

Estrogen Receptor Bio-Activities Determine Clinical Endocrine Treatment Options in Estrogen Receptor-Positive Breast Cancer

Technology in Cancer Research & Treatment
Volume 21: 1-19
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DOI: 10.1177/15330338221090351
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Abstract

In estrogen receptor positive (ER+) breast cancer therapy, estrogen receptors (ERs) are the major targeting molecules. ER-targeted therapy has provided clinical benefits for approximately 70% of all breast cancer patients through targeting the ER α subtype. In recent years, mechanisms underlying breast cancer occurrence and progression have been extensively studied and largely clarified. The PI3K/AKT/mTOR pathway, microRNA regulation, and other ER downstream signaling pathways are found to be the effective therapeutic targets in ER+ BC therapy. A number of the ER+ (ER+) breast cancer biomarkers have been established for diagnosis and prognosis. The *ESR1* gene mutations that lead to endocrine therapy resistance in ER+ breast cancer had been identified. Mutations in the ligand-binding domain of ER α which encoded by *ESR1* gene occur in most cases. The targeted drugs combined with endocrine therapy have been developed to improve the therapeutic efficacy of ER+ breast cancer, particularly the endocrine therapy resistance ER+ breast cancer. The combination therapy has been demonstrated to be superior to monotherapy in overall clinical evaluation. In this review, we focus on recent progress in studies on ERs and related clinical applications for targeted therapy and provide a perspective view for therapy of ER+ breast cancer.

Keywords

estrogen receptor-positive breast cancer, estrogen receptor, mutation, endocrine therapy, biomarkers, resistance mechanisms, clinical trials, targeted therapy, combination therapy

Abbreviations

AF-1, activation function 1; AF-2, transcription activation function 2; AIs, aromatase inhibitors; BRCA1/2, breast cancer gene 1 and 2; CDK4/6, cyclin-dependent kinase 4/6; CTCs, circulating tumor cells; DBD, DNA-binding domain; ddPCR, drop-digital polymerase chain reaction; DFS, disease-free survival; DOX, doxorubicin; ER, estrogen receptor; ERE, estrogen response element; ET, endocrine therapy; FGFR, fibroblast growth factor receptor; FUL, fulvestrant; GFR, growth factor receptor; GPER, G-protein coupled estrogen receptor; HER2, human epidermal growth factor 2; HR, hormone receptor; HSP90, heat shock protein-90; IGF-1R, insulin-like growth factor 1 receptor; LBD, ligand-binding domain; LBP, ligand-binding pocket; MAPK, mitogen-activated protein kinase; MBC, metastatic breast cancer; NCoR, nuclear receptor co-repressor; NGS, next-generation sequencing; OS, overall survival; PFS, progression-free survival; PIK3CA, phosphatidylinositol 3-kinase catalytic alpha polypeptide gene; PR, progesterone receptors; PTX, paclitaxel; RB, retinoblastoma; SERCA, selective estrogen receptor covalent antagonist; SERDs, selective estrogen receptor degraders; SERMs, selective estrogen receptor modulators; SHARPIN, shank-associated RH domain interactions protein; SIPL1, shank-interactions protein-like1; SRC-3, steroid receptor co-activator 3; TAM, tamoxifen; TF, transcription factor; WT, wild-type

Received: September 24, 2021; Revised: February 23, 2022; Accepted: March 7, 2022.

Introduction

The incidence of breast cancer (BC) is increasing worldwide in recent years, posing a serious threat to women's health. About 75% of BC patients are clinically diagnosed with estrogen receptor positive (ER+) tumors. Regulation of ER activity

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and expression becomes a key topic in both basic and clinical BC research. There are 2 types of estrogen receptor (ER), one is the transmembrane type or G-protein coupled receptor type, known as GPER, the other is the nuclear receptor type. In this review, we focus only on the nuclear receptor type ER. The nuclear receptor type ER is encoded by 2 genes, *ESR1* and *ESR2*, and the corresponding protein products are ER α and ER β .¹ Increased ER α activity is positively associated with BC progression.² *ESR1* may mutate during therapy that leads to development of resistance to therapeutic drugs such as antiestrogen and/or ER drugs (endocrine therapy [ET]). ER β has a broad-spectrum tumorigenesis effect. Apparently, ER-negative (ER-) BC cannot be treated by ET because of a lack of ER expression.

Development of ET resistance is a major problem in the ER+ BC treatment. When the classical ET drugs, such as aromatase inhibitors (AIs), selective ER modulators (SERMs) and selective ER degraders (SERDs) are used for treatment, the ER+ tumor usually develops drug resistance in the late stage. Causes for the drug resistance include, but are not restricted to, *ESR1* mutation, *BRCA1/2* mutation,³ and upregulation of specific microRNAs (miRNAs) (eg, miR-221/222).⁴ This has resulted in the need for the establishment of predictive and prognostic markers for detecting the drug resistance of BC. The expression level of ER α ⁵⁻⁷ and the *ESR1* mutations^{8,9} has been used as predictive or prognostic biomarkers in the ER+ BC. Many other drug resistance biomarkers of the ER+ BC have been identified and will be described in detail in the following sections. Circulating tumor cells (CTCs), drop-digital polymerase chain reaction (ddPCR), and next-generation sequencing (NGS) are the main methods for detecting the related molecules expression levels or mutations of the drug resistance genes.

A combination of multiple antitumor drugs has been applied for the therapy of the ER+ BC in drug resistance or metastasis settings in clinical trials. For example, treatment with the cyclin-dependent kinase 4/6 (CDK4/6) inhibitors (palbociclib, ribociclib and abemaciclib) in combination with fulvestrant (SERD), which is approved by the Food and Drug Administration (FDA), has significantly improved survival of ET-resistant BC patients.¹⁰⁻¹²

Nowadays, numerous studies have reported new findings of the structure and function of ERs and the upstream and downstream pathways regulating ERs in BC cells. A number of clinical trials have shown the therapeutic efficacy of newly developed drugs. Many statistical data on combination therapies have been published. This review seeks to summarize the latest studies on the mechanism of the ET resistance of the ER+ BC and the therapy with newly developed drugs and clinical data in recent years.

Structure and Function of ERs

ER is a ligand-activated transcription factor (TF).¹ ER has 2 members: ER α and ER β that are encoded by genes *ESR1* and *ESR2*, respectively. *ESR1* is located at chromosome position 6q24-27, and *ESR2* at 14q22-24.¹³⁻¹⁵ The expression profile of *ESR1* is very different from that of *ESR2* in human tissues and cell types. *ESR1* is mainly expressed in the uterus, pituitary

gland, liver, hypothalamus, bone, mammary gland, cervix and vagina, while *ESR2* is predominantly expressed in ovary, lung, and prostate.¹⁶

The tertiary structures of the *ESR1* product ER α and the *ESR2* product ER β are highly similar with minor differences in some domains. Both receptors possess 5 structural domains: an N-terminal domain (NTD; A/B-domain) containing the transcription activation function 1 (AF-1) region that regulates ligand-independent transcriptional activity,¹⁷ a DNA-binding domain (DBD; C-domain) that has 2 “zinc-finger” motifs capable of interacting with the estrogen response element (ERE); a hinge region (D-domain) that connects the C-domain and the E-domain and serves as an interface for the receptor posttranslational modifications (PTMs); a ligand-binding domain (LBD; E-domain) containing the ligand-binding pocket¹⁸ and the transcription activation function 2 (AF-2) region that plays an essential role in ligand-dependent transcriptional regulation;¹⁷ and a C-terminal domain (CTD; F-domain) that regulates ligand-dependent dimerization.¹⁹ Although ER α and ER β contain similar domains, their A/B, D and F domains are quite different from each other (Figure 1).^{1,20}

Based on subcellular localization of ERs including cell membrane, cytoplasm and the nucleus, the physiological effects of ERs can be classified into 2 categories: nongenomic effects on cell membrane and genomic effects on the cytoplasm and nucleus. Nongenomic effects are complicated and make affects not only in ER+ BC, so they will not be dealt with in detail in this review. The genomic effects of ERs on the target gene transcription are through following 3 aspects: (i) direct binding to corresponding DNA ERE; (ii) interaction with other TFs to activate gene transcription; and (iii) a ligand-independent transactivation via phosphorylation of AF-1, which is a highly conserved DBD that binds to ERE.

Estrogen-ER binding triggers conformational changes in the LBD, which is an α -helical bundle, with the C-terminal helix, H12, forms ER dissociation from the molecular chaperone heat shock protein-90 and assembles into homodimers (ER α /ER α or ER β /ER β) and heterodimers (ER α /ER β), allows the complex to bind to DNA EREs. Then, recruitment event begins that specific coactivators or corepressors gather and associate with ERs, activating or inhibiting gene transcription.²¹ Estrogen binding increases the number of binding peaks in the genome. The mouse model of DBD mutation of ER α shows that direct DNA binding is needed in order to induce hormonal response and biological activity. Direct DNA binding also needs to be supplemented by other signaling mechanisms, such as pioneering factor FoxA1 and GATA2, which allows the recruitment of chromatin remodeling proteins, opens chromatin so that ER can enter its DNA regulatory sites following ER transcriptional complex assembly, polymerase II recruitment, and gene transcriptional initiation.^{22,23} A second method, ERs also regulate gene expressions through indirect or tethered mechanism with protein–protein interactions of other TFs such as AP-1, SP-1, NF- κ B²⁴ that have been bound to DNA, and then associate the receptor with other genes that do not contain ERE (ERE-independent way). Finally, in the

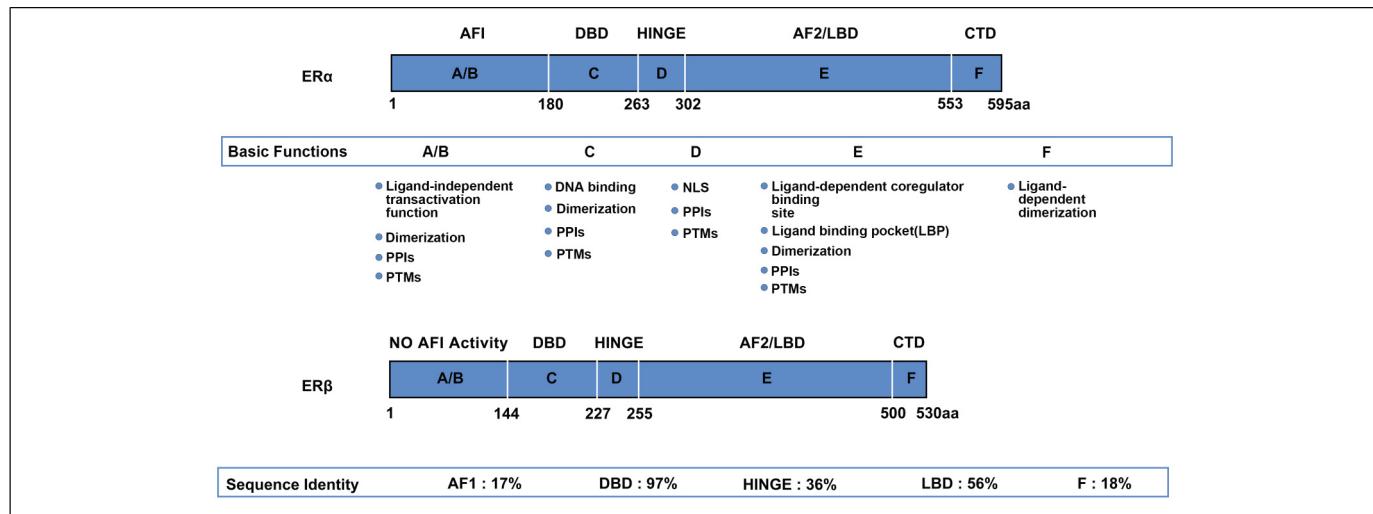


Figure 1. Domain structure of ER α and ER β . Basic modular domain structure and functions of ER α and ER β is very similar. The domain similarity of the 2 receptors is: the N-terminal domain (NTD; A-/B-domain) 17%; the DBD (C-domain) 97%; the hinge region (D-domain) 36%; the LBD (E-domain) 56%; and the CTD (F-domain) 18%, respectively. All the domains of the 2 receptors undergo PTMs. Some of domains are involved in PPIs, such as interaction with coregulator proteins. Both ER α and ER β contain a NLS in the hinge domain. In addition, the NTD of ER β has no AF1 activity, suggesting that ER β may not have the ligand-independent transcriptional activity. Abbreviations: DBD, DNA-binding domain; LBD, ligand-binding domain; CTD, C-terminal domain; PTM, posttranslational modification; PPI, protein–protein interaction; NLS, nuclear localization signal; NTD, N-terminal domain; ER, estrogen receptor.

absence of ligands, ERs can regulate activity and drive hormonal responses through ligand-independent activation of growth factors or other intracellular signaling pathways (thought to be involved in the phosphorylation of certain serine residues on the receptor, especially at AF-1 domain).²⁵ Overall, these may explain the complementarity of different cellular signaling pathways, indicating that ER has a great ability to change the phenotypes of cells.

Interestingly, in BC, the reference to ER generally refers to ER α rather than ER β , which is probably related to the difference in expression and function of the 2 subtypes in BC cells. Statistics show that about two-thirds of BCs are positive for ER α at the time of diagnosis.²⁶ In BC cells, E2 accelerates disease progression by promoting many processes such as sustaining proliferative signaling that defined by the hallmarks of cancer,² however, in comparison to ER α , ER β binds E2 with lower affinity and has lessened binding to nonconsensus EREs, which represent the majority of estrogen-responsive elements (eg, C-fos, c-jun, pS2, cathepsin D, and choline acetyltransferase cis-regulatory sequences).²⁷ Early studies using the ER (ER α and ER β) knockout mice also indicate that ER α plays the significant role in estrogen-mediated metabolic regulation, whereas ER $\beta^{-/-}$ mice show only a modest metabolic phenotype.²⁸ On the contrary, Rahul et al give opinions that ER β possesses broad-spectrum tumor suppressor activity including BC in the year 2020, which slow down the progression of BC by regulating the genomic and nongenomic effects through a series of complex mechanisms that have not yet been fully explored, and serve as an independent prognostic marker and therapeutic target.¹⁹

ER and BC

Not long ago, the International Agency for Research on Cancer (IARC) released the latest global cancer data that the total number of new cancers worldwide is expected to be 19.29 million in 2020. Among them, the number of new cases of BC reached 2.26 million, accounting for about 11.7% of new cancer cases, demonstrating the first time that BC has surpassed lung cancer to become “the largest cancer in the world.” Causes that result in BC include age, early menarche, late menopause radiation exposure, etc.²⁹ BC can be divided into 4 molecular subtypes on account of gene expression profiles: (i) luminal A, which is characterized by low tumor grade, ER-positivity, strong positive expression of progesterone receptor (PR) (PR \geq 20%), human epidermal growth factor 2 (HER2)-negativity, low expression of Ki67 (< 14%) and have a proliferation of slow; (ii) luminal B, which is ER-positive, PR-positive (low expression,<20%) or HER-2 positive or Ki67 high expression (\geq 14%), is considered more aggressive; (iii) basal-like tumors/triple-negative (ER-, PR-, HER2-) and (iv) HER2-enriched (ER-, PR-, HER2+).³⁰ Notably, ER+ BC accounts for about 70% of all BCs among the 4 categories. Estrogen-ER binding translocates to the cancer cell nucleus and initiates a signaling cascade, resulting in the proliferation and survival of BC cells. This mechanism reveals the important role of ET in the treatment of BC.

ER α and ER β Crosstalk in Breast Cancer

ER β expression was significantly correlated with the expression of ER α from the tissue microarray analysis of BC.³¹ Given that

the expression of ER α and ER β exists in the majority of BCs, one key question is to understand their crosstalk effects. First of all, ER α itself can directly bind to its homologous DNA binding element EREs. However, the transactivation potential of the ER β AF1 domain decreased and the cooperative interaction with its AF2 domain reduced,³² so ER β has a lower binding to EREs which represent the majority of estrogen-responsive elements. In addition, both ER α and ER β can also indirectly interact with other DNA-binding TFs such as AP-1.^{33,34} In the presence of estradiol (E2), ER α was found to upregulate the transcription of ERE-AP-1 composite response elements while ER β had the opposite effect.³⁵ Second, the study of Hall and McDonnell showed that ER β antagonized the effect of ER α on E2-responsive E2-AP-1 complex promoters in transient transfection experiments. It is therefore suggested that selective activation of ER β can inhibit cell proliferation induced by ER α .³⁶ Kim et al³⁷ using the estradiol response promoter containing 3 tandem GC-rich SP1 binding elements finding that both ER α and ER β proteins interact with SP1 through their C-termini. Indeed, the binding event of ER β with SP1 represses ER α transcription by recruiting a corepressor complex containing nuclear receptor co-repressor to the *ESR1* gene promoter.³⁸ Furthermore, the interaction between the 2 isoforms with the cell division protein cyclin D1 (*CCND1*) promoter or EGFR signaling also revealed the opposite interesting effect which ER β showed an inhibitory impact.³⁹⁻⁴¹ These suggest that ER β is a negative regulator of the proliferative and invasive effects. Last but not least, steroid receptor co-activator 3 (SRC-3)/AIB-1 which is an oncogenic co-activator in ER+ BC⁴² had a positive association with ER α in their expressions but inversed with ER β . Observation found induced SRC-3 recruitment and enhanced SRC-3/ER α but not SRC-3/ER β interaction in the location of ERE under certain endocrine drug treatments.⁴³ The selective interaction of SRC-3 with ER α but not ER β may explain some of the different cancer outcomes in the presence of drugs between the 2 ER isoforms.

ER and Endocrine Therapy Resistance

Despite the fact that most patients have the early-stage disease at the time of initial diagnosis, more than 25% of patients experience relapse and develop into metastatic BC (MBC). As stated previously, more than 70% of BCs are hormone receptor (HR, contains ER and PR) + and HER2-. Most of these tumors remain ER-positive, but the expression of ER in metastatic sites is lower than that in primary tumors.⁴⁴⁻⁴⁶ Blocking ER signal transduction is the principal treatment for ER+/HER2- BC. At present, effective clinical strategy to treat and arrest palindromia of ER+ BC is ET. ET cures about half of the patients in the nonmetastatic stage, and about 30% of metastatic patients have clinical benefits. Therefore, ET targeting ER activities has greatly reduced the mortality of BC. However, despite effective hormonal and targeted therapy, half of these patients will relapse or progress to incurable metastatic diseases.⁴⁷ The occurrence of endocrine resistance in patients with advanced

BC is inevitable. ESR1 mutations, ER α PTM by kinase, and ER androgen receptor (AR) crosstalk are involved in this process.

According to genomic alterations, endocrine-resistant breast tumors are divided into 4 groups: (i) tumors with *ESR1* gene changes (about 18%); (ii) tumors with impaired mitogen-activated protein kinase (MAPK) pathway (about 13%); (iii) tumors with mutations in TFs (about 9%); and (iv) tumors with unknown endocrine resistance (about 60%). Several mechanisms of *de novo* and acquired ET resistance mainly focus on the imbalance of ER pathway itself, including loss of ER expression, crosstalk between ER and other nuclear receptors, genomic alterations of tumor suppressors or drivers, gene fusions of *ESR1*, and missense mutations of *ESR1*.⁴⁸⁻⁵⁰

ESR1 Mutations

Since it was first described in the cell model in 1996⁵¹ to the present clinical data indicate that *ESR1* mutation is one of the most common mechanisms of endocrine resistance.^{47,52} *ESR1* mutations tend to cluster in 2 hot spots of the gene which encodes the ER LBD (about 80% of the encountered mutations), one in exon 5 (E380Q mutation) and the other in exon 8 of helix 12 at codons 536, 537, and 538 (Figure 2).^{52,53}

In addition, there are other mutations, such as K303R (located in the ER hinge region),⁵⁴ S463P or L536R/H/P/Q mutations, with a prevalence of less than 3%.^{55,56} The most common mutations (Y537, D538)^{8,9,55} have been identified ligand-independent that leads to constitutive activation of ER, thus activating transcriptional function and promoting hormone-independent tumor cell growth.^{53,57} Both D538G and Y537S (less expressed in Y537N and Y537C) mutations are located in the H11-H12 loop of ER α LBD and have unique transcription actions. By changing the hydrogen bonds at different positions, the conformation of the loop is modified to be more similar to that of wild-type (WT) ER-E2, resulting in the recruitment of co-activators such as SRC-1, SRC-3 in the absence of hormones and further stabilizing its conformation through different biophysical mechanisms.⁸ In vitro experiments showed that D538G mutation enhanced the migration ability of BC cells, which may be linked to the frequency of these mutations in the metastatic environment.⁵⁷ The activation degree of Y537S mutant is much higher than that of D538G, same with the drug resistance and phenotype invasion, which may explain the reason that Y537S constitutive transcriptional activity is higher than that of D538G. Other mutations lead to estrogen hypersensitivity (K303R, E380Q) or neutral, retaining hormone-dependent activation function (S432L, V534E).⁵⁴⁻⁵⁶ In addition, many of these mutations are rare and have not yet been functionally annotated.

The LBD *ESR1* mutation is a gain-of-function activation and occurs in the heterozygous state, which suggests that the functional states of the WT alleles are overridden by those of coexisting mutations.⁵⁸ This is in line with clinical sample data showing that up to 20% of endocrine-resistant BCs contain *ESR1* mutations, which appear to be rare in primary

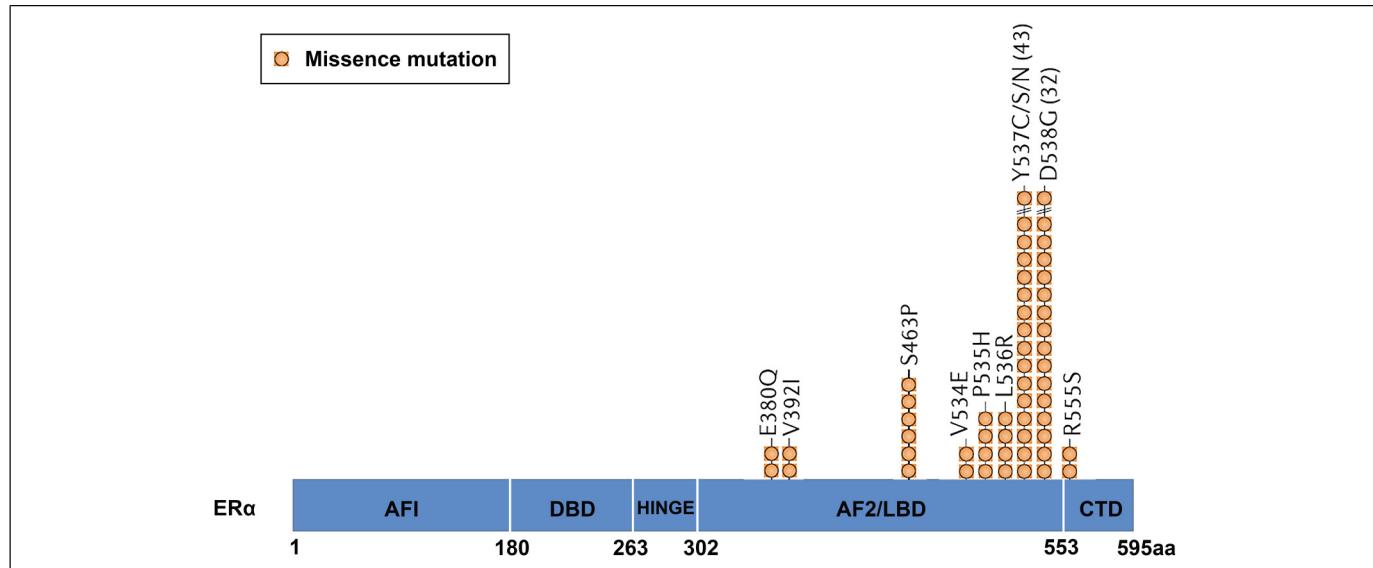


Figure 2. The most common mutations occur in the LBD of ER α . Approximately 80% of mutations are D538G, Y537S, Y537N, Y537C, or E380Q, located in the LBD of ER α . Abbreviations: LBD, ligand-binding domain; ER, estrogen receptor.

tumors.^{52,59} It implies that these mutations are either produced by clonal selection for very low abundance resistant clones, or are acquired later in the disease process under selection pressure from ET. BC cells harboring LBD *ESR1* mutations showed partial resistance to tamoxifen (TAM) and fulvestrant in vitro because higher doses of these endocrine drugs were needed to induce their antiproliferative effects in cells carrying such mutations.⁵³ Data also suggest that LBD *ESR1* mutations lead to complete resistance to AIs.⁵² Furthermore, apart from the most widespread mutations mentioned above, gene fusions are another well-known activating alteration that has been explored by RNA sequencing, such as *ESR1*-CCDC170, *ESR1*-YAP1, *ESR1*-POLH, *ESR1*-PCDH11X, and *ESR1*-AKAP12.^{60,61} Notably, none of them had the LBD as a common feature. The absence of the LBD greatly reduces the efficacy of the targeted endocrine drugs, and the subsequent increase in frequency of *ESR1* fusions in breast ER+ metastatic disease coexists with known missense alterations in *ESR1*, resulting in polyclonal resistance.⁶²

Kinase Signaling Pathways of the ER α Posttranslational Modifications

The PI3K-Akt-mTOR pathway is the most common altered pathway not only in BC but possibly also in all human cancers. This key signaling pathway regulates cell growth, proliferation, differentiation, survival and other vital cell functions.⁶³ Crosstalks between proteins involved in the PI3K pathway and the ER activation signaling are related to the development of ER+ BC resistance to ET.^{64–66} In addition, AKT improves the efficiency of ER S305 phosphorylation in the presence of *ESR1* K303R mutations is also closely related to TAM and AIs resistance.^{50,67,68}

Interactions between ER and GFR (such as insulin-like growth factor 1 receptor [IGF-1R], HER2, and fibroblast growth factor receptor) activate the downstream PI3K/AKT/mTOR signaling pathways,⁶⁹ and accelerate the development of resistance to ET.⁷⁰ About 12% of ER-positive tumors possess *HER2* gene amplification/overexpression which promotes cell proliferation, invasion and metastasis by activating MAPK and PI3K/AKT signaling pathways.^{71,72} IGF-1R is in charge of the insulin growth factor signaling pathway. The interaction between ER and IGF-1R will alter the antiproliferative effect of TAM by affecting the transcriptional activity of ER.

Overexpression of either p21 protein-activated kinase 1 (PAK1) or 2 (PAK2) is associated with ET resistance and worse clinical outcome. PAK1 induces the S305 ER site phosphorylation which enhances interaction with IGF-1, promoting cell growth.⁵⁰ The S305 phosphorylation by PAK1 protects the TAM-bound ER active conformation, similar to the AKT signaling.⁷³ Xiao T et al discovered an estrogen-induced negative feedback loop that normally constrains the growth of ER+ tumors. In the presence of E2, ER activates C-terminal SRC kinase expression, who represses SRC family kinases (SFKs)⁷⁴ and PAK2 activity. Inhibition of SFK and PAK2 represses oncogenic signaling pathways and estrogen-independent growth.

In general, ER α PTMs by kinases is actually one of the important reasons for drug resistance of ET in BC cases.

ER-AR Crosstalk

Almost 90% of ER+ BCs with endocrine resistance are AR-positive (AR+). AR interacts directly with ER α -LBD, promoting the ER α transcriptional activity and vice versa, increasing cell proliferation.⁷⁵ A recent ChIP-seq study found that

E2-induced AR and ER α -binding sites share 75% overlap.⁷⁶ Genomic DNA binding of ER α was only inhibited at those overlapping sites when BC MCF-7 cells were treated with AR antagonists.⁷⁶ Some studies also found that interaction between ER α and AR occurred through a long-range enhancer and promoter chromatin interaction.^{77,78} These findings imply that AR may preferentially regulate the expression of ER α -targeted genes based on the ER α -ERE sequences and that may induce metastasis⁷⁹ or decrease ER transcriptional activity.^{75,80} Additionally, AR overexpression contributes to the conversion of androgens to E2 by CYP19 aromatase⁸¹ which reduces the estrogen deprivation effect of endocrine drug AIs. However, AR-targeted therapy such as fluoxymesterone and testosterone propionate, have been used for the treatment of BC regardless of tumor AR expression levels since the 1940s.^{82,83} Kono et al retrospectively identified 103 patients with metastatic, ER-positive BC treated with fluoxymesterone and showed a clinical benefit rate of 43%.⁸⁴ Moreover, Davies et al found that tumors escape epithelial lineage confinement and transition to a high-plasticity state as an adaptive response to potent AR antagonism in prostate cancer, leading to AR-targeted therapy resistance phenotypes.⁸⁵ It is reasonable to speculate that a similar phenomenon may occur in ER+ BC.

Other ER-Mediated Endocrine Therapy Resistance Pathways

BC gene 1 and 2 (*BRCA1/2*) are tumor suppressor genes that play an important role in cell proliferation and DNA damage repair.³ Mutations in *BRCA1* and *BRCA2* lead to loss of tumor inhibition in BC. *BRCA1* and *BRCA2* mutations were found in about 5% of BC cases.^{86,87} Patients with a family history of BC, younger ages, or triple-negative BC have a high risk of the mutations. The *BRCA1* mutation drives patients to develop the triple-negative BC to a great extent, while the *BRCA2* mutation often induces expression of ERs.^{88,89}

Shank-interactions protein-like 1 (SIPL1) or shank-associated RH domain interactions protein (SHARPIN) is a novel oncogenic protein with extensive carcinogenic activity and associated with poor overall survival (OS) in BC patients.^{90–92} Role of SIPL1/SHARPIN in BC oncogenesis, especially ER+ BC, has not been thoroughly studied until recent years. It has been reported that overexpression of SIPL1/SHARPIN in BC cells reduces p53 protein levels and p53 target genes MDM2,⁹³ P21, P53NP1, and BTG2, and increases activity of MAPK and AMPK pathways,^{94,95} leading to resistance to TAM through AKT activation and NF- κ B signaling pathways.^{96,97}

Various oncogenic miRNAs regulated by estrogen/ER α interaction signaling have been found to cause endocrine drug resistance during treatments. It is interesting to note that different miRNAs expression in BC cells is correlated with diverse effects of resistance to endocrine drugs. For example, miR-21 and miR-221/222 are involved in both fulvestrant and TAM resistance, while miR-125b, miR-205, and miR-30a are all significantly upregulated in AI-resistant cell lines.^{4,98} In addition,

BC cells in 1 area which are sensitive to ET may eventually gain ET resistance by capturing miRNA-exosomes secreted from nearby ET-resistant cells.⁹⁹

In general, ET resistance is a complicated, not yet fully understood mechanism which brings huge challenges to clinical treatment.

Biomarkers in the ER+ Breast Cancer

ER and PR

ER (ER α) and PR have been used clinically for BC typing and ET selection for decades. It was speculated that the level of ER in BC was related to the benefit of antiestrogen therapy since the 1970s.⁵ To this day, ER remains to be the preferred reference marker for all newly diagnosed BC cases and for patients with metastatic/recurrent settings.^{6,7} PR is often measured along with ER, due to the initial observation that PR is induced by estrogen¹⁰⁰ and competitively binds and alters the chromatin binding sites of ER,¹⁰¹ changing the transcriptional target genes associated with proliferation into that with cell cycle arrest, apoptosis, and differentiation.^{102,103} Clinical studies also found that patients with ER+, PR+ BC are more likely to respond to ET than patients with ER+, PR-.¹⁰⁴ However, it is not clear that PR has an independent predictive value for adjuvant ET, so the detection of PR exists only as a supplementary reference for ER.^{105,106}

***ESR1* Mutation as a Predictive and Prognostic Biomarker**

Studies have suggested that *ESR1* mutations may be a poor prognostic indicator for ER+ MBC. This is because *ESR1* mutations accumulate during endocrine treatment and may produce a more aggressive phenotype through transcriptional changes. Most *ESR1* mutations are deemed to occur in the LBD, leading to persistent, ligand-independent activation of ER.¹⁰⁷ Patients with *ESR1* mutations had shorter progression-free survival (PFS) than patients who did not ($P = .0007$).¹⁰⁸ Takeshita et al¹⁰⁹ found that about 72.7% of MBC patients with *ESR1* mutations developed polyclonal mutations during treatment, suggesting differences in response to drugs for the individual *ESR1* mutations and furthermore, the unique clinical significance for each mutation. *ESR1* mutations may occur at low frequency in primary tumors, but be enriched in metastatic ones. Data from a Fergi clinical trial showed *ESR1* mutations in 9.7% (3/31) of metastatic samples not treated with AIs, comparing to 63% (12/19) of metastatic samples that treated.¹¹⁰

In the early stage, traditional tissue biopsies obtain patient samples through repeated invasive surgery, which has a high detection rate and accuracy. However, this may cause serious harm to patients, and take a long time (a month or more) to get the test results. Nowadays, with advancement of DNA sequencing technology, liquid biopsy has become the first clinical choice due to advantages of noninvasion procedures and short test time. ddPCR and NGS are the 2 most commonly

used methods for liquid biopsies. DdPCR has been the first choice for detecting *ESR1* mutations due to its high sensitivity and accuracy.¹¹¹ NGS can gain larger data, such as gene panels, without prior knowledge of mutations.¹¹² Both approaches are based on the detection of circulating tumor DNA (ctDNA) and cellular free DNA (cfDNA) in patient plasma to identify mutated *ESR1* DNA alleles.

HER2 and PI3CA

Overexpression or amplification of *HER2* and phosphatidylinositol 3-kinase catalytic alpha polypeptide gene (*PIK3CA*) genes detected by genomic assessment and tumor tissue or blood ctDNA analysis are found to be associated with a shorter median PFS.¹¹³ *HER2* gene amplification or overexpression accounts for 15% to 20% of invasive cases. *HER2* detection is now indispensable for all new cases of invasive BC and, if feasible, for recurrent / metastatic lesions. Although *HER2* was originally proposed as a prognostic biomarker for BC, its current use is primarily to predict neoadjuvant, adjuvant therapy, and anti-*HER2* treatment responses in advanced disease. In addition, since anti-*HER2* therapy exerts its anticancer activity at least in part by inhibiting activation of the PI3K signaling pathway through *HER2* overexpression, specific mutations in the p110 α catalytic subunit of PI3K (ie *PIK3CA* gene) can lead to resistance to the anti-*HER2* therapy with trastuzumab or lapatinib.^{114,115} Thus, *PIK3CA* is, to some extent, a secondary marker for predicting the efficacy of the anti-*HER2* therapy.

MicroRNAs

miRNAs are small noncoding RNA molecules composed of about 20–25 nucleotides, which are involved in the regulation of gene expression at the posttranscriptional level and in key processes such as cell proliferation, differentiation, angiogenesis, migration, and apoptosis.¹¹⁶ In serum/plasma, miRNAs are highly stable.¹¹⁷ The miRNAs expression profile has been used as a reference for molecular classification of BC potential biomarkers and guidance for personalized treatment for nearly a decade. Moreover, the roles of miRNAs in the development of BC are diversified. First, miRNAs are expressed differentially in subtypes of BC. Secondly, disease progression in BC patients is promoted by down-regulation of some tumor suppressor miRNAs (such as miR-206)¹¹⁸ and up-regulation of oncogenic miRNAs (such as miR-10b and miR-21).^{118,119} Finally, miRNAs intervene in standard first-line ET by regulation of ER α expression/activity and other oncogenic signaling pathways.

In addition to peripheral blood, the exosome is another site for detecting miRNAs clinically. Exosomes are 50–100 nm-sized vesicles derived from endosomes, secreted from a variety of cell types including cancer cells. The miRNAs are encapsulated in exosomes. Many clinical research data support the exosomal-derived miRNAs as an additional diagnostic tool for the prediction of BC.¹²⁰ The miRNA biomarkers

of ER+ BC are summarized in Table 1 and the clinical information of those miRNAs is summarized in Table 2.

Targeted Therapy for ER+ Breast Cancer

Targeting Aromatase by AIs

Aromatase is an enzyme of the cytochrome P450 family. This enzyme catalyzes the conversion of the adrenal substrate androstenedione to estrogen in peripheral tissues such as the breast and liver. The basic principle of using AIs (anastrozole, letrozole, and exemestane) in BC patients is to block estrogen production by inhibiting aromatase in the tumor and surrounding tissues.¹³⁷ AIs were once the first-line treatment of choice for postmenopausal women with HR+, ER2– metastatic BC (MBC). However, it is common in development of therapeutic relative resistance through acquisition of ligand-independent *ESR1* mutations during AI therapy for metastatic ER+ BC. The rate of *ESR1* mutations was significantly higher in ER+ MBC patients who progressed to AI resistance than in those who did not (25.8% vs 0%; $P = .015$).¹³⁸ Interestingly, a very low rate of *ESR1* mutations was in patients with MBC treated with AIs in adjuvant therapy, but not in metastatic therapy.¹³⁹ This conclusion was also confirmed in a French trial, PADA-1,¹⁴⁰ in which only 3.2% (26 of 811) of patients diagnosed with stage IV HR + BC had *ESR1* mutations detected in any pretreatment ctDNA. In these patients, the only variable significantly associated with *ESR1* mutation detection was exposure to AIs. However, the overall frequency of *ESR1* mutations detected in patients exposed to AIs was only 6.4%, which remains low.¹⁴¹ A plausible explanation for this high prevalence of *ESR1* mutations in metastatic settings after exposure to AI therapy and low prevalence of *ESR1* mutations in adjuvant settings is that hormonal deprivation by AIs may lead to selection of existing *ESR1* mutant subclones.¹⁴² Emerging research found that AI resistance may also be mediated by miRNAs in ER+ BC. In both the letrozole and the anastrozole resistant MCF-7 cell lines, miR-125b, miR-205, and miR-30a were significantly upregulated, while miR-424 downregulated. These miRNA signals are related to regulation of various signaling pathways, including MAPK, focal adhesion, insulin, HER, and mTOR signaling pathways that converge to AKT regulation.⁹⁹

Targeting ER by SERMs

SERMs (selective ER modulators) competitively binds ER to form inactive complexes by preventing coactivator interactions.^{143,144} TAM is the first generation SERM, which has a selective tissue-specific antagonism against ER α in mammary tissue. However, it shows agonism in the endometrium and exhibits agonistic pro-estrogenic properties on the uterine tissue.¹⁴⁵ This results in a seemingly paradoxical increase in the incidence of endometrial cancer (EC) during TAM treatment.¹⁴⁶ Raloxifene, a second-generation SERM, partially compensates this shortcoming and is associated with a lower

Table 1. miRNAs Overexpressed in ER+ Breast Cancer Used for Prognostic and Predictive Biomarkers.

miRNA overexpression	Prognostic		Prediction of		Reference
	Worse	Better	Response	Resistance	
let-7f	-	-	Letrozole	-	121
let-7c	-	Outcome, RFS, OS	-	-	122
let-7b	-	Outcome, RFS, OS	-	-	123
miR-10a, miR-375	-	DFS (TAM treated patients)	TAM	-	124,125
miR-26a,	-	-	TAM	-	126
miR-342	-	-	TAM	-	127,128
miR-10b	Metastasis promoter	-	-	-	129,130
miR-221	OS	-	-	H	131
miR-21	OS	-	-	-	132
miR-29b	-	Metastasis suppressor	-	-	133
miR-193b	-	Metastasis suppressor	-	-	134
miR-30a	-	Outcome, RFS, DFS	-	-	135
miR-30c	-	-	DOX, PTX	-	136

Abbreviations: RFS, relapse-free survival; OS, overall survival; TAM, tamoxifen; DFS, disease-free survival; DOX, doxorubicin; PTX, paclitaxel; H, trastuzumab; ER, estrogen receptor; miRNA, microRNA.

EC risk. Bazedoxifен is a third-generation SERM with SERD activity that triggers proteasomal degradation of ER by altering conformation of ER.¹⁴⁷ Bazedoxifен effectively inhibited BC cell growth regardless of whether the cells were sensitive or resistant to previous TAM treatment.

SERMs resistance is a major challenge in current BC treatment. There are considerable controversy and uncertainty regarding the mechanisms that lead to SERMs resistance. Currently, TAM is still the most common treatment option among multiple treatment regimens in primary ER α -positive BCs.¹⁴⁸ TAM extends the OS of approximately 85% of ER α -positive BC patients to more than 5 years after diagnosis.¹⁴⁹ However, when TAM treatment continues for 5–10 years, almost 1 in 3 women with primary disease receiving adjuvant TAM will develop resistance to the treatment within a variable time frame.¹⁵⁰ TAM resistance may be caused by genetic alterations, such as miRNAs¹⁵¹ and *ESR1* amplification.¹⁵² Although up-regulation of BECN1 promotes autophagy and suppresses the tumorigenic properties of ER+ BC MCF-7 cells,¹⁵³ data from ER+ BC patients treated with TAM and the TAM resistance MCF7 cell line have shown that high BECN1 expression is associated with TAM resistance, high expression of HER2 and reduced patient survival,¹⁵⁴ suggesting that BECN1 is involved in TAM resistance. The miRNAs MiR-221/222, which inhibits the expression of BECN1, thus may enhance TAM sensitivity of ER+ BC. In addition, miR-21, miR-378, miR-27b, miR-342 and other miRNAs are also involved in TAM resistance of ER+ BC cells in vitro. *ESR1* mutations reduce the inhibitory effect of SERMs due to structural changes in the H11-12 ring as well as changes in the H12 antagonist status.¹⁴² It seems that TAM resistance is a partial resistance,¹⁵⁵ increasing the therapeutic dose may be sufficient to overcome TAM resistance. Metastatic TAM-resistant BC, which still expresses functional and highly active ER α in most cases, is difficult to treat and currently has no standard treatment regimens.⁵⁹ By far the best

treatment options for treating metastatic TAM-resistant BC are still ET and high-dose TAM for preventing the proliferation of the cancer cells.

Targeting ER by SERDs

SERDs antagonize ER α and trigger receptor degradation via 26S proteasome, resulting in decreased ER α protein levels. This property makes SERDs as a unique type of inhibitors that block ER α signaling by reducing the protein level of ER α . Fulvestrant is the first and only SERD approved as a therapeutic drug for treatment of advanced BC.¹⁵⁶ Unlike TAM which exerts an agonistic effect, fulvestrant has no agonistic action.¹⁵⁷ Binding affinity of fulvestrant to ER is about 100 times higher than that of TAM.¹⁵⁸ Preclinical and clinical data have shown that fulvestrant is effective even in TAM resistant models.^{159,160} However, intramuscular administration of fulvestrant has poor bioavailability. Thus, development of oral SERDs is particularly important for ER+ BC treatment.

The initial study of fulvestrant approved by the US FDA in 2002 was based on a dose of 250 mg per month intramuscular injection.¹⁶¹ In some studies, a load dose of 500 mg was also given. Median-free survival in the CONFIRM trial was 5.5 and 6.5 months in the 250 and 500 mg dose groups, respectively (hazard ratio 0.80 [95% confidence interval 0.68-0.94]); $P = .006$. Median OS was 22.3 months in the 250 mg dose group and 26.4 months in the 500 mg dose group (hazard ratio 0.81 [95%CI 0.69-0.96]; nominal $P = .02$).^{162,163} Thus, 500 mg is recommended for postmenopausal women with HR + MBC patients who have failed previous hormone therapy. The first phase II study compared fulvestrant (500 mg/month) with the AI anastrozole (1 mg/day) in postmenopausal HR+ locally advanced BC or MBC.¹⁶⁴ The 6-month clinical benefit rate was 72.5% for fulvestrant versus 67.0% for anastrozole. In the follow-up analysis, the median time to progression of fulvestrant was 23.4 months, anastrozole was 13.1

Table 2. miRNAs Overexpressed in ER+ Breast Cancer Used in Clinic or Clinic Trials.

miRNA overexpression	Known mechanism	Sample sources	Number of samples	Methods	Reference
let-7f	Tumor suppressor miRNA in breast cancer (directly targeted the aromatase gene)	Clinical (obtained from the Celecoxib AntiAromatase Neoadjuvant Trial (CAAN Trial))	90 patients	qRT-PCR, Western blotting, Immunohistochemistry, Luciferase reporter assay	121
let-7c	Tumor suppressor miRNA in breast cancer (directly targeted the <i>HER2</i> gene)	Cell line (MCF-7) from TCGA	-	NanoString, qRT-PCR, Patient sample analysis, Western Blot	122
let-7b	Tumor suppressor miRNA in breast cancer (directly targeted the <i>BSG</i> gene)	Clinical (First Affiliated Hospital of Anhui Medical University, China)	102 samples between 2001 and 2002	TMA construction, <i>In situ</i> hybridization, Immunohistochemical staining	123
miR-10a, miR-375	MiR-10a is an Oncogenic miRNA in breast cancer (directly targeted the <i>HOXA1</i> gene); MiR-375 is a tumor suppressor miRNA in breast cancer (directly targeted the <i>MTDH</i> gene)	Clinical (Robert Bosch Hospital (RBK), Stuttgart, Germany)	2689 patients between 1986 and 2005	MicroRNA microarray, qRT-PCR	124,125
miR-26a,	Suppresses <i>ESR1</i> expression (directly targeted the <i>ESR1</i> gene)	Clinical	235 patients between 1981 and 1996	qRT-PCR	126
miR-342	Tumor suppressor miRNA in breast cancer (regulated genes in multiple tamoxifen actions including both apoptosis and cytostasis.)	Clinical (the Department of Pathology, Massachusetts General Hospital, Boston, MA)	791 patients	<i>In situ</i> Apoptosis Assay (TUNEL)	127,128
miR-10b	Oncogenic miRNA in breast cancer (inhibits synthesis of the HOXD10 protein, permitting the expression of the pro-metastatic gene product)	Collected at the University of Ferrara (Italy), Istituto Nazionale dei Tumori, Milano (Italy), and Thomas Jefferson University (Philadelphia, PA).	76 samples	miRNA microarray, Northern blotting	129,130
miR-221	Suppresses <i>ESR1</i> expression (directly targeted the <i>ESR1</i> gene)	Clinical (Department of Breast Surgery, Sun-Yat-Sen Memorial Hospital, China)	125 samples	qRT-PCR	131
miR-21	Oncogenic miRNA in breast cancer (associated with poor trastuzumab response.)	Clinical (Department of Breast Surgery, Sun-Yat-Sen Memorial Hospital, China)	32 patients	<i>In Situ</i> Hybridization, Immunohistochemistry, MicroRNA microarray, qRT-PCR, Northern blotting	132
miR-29b	Tumor suppressor miRNA in breast cancer (inhibits metastasis)	Cell lines (MDA-MB-231, T47D) from ATCC	-	qRT-PCR, Immunostaining and histology	133
miR-193b	Suppresses <i>ESR1</i> expression (directly targeted the <i>ESR1</i> gene)	Clinical (Department of Breast Surgery at Shanghai Cancer Hospital, China)	435 samples	qRT-PCR, MicroRNA microarray, Western blotting, Immunohistochemical staining	134
miR-30a	Tumor suppressor miRNA in breast cancer (decrease the vimentin-mediated migration and invasiveness)	Clinical (Chung Shan Medical University Hospital, Taichung, Taiwan, China)	221 patients	MicroRNA microarray, Western blotting, qRT-PCR, Dual luciferase reporter assay	135

(continued)

Table 2. (continued)

miRNA overexpression	Known mechanism	Sample sources	Number of samples	Methods	Reference
miR-3 30c	Predictor for clinical benefit of tamoxifen therapy	Clinical	246 patients between 1981 and 1995	qRT-PCR, Pathways and global testing	¹³⁶

Abbreviations: TMA, tissue microarray; ER, estrogen receptor; miRNA, microRNA.

Table 3. Endocrine and Targeted Drugs of Breast Cancer and Their Targets.

Drugs	Target	Stage	References
Aromatase inhibitors (anastrozole, letrozole, exemestane)	Aromatase	Approval (FDA)	137,138,183
Tamoxifen (SERM)	Estrogen receptor	Approval (FDA)	144,183
Fulvestrant (SERD)	Estrogen receptor	Approval (FDA)	156,183
Trastuzumab, lapatinib, pertuzumab, neratinib	HER2	Approval (FDA)	183
Cyclin-dependent kinase 4/6 inhibitors (palbociclib, ribociclib, abemaciclib)	cyclin-dependent kinase 4/6	Approval (FDA)	175,183
Alpelisib	PI3K	Approval (FDA)	183,184
Megestrol	progesterone receptor	Approval (FDA)	183
Goserelin	GnRH receptor	Approval (FDA)	183
Pamidronate	farnesyl pyrophosphate synthase	Approval (FDA)	183
Everolimus	mTOR	Approval (FDA)	183,185
Olaparib, Talazoparib	PARP	Approval (FDA)	183
Bevacizumab	VEGF	Approval (FDA)	183
Bazedoxifene(mixed SERM/SERD)	Estrogen receptor	Clinical trial	186
H3B-5942 (SERCA)	Estrogen receptor	Clinical trial	174
Fluoxymesterone, testosterone	Androgen receptor	Clinical trial	82
Bortezomib	Proteasome	Clinical trial	187
FK228, Vorinostat	Histone deacetylase	Clinical trial	188,189
Venetoclax	BCL-2	Clinical trial	190
Alisertib	Aurora Kinase A	Clinical trial	191
FRAX1036	PAK1	Clinical trial	192
Capivasertib, Ipatasertib	AKT	Clinical trial	193,194
Dasatinib, Saracatinib, Bosutinib	SRC	Clinical trial	195
Vorinostat, Entinostat, Tucidinostat	HDAC	Clinical trial	196,197
ARV-471 (Proteolysis targeting chimeras, PROTACs)	Estrogen receptor	Clinical trial	198
Buparlisib, Taselisib	PI3K	Clinical trial	184

Abbreviations: SERD, selective estrogen receptor degrader; SERM, selective estrogen receptor modulator; FDA, Food and Drug Administration; HER2, human epidermal growth factor 2; SERCA, selective estrogen receptor covalent antagonist; PAK1, protein-activated kinase 1; SRC, steroid receptor co-activator.

months.¹⁶⁵ Final OS analysis showed that the median OS of fulvestrant (54.1 months) was longer than anastrozole (48.4 months; hazard ratio 0.70 [95%CI 0.50–0.98]; $P = 0.04$).¹⁶⁶ The results of this study have shown for the first time that fulvestrant is more effective in first-line treatment than anastrozole. These findings suggest that fulvestrant is more effective than anastrozole in locally advanced BC or MBC patients who have not previously received ET.¹⁶⁷

Like TAM, fulvestrant resistance is also partly due to *ESR1* mutations. *ESR1* Y537S was identified as the mutation most likely to promote resistance to fulvestrant.^{168,169} Compared with other mutants, the *ESR1* Y537 mutant requires the highest dose to completely block transcriptional activity and cell proliferation.⁵⁶ The biochemical mechanisms of fulvestrant resistance have not yet been elucidated, new SERMs or SERDs or high doses of TAM or fulvestrant may be the effective

therapeutic strategies to overcome resistance associated with *ESR1* mutations.¹⁷⁰

In addition, some miRNAs are associated with fulvestrant resistance. MiR-221/222 was up-regulated in fulvestrant resistant cell lines.⁴ MiR-375, miR-21, and miR-214 may also be involved in fulvestrant resistance by regulating autophagy.^{171–173}

Targeting ER by Selective ER Covalent Antagonists

Selective ER covalent antagonist (SERCA) is a novel covalent ER α antagonist, and the experimental oral drug H3B-5942 is considered to be the first SERCA. H3B-5942 is capable of covalently binding cysteine residues (C530) both in ER α WT and ER α mutants, forcing ER α to fold into a unique conformation, thus effectively inhibiting ER α -dependent transcription in

Table 4. Ongoing Clinical Studies of Novel Drugs in ER+ BC Patients (Registered in Clinical Trials in clinical trials.gov from January 1, 2021 to August 25, 2021).

NCT Number	Status	Conditions	Interventions
NCT04802759	Recruiting	<ul style="list-style-type: none"> Inoperable, locally advanced or metastatic, ER-positive BC 	<ul style="list-style-type: none"> Drug: Giredestrant, abemaciclib, ipatasertib, inavolisib, ribociclib, everolimus
NCT04738292	Recruiting	<ul style="list-style-type: none"> ER-positive BC HER2-negative BC Metastatic cancer 	<ul style="list-style-type: none"> Drug: Onapristone, fulvestrant
NCT04727632	Recruiting	<ul style="list-style-type: none"> Estrogen receptor positive BC 	<ul style="list-style-type: none"> Drug: Fluoroestradiol
NCT04711252	Recruiting	<ul style="list-style-type: none"> ER-positive HER2-negative BC 	<ul style="list-style-type: none"> Drug: AZD9833, anastrozole, anastrozole placebo, AZD9833 placebo, palbociclib, LHRH agonist
NCT04601116	Recruiting	<ul style="list-style-type: none"> BC Female Estrogen receptor positive tumor 	<ul style="list-style-type: none"> Drug: Atorvastatin 80 Mg Oral Tablet, Placebo oral tablet
NCT04443348	Recruiting	<ul style="list-style-type: none"> Triple Negative BC Hormone Receptor Positive (HR +), HER2- negative BC Biopsy-proven, positive lymph node(s) 	<ul style="list-style-type: none"> Radiation: Radiation therapy boost Drug: Pembrolizumab, paclitaxel, carboplatin, cyclophosphamide, doxorubicin, capecitabine
NCT04669587	Recruiting	<ul style="list-style-type: none"> Estrogen receptor-positive HER2-negative Locally advanced BC Metastatic BC 	<ul style="list-style-type: none"> Drug: ZB716, palbociclib
NCT04964934	Recruiting	<ul style="list-style-type: none"> ER-positive HER2-negative BC 	<ul style="list-style-type: none"> Drug: AZD9833, AZD9833 Placebo, anastrozole, anastrozole placebo, letrozole, letrozole placebo, palbociclib, abemaciclib, LHRH agonist

ER, estrogen receptor; BC, breast cancer; HER2, human epidermal growth factor receptor 2; LHRH, luteinizing hormone-releasing hormone; +, positive; -, negative.

primary and MBC cells. In vivo, H3B-5942 showed antitumor activity superior to fulvestrant therapy in BC xenograft models with *ESR1* WT or *ESR1* Y537S mutation.¹⁷⁴ Further clinical trials of H3B-5942 and development of new generation of SERCAs are currently under study.

CDK4/6 inhibitors

CDK4/6 are cyclin-dependent kinases (CDKs) that regulate the G1-to-S phase of the cell cycle and play a key role in ER+ BC.¹⁷⁵ CDK4/6 inhibitors inhibit the phosphorylation of the tumor suppressors retinoblastoma (RB) protein. This, in turn, promotes the binding of RB to E2F and blocks E2F-mediated

oncogenic transcription, thereby preventing cell cycle progression from G1 phase to S phase. Three CDK4/6 inhibitors, palbociclib, ribociclib, and abemaciclib, are currently approved or in clinical trials. They are all commonly used in combination with other drugs, such as AIs and fulvestrant. Palbociclib is the first approved CDK4/6 inhibitor drug. Abemaciclib has been approved by the FDA as a monotherapy for refractory, severely pretreated ER+/HER2-MBC patients. In addition, CDK4/6 inhibitors exert anticancer effects by interfering with the immune system. CDK4/6 inhibitors enhance PD-L1 antigen presentation and cytotoxic T-cell activity in tumor cells but inhibit the proliferation of regulatory T cells,¹⁷⁶ suggesting that treatment with CDK4/6 inhibitors may increase

response to immunotherapy.¹⁷⁷ CDK4/6 inhibitors have emerged as the first-line and second-line treatment of choice in postmenopausal and premenopausal/peri-menopausal women with ER+/HER2– MBC. Unfortunately, up to 20% of ER+/HER2– MBC cases are intrinsically resistant to CDK4/6 inhibitors, and virtually all patients who initially respond to the drugs will develop acquired resistance. *ESR1* mutations and activation of the PI3K/AKT/mTOR pathway are common events in the drug-resistance.^{178,179} Currently, the mechanisms of intrinsic and acquired resistance to CDK4/6 inhibitors are still poorly understood.¹⁸⁰ Mechanism studies and combination therapy are ongoing.

Other Drugs and Combined Therapies

ET combined with a variety of targeted inhibitors has been widely tried in the clinical treatment of BC. It should be noted that the endocrine treatment is only one of the solutions of ER+ BC, chemotherapy is also clinically used to treat MBC or combined with endocrine drugs, such as capecitabine, an oral fluoropyrimidine which has lower side effects, is approved as monotherapy for MBC patients who are resistant to paclitaxel and further anthracycline therapy.¹⁸¹ For more information about chemotherapy see.¹⁸² The inhibitors targeting ER signaling pathways have been used in combination with ET and shown to increase the sensitivity of BC treatment and prolong patients' PFS. Three separate phase III clinical trials (PALOMA-3, Monaleesa-3 and MONARCH2) evaluated fulvestrant in combination with the CDK4/6 inhibitors palbociclib, ribociclib, and abemaciclib, respectively. The combination of fulvestrant with each of CDK4/6 inhibitors significantly extended PFS compared to fulvestrant alone.^{10–12} Therefore, CDK4/6 inhibitors had been approved in combination with fulvestrant for the first-line treatment of HR+/HER2– ABC or MBC with endocrine resistance. The same conclusion was achieved in a combination of CDK4/6 inhibitors with AIs in postmenopausal patients with the same disease setting. A brief summary of the endocrine and targeted drugs of BC and the details of ongoing clinical trials are presented in Table 3 and Table 4.

Conclusions

Overactivation of ER α makes ER+ BC more invasive and refractory. It is important to find out more precisely predicted and prognostic biomarkers and to develop novel drugs for ER+ BC and ET resistance therapy. To date, solutions targeting multiple mechanisms (*ESR1* mutations, proteasomal inhibition, kinases, coactivators, etc) of ER biological activities have been established for the BC patients with ER+ setting as well as ET resistance. Because of in-depth exploration of ER signaling pathways, new drugs targeting these mechanisms have been developed with satisfactory results in clinic or clinical trials. In addition, the ER/AR, ER/PR or ER α /ER β crosstalks may define novel targets for ER+ BC therapeutic innovation, especially for ET resistance. Currently, these crosstalks in ET

resistance have not been fully investigated. Endocrine drugs combined with targeted inhibitors have shown to be more effective than monotherapy in clinical treatments. For example, a combination of fulvestrant with targeted inhibitors, such as CDK 4/6 or PI3K inhibitors, is a rational approach for ER+ BC treatment. The only SERD drug fulvestrant, due to its high ER binding affinity and mild side effects, is a promising endocrine drug for ER+ BC therapy, particularly for the *ESR1*-mutation patients with relapse on or after adjuvant AIs. However, the current limited bioavailability of intramuscular fulvestrant limits the effectiveness of the drug, and it is necessary to develop oral SERDs to overcome this limitation. In the future, the key steps in improving ET for ER+ BC are to overcome the drug resistance, discover more therapeutic targets of ER+ BC and develop more effective combination therapies.

Acknowledgments

The authors would like to thank Dr Wannian Yang for his critical comments on this manuscript.

Declaration of Conflicting Interests

The authors declared no potential conflicts of interest with respect to the research, authorship, and/or publication of this article.

Funding

The authors disclosed receipt of the following financial support for the research, authorship, and/or publication of this article: This work was supported by the National Natural Science Foundation of China, (grant number Nos. 81871888, 82172942).

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