cells

The *cancer stem cell (CSC)* theory posits that tumors contain a subpopulation of cells that share properties of normal stem cells including self-renewal, tumor initiation, indefinite replicative potential, and the ability to generate differentiated progeny [13]. Importantly, CSCs compared to the bulk tumor cells are proposed to have heightened resistance to conventional chemotherapies due to relative quiescence and elevated expression of multidrug resistance pumps [14, 15]. Breast CSCs in particular show selective resistance to radio-, chemo- and endocrine therapies [16–19]. The notion of a rare static breast CSC population is challenged by developing evidence that the breast CSC phenotype is not necessarily pre-existing, but can be acquired through cytokine signaling and environmental cues [20–22]. This has important implications for hormone receptor positive breast cancers, where endogenous or exogenous hormone exposure could influence the number and activity of CSCs. In fact, our evolving concept of the CSC theory suggests that a combination of CSCs and environmental and clonal pressures collaborate to shape individual tumor phenotype [23, 24].

Several biomarkers have been identified for breast CSCs, albeit with no clear consensus. The seminal paper by Al-Hajj et al. defined breast CSCs as having the surface marker signature CD44+CD24−/lowEpCAM+ (termed CD44+CD24− hereafter) [25]. Primary breast tumor cells with this signature were able to initiate tumors from small numbers of cells in immune deficient mice [25]. CD44+CD24− cells are more abundant in triple negative breast cancers (TNBC) that lack estrogen receptors (ER, alpha) and progesterone receptors (PR), and are less prevalent (0–5 %) in luminal subtype ER+PR+ breast cancers [19, 26, 27]. Furthermore, within a tumor, CD44+ CD24− cells express low ER and PR mRNA compared to CD44−CD24+ cells [28]. Activity of the enzyme aldehyde dehydrogenase (ALDH) was subsequently defined as a marker of normal breast stem cells and breast tumor initiating cells [29]. The ALDH+ and CD44+CD24− populations are not identical in tumors, but share an overlapping population that has the most potent tumor initiating activity [29]. ALDH+ cells have also been reported as ER negative [29, 30]. However, a recent report finds ALDH

+ cells exist in both mesenchymal and luminal-like states, although ER expression was not measured [31]. Our group originally reported that luminal ER+PR+ breast cancers contain a subpopulation of cells that express the epithelial intermediate filament protein cytokeratin 5 (CK5), a marker of normal human breast stem and luminal progenitor cells [32–36]. CK5+ cells, compared to the bulk CK5− tumor cells, are endocrine and chemotherapy resistant, and have enhanced mammosphere-forming and tumor-initiating potential [17, 37, 38]. CK5+ cells generally lack expression of ER and PR [37] and their population partially overlaps with CD44+ cells, though non-identical populations exist [37, 38]. Other biomarkers for breast CSCs have been mentioned in the literature less frequently; we focus our discussions here on these three well-described markers.

Progestins, Progesterone Receptors, and Breast Cancer Stem Cells

PR has been measured in breast cancer since the 1970s with the advent of radio ligand binding assays [39]. The presence of PR portends better prognosis and responsiveness to endocrine therapy, and has generally been thought to be an indicator of functional ER [40]. However, activated PR is detrimental for late stage breast cancers, providing some rationale for dual targeting of ER and PR in advanced tumors [41]. PR has two naturally occurring isoforms transcribed from the same gene, a truncated PRA and a longer PRB form [42]. Both isoforms are generally co-expressed in PR+ cells. However, a higher PRA:PRB ratio signifies less favorable outcome for breast cancer [43, 44]. PR ligands include the ovarian hormone progesterone as well as synthetic progestins such as medroxyprogesterone acetate (MPA).

The unexpected findings of the Women's Health Initiative and the Million Women Study that combination estrogen/progestin but not estrogen alone increased the risk of invasive breast cancer changed our perception of progestins as predominantly onco-protective hormones [45, 46]. Progestin-mediated proliferative stimuli on the post-menopausal normal breast were originally suspected as causing increased breast cancer risk [47]. However, an alternative theory supposes that progestins expand a transformation sensitive pool of normal stem cells, or activate occult malignant stem cells, accelerating the appearance of ER+PR+ tumors [48, 49]. This aligns with early studies by Charles Huggins et al. establishing that administration of progesterone (but not estrogen alone or estrogen plus progesterone) to female Sprague Dawley intact rats fed a single dose of the mutagen 17, 12 dimethylbenz(a)anthracene (DMBA) greatly accelerated time to mammary tumor formation [50]. It was later shown that PR knockout (PRKO) animals had significantly less DMBAinduced mammary tumors than wild-type animals, suggesting PR are crucial for carcinogeninduced mammary tumor formation in rodents [51]. Thus, it is established that progestins and PR play important roles in rodent mammary tumorigenesis, which could potentially occur through modulation of stem cells. The role of progestins in human breast tumorigenesis is less well established. HRT trials suggest that progestins are tumorigenic in post-menopausal women, although there is some speculation that progestins may be accelerating the growth of existing micro-malignancies [49, 52]. In this review, we discuss the role of progestins in established breast cancers.

Progesterone and synthetic progestins increase populations of phenotypical breast CSCs in ER+PR+ breast cancer cell lines. This was first demonstrated in PR-rich T47D xenograft tumors grown in mice supplemented with estrogen alone or estrogen plus the synthetic progestin MPA; the progestin treated tumors had increased numbers of CK5+ tumor cells [37]. Progesterone induction of CK5+ cells occurs within 24 h in multiple luminal breast cancer cell lines including MCF7, ZR75-1, and BT474, but is most potent in T47D cells; these cells have amplification of the PR gene, and express PR in a non-estrogen-dependent manner [17, 53, 54]. In T47D cells, the post-treatment CK5+ population can be up to 20 % of the total cells. Progesterone treatment also increased the total CD44+ cell population by 8–12 fold, measured by flow cytometry, in luminal breast cancer cell lines [53, 54]. MCF7, BT474, and ZR75 cells require pre-treatment with estrogens to induce PR protein levels prior to assessing progesterone action. In these cell lines, estrogen alone did not increase the CD44+ population, whereas estrogen plus progesterone increased the number of CD44+ cells [53, 54]. These experiments measured only the total CD44+ population; luminal breast cancer cell lines are near ubiquitous for CD24+ cells. A recent paper by Hilton et al. [55] demonstrated that treatment with progesterone or the synthetic progestins ORG2058 or MPA increases the CD44+CD24− population in T47D and HCC1428 breast cancer cells. One recent study reported that progesterone treatment increased the ALDH+ population from 1 to 3.5 % in T47D cells [56]. Thus, there is sufficient evidence that in breast cancer cell lines and cell line-derived xenograft models, progesterone or its synthetic analogs can increase breast CSCs as defined by three common markers. There are some exceptions; BCK4 cells, an ER+PR+ breast cancer cell line isolated from a pleural effusion [57], do not increase CK5 protein levels in response to progesterone (with or without estrogen).¹ Also, in our collection of breast cancer patient derived xenografts (PDX) [58], we find tumor lines that are both sensitive and resistant to progestin expansion of $CK5+$ cells². Thus, the context in which progestins and PR increase breast CSCs warrants further investigation.

Progesterone-expanded breast cancer cells show functional stem cell properties. Our laboratory has engineered T47D cells with stable integration of the human CK5 promoter linked to GFP, allowing FACS isolation of enriched CK5+ and CK5− fractions [38, 59]. We demonstrated that isolated CK5+ compared to CK5− cells following progesterone treatment have increased mammosphere forming capacity [38]. Progesterone-expanded CK5+ vs. CK5− T47D cells also show increased tumor initiation capacity in vivo with limiting dilution analysis.³ CK5+ cells also produce outgrowths of $ER+PR+$ cells [37], suggesting they are capable of recapitulating tumor heterogeneity. Taken together, these data support that progesterone increases functional CSC activity.

There is some speculation over whether synthetic progestins impart a higher risk for breast cancer than the natural hormone progesterone during hormone replacement regimens [60]. Studies in breast cancer cells identify that both progesterone and progestins increase CSCs similarly. In PR-rich T47D breast cancer cells, both progesterone and MPA regulate a similar program of genes [61]. Likewise, both hormones expand CK5+ cells in T47D

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xenograft breast tumors [36], and several progestins increase the CD44+CD24− population in T47D breast cancer cells [55]. As progestins, particularly MPA, can target both PR and AR, studies in new patient-derived tumor models with various PR and AR expression may shed light on their contributions to breast CSC expansion.

Estrogens, Estrogen Receptors, and Breast Cancer Stem Cells

Estrogen receptor alpha (ER) remains the single most important prognostic and predictive factor determining breast cancer treatment and outcomes. Like PR, ER measurement also commenced in the early 1970s via radio ligand binding assay [62]. ER is expressed in \sim 75 % of breast tumors and indicates candidacy for treatment with therapies that target ER through selective ER modulation or degradation (SERMs and SERDs, respectively) or reduction in estrogen production (aromatase inhibitors, AI). These endocrine therapies remain the cornerstone of breast cancer treatment for most patients [63]. Estrogens are the primary mitogens in hormone-dependent breast cancers, with compensatory proliferative pathways in refractory endocrine resistant tumors [64]. While estrogens are pro-proliferative in breast cancer, ER is also positively associated with luminal differentiation markers such as GATA3, CK18, and MUC1 [65]. This is in contrast to the normal human breast where ER+ luminal cells are quiescent while ER− luminal cells are actively proliferating [66].

Estrogens are proposed to play a permissive role in the expansion of normal murine mammary stem cells by stimulating expression of PR [10, 11]. In breast cancers, several studies have reported that estrogens alone do not increase CD44+ or CK5+ CSCs [38, 53, 54, 67]. There are, however, a few studies that have linked estrogens and ER to increased CD44+CD24− breast cancer cells. One study reported that estrogen treatment of MCF7, T47D, and HCC1428 breast cancer cells increased the CD44+CD24− population up to eight-fold [68]. This was hypothesized to occur through a paracrine feedback mechanism involving estrogen induction and secretion of fibroblast growth factor 9 (FGF9), increased expression of the transcription factor Tbx3 in non-CSCs, and further stimulation of Wnts and FGFs to expand the CSC pool. In ER− breast cancers, Tbx3 expression stabilizes paracrine FGF and Wnt signaling to regulate CSC subpopulations [68].

Several studies have reported that estrogens can influence breast CSCs through both nongenomic signaling and variant ERs. G protein-coupled receptor 30 (GPR30), a seventransmembrane domain receptor, mediates non-genomic estrogen signaling and is expressed in both ER+ and ER− breast cancer cells and tumors [69, 70]. GPR30 regulates the Hippo signaling pathway through activation of tafazzin (TAZ), a phospholipid transacylase [69]. Using an isogenic derivative of the human immortalized epithelial MCF10A cell line (Rastransformed MCF-10A-T1k cells), CD44+CD24− cells expressed higher levels of TAZ; knockdown of TAZ in these cells significantly reduced the CD44+CD24− population and mammosphere formation capacity [71]. TAZ is also overexpressed in the CSC fraction of primary breast cancers and has been linked to CSC-mediated metastasis [72]. Knockdown of TAZ decreased chemoresistance and the tumorigenic capacity of primary breast CSCs [72].

The ER variant ER-α36 has been implicated in regulating breast CSCs. ER-α36 lacks the ligand-dependent and –independent transactivation domains (ATF-1 and -2), while retaining

the DNA binding, dimerization, and ligand-binding domains [73]. In MCF7 and T47D cells, ER-α36 promoted tamoxifen resistance by increasing the self-renewal capacity of CD44+CD24− cells [74, 75]. Knockdown of ER-α36 in T47D and MCF7 cell lines decreased the overall CD44+CD24− population and blocked tamoxifen- or fulvestrantmediated increases in CD44+CD24− cells. ER-α36 knockdown also decreased mammosphere formation of the same cells [74, 75]. Knockdown of ER-α36 in the HER2+ breast cancer cell line SKBR3 reduced HER2 expression and the ALDH+ CSC population [76]; HER2 has been implicated as a driver of ALDH+ breast CSCs [77]. These data support a role for variant ER-α36 in regulating breast CSCs in both ER+ and HER2+ER− tumors.

Several reports have cited that SERMS, SERDs, and AIs enrich for cells with a CD44+CD24− or CK5+ phenotype. Tamoxifen, fulvestrant, or estrogen depletion increased the percent of CK5+ cells in T47D cell cultures [17]. In a small cohort of patients undergoing neoadjuvant therapy with the AI exemestane plus tamoxifen, CK5 expression increased in post-compared to pre-therapy tumor biopsies from the same patients [17]. Tumors treated with the AI letrozole were enriched in CD44+CD24− mammosphere forming cells post-therapy [18]. Tamoxifen-resistant MCF7 cells have increased CD44+CD24− and ALDH+ populations compared to the parental line and high levels of Sox2, one of four transcription factors involved in induced pluripotent stem cell production. The development of Tam resistance in these cells is driven by Sox2 activation of Wnt signaling, possibly through expansion of CSC populations [78]. Knockdown of Sox2 or inhibition of Wnt signaling reduced CSC populations, inhibited mammosphere formation, and restored tamoxifen sensitivity [78]. These studies suggest that antagonizing estrogen action in breast cancer cells and tumors increases CSCs. This could occur through selection and expansion of the mostly ER− CSC pool, or upregulation of self-renewal signaling pathways such as Wnt.

Androgens, Androgen Receptors, and Breast CSCs

AR is present in 70–80 % of breast cancers [79–81], making it more commonly expressed than either ER or PR. Overall AR, like ER and PR, is associated with more favorable prognosis and a well differentiated phenotype in breast cancer, although this may be subtype specific. AR is co-expressed with ER in 80–90 % of luminal breast cancers where it generally correlates with better prognosis [79, 82–85]. AR has also been detected as a potential co-regulator for ER, both in previous work using two-hybrid systems [86] and more recently using ChIP and proximity ligation assays (PLA) [87]. AR is also found in ER − breast cancer subtypes including HER2+ER− tumors and a subset of TNBC termed luminal AR [81, 88]. Recent data implicate AR as a compensatory mechanism for breast cancer growth in ER− disease; these findings have led to the development of AR-targeted therapeutic approaches for breast cancer [89–91]. Clinical trials are currently centered on the anti-androgen enzalutamide for treatment of AR+ TNBC or endocrine-refractory ER+ tumors [89, 91].

The contribution of androgens and AR in regulating breast CSCs remains only marginally explored. A recent report cited that dihydrotestosterone (DHT) treatment led to a small increase (1–3 %) in the CK5+ population in MCF7 but not T47D cells [67]; the latter may

have nonfunctional AR [92]. This same study demonstrated that glucocorticoids and mineralocorticoids can also expand the CK5+ subpopulation in luminal breast cancer cell lines [67]. This intuitively makes sense as PR, GR, AR, and the mineralocorticoid receptor (MR) share similar DNA binding consensus sequences. In AR+ TNBC cell lines, AR is important in maintaining the CSC population as knockdown of AR and treatment with the antiandrogen enzalutamide each reduce the ALDH+ population and mammosphere formation [93]. It is therefore also likely that AR can regulate breast CSCs in a context-dependent manner.

Many synthetic progestins have partial affinity for AR and can mimic androgen activity in breast cancer cells, as well as cause androgenic side effects in women taking these drugs [94, 95]. Therefore it is possible that progestin-mediated increases in breast CSCs could occur partially through AR. This could be particularly important in breast neoplasms that are AR+PR− or have a higher AR to PR ratio (AR>PR). Furthermore, in HRT-treated women, synthetic progestins had stronger association with increased breast cancer risk than progesterone [96, 97], implicating dual stimulation of AR and PR could be involved. Under some circumstances, AR blocks ER action in breast cancer cells by binding at ER target genes, and acts as an antiestrogen to inhibit growth [98]. This underscores the complexities of AR action in breast cancer, which are likely to be context-dependent [99]. As crosstalk and cooperative interactions between ER, PR, and AR signaling are unraveled, it may become clear that the balance of the three receptors contributes to the regulation of breast CSC_s.

Downstream Signaling Pathways and Transcription Factors that Facilitate the Progesterone-Mediated Increase in Cancer Stem Cells

In breast cancer cells, progesterone treatment leads to downstream increases in multiple transcription factors, growth factors, and other proteins that could contribute to an increase in CSCs (illustrated in Fig. 1). Progesterone potently upregulates genes involved in normal mammary development such as prolactin receptor (PRLR) and Signal Transducer and Activator of Transcription 5A (Stat5a). Progesterone and MPA also upregulate or activate signaling pathways involved in CSC self-renewal in T47D breast cancer cells such as members of the Notch signaling pathway (Notch2 and Jagged 1) [61, 100]. Notch signaling is also elevated in CK5+ compared to CK5− breast cancer cells [101]. Progesterone also activates mitogenic Wnt signaling in human breast cancer cell lines through Wnt1, which leads to epidermal growth factor receptor (EGFR)-mediated downstream activation of Erk1/2 mitogen-activated protein kinase (MAPK) activity [102]. EGFR is upregulated and activated by progesterone in breast cancer [103]. While EGFR has not been directly linked to breast CSCs, it is co-expressed with CK5 in both luminal and basal-like breast cancers [101, 104]. HER2 is a reported driver of ALDH+ CSCs in non-HER2 amplified tumors [77, 105], and although the HER2 gene has not been reported as directly regulated by progestins, activated PRs increase HER2 signaling during tumor progression [106]. These data implicate that several progesterone-activated signaling pathways contribute to breast CSC expansion; precise mechanisms of action require further investigation.

Several other transcription factors are reported to positively or negatively influence progesterone/PR− induced CK5 expression. Progesterone-mediated expression of CK5 is preceded by upregulation of BCL6, an oncogene and transcriptional repressor [107]. Prolactin inhibits progesterone-mediated upregulation of CK5 through Stat5a-dependent repression of BCL6 transcription, indicating negative crosstalk between PRLR and PR [107, 108]. This suggests that loss of BCL6 protein may lead to increases in other factors that block PR transcription of the CK5 gene. Krüppel-like factor 5 (KLF5) is another transcription factor upregulated by progesterone in breast cancer cells [61, 100]; knockdown of KLF5 impaired progesterone-mediated induction of CK5, whereas overexpression of KLF5 in the absence of progesterone was able to increase CK5 expression [109]. Progestins also downregulate the transcription factor (and Notch target gene) GATA3, which is associated with maintaining the luminal epithelial phenotype [110]. Using a high content screen, we found that several retinoic acid (RA) compounds were potent inhibitors of progesterone induction of CK5 in T47D breast cancer cells [59]. RA is a strong prodifferentiation hormone in multiple cell types and, contrary to progesterone, can prevent carcinogen-induced mammary tumor formation in rats [111]. Interestingly, RA downregulates PR mRNA and protein levels, and inhibits progestin-stimulated transcription of a PR-regulated reporter construct [112, 113], suggesting negative crosstalk between retinoic acid receptor (RAR) and PR signaling in regulating a breast CSC phenotype. Overall, these studies have identified that several progesterone-regulated transcription factors cooperate in regulating breast CSC populations, while other transcription factors may counterbalance the action of progesterone/PR.

Steroid Hormone-Regulated microRNAs and Breast CSCs

MicroRNAs (miRNAs) are small regulatory RNA molecules that regulate expression of specific target genes by base-pairing to their mRNAs and interfering with translation and/or inducing degradation. Progestins, estrogens, and androgens all regulate miRNAs [114–117], several of which have been linked to CSC formation in breast cancer cells (Fig. 1). The miR-29 and miR-200 families have specifically been studied for their roles in progesteroneinduced breast CSC formation. All three miR-29 family members (miR-29abc) are rapidly (within 6 h) downregulated by progestin treatment in breast cancer cells [53]. This downregulation coincides with an increase in protein levels of the transcription factor KLF4, which was found to be a specific target of miR-29a [53]. Inhibition of miR-29a or miR-29b alone was sufficient to increase the CD44+ breast cancer cell population [53, 118] and tumor-initiating ability of breast cancer cells [53]. miR-29a inhibition also potentiated the progestin-mediated increases in both the CD44+ and CK5+ breast cancer cell populations [53]. Progesterone also downregulates GATA3 in breast cancer cells [110], which has been shown to increase miR-29b expression to promote a differentiated phenotype and suppress metastasis [118]; the progestin-induced down-regulation of miR-29b could therefore increase the breast CSC population partially through lowering GATA3.

Progesterone also rapidly downregulates miR-141, a member of the miR-200 family of tumor suppressors [54]. Inhibition of miR-141 also increased the number of CD44+ breast cancer cells, and potentiated progesterone-dependent increases in the CD44+ and CK5+ populations. A combination of miR-141 inhibition plus progesterone treatment increased the

tumor initiating capacity of breast cancer cells [54]. MiR-141 was found to directly target both PR and Stat5a mRNA. Knockdown or inhibition of Stat5a using siRNA or the small molecule Pimozide, respectively, reduced the ability of progesterone to increase CK5+ cells [54]. Interestingly, miR-141 as well as other miR-200 family members are underexpressed in CD44+CD24− breast cancer cells [119], suggesting their suppression helps maintain a more stem-like phenotype.

ER-regulated miRNAs in breast cancer cells have been reported by multiple laboratories [114]. While there are no specific studies on ER miRNAs and breast CSCs, ER upregulates several miRNAs involved in maintenance of differentiation including the let-7 miRNA family, proposed to repress self-renewal and promote differentiation in normal and cancer cells [120]. Interestingly, ER upregulates the miR-29 family; this is opposite to the effects of progesterone. One study showed that ER downregulates miR-221/222 [121], a miRNA that represses ER expression [122], and is found in higher levels in CD44+CD24− breast cancer cells [119]. The role of AR-regulated miRNAs in breast CSCs remains unexplored. A few studies have assessed dihydrotestosterone (DHT)-regulated miRNAs in MCF7 and MDA-MB-453 breast cancer cell lines [116, 123, 124]. The majority of miRNAs were downregulated, similar to that described for progestins [124]. AR also downregulates the pro-differentiation miRNA let-7a; overexpression of let-7a inhibited the growth of TNBC cells [123]. Collectively, these studies suggest that ER upregulates miRNAs that maintain a more differentiated phenotype while PR, and perhaps AR, suppress miRNAs that support breast cancer cell differentiation. Further investigation is required to address how hormone regulated miRNAs, and other non-coding RNAs, influence a breast CSC phenotype.

Intrinsic vs Extrinsic Signaling in Progesterone-Mediated Expansion of Breast CSCs

The mechanism of progestin-mediated increases of breast CSCs likely involves both intrinsic and extrinsic signaling. Using a GFP reporter driven by the human CK5 promoter and time-lapse microscopy, we showed that previously CK5− cells become CK5+ upon progesterone treatment [125]. This argues against expansion of pre-existing CK5+ cells through cell division and suggests that progesterone directly stimulates reprogramming from a CK5− to CK5+ state. Interestingly, these CK5+ cells lose expression of ER and PR [38]. To truly test if this occurs in a cell-intrinsic manner will require single cell experimentation. Progestins regulate multiple secreted factors that could act on the producing cell or on neighboring cells to stimulate CK5 expression. Although progestin treatment increases the fraction of cells with breast CSC markers several fold, this still only comprises 5–20 % of the total cell population. Therefore, only specific cells are primed for progesterone reprogramming, implying surrounding cells could contribute via extrinsic signaling but not change phenotype themselves. Altered transcriptomes, pioneer and cofactor expression, and DNA epigenetics in individual cells may all contribute to susceptibility to dedifferentiation. This would be even more pronounced in solid tumors where genetic diversity plays large role in tumor progression. Our knowledge of which cells become CSCs is limited.

Paracrine signaling plays a critical role in progesterone-driven expansion of mammary stem cells (MaSCs) in murine mammary glands [10, 11]. This is mediated through several

secreted factors including receptor activator of nuclear factor kappa-B ligand (RANKL), a potent progesterone regulated gene during mammary development and during pregnancy at peak progesterone levels [10]. Progesterone simultaneously increases RANKL in the luminal cell compartment and RANK receptor in the myoepithelial and mammary stem cell compartments [10, 11]. RANKL is also a key paracrine mediator in progestin-dependent mammary tumorigenesis [126, 127]. Along with RANKL, Wnt4 is upregulated by progesterone in the luminal cell compartment [10]; more recently, Wnt4 was identified as a downstream control factor of progesterone-mediated MaSC function [128]. Recent reports have also identified a role for progesterone-mediated CXCR4 paracrine signaling in normal mammary stem and progenitor cells. In normal mouse mammary glands, inhibition of CXCR4 led to a decrease of progesterone-directed expansion of progenitor cell populations and a reduction in colony-forming capacity [129]. Overall, these data implicate a critical role for paracrine signaling in progesterone regulation of murine MaSCs.

Despite the role of signaling in mediating progesterone signals in the murine mammary gland and during mammary tumorigenesis, their role in progesterone signaling in humans is less well studied. RANKL was not a significantly progesterone-regulated gene in genomewide profiling of human breast organoids [12]. A recent report identified that progesterone increased RANKL in human breast microstructures, but not in isolated HMECs [130]. Furthermore, RANKL expression in human breast specimens was associated with high serum progesterone levels [130]. Despite these observations, multiple studies have not identified RANKL mRNA or protein levels as increased by progestin treatment in PR+ breast cancer cell lines [61, 100, 130–133]. Forced overexpression of RANK and stimulation with RANKL in multiple breast cancer cell lines, however, increased the CD44+CD24− population, as well as increased migration and invasion [133]. Progestins do increase RANKL family members TNFSF10 (TRAIL) and TNSFS10a (TRAIL receptor) [61, 100], and thus could be signaling through a similar system. In normal human breast tissue, cell populations that express growth hormone receptor (GHR) were found to overlap with progenitor cell populations and show some functional properties of stem cells, including the ability to form mammospheres and differentiate into multiple lineages [134]. While these GHR+ cells are hormone receptor negative, progestins act on ER+PR+ cells in the normal breast to induce GH secretion; inhibition of this signaling pathway significantly reduced MCF7 xenograft growth in vivo [134]. In human breast cancer, CXCR4 is linked to poor prognosis and metastasis. While there is no evidence for progestin-mediated regulation of CXCR4 in breast cancer, studies in breast cancer cell lines have shown higher CXCR4 levels in the CD44+CD24− CSC population, and inhibition of CXCR4 decreased mammosphere formation in MCF7 cells [135]. Thus while progesterone signaling appears to switch on a cell-intrinsic ability to transition to CSCs, the involvement of extrinsic factors from neighboring cells cannot be excluded and requires further investigation.

Conclusions

An integral connection between steroid hormones and their cognate receptors in breast tumorigenesis and progression has been established during more than a century of work. More recently, it has been discovered that hormones regulate the balance of stem cell populations in the normal and malignant breast. In the normal breast, it is speculated that

increased stem cell populations lead to increased breast cancer susceptibility. It is also speculated that increasing breast CSC populations influences both drug resistance and tumor recurrence. The fact that luminal subtype ER+PR+ tumors can have particularly long latency periods prior to recurrence underscores how increasing long-lived cells even a few fold may contribute to this clinical problem. On the whole, evidence suggests that progestins are the dominant force increasing normal and breast CSC populations, with estrogens playing a more permissive role. The increasing studies of androgens and AR in breast tumor biology are certain to uncover how they contribute to breast CSC levels. Here we have described what is currently known concerning downstream mechanisms of steroid hormone and receptor regulation of breast CSCs. These include direct and indirect regulation of genes, mostly transcription and signal transduction factors, and post-transcriptional regulation of transcription factors through hormone-regulated miRNAs. The progesterone-mediated increase in breast CSCs is likely less dependent on paracrine signaling, as opposed to stem cell upregulation in the normal murine mammary gland. As new inroads into interactions between ER, PR, and AR are made, it is likely that the balance of steroid hormones and their receptors controls heterogeneous populations in breast cancers, and can influence their long term fate.

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Abbreviations

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Fig. 1.

Schematic of described mechanisms involved in steroid hormone regulation of cancer stem cell populations. Estrogens bind estrogen receptor alpha (ER) to increase transcription of target genes FGF9, let-7, and miR-29abc. FGF9 is involved in paracrine, and possibly autocrine, signaling to increase transcription of the transcription factor Tbx3. Estrogens can also bind GPR30 to initiate EGFR and Hippo signaling pathways. Progesterone or progestins bind progesterone receptor (PR) to increase expression of transcription factors (Stat5, Bcl6, Klf5, and Klf4), Notch pathway members (Notch2, Jagged1), and members of the Wnt family (Wnt-1). Wnts and other extrinsic factors may be secreted to influence dedifferentiation of the secreting or neighboring cells. Both progesterone and progestins bind PR to downregulate GATA3, miR-141, or miR-29abc, and increase CSC populations; GATA3 upregulates expression of miR-29b. Androgens or progestins bind androgen receptor (AR) to suppress let-7 microRNA transcription. ER downregulates miR-221/222, which represses translation of ER, miR-29abc blocks translation of Klf4, and miR-141 blocks translation of both Stat5 and PR. Prolactin binds prolactin receptor (PRLR) to block expression of the transcription factor BCL6, which suppresses progestin-dependent induction of CK5