A review of estrogen receptor/androgen receptor genomics in male breast cancer

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Abstract

Male breast cancer is a rare disease, of which little is known. In contrast to female breast cancer, the very vast majority of all cases are positive for estrogen receptor alpha (ERα), implicating the function of this steroid hormone receptor in tumor development and progression. Consequently, adjuvant treatment of male breast cancer revolves around inhibition of ERα. In addition, the androgen receptor (AR) gradually receives more attention as a relevant novel target in breast cancer treatment. Importantly, the rationale of treatment decision making is strongly based on parallels with female breast cancer. Yet, prognostic indicators are not necessarily the same in breast cancer between both genders, complicating translatability of knowledge developed in female breast cancer toward male patients. Even though ERα and AR are expressed both in female and male disease, are the genomic functions of both steroid hormone receptors conserved between genders? Recent studies have reported on mutational and epigenetic similarities and differences between male and female breast cancer, further suggesting that some features are strongly conserved between the two diseases, whereas others are not. This review critically discusses the recent developments in the study of male breast cancer in relation to ERα and AR action and highlights the potential future studies to further elucidate the genomic regulation of this rare disease.

Introduction

Male breast cancer is rare, accounting for around 1% of all breast cancers (Siegel et al. 2016) and is frequently positive for ERα (91–95%) and/or PR (80–81%) (Giordano et al. 2004, Anderson et al. 2010, Nilsson et al. 2013). The most well-known anti-estrogenic therapy is tamoxifen, which competitively blocks estradiol binding to the receptor, effectively inducing an alternative conformation of ERα ligand-binding domain (Shiau et al. 1998), which prevents the formation of an active transcription complex (Zwart et al. 2007) and inhibiting the onset of tumor cell proliferation programs (Severson et al. 2016). Aromatase inhibitors are also used in the treatment of ERα-positive breast cancer to prevent the conversion of testosterone to estrogen, thus depleting the patient and therefore the tumor of estrogens, and blocking ERα-driven cell proliferation (Zimniski et al. 1993). Both tamoxifen and AIs are prescribed in the adjuvant treatment of female breast cancer (Baum et al. 2002, Regan et al. 2011). In male breast cancers, tamoxifen (Aisner et al. 1979) and aromatase inhibitors (Doyen et al. 2010) are both effective.

Androgen receptor (AR) is also frequently positive in both male and female breast cancers (Isola 1993, Peters et al. 2009, Hu et al. 2011, Chia et al. 2015). In ERα-positive female breast cancer, AR is practically always...
expressed (Wang et al. 2014, Sas-Korczynska et al. 2015) and has been linked to differential outcome (Jiang et al. 2016). Interestingly, ERα-negative male breast cancers can express AR as well, in about 8–12% of the cases, termed molecular apocrine breast cancer (Farmer et al. 2005, Doane et al. 2006, Lakis et al. 2014). Gene expression profiles in ERα−/AR+ breast cancers are similar to ERα+/AR+ breast cancers (Doane et al. 2006), suggesting that AR may compensate in the absence of ERα. These results are further confirmed by ChIP-seq analyses, which revealed a potential of AR to compensate for the lack of ERα expression by binding the same genomic regions to regulate expression of many of the same genes (Robinson et al. 2011).

Recently, multiple reports shed further light on the genomics, transcriptomics and epigenetic gene regulation of male breast cancer. Furthermore, clinical trials have been initiated to specifically block ERα and/or AR in male breast cancer. These new observations together with parallels as well as differences with the female disease call for a review paper to update us on the most recent developments in the field of male breast cancer in relation to genomic features and novel therapeutics.

**Clinical features**

Although the development of the male breast is distinctly different from that of the female breast, male breast cancers are typically treated in the same fashion as female breast cancers in post-menopausal women (Korde et al. 2010). The underlying biology of the vast majority of male breast cancers is thought to be fully dependent on endocrine stimulation as both ERα and AR are typically expressed in these tumors (Hong et al. 2016). The majority of circulating estrogens in men (~80%) originate from peripheral aromatization of adrenal and testicular androgens. The remaining ~20% comes from direct production in the testes (Doyen et al. 2010). Administration of monotherapy aromatase inhibitors is not advised because of the risk of secondary resistance due to a likely feedback mechanism allowing for additional substrate (testicular androgens) for aromatization, which has been associated with increased estradiol levels at progression (Doyen et al. 2010). It has been suggested AIs could be more effective in combination with a pituitary gonadotropic-releasing hormone (GnRH) analogue to block this feedback loop leading to an efficacious suppression of estrogen production (Sousa et al. 2013).

Because of the rarity of breast cancer in males, there are few clinical trials involving exclusively male breast cancer patients making it difficult to determine the benefit of particular treatments. Tamoxifen is effective in male breast cancer patients, but recurrence does occur at a similar frequency as compared to female breast cancer (Kiluk et al. 2011). Although tamoxifen is a beneficial treatment, it is not without clinical issues including side effects such as reduced libido and impotence (Arnould et al. 2006), which may lead to a clinical or patient decision to stop treatment (Fentiman et al. 2006). In addition, the prognostic indicators are not necessarily the same between male and female breast cancers, making it difficult to determine which patients truly require treatment (Abreu et al. 2016, Leone et al. 2016).

AR is known for many years as driver of tumorigenesis in prostate cancer via receptor activation by ligand binding and subsequent downstream expression of genes critically involved in tumor cell proliferation (Brinkmann et al. 1999, Xu et al. 2006, Wang et al. 2009, Itkonen & Mills 2012). Function of AR and AR-mediated gene expression are evolutionary related to ER biology (Mangelsdorf et al. 1995, Shang et al. 2002, Wang et al. 2005, 2007). Current therapies to block AR action in prostate cancer are aimed to inhibit testosterone production by abiraterone (Li et al. 2015), prevent the nuclear import of the receptor (enzalutamide (Tran et al. 2009)) and/or block coactivator recruitment (bicalutamide (Schellhammer 2002)). These novel therapies have successfully been used in primary and metastatic prostate cancers (Perlmutter & Lepor 2007, Zhao et al. 2016b). Recently, the selective antagonist apalutamide has been developed to bind AR thus rendering it unable to bind cofactors and inhibiting downstream effects (Clegg et al. 2012). As breast cancer expresses AR as well, these existing therapeutics that were originally designed for the treatment of prostate cancer are considered promising regimens in the management of breast cancer. Consequently, several clinical trials examining the efficacy of AR inhibition alone or in combination with other treatments such as anti-estrogen therapy (Table 1) are currently ongoing in both female and male breast cancer.

**Molecular features**

Although the paucity of male breast cancer patients makes it a difficult disease to study, recent work from several groups has undertaken the molecular characterization of male breast cancer. Breast cancer is well described at the transcriptional and (epi)genomic levels. Molecular characteristics are known to differ between male and female breast cancers (e.g. BRCA2 germline mutation frequency (Johansson et al. 2014, Silvestri et al. 2016)). This indicates additional molecular
Table 1 Current running clinical trials (clinicaltrials.gov) examining androgen receptor inhibition in breast cancer.

<table>
<thead>
<tr>
<th>Study</th>
<th>Patient group (gender)</th>
<th>Trial and treatment setting</th>
<th>Treatment</th>
<th>Androgen inhibition</th>
<th>Estrogen inhibition</th>
</tr>
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<tbody>
<tr>
<td>NCT02567986</td>
<td>ER+/TN-AR+ (female)</td>
<td>Phase II, neoadjuvant</td>
<td>Enzalutamide monotherapy</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>NCT02353988</td>
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<td>No</td>
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<tr>
<td>NCT01990209</td>
<td>AR+ (both)</td>
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<td>Orteronel monotherapy</td>
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<tr>
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<tr>
<td>NCT02605486</td>
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<td>Palbociclib + bicalutamide</td>
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<td>No</td>
</tr>
<tr>
<td>NCT01638247</td>
<td>ER+ and/or PR+ (male)</td>
<td>Phase II, adjuvant,</td>
<td>Tamoxifen + GnRH analogue vs Al + GnRH analogue</td>
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<td>Yes</td>
</tr>
<tr>
<td>NCT02457910</td>
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<td>Phase I/II, metastatic</td>
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<td>NCT02689427</td>
<td>TN-AR+ breast cancer (both)</td>
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<td>Enobosarm monotherapy</td>
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<tr>
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<td>NCT0075885</td>
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<td>Abiraterone acetate</td>
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<tr>
<td>NCT0207512</td>
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<tr>
<td>NCT02091960</td>
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<td>Phase II, metastatic</td>
<td>Enzalutamide + trastuzumab</td>
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<td>NCT01842321</td>
<td>Molecular apocrine/HER2-(female)</td>
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<td>Yes</td>
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<td>ER+ (female)</td>
<td>Phase II, metastatic</td>
<td>Abiraterone acetate</td>
<td>No</td>
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</tr>
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features may differentiate between genders, potentially leading to additional or new treatments for male breast cancer. The vast majority of male breast cancers express AR (Murphy et al. 2006, Shaaban et al. 2012), and the receptor is considered a valid drug target in this setting, as evidenced by recent initiation of multiple clinical trials (Table 1). FBC trials are also listed in this table for reference. In ERα-positive breast cancer cells, AR has been shown to limit ERα-mediated growth (Cops et al. 2008, Peters et al. 2009) indicating the propensity to confer better response in patients who are positive for both receptors. This finding is supported in MBC by clinical work in which ERα-positive/AR-positive patients had significantly better outcome compared to ERα-positive/AR-negative patients, and their hormone receptor immunohistochemical profiles illustrated co-clustering based on ER (both ERα and ERβ) and AR expression (Shaaban et al. 2012). In FBC on the other hand, ERα clustered with progesterone receptor, whereas AR clustered with ERβ, suggesting an intrinsic difference in hormone receptor biology and hormone receptor dependencies between genders. Specifically in MBC, AR has been shown to be a valid target for treatment in the metastatic setting (Di Lauro et al. 2015).

To add complexity to the role of AR in breast cancer, preclinical studies have demonstrated AR may have both proliferative (De Amicis et al. 2010) and anti-proliferative (Szelei et al. 1997, Andò et al. 2002, Cops et al. 2008, Peters et al. 2009) properties. Not surprisingly, as these receptors are transcription factors with broad effects on transcription, differential binding at these sites can be indicative of outcome in both breast and prostate cancer. Further research is needed to characterize the binding sites of AR in both male and female breast cancer so the responsive genes can better be determined from a more functional standpoint, leading to increased knowledge of the action of AR in breast cancer and its likely weak points, which may be exploited therapeutically.

In contrast to male disease, female rates of ERα and/or PR-positivity are higher (Giordano et al. 2004, Anderson et al. 2010, Nilsson et al. 2013). Notably, AR is highly expressed in male breast cancers (Zhou et al. 2014) and has been found to be indicative of good outcome in male breast (Shaaban et al. 2012) and poor outcome in hormone-refractory prostate cancer (Buhmeida et al. 2006). These discordant results may be indicative of inherent differences between breast and prostate cancer or they may highlight the importance of treatment setting...
in these studies as ERα/AR dual positivity has recently been shown to be associated with improved outcome (Li et al. 2016).

A recent study by Johansson and coworkers examining the gene expression profiles of MBC identified two novel subgroups using unsupervised hierarchical clustering, that are associated with different clinical and biological features (Johansson et al. 2012). These two subgroups of MBC, the luminal M1 and luminal M2 subgroups, do not completely overlap with FBC luminal A/B classifications suggesting potential ERα-related differences in MBC, which may be clinically relevant. As gene expression is typically related to protein expression, examination of the differences between MBC and FBC were studied at the HR immunohistochemical level in a large series of 514 matched cases (Shaaban et al. 2012). Strikingly, hierarchical clustering revealed in FBC ERα clustered together with PR, whereas in MBC, ERα clustered with AR suggesting a clinically actionable difference between genders in hormone receptor biology.

The frequency of BRCA2 mutations is notably higher in MBC than FBC (Rizzolo et al. 2013, Silvestri et al. 2016). In a recent study, Biesma and coworkers found 22% of MBC samples investigated (15/69) had a BRCA2-like profile based on DNA copy number data indicating a significant proportion of MBCs may be susceptible to PARP inhibition therapy or specific chemotherapy regimens aimed at DNA double-strand breaks (Biesma et al. 2015). In addition, with the exception of gains on chromosome X in MBC, this work found few differences between MBC and FBC (luminal-like) with respect to copy number changes (Biesma et al. 2015). This is a particularly interesting finding as AR is found on chromosome X and may therefore be upregulated in these samples. A recent study of similar size (59 MBC samples) also found that MBCs and FBCs of similar subtype shared many recurrent copy number aberrations (Piscuoglio et al. 2016). Unfortunately, this study did not determine BRCA2-like status based on copy number profiles despite reporting 5% of the samples as germline BRCA2 mutated, so validation of high frequency of BRCA2-like status in MBC (Biesma et al. 2015) and potential AR upregulation could not be investigated.

In an integrative analysis, Johansson and coworkers used an algorithm to detect candidate driver genes for tumorigenesis in MBC by combining copy number and gene expression data in both MBC and FBC samples, which revealed differences in the pathways and processes associated with the drivers between MBC and FBC suggesting differential regulatory processes between the two cancers (Johansson et al. 2013). Indeed, an extensive examination of genome-wide DNA methylation profiles in MBC has indicated there are two major subgroups, ME1 and ME2, which were associated with the gene expression subgroups luminal M1 and luminal M2 (Johansson et al. 2015). ME1 tumors were enriched for hypermethylation at polycomb target genes with respect to ME2, with ME1 and its associated gene expression subgroup luminal M1 to be associated with more aggressive tumors. Moreover, this work identified hypermethylated genes in the ME1 subgroup to be associated with androgen response suggesting a possible link to AR function.

To examine further likely driver genes in MBC tumorigenesis, Piscuoglio and coworkers determined the mutational landscape in MBC in relation to FBC. In this study, 59 samples were subjected to detection of somatic mutations for a subset of 241 genes that are frequently recurrently mutated in cancer or involved in DNA repair pathways (Piscuoglio et al. 2016). Genes identified as most frequently mutated included GATA3, a known interactor of ERα (Theodorou et al. 2013) and regulator of luminal cell differentiation associated with ERα-positive FBC breast cancer. Unfortunately, because this work only examined a very small subset of pre-selected genes, the analysis was intrinsically biased without an opportunity to discover new genes, which may be mutated in MBC. Genome-wide sequencing would solve the problem of biased gene selection, but a drawback is that a significant proportion of mutations in DNA do not give rise to functional or stable transcripts (Shah et al. 2012). Using RNA-seq of MBC samples can give both genome-wide mutational data and identify mutations that are found in a stable transcript and thus most likely to have a biological consequence on the protein level, lending additional weight to mutational findings.

Although ERα is the main driver of MBC, affecting downstream transcription and tumor cell proliferation, the functionality of ERα in MBC has remained completely unexamined. In FBC, genome-wide ERα/DNA binding profiles determined by chromatin immunoprecipitation coupled with massively parallel sequencing (ChIP-seq) have been found to be dynamic upon tamoxifen exposure (Severson et al. 2016) and more importantly are associated with differential outcome (Ross-Innes et al. 2012, Jansen et al. 2013). H3K27ac signal, a histone modification indicative of active enhancers at ERα-binding regions, is similar between male and female tissues suggesting the inherent transcriptional programming between genders is comparable (ENCODE Project Consortium 2012). As MBC is generally ERα driven, we suggest a similar action of ERα in MBC to FBC, which may also indicate the potential
for outcome determination of male breast cancers on the basis of differential ERα binding. In addition, several groups have profiled AR/DNA binding in prostate cancer and have shown associations of distinct AR signatures with outcome (Stelloo et al. 2015, Nevedomskaya et al. 2016, Zhao et al. 2016a). These findings indicate that these techniques can be applied to breast tumor samples as well, to better characterize the functional binding patterns of both ERα and AR in male breast cancer in relation to patient prognostication.

Discussion

Both in science as well as clinical practice, we tend to couple distinct diseases to genders and specific gene products. Breast cancer is almost automatically linked with female and estrogen receptor alpha (ERα) action. Although this is intrinsically true, it is by far not the full story, as breast cancer is neither gender-exclusive nor fully ERα mediated. Analogous to this, androgen receptor (AR) action is not confined to the prostate alone, but is highly expressed in most breast cancers of both genders. A common feature between male and female breast cancer is that resistance to endocrine therapeutics is frequently observed. As endocrine therapy resistance is clinically identified at the level of recurrent disease, a clear clinical need exists to identify markers for endocrine resistance at an early stage, so that patients with a predicted resistance can be treated with an alternative treatment instead. ERα and AR both have thousands of known DNA-binding sites in breast and prostate cancer, respectively (Carroll et al. 2006, Chng et al. 2012, Jansen et al. 2013, Zwart et al. 2013, Stelloo et al. 2015, Severson et al. 2016). Differential binding at these sites can be indicative of outcome in both breast and prostate cancer. In male breast cancer, such analyses have not been reported to date, and it would be highly relevant to identify biomarkers based on ERα and/or AR behavior in male breast cancers to identify weak points that may be exploited therapeutically.

Although MBC is typically considered ERα driven, there are distinct molecular features found in male breast cancer, which could be used as targets for currently available or yet undeveloped therapies. As most male breast cancers are positive for AR, this steroid hormone receptor could be considered an interesting drug target that may work in synergy with blocking ER action. AR-targeted therapeutics are currently being tested in multiple clinical trials accruing both male and female patients, either as monotherapy or as a combination therapy together with ERα inhibitors. Still, surprisingly little is known about the biological interaction between ERα and AR in female breast cancer, being completely unexplored in the male setting. Therefore, it remains to be determined whether such treatments will be supported by translational studies. In contrast to female breast cancers, cell line model systems for male breast cancer do not exist, greatly complicating preclinical analyses and the search of novel drug targets in this rare disease. With the recent development of ex vivo intervention technologies (Centenera et al. 2012, 2013, Dean et al. 2012, Ochnik et al. 2014), these issues may be resolved in the future, enabling us to effectively bridge biology with clinical practice in a disease as rare as male breast cancer.

Declaration of interest

The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of this review.

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References


breast.2014.02.013)
Leone JP, Zwenger AO, Iturbe J, Leone J, Leone BA, Vallejo CT &
Bhargava R 2016 Prognostic factors in male breast cancer: a
population-based study. Breast Cancer Research and Treatment 156
Li Z, Bishop AC, Alyamani M, Garcia JA, Dreicer R, Bunch D, Liu J,
Upadhyay SK, Auchus RJ & Sharifi N 2015 Conversion of aromatere
to D4A drives anti-tumour activity in prostate cancer. Nature 523
347–351. (doi:10.1038/nature14406)
Li W, O’Shaughnessy JA, Hayes DF, Campone M, Bondarenko I,
Zbarskaya I, Brain E, Stelloo S, van der Poel HG, de Jong J, Wessels LFA,
Li W, O'Shaughnessy JA, Hayes DF, Campone M, Bondarenko I,
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Li W, O'Shaughnessy JA, Hayes DF, Campone M, Bondarenko I,
Zbarskaya I, Brain E, Stelloo S, Nevedomskaya E, van der Poel HG, de Jong J, Wessels LFA,


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