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Estrogens and breast cancer: mechanisms involved in obesityrelated development, growth and progression

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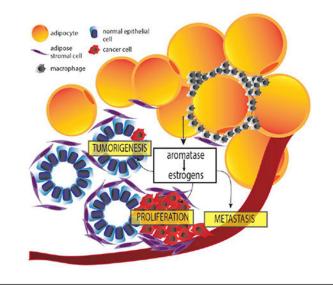
Abstract

Obesity is a risk factor for estrogen receptor-positive (ER+) breast cancer after menopause. The pro-proliferative effects of estrogens are well characterized and there is a growing body of evidence to also suggest an important role in tumorigenesis. Importantly, obesity not only increases the risk of breast cancer, but it also increases the risk of recurrence and cancer-associated death. Aromatase is the rate-limiting enzyme in estrogen biosynthesis and its expression in breast adipose stromal cells is hypothesized to drive the growth of breast tumors and confer resistance to endocrine therapy in obese postmenopausal women. The molecular regulation of aromatase has been characterized in response to many obesity-related molecules, including inflammatory mediators and adipokines. This review is aimed at providing an overview of our current knowledge in relation to the regulation of estrogens in adipose tissue and their role in driving breast tumor development, growth and progression.

Graphical Abstract

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1. Sources of estrogens in pre- and postmenopausal women

Estrogens play an important role in a number of physiological processes, including regulating energy metabolism, stress responses, mineral balance, as well as sexual development [1]. In premenopausal women, estrogens are predominantly produced by the ovary [2]. The hypothalamus releases gonadotropin-releasing hormone (GnRH), which stimulates the secretion of follicle-stimulating hormone (FSH) and luteinizing hormone (LH). FSH stimulates the biosynthesis of estrogens in growing ovarian follicles, which then act on the hypothalamus to induce the production of LH. An acute rise in LH triggers ovulation and the development of the corpus luteum. After menopause, the ovaries produce negligible levels of estrogens. The importance of gonadal steroidogenesis in normal breast development and in the origin of breast cancer is emphasized by the fact that early menstruation and late menopause (before the age of 40) result in a significant reduction in the risk of developing breast cancer [4]. It is somewhat paradoxical, therefore, that the majority of breast cancers occur after menopause, when circulating estrogen levels are low.

The *de novo* biosynthesis of sex hormones necessitates cholesterol, which is the precursor to all adrenal and gonadal steroid hormones [5]. The first process in steroidogenesis is the transport of cholesterol to the inner mitochondrial membrane by the steroidogenic acute regulator (StAR). Next, cholesterol is converted to pregnenolone by the cytochrome P450 side-chain cleavage enzyme. The formation of the testosterone precursor androstenedione from pregnenolone is dependent on the action of 3 β -HSD to produce progesterone and CYP17A1, which converts progesterone to androstenedione via a two-step mechanism. Androstenedione is then converted to testosterone by 17 β HSD enzymes, and can then be aromatized to estradiol (17 β -estradiol/E2). In postmenopausal women, however, it is circulating dehydroepiandrosterone sulfate (DHEA-S) from the adrenals that is the source of androgen for estrogen formation at peripheral sites. The local biosynthesis of estrogens within the breast [6, 7] and circulating levels of estrogens in blood [8, 9], believed to be a reflection of adipose-derived steroid production, are directly associated with driving breast

tumor cell proliferation [10]. The intracrinology that occurs in the breast as a result of the complex interaction of enzymes responsible for the activation and inactivation of steroid hormones has been the focus of many studies to explain the increased risk of breast cancer after menopause, when gonadal estrogen biosynthesis has ceased [11, 12]. Specifically, the breast expresses all enzymes required for the conversion of DHEA-S to E2, including steroid sulfatase, 3β -HSD, 17β HSD1 and aromatase [13, 14]. Of these enzymes, the best characterized in terms of its regulation in obesity is the enzyme involved in the rate-limiting step in estrogen biosynthesis, aromatase.

2. Aromatase

Cytochrome P450 aromatase (P450arom) is a microsomal enzyme that is expressed in the endoplasmic reticulum and catalyzes one of the final steps in estrogen biosynthesis by converting 19-carbon steroids (androgens, e.g. androstenedione and testosterone) to 18-carbon steroids (estrogens, e.g. estrone and estradiol) [15]. Aromatase is found in many tissues, including the gonads, brain, adipose tissue, placenta, blood vessels, skin, bone and in breast cancer tissue [16]. Its expression in breast adipose is hypothesized to be a major driver of estrogen-dependent breast cancer after menopause. The aromatase (*CYP19A1*) gene is located on chromosome 15q21.2 and is approximately 123kb long with nine coding exons (II-X) and a 93kb regulatory region.

Eight tissue-specific promoters regulate the expression of the *CYP19A1* gene yielding transcripts with unique 5'-untranslated regions [17]. These are promoters I.1 (placenta major, « 93kb), I.2a (placenta minor, « 78kb), I.4 (skin, adipose tissue and bone, « 73kb), I.7 (endothelial cell and breast cancer, « 36kb), I.f (brain, « 33kb), I.6 (bone, « 0.7kb), I.3 (adipose tissue and breast cancer, « 0.2kb) and II (ovary, adipose tissue, breast cancer and endometriosis, within 1kb) [15, 17]. In normal breast adipose tissue, low levels of aromatase are derived from activation of the distal promoter I.4, known to be regulated by glucocorticoids and class 1 cytokines, such as interleukin 6 (IL-6), interleukin 11 (IL-11), leukemia inhibitory factor (LIF) and oncostatin M (OSM), via the Janus kinase-1/signal transducer and activator of transcription 3 (JAK1/STAT3) pathway [18]. Promoter I.4 is also activated protein (MAP) kinase-AP1 pathway [18]. However, in the breast adipose tissue of women with breast cancer, the majority of transcripts are derived from the coordinated activation of promoters I.3 and II in a cAMP-dependent manner [18, 19].

2.1 Aromatase regulation in obesity

The prevalence of obesity has been steadily rising worldwide, and there is now strong evidence to support a causal link between obesity and the development of many cancers, including breast, ovarian, renal, pancreatic, leukemia, multiple myeloma, and esophageal cancers [20–25]. For breast cancer, the link is strongest for postmenopausal women and for the development of ER+ breast cancer, suggesting an important role of estrogens in driving obesity-associated breast cancer growth and development [20, 24]. After menopause, adipose tissue is the primary source of estrogen production in the body [26–28]. Interestingly, BMI is found to be positively associated with tissue levels of estrogens [29,

30]. Therefore, as fat mass increases with increasing body weight, aromatase expression and consequently estrogen levels, are also elevated, an effect that is more prominent in postmenopausal women [31–37].

A number of studies have further explored the positive association between obesity and local estrogen production by highlighting specific factors dysregulated in obese adipose tissue that induce aromatase expression in adipose stromal cells (ASCs) (Figure 1). Following up on the seminal findings that proinflammatory mediators and cytokines (e.g. PGE_2 , $TNF\alpha$, IL-1, IL-6, COX-2) play key roles in regulating estrogen production in ASCs [18, 19, 38–42], several recent mechanistic studies have provided greater insight into the regulation of aromatase by some of these factors in obese adipose tissue. For example, using both cell culture and clinical samples Wang et al. showed that p53 is a negative regulator of aromatase expression in ASCs and treatment with PGE2, which is elevated in obesity, inhibits p53 resulting in elevation in aromatase [43]. PGE₂ was also shown to stabilize HIF1 α , leading to the binding and stimulation of aromatase PII [44]. More recently, Subbaramaiah et al. found that PGE₂ downregulates SIRT1 in a human ASC cell line leading to the upregulation of HIF1a [45]. Further supporting the role of PGE₂ in induction of aromatase, IL-6 in sera from obese subjects was found to induce breast cancer cell PGE₂ secretion, which in turn induced aromatase expression in primary ASCs. This effect was nullified by both depletion of IL-6 from sera or treatment with celecoxib, an inhibitor of the enzyme COX-2 which catalyzes the conversion of arachidonic acid to PGE_2 [46]. These findings provide a new level of complexity regarding the role of IL-6 in regulating aromatase expression in ASCs, as previous findings demonstrated that it can increase the activity of promoter I.4 in the presence of the IL-6 soluble receptor [18]. Adipokines have also been examined for their role in regulating aromatase.

Leptin, an adipokine increased in obesity, inhibits p53 in human breast derived ASCs, leading to an increase in aromatase expression [47]. This finding complemented prior work demonstrating that PGE₂ and leptin stimulate aromatase expression by suppressing the activity of energy sensors LKB1/AMPK, thereby alleviating their suppressive effects on CREB-regulated transcriptional co-activators (CRTCs) which stimulate aromatase [48, 49]. Interestingly, LKB1 and AMPK are stimulated by adiponectin, an adipokine produced by healthy adipocytes, leading to suppression of the PII-specific expression of aromatase. This suggests that AMPK-activating drugs may selectively inhibit aromatase in adipose tissue, including breast. More recently, the orexigenic hormone ghrelin and its unacylated form, des-acyl ghrelin, which are reduced in obesity, were also shown to suppress PII-driven aromatase expression mediated via suppression of cAMP [50].

The regulation of PI.4 has also been examined in the context of obesity. Promoter I.4specific transcripts, present in adipose tissue, can be stimulated by inflammatory mediators, including IL-6, IL-11, leukemia inhibitory factor, oncostatin M, as well as TNFa [51, 52]. Using preclinical models and human breast tissue, the TNFa-mediated induction of aromatase was shown to require ERK1/2 activation, an effect that was blocked by the antiinflammatory cytokine IL-10 [53]. Taken together, these studies propose new mechanisms that explain the elevation in estrogen produced by breast adipose tissue in obese postmenopausal women.

It is important to highlight that since aromatase is produced by dysfunctional breast adipose tissue, obesity as defined by BMI may not be the best predictor of local estrogen levels since it does not account for volume of body fat or quality of fat. For example, a recent study found that breast white adipose tissue inflammation and other systemic correlates of metabolic syndrome (e.g. leptin) were strongly correlated with aromatase expression and activity in women with a normal BMI (24.9 kg/m²)[54]. In a prospective study of 12,159 postmenopausal women in Sweden, body fat % was a better predictor of breast cancer incidence than BMI [55]. It is possible that this discrepancy is due to body fat % being a superior readout of estrogen levels which are closely tied to breast cancer risk.

3. Estrogens, estrogen receptors and breast cancer

Estrogens have been shown to function predominantly by interacting with two estrogen receptors (ERs), ERa and ER β [56]. Estrogen receptors are fundamental for mammary gland maturation and physiological events such as puberty and pregnancy. ERa is found in nearly 50-80% of breast cancers, and its expression correlates with better prognosis and a lower chance of recurrence [57, 58]. ER β has also been detected in breast tumors, and is suspected to contribute to hormonal sensitivity and resistance [59, 60]. Studies show decreased ER β RNA levels in invasive breast cancers in comparison with the normal mammary gland [60]. Although the role and mechanism through which decreased ER β expression results in tumorigenesis is unknown, results from several studies suggest a stimulatory role of ERa and an inhibitory role of ER β in relation to proliferation of estrogen-dependent cells [61, 62].

3.1 Estrogens as mutagens and effects on breast epithelium

Estrogens are a significant driver of ER+ breast cancer, with studies suggesting a role in ER – breast cancer as well [63–65]. Neighboring the estrogen-producing ASCs are breast epithelial cells, which are hormone-sensitive and express the ER. Estrogens play an important in role in the normal development of breast epithelium by stimulating proliferation and ductal morphogenesis [66]. However, when exposed to high levels of estrogens such as in the setting of obesity, the pro-proliferative effect of these steroids may cause accumulation of replication errors leading to mutations and the development of breast cancer (Figure 2). Proliferating cells also have higher energy demands that require increased mitochondrial activity, which could potentially lead to an elevation in reactive oxygen species (ROS) as a byproduct of cellular respiration. Felty *et al.* found that estradiol can directly stimulate the production of intracellular ROS from mitochondria in several breast cancer cell lines [67].

Additionally, estrogens can be metabolized to catechols followed by further oxidation to semi-quinones and quinones through a process of redox cycling that produces ROS. This is important in the context of tumorigenesis because estrogen quinones are mutagenic and can interact directly with DNA to form adducts, a form of DNA damage [68–70]. Several studies have shown that treating normal breast epithelial cells (MCF-10A) with estrogen metabolites induces elevation in intracellular ROS leading to oxidative DNA damage [71–73]. By interacting directly with DNA, estrogen metabolites do not require the estrogen receptor to exert their mutagenic effects, which may explain the role of estrogen in promoting some ER

- breast cancers. Indeed, Savage *et al.* found that estrogen and estrogen metabolites caused DNA double strand breaks (DSB) in both normal breast epithelial cells and ER- breast cancer cells [74]. Given the abundance of evidence for mutagenic and mitogenic effects of estrogens, the obesity-induced elevation in local estrogen production is likely to drive DNA damage in breast epithelial cells leading to a greater risk of tumorigenesis.

Interestingly, there is a growing body of literature implicating estrogens in the disruption of the DNA damage response (DDR) and DNA repair machinery. For example, some studies have indicated that ERa downregulates ATM and ATR, important initiators of the DDR [75–77]. This is hypothesized to result in defective processing of DNA damage. The mechanisms by which estrogen signaling alters DDR and DNA repair has been reviewed in detail [78] and provides a novel theory for how estrogens promote breast cancer, i.e. not only by inducing DNA damage but also potentially diminishing the cell's ability to sense and repair damage.

3.2 Mechanism of breast cancer growth in response to estrogen

In breast cancer, estrogens can act via genomic and non-genomic mechanisms. Genomic actions of ERs are associated with the regulation of estrogen-response element (ERE)-dependent and ERE-independent gene expression [79–81]. In ERE-dependent genomic activation, estrogen binding to its receptor is associated with increased interaction with coactivator proteins in order to bind to the ERE in DNA, resulting in changes in gene expression that regulate growth, differentiation, apoptosis and angiogenesis [80]. However, estrogens can also facilitate gene transcription via pathways that do not require EREs. In ERE-independent genomic activation, the estrogen-ER complex can also interact with other DNA bound transcription factors such as Fos/Jun in order to bind to AP-1 or SP1 sites in the promoter regions of target genes, thereby resulting in activation of gene transcription [79, 81].

Non-genomic effects are actions mediated via activation of ER localized closely to or at the plasma membrane [82–84]. Membrane-associated ER may interact with many proteins including adaptor proteins, G-proteins, Src, growth factor receptors (EGFR, IGFR1, HER2), cytoplasmic kinases (MAPKs, PI3K, AKT) as well as signaling enzymes (adenyl cyclase) [85–89]. The actions mediated by this mechanism are independent of gene transcriptional changes [85–89].

Recent findings show that non-genomic effects also involve the orphan GPCR-like protein, GPR30 (G protein coupled receptor 30) [90, 91]; also named GPER [92]. It has been reported that estrogens can act on membrane GPER in order to stimulate release EGF or EGF-related ligands leading to a transient activation of the EGFR, which in turn activates MAPK and PI3K signaling pathways [93, 94]. Interestingly, activation of GPER leads to the stimulation of adenylyl cyclase activity and increases in cAMP formation, which then leads to a marked inhibition of cell proliferation [95]. It is hypothesized that GPR30 inhibits MAPK activity and can also increase intracellular calcium stores, resulting in apoptosis and inhibition of MCF7 cell proliferation [96, 97]. Thus, GPR30 could be a novel potential target for ER+ breast cancers.

There is also an important cross-talk between ER genomic and non-genomic signaling pathways. Estrogen binding to nuclear ER can increase transforming growth factor (TGFa) and amphiregulin expression. Once TGFa and amphiregulin are bound, they stimulate EGFR in order to activate MAPK and AKT [79, 81, 98]. Conversely, several cytokines, growth factors, EGFR ligands and IGF1R-related pathways activate MAPK/ERK, PI3K/ AKT, p90rsk and p38 MAPK, which lead to ER phosphorylation. The phosphorylation of the AF-1 serines 118,167 and threonine 311, or other domains, results in the activation of ER [99–103].

Both genomic and non-genomic signaling pathways of the ER play a critical role in breast cancer development, progression, and survival. This is due in part to the regulation of the anti-apoptotic gene BcI2, pro-apoptotic gene caspase and cell cycle regulator cyclin D1 [104–106]. Additionally, estrogens increase the growth of breast tumors by increasing the number of G0/G1 cells entering into the cell cycle, therefore resulting in greater proliferation [107, 108]. Moreover, PI3K interacts with Src in order to promote S-phase entry of MCF7 cells in the presence of estradiol [109].

3.3 Role of estrogens in breast cancer metastasis

Estrogens have also been shown to influence breast cancer progression. For example, estrogen treatment has been shown to cause cytoskeletal remodeling, and contribute to cancer cell migration and invasion in vitro [110]. As mentioned above, estrogens not only influence the etiology of ER+ breast tumors, but also of ER- breast cancers. In ER- breast cancer cells, estrogen actions on GPER1 lead to increased invasion and migration, promoting a prometastatic phenotype [111]. ERa splice variants have also been shown to mediate extra-nuclear effects of estrogens through activation of PKC signaling pathway and promote metastasis in ERa-positive and ERa-negative breast cancer cell lines [112]. Estradiol-induced proteins like G1P3 are able to rescue cells undergoing anoikis [113], favoring prometastatic estrogenic effects. Estradiol-induced expression of Proteinase Inhibitor-9 (PI-9) with inhibitory activity against Granzyme-B contributes to breast cancer immune escape [114]. Another estrogen contribution to metastasis is related to premetastatic niche formation and bone marrow derived myeloid (BMD) cells recruitment. ERa expression in BMDs is necessary for estrogen-mediated tumor promotion of ER- breast cancer [115]. Estrogens might contribute to BMD recruitment through VEGF-A and/or SDF1a that were previously described as downstream mediators of estradiol/ER-induced angiogenesis and macrophage chemotaxis, respectively. Sartorius et al. demonstrated that estradiol promotes brain metastasis of ER- breast cancer cells by modulating astrocyte function, suggesting that existing endocrine therapies may provide some clinical benefit towards reducing and managing brain metastases in patients with ER- breast tumors [116].

A number of epidemiological studies supports these laboratory-based studies. For example, endocrine therapy has been shown to decrease the risk of developing ER+ contralateral breast cancer [117]. Interestingly, in this study, the authors found that patients on antiestrogen therapy presented a higher risk of contralateral ER- breast cancer. In a retrospective analysis of metastatic behavior of breast cancer subtypes [118], data demonstrate that women with ER+ tumors are more likely to develop bone metastases and

have improved disease-free survival compared to women who have ER– tumors. Their study support a close relationship between ER+ tumors and metastasis-specific survival, a finding that is consistent with data from previous studies [119].

4. Endocrine therapy

ERa and progesterone receptor (PR) expression have the greatest predictive value for response to hormonal therapy [120]. Despite breast cancer being the most commonly diagnosed cancer among women, cancer-related mortality rates are declining, in part, due to advances in adjuvant therapy [121]. Endocrine or hormonal therapies, including aromatase inhibitors, have revolutionized treatment for breast cancer patients. Current endocrine therapy holds major therapeutic value, especially for ER+ breast cancer patients.

4.1 Tamoxifen

The initial findings by George Beatson regarding the important role estrogen plays in breast development have served as the basis for research, development, and discovery of tamoxifen in 1967 by Harper and Walpole [122, 123]. Tamoxifen is a selective ER modulator (SERM) used to treat estrogen-dependent breast cancer and reduce the risk of cancer recurrence in premenopausal and postmenopausal women [124]. This drug was approved by the food and drug administration (FDA) in 1998 and is known by the brand names Nolvadex and Soltamox. Tamoxifen is a non-steroidal antiestrogen with triphenylethylene structure [125]. As a prodrug, tamoxifen has little affinity for the ER. It is metabolized in the liver into an active metabolite, 4-hydroxytamoxifen [126] which acts as an antagonist of the ER in breast tissue, leading to the inhibition of binding with coactivator proteins, thereby blocking the G₁ phase of the cell cycle and preventing cell proliferation. Another tamoxifen metabolite 4-hydroxytamoxifen (endoxifen) is present at greater concentrations in plasma than 4-hydroxytamoxifen, and thus may be just as important, if not more, to the anti-estrogenic action of tamoxifen [127, 128].

In ER-positive breast cancer, most clinical studies demonstrate that tamoxifen should be taken continuously for five years or ten years. According to the worldwide Adjuvant Tamoxifen: Longer Against Shorter (ATLAS) trial, it was suggested that patients who are treated with tamoxifen for ten years have reduced risk of breast cancer recurrence and cancer-associated death compared with patients who are treated with tamoxifen for only 5 years [129]. Another clinical trial, the aTTom trial, showed that patients who were continuously treated with tamoxifen for ten years also had significantly reduced risk of breast cancer recurrence compared with patients who took tamoxifen for 5 years [130]. Although tamoxifen treatment helps to reduce the risk of cancer recurrence, side effects, including endometrial and uterine cancers [131, 132], loss of blood flow to parts of the brain and significant loss of bone mineral density in premenopausal women [125, 133], have been reported, thereby highlighting a need for safer alternative therapies.

4.2 Fulvestrant

Fulvestrant (ICI 164384) is a selective ER degrader (SERD). It is classified as a pure steroidal antiestrogen (European medicines agency, brand name Faslodex) [134]. It is a class

of drug that targets estrogen receptors approximately 100 times faster than tamoxifen [134] and immediately causes degradation of the ER in breast cancer cells which reduces their ability to be activated by estrogen as well as the ability of ER to be activated via estrogen-independent mechanisms [135]. The loss of the estrogen receptor in breast cancer results in inhibition of breast cancer cell growth. *In vitro*, fulvestrant inhibits the growth of tamoxifen-resistant ER positive MCF7 breast cancer cells [136]. *In vivo*, fulvestrant also inhibits tamoxifen-resistant and ER positive MCF7 breast cancer xenografts [137]. In clinical studies, a correlative downregulation of ER with increasing dose was observed in postmenopausal women with primary breast cancer treated with single doses of fulvestrant for 15-22 days before surgery [138].

The FDA has approved this drug for the treatment of hormone receptor-positive metastatic breast cancer. Breast cancer patients receive this therapy once a month via intramuscular injection [139]. However, side effects such as diarrhea, hot flushes and throat inflammation have been reported that can affect the quality of life of breast cancer patients [140]. It is recommended for use in postmenopausal women who cannot be effectively treated with tamoxifen or aromatase inhibitors, as fulvestrant acts independently of estrogens [141–144].

4.3 Aromatase inhibitors

Aromatase inhibitors (AIs) are a class of drugs that block the action of the aromatase enzyme [145] in order to reduce the amount of estrogen in the body. There are two types of AIs, irreversible steroidal inhibitors such as exemestane (brand name, Aromasin®) [146], and non-steroidal inhibitors such as anastrozole (brand name, Arimidex®) [147] and letrozole (brand name, Femara®) [148]. These three inhibitors were all approved by the FDA and most clinical studies prove that treating breast cancer with exemestane [149], anastrozole [150] or letrozole [151] highly reduces breast cancer recurrence compared with tamoxifen treatment. The levels of FSH increase as a consequence of estrogen suppression. For this reason, AIs are contra-indicated in premenopausal women as use can lead to the development of polycystic ovaries and incomplete inhibition of ovarian estrogen biosynthesis. AI use is also associated with well-documented side effects such as osteoporosis [152], joint and muscle pain [153, 154] and hot flushes [155] because of the whole-body inhibition of aromatase and estrogen production.

5. Endocrine resistance

While endocrine therapy has enhanced the lives of many breast cancer patients, emergence of resistance is inevitable with advanced breast cancer and is to be expected over time. Endocrine resistance in cancer cells can be divided broadly into two main categories – *de novo* and acquired resistance. Breast tumors that show no response to first line hormonal therapy are examples of *de novo* resistance. On the other hand, tumors that exhibit a response initially to endocrine therapy, but then later recur are examples of acquired or secondary resistance.

Endocrine resistance may be considered to reflect four possible mechanisms: 1) Pharmacological resistance; 2) Changes in expression of ERa and its co-regulators; 3)

Alterations in expression of cell cycle signaling molecules; 4) Alternate growth receptor pathways, which is especially relevant in the context of obesity.

The first possible theory for developing hormonal resistance is by means of pharmacological mechanisms. As previously mentioned, tamoxifen is a pro-drug that undergoes extensive oxidation in the liver, primarily by CYP3A and CYP2D6 [126]. However, polymorphisms in tamoxifen-metabolizing genes affect the efficacy of the enzymes and thus plasma concentrations of the active metabolites of tamoxifen. Retrospective clinical data suggests that women with CYP2D6 4*/4* genotype have null or reduced enzyme activity, resulting in higher risk of tumor relapse [156].

The second possible mechanism for developing endocrine resistance is through mutations in the ESR1 gene, which encodes ERa. Expression of ERa has long been used to predict clinical response to anti-estrogen therapy. The mutations mainly occur at two residues in the ligand-binding domain, which replaces tyrosine with serine or asparagine at residue 537 and replaces aspartic acid with glycine at residue 538 [157]. A study found a mutation rate of 12% among 76 patients with metastatic ER+ breast cancer, and a 20% mutation rate among individuals with heavily pretreated disease [158]. Analysis of ESR1 mutations was performed on plasma samples from patients participating in the PALOMA3 and SoFEA studies, and a mutation rate of 25% was observed in patients with breast cancer progression on endocrine therapy, and an even higher mutation rate of 29% in patients who received prior AI therapy [159]. Similarly, a mutation rate of 39% was detected in patients with prior AI sensitivity. These findings suggest that although ESR1 mutations are a rare cause of primary endocrine resistance, the mutations arise more commonly with acquired secondary resistance to AI therapy [159]. Several studies have sought to clarify the role of ERB, if any, in relation to response and resistance to endocrine therapy. Despite some conflicting evidence, it has been suggested that low levels of ER β expression are related to tamoxifen resistance [59].

Additionally, overexpression of the ER co-activator AIB1 (or SRC3 or NCoA3) and down regulation of the co-repressor NCoR is associated with tamoxifen resistance [160–162]. Finally, increased levels of transcription factors such as NFkB and AP-1, which increase the interaction of ER with specific gene promoters, have also been linked to endocrine resistance [163, 164].

Endocrine resistance can also occur as a result of alterations in key cell cycle checkpoints [165]. The cell cycle involves a complex sequence of events through which a cell duplicates, and involves many regulatory proteins such as cyclin proteins, and cyclin-dependent kinases, oncogenes and tumor-suppressor genes, and mitotic checkpoint proteins. The balance of proliferative and anti-proliferative signals determines if a cell will progress from the G1 phase to the S phase, or withdraw into the dormant phase [166]. Anti-proliferative signals are communicated via the retinoblastoma (Rb) tumor suppressor protein, while Rb itself is regulated via complexes of cyclin and cyclin-dependent kinases [167]. Cyclin-dependent kinase 4, in complex with cyclin D1, D2 or D3, controls the phosphorylation of Rb, which in turn regulates the progression of the cell from G1 to S phase [168]. By means of CDK4 inactivation, or cyclin D1 and E1 amplification, tumor cells are able to circumvent cell cycle

regulation [169, 170]. Interestingly, cyclin D1 amplification is a common occurrence in estrogen-receptor positive breast cancers with 58% and 29% incidence rate in luminal B and luminal A cancers, respectively (Cancer Genome Atlas Network, 2012). Similarly, reduced expression of p21 and p27 (negative cell cycle regulators) and inactivation of Rb are also associated with poor response to hormonal therapy, especially tamoxifen [171, 172]. As a result, endocrine therapy and CDK4/6 inhibitors, in combination or sequentially, are now a viable option for the treatment of hormone receptor-positive breast cancer as a first line therapy and following development of resistance to endocrine therapy [173].

Another possible mechanism for developing endocrine resistance is by the means of enhanced autophagy, which is an intracellular process that recycles damaged or unnecessary organelles (macroautophagy) or proteins (microautophagy). Under conditions of compromised autophagy, it was noted that cytotoxic effects of 4-hydroxytamoxifen (4-OHT) were significantly increased [174]. Inhibition of autophagosome function stimulated a strong caspase-dependent cell death in the 4-OHT treated, anti-estrogen resistant cells [174, 175]. Thus, impaired autophagy increases sensitivity to endocrine therapy, and inhibition of the autophagosome may be a potential target to overcome resistance and improve efficacy of hormonal treatment of ER+ breast cancers.

Finally, overexpression and amplification of growth factor receptors, such as FGFR1 (fibroblast growth factor receptor -1), IGF1R (insulin growth factor -1 receptor), HER2 (human epidermal growth receptor -2), HER3 (human epidermal growth receptor -3), and EGFR (epidermal growth factor receptor) [176–179], which converge on the PI3K/Akt/ mTOR and Raf/Mek/Erk pathways, have been shown to be associated with sustained tumor proliferation and survival independent of estrogen [176–179]. These pathways provide alternative survival stimuli to the tumors, and can emerge to act as ER-independent drivers of tumor growth, thus conferring resistance to endocrine therapy. In addition, these pathways can be activated by amplification of the receptors and/or their respective ligands. Alternatively, deregulation of downstream signaling molecules such as an activating mutation in the PI3K p110 catalytic subunit or the loss of expression of PTEN tumor suppressor can also lead in activation of the pathways [180].

5.1 Endocrine resistance in obesity

Several studies have shown that obese women are more likely to face a poor breast cancer prognosis as compared to lean women, and a greater chance of breast cancer recurrence [181–183]. In the Anastrozole, Tamoxifen Alone or in Combination (ATAC) [150, 184, 185] and Australian Breast Cancer Study Group (ABCSG)[186] trials there was evidence that the relative benefit of anastrozole vs. tamoxifen was greatest when BMI was normal vs. elevated. A 2014 meta-analysis concluded that there is an association between BMI and outcome, and that there is increased risk of mortality in individuals with BMI over 25 kg/m² at diagnosis [187]. Different studies have evaluated the efficacy of AI inhibitors in suppressing circulating estrogen levels and its relation with BMI. Interestingly, Elliott *et al.* found that BMI and estradiol were higher in metastatic patients [188], and Lonning *et al.* showed that estrone levels positively correlate with BMI in women receiving AIs [189]. In a study by Sestak *et al.*, obese women were less likely to observe benefits of AI treatment

despite a significant reduction in circulating estrogens [190]. Therefore, it seems that higher BMI may contribute to reduced efficacy of AIs.

Many circulating factors found in the serum of obese postmenopausal women can amplify crosstalk between nongenomic ERa signaling and PI3K/Akt/mTOR and Raf/Mek/Erk pathways which promotes breast cancer progression [191]. For example, cells grown in media supplemented with sera from obese patients have greater IGF-1R activation in comparison to control sera [191]. As mentioned previously, FGFR1 is a known mediator of endocrine therapy resistance [177, 179, 192]. The FGFR1 regulatory pathway is one of the pathways that shows shared activation in patients with obesity and those with resistance to AI therapy [193]. Phosphorylation of FGFR1 and FGFR1 ligand expression is increased with obesity, metabolic dysfunction, weight gain and adipocyte hypertrophy [193]. Weight gain leads to a positive energy balance, and in the context of obesity/metabolic dysfunction, promotes FGFR ligand production from adipose tissue, which may also result in the activation of receptors in nearby breast cancer cells to promote growth after estrogen deprivation [193]. Leptin has also been shown to induce cell proliferation through activation of MAPK signaling, and its receptors are expressed in both normal breast tissue and solid tumors [194]. Additionally, leptin can mimic the effects of ERa transactivation in an ER+ breast cancer cell line, including down-regulation of ER mRNA and protein levels and upregulation of the estrogen-dependent gene pS2 [195]. Since serum leptin concentrations are correlated with the percentage of body fat [196], obese individuals have a higher chance of developing endocrine resistance due to the mechanism described above. Moreover, leptin stimulates the expression of aromatase through enhanced binding of CREB, CRTC and AP-1 to specific sites in the promoter region [48, 197], thus amplifying in situ production of E2 and driving breast tumor growth.

Nevertheless, a number of studies found no association between BMI and breast cancer outcomes. Coscia *et al.* showed a reduction in plasma estrone and estradiol following anastrozol treatment, but no significant changes in steroid concentration in association with BMI [198]. Two recent studies showed no significant relationship between high BMI and the efficacy of two different aromatase inhibitors [199, 200]. In a cohort where more than two thirds of postmenopausal women receiving adjuvant letrozole therapy were obese, there was no association for worse outcome in the obese women compared with lean women receiving the same treatment [200]. Zewenghiel *et al.* found no statistically significant difference between the three BMI categories (normal weight, overweight and obesity) and time to progression during fulvestrant treatment in their 173 patient cohort [199]. Therefore, additional studies are required to determine which patient group and/or treatment may be impacted by BMI before altering disease management.

6. Conclusions and future directions

Obesity is now an established risk factor for breast cancer in postmenopausal women. The local production of estrogens in the breast adipose tissue is suspected to be a key driver of breast cancer development and growth, and a mediator of resistance to endocrine therapy. Additional factors in obesity are also important for disease development and progression, and a better understanding of the mechanisms at play will inform management of breast

cancer in an increasingly obese female population. Additional studies are also required to determine whether pharmacological or lifestyle interventions will reduce the risk of breast cancer development and progression in this obese population.

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SBMB_2019_10 Manuscript Highlights

- Obesity is linked to an increased risk of developing hormone receptor positive breast cancer
- Estrogens stimulate cancer development, growth and progression
- The local production of estrogen in adipose tissue drives the growth of breast cancer after menopause

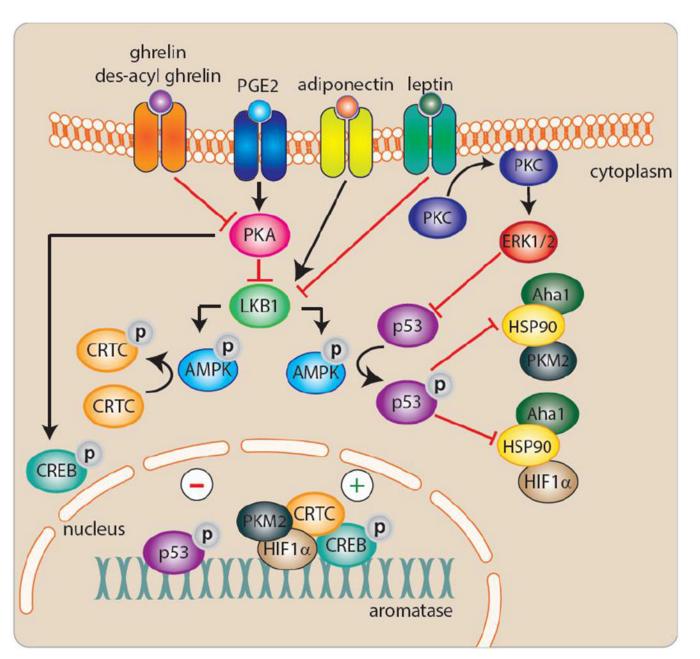


Figure 1: Molecular regulation of aromatase in obesity.

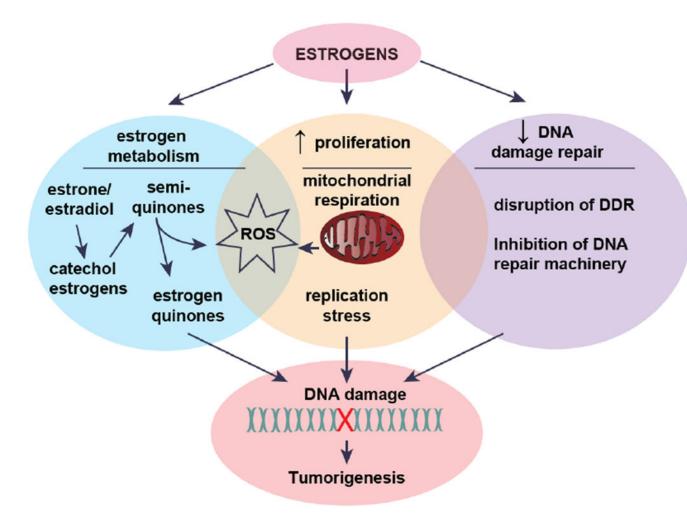


Figure 2: Estrogens and tumorigenesis.