

# Derailed Estrogen Signaling and Breast Cancer: An Authentic Couple

Bramanandam Manavathi, Oindrilla Dey, Vijay Narsihma Reddy Gajulapalli, Raghavendra Singh Bhatia, Suresh Bugide, and Rakesh Kumar

Molecular and Cellular Oncology Laboratory (B.M., O.D., V.N.R.G., R.S.B., S.B.), Department of Biochemistry, School of Life Sciences, University of Hyderabad, Hyderabad 500046, India; Cancer Research Program (R.K.), Rajiv Gandhi Centre for Biotechnology, Thiruvananthapuram 695014, India; and Department of Biochemistry and Molecular Biology (R.K.), The George Washington University, Washington, D.C. 20052

Estrogen or 17 $\beta$ -estradiol, a steroid hormone, plays a critical role in the development of mammary gland via acting through specific receptors. In particular, estrogen receptor- $\alpha$  (ER $\alpha$ ) acts as a transcription factor and/or a signal transducer while participating in the development of mammary gland and breast cancer. Accumulating evidence suggests that the transcriptional activity of ER $\alpha$  is altered by the action of nuclear receptor coregulators and might be responsible, at least in part, for the development of breast cancer. In addition, this process is driven by various posttranslational modifications of ER $\alpha$ , implicating active participation of the upstream receptor modifying enzymes in breast cancer progression. Emerging studies suggest that the biological outcome of breast cancer cells is also influenced by the cross talk between microRNA and ER $\alpha$  signaling, as well as by breast cancer stem cells. Thus, multiple regulatory controls of ER $\alpha$  render mammary epithelium at risk for transformation upon deregulation of normal homeostasis. Given the importance that ER $\alpha$  signaling has in breast cancer development, here we will highlight how the activity of ER $\alpha$  is controlled by various regulators in a spatial and temporal manner, impacting the progression of the disease. We will also discuss the possible therapeutic value of ER $\alpha$  modulators as alternative drug targets to retard the progression of breast cancer. (*Endocrine Reviews* 34: 1–32, 2013)

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## I. Introduction

**B**reast cancer is heterogeneous in nature that originates from the mammary epithelial cells. Despite advances made in the understanding of the molecular and cellular events that underlie the disease, it remains the leading cause of cancer deaths among females worldwide (1). A woman's risk of breast cancer is influenced by her reproductive history, *i.e.*, lifetime exposure to reproduc-

Abbreviations: AIB1, Amplified in breast cancer-1; AKT, serine/threonine protein kinase; ALDH, aldehyde dehydrogenase; ATM, ataxia telangiectasia mutated; ATR, ataxia telangiectasia and rad3-related protein; BCAS3, breast carcinoma amplified sequence 3; BRCA1, breast cancer 1; BrCSC, breast cancer stem cell; BT-IC, breast tumor-initiating cell; CDK4, cyclin-dependent kinase; Ciz1, CDKN1A-interacting zinc finger protein 1; DACH1, dachshund homolog 1; DBC1, deleted in breast cancer 1; DNAPK, DNA-dependent protein kinase; E2, estrogen or 17 $\beta$ -estradiol; Efp, estrogen-responsive finger protein; EGFR, epidermal growth factor receptor; EMT, epithelial-mesenchymal transition; ER, estrogen receptor; ERE, estrogen response element; GPR30, G protein-coupled receptor 30; GREB1, growth regulation by estrogen in breast cancer 1; GSK3 $\beta$ , glycogen synthase kinase 3 $\beta$ ; HAT, histone acetyl transferase; HDAC, histone deacetylase; HPII, hematopoietic PBX-interacting protein 1; MaSC, mammary stem cell; miRNA, microRNA; MTA, metastasis-associated protein; MTA1s, MTA1 short form; NCOR1, nuclear receptor corepressor 1; NuRD, nucleosome remodeling and histone deacetylation complex; PAK1, serine/threonine p21-activated kinase; PELP1, proline, glutamic acid and leucine-rich protein; PHB, prohibitin; PI3K, phosphatidylinositol 3 kinase; PKA, protein kinase A; PR, progesterone receptor; PRMT1, protein arginine N-methyltransferase 1; REA, repressor of ER activity; SAFB, scaffold attachment factor B; SCID, severe combined immunodeficiency; SERM, selective ER modulator; SIRT1, sirtuin 1; S6K1, S6 kinase 1; SP, specificity protein; TFF1, trefoil factor 1; UTR, untranslated region.

tive hormone milieu, primarily estrogen (2).  $17\beta$ -Estradiol or estrogen (we refer to both hereafter as E2), a steroid hormone that plays a significant role in mammary gland development, serves as one of the main risk factors for breast cancer development. E2 actions are mainly mediated by two receptors, estrogen receptor- $\alpha$  (ER $\alpha$ ) and - $\beta$  (ER $\beta$ ). Experimental and clinical evidence suggests that ER $\alpha$  subtype is the major culprit for the development of the majority of the breast cancers (3–5). Therefore, antiestrogens that antagonize E2 binding to the receptor and E2 synthesis inhibitors (aromatase inhibitors) were developed to treat breast cancers (6).

The ER $\alpha$  is a ligand-dependent transcription factor that regulates genes involved in cell proliferation, differentiation, and migration (7). Therefore, deregulated actions of ER $\alpha$  signaling are associated with breast cancer development (8). In addition to the classical genomic actions exerted by ER $\alpha$ , emerging studies suggest that extranuclear signaling, coregulators, posttranslational modifications, and now microRNA (miRNA) add several levels of complexity to the action of ER $\alpha$  in breast cancer cells. Because deregulated expressions/actions of all of these modulators of ER $\alpha$  are found to correlate with breast cancer risk, the mammary epithelium is at high risk for transformation into a cancer cell. Therefore, the interrelationship between the ER $\alpha$  signaling and breast cancer development looks strong and attractive because the majority of breast cancers are ER $\alpha$ -dependent. In brief, breast cancer is a signaling disorder wherein deregulation of critical signaling pathways contributes to breast cancer pathogenesis. Here, we will summarize new insights into the E2-ER $\alpha$  signaling axis and its deregulation in breast cancer.

## II. E2 Signaling in Mammary Gland Development

The human mammary gland undergoes several major developmental changes involving cell proliferation, differentiation, apoptosis, and morphogenesis in coordination with the influence of various endocrine and paracrine factors (9, 10). Using endocrine disruption and replacement studies in rodents, it was established that female reproductive hormones such as E2 and progesterone are key regulators of postnatal development of mammary gland (11). The mammary gland at birth is underdeveloped, but with the onset of puberty, E2 initiates the maturation of the mammary gland together with progesterone (9, 12). In particular, E2 triggers ductal elongation during puberty (13, 14). The precise role of E2-mediated actions in mammary gland came from receptor knockout studies in mice. Deletion of ER $\alpha$ , which mediates the E2 action in mice, results in a rudimentary ductal system that fails to branch

out (15). Therefore, in ER $\alpha$ -null mice, mammary glands are normal before puberty (16). However, after the onset of puberty, terminal end buds remained absent, and ducts failed to invade into the fat pad beyond the nipple, indicating the strong influence of ER $\alpha$  in initiation of mammary gland development (17). Recent studies also established that ER $\alpha$  not only regulates ductal morphogenesis during puberty but is also involved in alveologenesis during pregnancy and lactation (18). By contrast, ER $\beta$ -null mice show no difference in morphology compared with the mammary glands of wild-type littermates, indicating that ER $\alpha$  (but not ER $\beta$ ) regulates mammary gland development (19). These findings explicitly established the importance of ER $\alpha$  in mediating E2 actions in the development of mammary gland. Interestingly, ER $\beta$  seems to antagonize proliferative activity of ER $\alpha$  in breast cancer cells, suggesting that ER $\beta$  plays a tumor-suppressive role with respect to breast tumor development (20, 21).

## III. ER $\alpha$ Genomic Signaling in Breast Cancer

### A. ER $\alpha$ genomic action in breast cancer

The first link between steroid hormone signaling and breast cancer came from Beatson's observation in 1896 (22). He reported in *Lancet* that the metastatic breast cancer patients who underwent bilateral oophorectomy showed regression of tumors implying the rationale for hormone therapy for the treatment of breast cancer (22). Several decades later, O'Malley *et al.* (23) observed changes in transcriptional message upon E2 stimulation of the chick oviduct, suggesting the role of E2 in transcription regulation. Immediately after this finding, an extensive search for an ER was pioneered in 1971 by Jensen *et al.* (24). As a result, a specific ER was discovered that was present in breast tumors, and its expression level could correlate to endocrine disruptions, thereby establishing a link between cancer and E2 (24). Later on, overwhelming evidence showed the overexpression of ER $\alpha$  in 60–70% of breast cancers, and so this receptor has been treated as a therapeutic target for breast cancers (25–27).

The ER $\alpha$  (classified as NR $_3A_1$ ) is a ligand-dependent transcription factor that belongs to the nuclear receptor superfamily of proteins with defined functional domains that can both activate and repress the expression of genes (28). In the absence of ligand, ER $\alpha$  is sequestered in complex with an inhibitory heat shock protein in target cell nuclei. Upon ligand binding, the receptor detaches from the heat shock protein complex and undergoes dimerization (29). The interaction of ER $\alpha$  with target gene promoters can occur either directly, through specific estrogen response elements (ERE), or indirectly through contacts

with other DNA-bound transcription factors such as activation protein 1, specificity protein (SP) 1, or nuclear factor  $\kappa$ -light-chain-enhancer of activated B cells. Once tethered to DNA, the receptor can either positively or negatively regulate target gene transcription (30). ER $\alpha$  regulates many genes that are involved in mammary gland development, and their altered expression is associated with breast cancer progression (31). Initially, the single gene approach has identified few target genes for ER $\alpha$ . The egg-white proteins in chicken oviduct and *Xenopus laevis* vitellogenin gene are among the first ER $\alpha$  target genes to be identified (32, 33). Later, pS2/trefoil factor 1 (TFF1), c-MYC, and cyclin D1 were identified as E2-responsive genes in breast cancer cells (34–36). The functions of pS2/TFF1 in breast cancer are not fully understood; however, a few reports show that ectopic expression of pS2/TFF1 in MCF7 cells is associated with increased cell proliferation, anchorage-independent growth, migration, and motility (37). pS2 is selectively expressed in breast cancers and positively correlates with the ER $\alpha$  status in different grades of breast tumors (38–40). In the recent past, many novel ER $\alpha$  target genes have been identified, *e.g.*, *FOXM1*, *Efp*, *PELP1*, *CIZ1*, *GREB1*, *etc.* Several of these gene expressions are associated with breast cancer progression. For instance, *FOXM1* mediates mitogenic functions of E2, and its deregulation contributes to anti-estrogen resistance (41). Estrogen-responsive finger protein (*Efp*) is an E2-responsive gene (42). *Efp* possesses a RING finger B-box coiled-coil (RBCC) motif and displays ubiquitin ligase activity. *Efp* promotes breast cancer cell growth by targeting 14-3-3 $\delta$ , a p53 target gene that inhibits cell cycle progression, for proteasomal degradation (43). *Efp* expression is positively associated with lymph node status and ER $\alpha$  status, while negatively correlated with 14-3-3 $\sigma$  (44). Proline, glutamic acid, and leucine-rich protein (*PELP1*), which serves as a coactivator of ER $\alpha$ , is also a genomic target of E2; it is involved in ER $\alpha$  cross talk with the cell cycle machinery and mediates E2-induced breast cancer cell proliferation, and its overexpression confers tamoxifen resistance (45–47). Likewise, CDKN1A-interacting zinc finger protein 1 (*Ciz1*), a coactivator of ER $\alpha$ , is responsive to E2 and confers hypersensitivity to E2 in breast cancer cells upon its overexpression (48). Growth regulation by estrogen in breast cancer 1 (*GREB1*) is another ER $\alpha$  target gene that mediates E2-induced proliferation in breast cancer cells (49). Similarly, metastasis-associated protein 3 (*MTA3*) is activated by E2 and regulates epithelial-mesenchymal transition (EMT) and breast cancer metastasis (50, 51).

With successful completion of the human genome project and introduction of novel technologies, a plethora of novel targets of ER $\alpha$  has been identified. Using chromo-

somal walking and carboxy terminus of HSP70-binding protein, Brown and colleagues (52) revealed that only a minor fraction of ER $\alpha$  binding sites are located in promoter regions, whereas a vast majority is located at long distances from target genes. Similarly, using the circular chromosome conformation capture method, it has been shown that multiple ER $\alpha$  binding sites interact at classical ER $\alpha$  target genes of pS2/TFF1, GREB1, carbonic anhydrase 12 (CA12), and B-cell lymphoma 2 via looping to regulate transcription (53–55). Fullwood *et al.* (56) mapped the chromatin interaction network bound to ER $\alpha$  in the human genome by utilizing chromatin interaction analysis by paired end tag sequencing and discovered that most high-confidence ER $\alpha$ -binding sites are anchored at gene promoters through long-range chromatin interactions like looping (Fig. 1). Similar three-dimensional chromatin interaction studies in cancer patient samples revealed that the clinical outcome of the breast cancers is decided at the level of chromatin interaction by ER $\alpha$  (57). Furthermore, this study also demonstrates that drug-resistant breast cancers still recruit ER $\alpha$  to the chromatin but with different binding abilities, and such a differential ER $\alpha$ -binding pattern in patients with poor outcome is not due to the selection of a rare subpopulation of cells as previously thought, but is due to the FOXA1-mediated reprogramming of ER $\alpha$  binding. Thus, different clinical outcomes in breast cancer will derive from distinct combinations of cis-regulatory elements regulated by ER $\alpha$  in cancer cells.

## B. ER $\alpha$ coregulators in breast cancer

Accumulating evidence shows that ER $\alpha$  target gene expression results from the coordinated actions of ER $\alpha$  and its coregulators, which include both coactivators and corepressors (58–60). Most of these coregulators contain a LXXLL motif (L, leucine; X, any amino acid) that interacts with the ligand binding domain of ER $\alpha$ . These coregulators more often are associated with various enzymatic properties, *e.g.*, acetyltransferase, deacetylases, methyltransferase, phosphokinase, ubiquitin ligase, and ATPases, that regulate chromatin remodeling, thereby directly or indirectly regulating target gene expression (60–62). For instance, coactivator p300, a histone acetyl transferase (HAT), acetylates histones on ER $\alpha$ 's target gene chromatin, which facilitates opening of ER target chromatin and recruitment of transcription initiation complex that activates E2-responsive gene transcription (61). SWI/SNF (SWI $\alpha$ /Sucrose Non-Fermentable) complex, an ATP-dependent chromatin remodeling complex, is also known to regulate ER $\alpha$  transcriptional activity (63).

Figure 1.

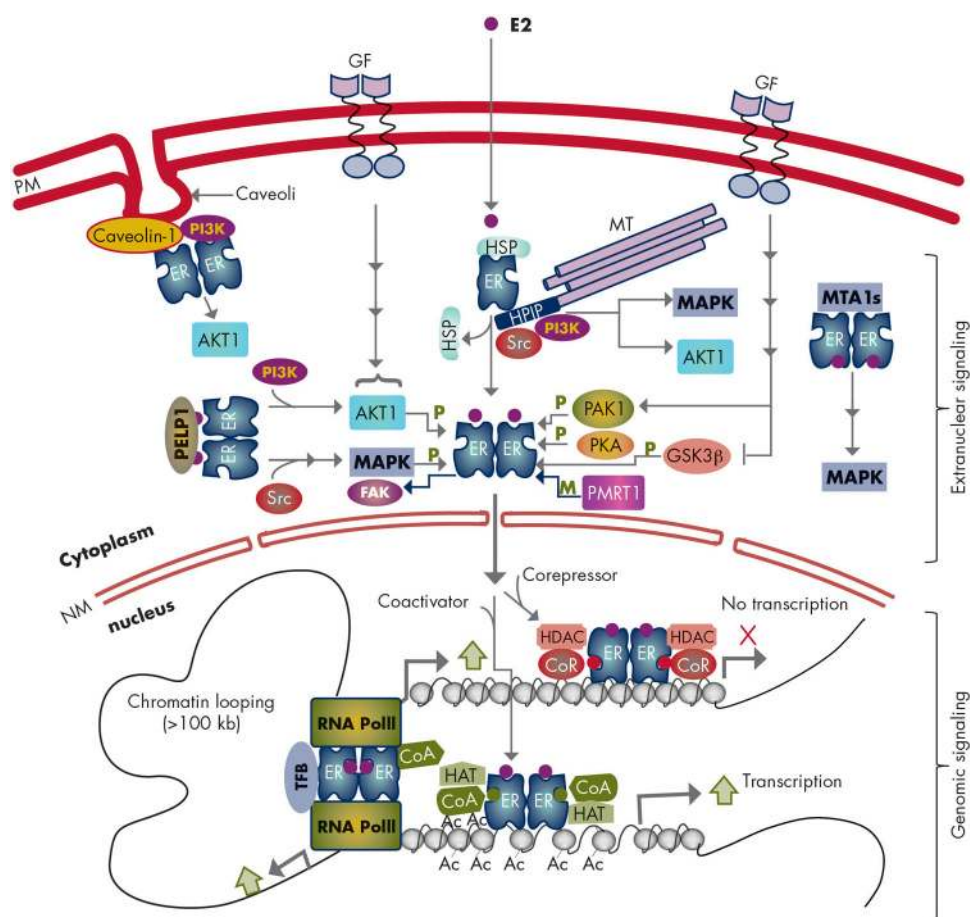


Figure 1. Hypothetical model illustrates the E2-ER $\alpha$  signaling pathway involving both genomic and extranuclear signaling pathways. *Extranuclear signaling of E2/ER $\alpha$* : Several signaling proteins like PI3K, Src, HPIP, MTA1s, etc., interact with ER $\alpha$  in the cytoplasm to activate E2 extranuclear signaling. Rapid E2 signaling promotes interaction of ER $\alpha$  with caveolin-1 in the caveoli and activates the PI3K/AKT pathway. Sequestration of ER $\alpha$  by HPIP in the cytoplasm through a microtubule scaffolding mechanism facilitates PI3K/Src recruitment, and activation of AKT/MAPK pathways occurs in response to rapid E2 signaling. MTA1s also activate E2 rapid signaling through cytoplasmic sequestration of the receptor. In response to rapid E2/ER $\alpha$  signaling, PELP1 could activate AKT and MAPK pathways by interaction with PI3K and Src kinase, respectively. Activation of downstream signaling kinases such as AKT, MAPK, PAK1, etc., by growth factor signaling led to phosphorylation of ER $\alpha$ , which could further impact its nuclear activity. Phosphorylation of ER $\alpha$  by GSK3 also enhances ER $\alpha$  transcriptional activity. Methylation of ER $\alpha$  at arginine 260 by PRMT1 involves activation of FAK signaling in response to E2 rapid signaling. *Genomic signaling of E2/ER $\alpha$* : Ligand binding to ER $\alpha$  ensures heat shock protein (HSP) dissociation and the receptor's nuclear entry. Upon nuclear translocation, ligand-bound receptor binds to its target genes to activate the transcription. If the HDAC complex is recruited to ER $\alpha$  chromatin, ER $\alpha$ -dependent transcription is repressed, whereas HAT complex recruitment activates ER $\alpha$ -dependent transcription. This model also illustrates that ER $\alpha$  can regulate the gene expression by extensive chromatin looping to bring genes together for coordinated transcriptional regulation. PM, Plasma membrane; NM, nuclear membrane; P, phosphorylation; M, methylation; GF, growth factor; MT, microtubules; CoA, coactivator; CoR, corepressor; ER, estrogen receptor  $\alpha$ ; HDAC, histone deacetyl transferase; RNA Pol II, RNA polymerase II; TFB, transcription factor binding proteins; FAK, focal adhesion kinase.

### 1. Coactivators in breast cancer

There is compelling evidence that deregulation of coregulator expression is associated with tumor progression, cancer cell migration, invasion, metastasis, and drug resistance (64–68). Table 1 summarizes the list of coregulators deregulated in breast cancer. According to ONCOMINE data, 38% of coregulators have shown deregulated expression in various diseases including cancer (98). Likewise, overexpression of coregulators like amplified in breast cancer-1 (AIB1)/SRC3, GRP1, PELP1, MUC1, breast carcinoma amplified se-

quence 3 (BCAS3), Ciz1, SRA, etc., has been shown to induce breast carcinogenesis (68, 98). AIB1/SRC3 and BCAS3 are both ER $\alpha$  coactivators known to be amplified, overexpressed, and associated with tamoxifen resistance in breast cancers (69, 70, 99, 100). A recent clinical study using 560 human breast tumor tissues found the AIB1 expression along with expression of genes involved in cell migration and invasion such as polyomavirus enhancer activator 3 and matrix metalloproteinases 2 and 9, suggesting a positive correlation of AIB1 expression with tumor metastasis

**TABLE 1.** List of deregulated ER $\alpha$  coregulators in human breast cancers

Coregulators deregulated in breast cancer	Ref.
Coactivator	
AIB1/SRC-3	69
BCAS3	70
BRG1	71
CARM1	72
CBP	64
CITED1	73
Cyclin D1	74
DBC1	75
E6-AP	76
GCN5L2	65
MUC1	77
p300	78
PELP1	79
SRA	80
SRC1/GRIP1	81, 82
SRC2/TIF2	83
Corepressor	
ATBF1	84
BRCA1	85
BRCA2	86
MTA1	87
MTA1s	88
MTA2	89
MTA3	51
NCOR1	65
NSD1	90
REA	91
RIP140	92
SAFB1/2	93
Smad4	94, 95
SMRT	96
DACH1	97

(101). The AIB1 coactivator activates ER $\alpha$ -dependent transcription by recruiting HAT such as p300 and P/CAF to ER $\alpha$  target gene chromatin (102). AIB1 interact with ER $\alpha$  in a ligand-dependent fashion, and such interaction and coactivator activity of AIB1 is potentiated by CK1 $\delta$  and PKC $\zeta$ -mediated phosphorylation of AIB1 in breast cancer cells (103, 104). Because suppression of AIB1 levels leads to ER $\alpha$  stabilization in the presence of E2, a reduced recruitment of ER $\alpha$  to its target gene promoters was also reported (105). AIB1 thus plays a dual role in regulating ER $\alpha$  activity, one in recruiting HAT involved in chromatin remodeling and the other in regulating ER $\alpha$  protein degradation mediated by the ubiquitin-proteasome pathway. BCAS3 is an E2-inducible gene, and its overexpression confers impaired responses to tamoxifen in hormone receptor-positive premenopausal breast cancers (100). BCAS3 associate with a transcriptional complex comprised of ER $\alpha$ , histone H3, and HAT protein P/CAF (p300/CBP-associated factor) to activate ER $\alpha$  target genes. Nevertheless, BCAS3 coactivator functions are

dependent on PELP1 protein, another ER $\alpha$  coactivator (70). It seems a transcriptional coactivator complex with PELP1 and P/CAF is recruited by ER $\alpha$ /BCAS3 complex to activate ER $\alpha$ -dependent transcription.

Deleted in breast cancer 1 (DBC1) is a recently identified novel coactivator of ER $\alpha$  (106). DBC1 potentiates ER $\alpha$  transcriptional activity by inhibiting the association of sirtuin 1 (SIRT1), a nicotinamide adenine dinucleotide-dependent deacetylase, with ER $\alpha$  and SIRT1-mediated deacetylation of ER $\alpha$ . DBC1 and SIRT1 expressions are also associated with distant metastatic relapse and shorter relapse-free survival in breast cancer patients (75). Ciz1 is a novel coactivator of ER $\alpha$ , known to participate in DNA replication and cell cycle regulation. Ciz1 regulate the activity of ER $\alpha$  by directly promoting the ligand bound receptor to ER $\alpha$  target genes (48). Interaction of CIZ1 with ER $\alpha$  enhances receptor sensitivity to E2 which impacts on breast cancer cell growth. Recently, actinin  $\alpha$  4, a cytoskeletal modulator, has been identified as a novel atypical ER $\alpha$  coactivator that regulates transcription networks to control cell growth. Actinin  $\alpha$  4 interacts with ER $\alpha$  through a functional LXXLL receptor interaction motif present in the coactivator and potentiates ER $\alpha$  gene expression in MCF7 cells (107). The DEAD-box RNA helicases p68 (DDX5) and p72 (DDX17), which are primarily involved in RNA splicing, also act as ER $\alpha$  coactivators in breast cancer cells. Although helicase activity is not required for their coactivator function, they act in synergy with SRC-1, another ER $\alpha$  coactivator (108). p72 interacts with ER $\alpha$  in a ligand-dependent manner in the nucleus. Therefore, p72 is important for ligand-dependent transcriptional activity of ER $\alpha$  and E2-dependent cell growth in breast cancer cells. Furthermore, p72 expression, but not p68 expression, is associated with an increased period of relapse-free and overall survival in ER $\alpha$ -positive primary breast cancers (108). MUC1, a transmembrane glycoprotein normally expressed on the apical borders of secretory mammary epithelia, is also a potent coactivator of ER $\alpha$ . A positive correlation between MUC1 and ER $\alpha$  levels in breast tumors is also established (77). MUC1 regulates ER $\alpha$  activity by directly binding to the DNA binding domain of ER $\alpha$  and stabilizes ER $\alpha$  by blocking its ubiquitination and degradation in breast cancer cells (109).

## 2. Corepressors in breast cancer

In contrast to coactivators, corepressors recruit histone deacetylases (HDAC) to ER $\alpha$  target gene chromatin, which leads to chromatin condensation and inhibition of ER $\alpha$  target gene expression in breast cancer cells (110). The corepressors thus counterbalance the action of coactivators to control the magnitude of E2 responses, leading to inhibition of ER $\alpha$  target gene expression. Therefore,

loss of ER $\alpha$  corepressors promotes breast cancer (111). Many corepressors of ER $\alpha$  have been identified, and their activities associated with breast cancer were characterized (Table 1). For instance, metastasis associated protein 1 (MTA1) containing nucleosome remodeling and histone deacetylation complex (NuRD) suppresses ER $\alpha$ -mediated gene expression, resulting in an invasive breast cancer phenotype (112). Because the NuRD complex possesses HDAC activity, the MTA1-NuRD complex brings chromatin condensation by deacetylating ER $\alpha$  target chromatin, which leads to RNA polymerase II dissociation from target gene chromatin and loss of transcription. The tamoxifen-ER $\alpha$  complex has been shown to recruit the MTA1/NuRD chromatin-remodeling complex onto ER $\alpha$  target genes (96). MTA1 overexpression is associated with highly aggressive breast cancer types with poor survival rate (114). Similarly, repressor of ER activity (REA) plays an essential role in mammary gland morphogenesis and functional activities (115). REA suppresses ER $\alpha$  transcription activity by recruiting HDAC1 onto ER $\alpha$  target genes (116). Clinical evidence shows positive correlation between REA expression and ER $\alpha$  levels in 40 human breast tumor biopsies used for the study (91).

Nuclear receptor corepressor 1 (NCOR1) is another well-defined corepressor of ER $\alpha$ . It inhibits ER $\alpha$  transcriptional activity by binding to the ligand binding domain of ER $\alpha$  through a I/LXXI/VI motif (I, isoleucine; V, valine; X, any amino acid), also known as CoRNR (corepressor of nuclear receptor) box, which is similar to the NR box such as the LXXLL motif found in ER $\alpha$  coactivators (117). Low expression of NCOR1 is associated with significantly shorter relapse-free survival in breast cancer patients, implying that loss of NCOR1 enhances breast cancer development (65). Further decreased NCOR1 protein expression is correlated with acquired tamoxifen resistance in a mouse model of breast cancer (118). Both scaffold attachment factor B (SAFB) 1 and SAFB2 suppress ER $\alpha$  target gene expression in breast cancer cells by associating with NCOR1 (119). Similarly, low expression of scaffold attachment factors such as SAFB1 and SAFB2 is associated with poor overall survival in patients who did not receive adjuvant therapy (93). Dachshund homolog 1 (DACH1), a cell fate decision factor, is a novel corepressor of ER $\alpha$  (97). DACH1 represses ER $\alpha$  signaling by blocking of coactivator-receptor interactions, *i.e.*, PELP1-ER $\alpha$  interactions, which results in increasing the relative abundance of HDAC1 on ER $\alpha$  target genes to suppress the ER transcription. Expressions of ER $\alpha$  and DACH1 are also reported to be inversely correlated in human breast cancers (97). Depletion of endogenous prohibitin (PHB), a tumor suppressor, is shown to enhance the expression of ER $\alpha$  target genes in MCF7 breast cancer cells. Mice

that are heterozygous for PHB null allele exhibit a hyperproliferative mammary gland phenotype, indicating that PHB absence causes breast cancer (120). From the above examples, it is clearly evident that coregulators, both coactivators and corepressors, modulate ER $\alpha$  transcriptional activity, and their expression is associated with breast cancer progression. Therefore, assessment of ER $\alpha$  coregulator status and activity is crucial to determine the role of ER $\alpha$  in breast cancer progression and to predict prognosis and response to therapy.

### C. E2 signaling, BRCA, and breast cancer risk

Gain-of-function mutations in oncogenes or loss-of-function mutations in tumor suppressor genes are known to cause cancers. Both *BRCA1* (breast cancer 1) and *BRCA2* are tumor suppressor genes, and loss-of-function mutations in these two proteins are predisposed to breast cancer development because they are key components of the genome maintenance network (121). Several studies demonstrated that *BRCA1* expression is absent or decreased in approximately 40% of sporadic breast cancers (122–124). The physiological link between *BRCA1* and E2 was established through mouse models. *Brca1* knockout mice confer hypersensitivity to E2, and accelerated development of mammary hyperplasias, preneoplastic mammary lesions, and adenocarcinomas was observed (125). It is clearly established that *BRCA1* mutations and E2 use are risk factors for the development of breast cancer (126). Most sporadic breast cancers show reduced or absent *BRCA1* expression due to promoter methylation, loss of one *BRCA1* allele, *etc.* (123, 124), but the majority of *BRCA1* mutant cancers are ER $\alpha$ - and progesterone receptor (PR)-negative (129). Nevertheless, several lines of evidence support the pivotal role played by steroid hormones and their receptors in the development of *BRCA1*-mutant cancers. For instance, *BRCA1* mutation carriers exhibited substantial reduction (about 50%) in breast cancer risk (130), and removal of ovaries reduced the incidence of mammary cancer in mice with a mammary-targeted deletion of full-length *Brca1* gene (131). Pregnancy appears to increase the risk of breast cancer in *BRCA1* carriers due to high circulating levels of E2 and progesterone, implying that steroid hormones may confer increased breast cancer risk in *BRCA1* carriers (132).

Interestingly, both *BRCA1* and *BRCA2* are E2-responsive genes, and *BRCA1* in turn regulates ER $\alpha$  activity through posttranslational mechanisms (133, 134). For instance, *BRCA1/BARD1* complex monoubiquitinates ER $\alpha$  in MCF7 cells, and thus, ubiquitinated ER $\alpha$  becomes transcriptionally inactive (134, 135). Because p300 acetylates ER $\alpha$  and *BRCA1* inhibits p300 expression, ER $\alpha$  acetylation mutant is resistant to *BRCA1*-mediated repression

of ER $\alpha$  activity (134, 136, 137). E2-ER $\alpha$  influences BRCA1/2 expression, and BRCA inhibits ER $\alpha$  activity through a monoubiquitination mechanism, implying the existence of a negative feedback mechanism that regulates functional interaction between ER $\alpha$  and BRCA in breast cancer cells. Loss of BRCA1 expression also led to tamoxifen resistance. This is due to increased coactivator and decreased corepressor recruitment onto ER $\alpha$ -regulated gene promoters under BRCA1 silencing (138). In addition to its direct ubiquitin ligase activity on ER $\alpha$ , BRCA1 also regulates ER $\alpha$  gene, *i.e.*, ESR1 expression, in association with transcription factor Oct-1 (139). This mechanism may explain why most sporadic tumors express wild-type BRCA1 and are ER $\alpha$ -positive. Based on these considerations, a model has been proposed for BRCA1-mutant breast cancer formation (140). According to this model, ER/PR-positive mammary epithelial cells deficient for BRCA1 are hypersensitive to endogenous E2 and progesterone and secrete growth factors that stimulate proliferation of nearby ER/PR-negative mammary epithelial cells. Thereby continual hormonal stimulation results in ER/PR-negative hyperplasia. In BRCA1 deficiency, these lesions eventually become autonomous and progress to invasive cancer.

#### D. E2 signaling on cell cycle machinery and breast cancer development

In general, loss of control over cell cycle progression results in cancer development. The cyclin proteins play a major role in G<sub>1</sub> to S phase transition during cell cycle progression and are critical components of endocrine and paracrine factor-induced mitogenesis in breast epithelial cells (141, 142). Of different cyclins, cyclin D1 is a target of E2 signaling (36). Mammary epithelial cell-specific overexpression of cyclin D1 leads to mammary carcinoma, whereas in cyclin D1-deficient mice, mammary gland development is arrested before lobuloalveolar development, implicating the significance of cyclin D1 in mammary gland (143). Cyclin D1 is encoded by *CCDN1* gene, which is located in chromosome 11q13—a region of the genome commonly amplified in a range of human carcinomas, including about 15% of breast cancers (74, 144).

Although cyclin D1 promoter lacks either ERE or ERE-like elements, E2-ER $\alpha$  regulates cyclin D1 expression by recruiting various transcription factors involving ATF-2 and c-Jun (36, 145). A recent report showed that hexamethylene bisacetamide inducible protein 1 inhibits ER $\alpha$ -mediated expression of cyclin D1 in mammary cells by curbing the recruitment of the transcription factor complex comprised of ER $\alpha$ , positive transcription elongation factor b, and serine 2-phosphorylated RNA polymerase II onto *CCDN1* promoter, implying that hexamethylene bi-

sacetamide inducible protein 1 is a critical regulator of E2-induced cyclin D1 expression in breast cancer cells (146). Because cyclin D1 regulates cyclin-dependent kinase (CDK) 4 activity and retinoblastoma protein functionality, which decides the transcriptional activity of E2F transcription and S phase progression, it is expected that up-regulation of cyclin D1 gene expression in response to E2 promotes G<sub>1</sub> to S transition by activating CDK4 through cyclin D1 induction (147). Therefore, the treatment of breast cancer cells with antiestrogens is associated with an acute decline in cyclin D1 mRNA and protein expression accompanied by a decline in cyclin D1-CDK4 activity and decreased phosphorylation of retinoblastoma (148–151). Cyclin D1 can also interact with ER $\alpha$  in a CDK-independent manner through the cAMP/protein kinase A (PKA)-mediated pathway (152). Overexpression of cyclin D1 protein and mRNA correlates strongly with ER $\alpha$  synthesis in tumor tissues and relates inversely to the level of cyclin E1 (153). Consistent with this possibility, one small clinical study suggested that the duration of response to tamoxifen was significantly longer in ER $\alpha$  patients with low cyclin D1 than those with high cyclin E1 (154). E2 regulates cell cycle progression not only through the cyclin D1/CDK4 pathway but also by regulating CDK2 activity, another cell cycle regulatory protein, by repressing p27<sup>KIP1</sup>, an inhibitor of CDK2, in MCF7 cells. This results in increased activity of cyclin A/CDK2 in the late G<sub>1</sub> phase of the cell cycle (155). In a recent clinical study, evaluation of p27<sup>KIP1</sup> in 328 breast cancers from premenopausal patients revealed that down-regulation of p27<sup>KIP1</sup> is associated with high proliferation and tamoxifen resistance (156). These facts suggest that E2/ER $\alpha$ -regulated cyclins can be considered key targets for developing ER-positive breast cancer therapies.

#### IV. E2 Extranuclear Signaling in Breast Cancer

In the last decade, extensive research on E2 signaling made a few interesting discoveries that could explain some novel pathophysiological anomalies associated with breast cancer. Although the majority of the ER is localized in the nucleus, several biochemical and microscopic analyses have suggested the existence of different pools of ER $\alpha$  in the cellular environment, including the plasma membrane, the mitochondria, and the endoplasmic reticulum (157). The cytoplasmic pool of ER $\alpha$  results in rapid actions of E2 via signal transduction pathways (157, 158) (Fig. 1). Palmitoylation at cysteine 447 localizes ER $\alpha$  to the plasma membrane and is responsible for the ligand-induced activation of MAPK and phosphatidylinositol 3 kinase (PI3K)/serine/threonine protein kinase (AKT) pathways in breast cancer cells

(159). Another mechanism proposed is that protein arginine N-methyltransferase 1 (PRMT1) methylates ER $\alpha$  at arginine 260 in the DNA-binding domain of the receptor mediating the extranuclear function of the receptor, which would then interact with Src/focal adhesion kinase and p85 and propagate the signal to downstream transduction cascades (160). It provides compelling evidence to support the existence of a functional extranuclear signaling pathway for E2 in breast cancer cells.

In breast cancer cells, rapid E2 actions stimulate various growth factor receptors such as IGF-I receptor and epidermal growth factor receptor (EGFR) and activation of effector molecules such as Src and PI3K through adaptor protein, SHC-transforming protein 1 and AKT, and MAPK (46, 161). The cross talk between E2 and growth factor signaling suggests that adaptor proteins play a key role in the extranuclear actions of ER $\alpha$ . For instance, the mammalian target of rapamycin/S6 kinase 1 has been found crucial for IGF-I receptor and ER $\alpha$  cross talk (162). The 40 S ribosomal S6 kinase 1 (S6K1) phosphorylates ER $\alpha$  at serine 167, and so inhibition of S6K1 kinase activity abrogates IGF-I-stimulated S6K1/ER $\alpha$  association and ER $\alpha$  target gene transcription (163). This leads to the suppression of IGF-induced colony formation and breast cancer cell proliferation. S6K1 overexpression is associated with poor prognosis of ER-positive breast cancers, implying that the cross talk between ER $\alpha$  and the IGF-I/S6K signaling pathway is crucial for development of breast cancers (163).

Extranuclear actions have a profound impact on breast cancer cell proliferation, migration, drug resistance, and apoptosis blockade (164, 165). Rapid E2 actions lead to the activation of MAPK through kinase (166). This study has shown that MAPK blockers inhibit breast cancer cell proliferation and tumor growth, indicating that the rapid E2-activated ER $\alpha$ /Src/MAPK pathway is functional in breast cancer cells. Similarly, integrin-linked kinase also participates in extranuclear signaling of E2 through the PI3K pathway and regulates breast cancer cell migration (167). PI3K inhibitors such as LY294002 also blocked PI3K/integrin-linked kinase/ER $\alpha$ -mediated breast cancer cell migration (167). Another recent finding shows that ER $\alpha$  regulates deacetylation of tubulins in association with HDAC6 through the E2 extranuclear signaling pathway and promotes breast cancer cell migration (168). In another report tamoxifen is shown to induce tubulin deacetylation implying that extranuclear signaling through tubulin deacetylation conferring endocrine resistance in breast cancer cells. In addition, Fernando and Wimalasena (169) have shown that E2 induces Bcl-2-associated death promoter phosphorylation through both the Ras/PI3K/AKT and the Ras/ERK/p90RSK1 pathways, suggesting that functional activation of the PI3K/AKT

pathway may be required for E2 to block apoptosis induced by TNF, hydrogen peroxide, and serum withdrawal. This model suggests the antiapoptotic activity of E2 extranuclear rapid action to support the survival of the breast cancer cell.

Emerging evidence suggests that various genomic coregulators of ER $\alpha$  can also act as extranuclear coregulators and can integrate genomic and extranuclear signaling pathways (170). ER $\alpha$  coregulators such as PELP1, MTA1 short form (MTA1s), hematopoietic PBX-interacting protein 1 (HPIP), and p130Cas are known to influence both functions of ER $\alpha$ . PELP1 was originally identified as Src homolog 2 domain-interacting proteins (45, 171). PELP1 contains 10 LXXLL motifs that participate in interaction with nuclear receptors and three proline-rich motifs that could participate in interaction with SH3 domain-containing proteins. PELP1 can act as an extranuclear adaptor protein between ER $\alpha$  and Src, thereby allowing E2-dependent activation of Src and the downstream ERK/MAPK signaling cascade (46). Interestingly, this pathway confers tamoxifen resistance in breast cancer cells through the activation of both PI3K/AKT and Src/MAPK pathway (46). In fact, PELP1-transgenic mice, which express cytoplasmic PELP1 in mammary gland-formed tumors, displayed tamoxifen resistance, suggesting that extranuclear actions are responsible for such drug resistance (172). PELP1 has also been implicated in aromatase regulation in breast cancer cells by involving short extranuclear autocrine loop between E2 and aromatase expression (173). This supports that extranuclear signaling of E2 indeed regulates aromatase activity (174).

Another protein that is known to integrate extranuclear signaling of ER $\alpha$  into genomic signaling is HPIP. HPIP, also known as pre-B-cell leukemia homeobox interaction protein (PBXIP1), is a microtubule-binding protein that interacts with ER $\alpha$  (175). HPIP binds to ER $\alpha$  through the LXXLL motif located on its C-terminus part of the protein. HPIP localizes predominantly to cytoplasm and interacts with cell survival signaling proteins such as PI3K and Src. E2 stimulates the formation of a signalosome consisting of ER $\alpha$ , Src, PI3K, and HPIP on the microtubules network to activate AKT/MAPK pathways in breast cancer cells (175). Treatment of breast cancer cells with nocodazole (a microtubule-depolymerizing agent) or HPIP silencing by HPIP-specific small interfering RNA enhanced ERE-dependent transcription, whereas paclitaxel (a microtubule-polymerizing agent) suppressed ERE-dependent transcription (ERE-Luciferase assay), suggesting the sequestration of the steroid receptor through the HPIP-microtubule network. A contradictory finding showed that E2-ER $\alpha$ /HPIP-activated Src/PI3K pathways can also integrate into genomic func-



tions of ER $\alpha$  by enhancing the receptor phosphorylation at serine 167 (176). This discrepancy could be due to different functional assays used by two groups. HPIP is also highly overexpressed in infiltrative ductal carcinoma of breast and confers taxol resistance to breast cancer cells (B. Manavathi, personal communication).

MTA1s is a frameshift-derived shorter form of MTA1 protein. The LXXLL motif, located on the C terminus of the protein, participates in interaction with ER $\alpha$ , and this interaction is enhanced in response to E2. Lack of nuclear localization signal ensures MTA1s cytoplasmic localization and sequestration of ER $\alpha$  in the cytoplasm that enhances extracellular functions of the receptor in the target cells while impairing genomic functions (88). In this context, E2 activates casein kinase I- $\gamma$ 2 transcription, which in turn phosphorylates MTA1s in breast cancer cells, thus enhancing the MTA1s ability to restrict ER $\alpha$  to the cytoplasm (177). The MTA1s expression is associated with human breast tumors with no (or low) nuclear ER $\alpha$ . Another protein that regulates both genomic and extranuclear activities of ER $\alpha$  is p130Cas. The p130Cas (Crk-associated substrate) is an adaptor protein and is a prime substrate of the Src kinase. Being an adaptor, p130Cas links the actin cytoskeleton signaling to the extracellular matrix during cell migration and cell invasion (178). p130Cas interacts with ER $\alpha$  in the cytoplasm, which leads to hyperstimulation of the Src/MAPK pathway and cyclin D1 induction in breast cancer cells (179). Thus, p130Cas-mediated E2 extranuclear signaling regulates E2-dependent cell cycle progression by modulating cyclin D1 expression.

E2 rapid signaling also participates in DNA damage response. In general, if damaged DNA is not repaired, genomic integrity can be compromised, and unrestrained proliferation of aberrant cells may occur. Inhibition of normal DNA repair signaling may simulate genetic loss of DNA damage response signaling molecules such as ataxia telangiectasia mutated (ATM), ataxia telangiectasia and rad3-related protein (ATR), DNA-dependent protein kinase (DNAPK), BRCA1 and -2, p53, and Chk2 and predispose normal cells to acquire transforming mutations (180). A recent report showed that in ER-positive breast cancer cells, DNA damaging agents including UV, ionizing radiation, and hydroxyurea rapidly activate ATR-dependent phosphorylation of endogenous p53 and Chk1 (181). Interestingly, this pathway involves extranuclear actions of E2 via plasma membrane-localized ER $\alpha$  and activation of PI3K and AKT signaling pathway. E2 delays DNA repair and increases chromosomal damage by regulating ATR and Chk1 activation in breast cancer epithelial cells. Ligand bound ER $\alpha$  regulates ATR activity by potentiating AKT-mediated phosphorylation of DNA to-

poisomerase 2-binding protein 1 at serine 1159, which prevents binding of topoisomerase 2-binding protein 1 with ATR after DNA damage. Since the association of Chk1 with Claspin is important for Chk1 activity, E2-ER $\alpha$  regulates Chk1 activity via AKT-mediated phosphorylation of Chk1 which prevents its association with Claspin and signaling to the G<sub>2</sub>/M checkpoint (181). Because ATM protein expression is found to be aberrantly reduced more frequently among BRCA1- and BRCA2-expressing tumors than in non-BRCA1 and -2 tumors, reduced ATM expression was found more often in ER $\alpha$ - and PR-negative breast cancer, indicating loss-of-function interaction among these molecules (182). This explains how E2 signaling can also affect DNA repair systems to delay the repair mechanism to support breast cancer cell growth.

## V. ER $\alpha$ Posttranslational Modification and Its Impact on Breast Cancer Progression

Posttranslational modifications such as phosphorylation, methylation, ubiquitination, sumoylation, also regulate ER $\alpha$  activity and is shown to have potential implications in breast cancer development and drug resistance (183) (Fig. 2). Several kinases including MAPK, AKT, glycogen synthase kinase 3 $\beta$  (GSK3 $\beta$ ), serine/threonine p21-activated kinase (PAK1), and PKA are known to phosphorylate ER $\alpha$  at distinct sites located in particular at the N-terminal region (183). For example, MAPK has been shown to phosphorylate ER $\alpha$  at serine 118, located in the activation function-1 domain of the receptor (184, 185). Phosphorylation at serine 118 directs gene-specific recruitment of ER $\alpha$  and its coregulators on ER $\alpha$  target promoters (186). The presence of ER $\alpha$  phosphorylation at serine 118 in human breast tumors further implies a clinical relevance to this modification with the disease (187). Likewise, growth factor-activated signaling kinases, such as PAK1 or PKA, phosphorylate ER $\alpha$  at serine 305 located in the transactivation function-2 domain and promote transactivation functions in the absence of ligand (188, 189). Transgenic mice expressing ER $\alpha$  serine 305E mutant gene in the mammary gland exhibit mammary hyperplasia (188). Furthermore, it has been shown that this phosphorylation is sufficient to activate the cyclin D1 in breast cancer cells (190). The serine 305 site in ER $\alpha$  has also been implicated in modifying the action of tamoxifen in breast cancer cells by regulating ER $\alpha$  phosphorylation at serine 118 (191). ER $\alpha$  serine 305 phosphorylation levels in advanced breast cancers indeed associate with sensitivity to tamoxifen in breast tumors (192). A recent report shows that prolactin also contributes to ligand-independent activation of ER $\alpha$  through activation of receptor phosphor-

Figure 2.

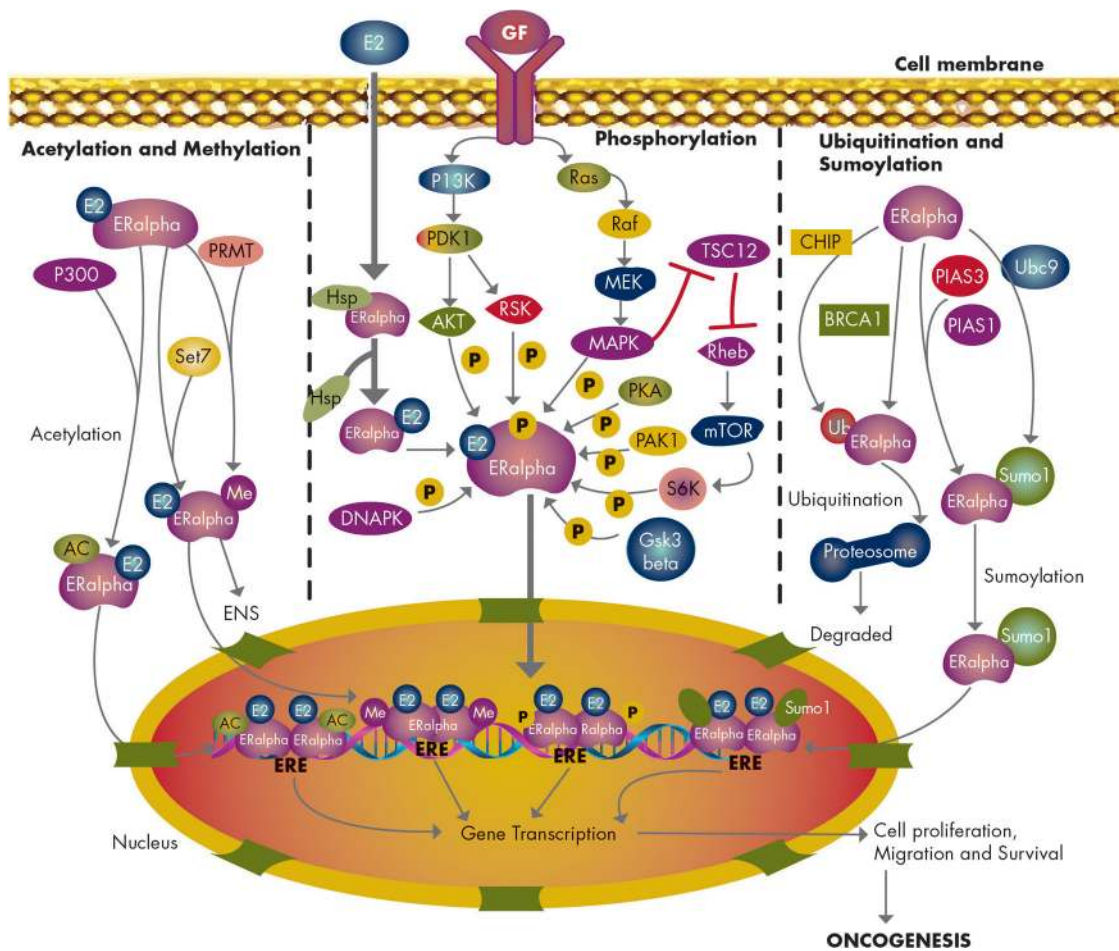


Figure 2. Posttranslational modifications of ER $\alpha$ . Most of the known growth factor responsive kinases like AKT, RSK, MAPK, PKA, PAK1, and S6K phosphorylate ER $\alpha$  at specific serine or threonine residues and are known to activate its transcriptional activity. Phosphorylation of ER $\alpha$  by DNAPK and GSK3 $\beta$  inhibits its proteasomal degradation and thereby enhances its nuclear activity. Acetylation of ER $\alpha$  at lysines 266, 268, 302, and 303 by p300 enhances transcriptional activity of ER $\alpha$ . Methylation of ER $\alpha$  at arginine 260 by PRMT1 promotes E2 extranuclear signaling (ENS), whereas ER $\alpha$  methylation at lysine 302 by SET7 methyltransferase led to transcriptional activation of ER $\alpha$ . PIAS1 and PIAS3, in association with Ubc9, sumoylate ER $\alpha$  and promote its transcriptional activity. CHIP regulates polyubiquitination of ER $\alpha$ , which leads to proteasomal degradation of the receptor, whereas BRCA1 monoubiquitinates ER $\alpha$  and reduces its transcriptional activity. RSK, Ribosome S6 kinase; Ubc9, SUMO-conjugating enzyme; CHIP, carboxy terminus of HSP70-binding protein.

ylation at serine 118 (193). AKT1, another serine/threonine kinase that acts downstream to growth factor signaling, also phosphorylates ER $\alpha$  at serine 167 through growth factor signaling activation (194). Clinical studies using patients treated with tamoxifen showed a positive relationship among AKT activation, ER $\alpha$  phosphorylation at serine 167, and tamoxifen resistance (194–196). These studies provided additional evidence for the role of PI3K/AKT-mediated tamoxifen resistance in breast cancers. Interestingly, a recent clinical study found an improved survival rate in ER-positive breast cancer patients who showed low phosphorylation of ER $\alpha$  serine 118 and high phosphorylation of ER $\alpha$  serine 167 (197). This suggested that we can distinguish the patients who are likely

to benefit from endocrine therapy alone from those who are not. GSK3 $\beta$ , also a serine/threonine kinase that opposes AKT1 functions, has been shown to phosphorylate ER $\alpha$  at serines 102, 103, 106, and 118 and to stabilize ER $\alpha$  from proteasome degradation, thereby enhancing ER $\alpha$  transcriptional activity (198). Similarly, DNAPK, a DNA repair enzyme, also phosphorylates ER $\alpha$  but only at serine 118. Phosphorylation results in stabilization of ER $\alpha$  because inhibition of DNAPK resulted in its proteasomal degradation (199). In addition to the above well-defined sites, a recent proteomic approach identified a few new phosphorylation sites in ER $\alpha$ , which include serine at 212, 294, 554, and 559 (200). However, the functional consequences of these residues on ER $\alpha$  activity are not known

yet. The ER $\alpha$  phosphorylation at ligand binding domain (AF2) Tyr 537 by Src and MAPK also promotes cell proliferation and hormone-independent activation of ER $\alpha$  (201–203). Phosphorylation of ER $\alpha$  at Thr 311 (located in ligand binding domain) by p38 protein kinase and MAP kinase kinase kinase, regulates nuclear export of ER $\alpha$ , and also inhibits the interaction with of the receptor with p160 (204). However, the relevance of these phosphorylation sites in ER $\alpha$  with breast cancer is yet to be analyzed. A detailed list of ER $\alpha$  modifications and enzymes involved in the modification is reviewed in Ref. 183.

ER $\alpha$  also subjected to acetylation modification and its functional significance has been well documented (205). It has been shown that ER $\alpha$  is directly acetylated by the coactivator p300 at the well-conserved lysine residues at 266, 268, 302, and 303 (137, 206). Particularly, acetylation of lysine at 302 and 303, which are located in the hinge region of ER $\alpha$  appears to play a key role in enhancing ligand sensitivity and subsequently ER $\alpha$ 's transcriptional activity (206). Interestingly, clinical studies determined that the lysine residue is in a mutation-susceptible site in breast cancers. In 34% of atypical breast hyperplasia samples, a Lys-to-Arg substitution was found at residue 303 (K303R) of the ER $\alpha$  (208). This mutant also confers hypersensitivity to E2 and induces resistance to an aromatase inhibitor via the PI3K/AKT kinase pathway (209). Because acetylation is a reversible process, it indicates the existence of an ER $\alpha$  deacetylase in cells. SIRT1, along with nicotinamide adenine dinucleotide, is shown to deacetylate ER $\alpha$  and inhibit E2-dependent cell proliferation (210). Interestingly, lysine 302 of ER $\alpha$  is also a site for monoubiquitination by BRCA1 (135). Down-regulation of BRCA1 activates ER $\alpha$  because of the absence of monoubiquitination, whereas overexpression of BRCA1 down-regulates ER $\alpha$  activity, indicating that ER $\alpha$  activity is controlled by the relative degree of acetylation *vs.* ubiquitination of ER $\alpha$  at 302 (134, 211). Monoubiquitination at K302 and K303 is associated with reduced ER $\alpha$  transcriptional activity, phosphorylation at serine 118, AKT activation, and ER $\alpha$ -induced cell proliferation (212). Furthermore, lysine 266 and 268 of ER $\alpha$  are also sites for sumoylation. Sumoylation at these sites appears to enhance ER $\alpha$  transcriptional activity in breast cancer cells (213, 214). In addition to lysine 266 and 268, lysines 299, 302, and 303 of ER $\alpha$  also seem to be sumoylated; therefore, mutation of these sites further reduces transcriptional activity of ER $\alpha$  (213). ER $\alpha$  also undergoes methylation at arginine 260 by PRMT1 in the cytoplasm (215). In addition, methylation at lysine 302 by SET7 methyltransferase was reported to stabilize ER $\alpha$  and efficient recruitment of the ER $\alpha$  to its target genes (216). ER $\alpha$  is methylated in normal epithelial breast cells and is hyper-

methylated in a subset of breast cancers, indicating that ER $\alpha$  methylation could serve as a prognostic marker to a subset of breast cancers (215). Altogether, these observations indicate that ER $\alpha$  posttranslational modifications regulate ER $\alpha$  activity in breast cancer cells, implying that their deregulation is also responsible for breast carcinogenesis.

## VI. Cross Talk between miRNA and E2 Signaling in Breast Cancer

miRNA are a class of endogenous short noncoding RNA of 22–24 nucleotides in length and capable of regulating the expression of protein-coding genes at the posttranscriptional level by cleaving target mRNA and/or repressing their translation (217). More than 50% of human miRNA genes are located at chromosomal regions with high frequencies of amplification or deletion that are genetically altered in cancers (218). Emerging studies show that miRNA function as oncogenes or tumor suppressors to modulate multiple oncogenic cellular processes, including cell proliferation, apoptosis, invasion, and migration by targeting various important cell regulators including p53, Her2, Myc, *etc.* (219–221). It has also been shown that miRNA, *e.g.*, miR-101a, miR-126–3p, miR-212, and miR-132 regulate mammary gland development, indicating the importance of these miRNA in normal physiology (222). Because ER $\alpha$  is one of the major culprits for endocrine-related breast cancer development, it naturally creates a curiosity to look for miRNA that target ER $\alpha$ .

### A. E2 signaling on miRNA expression

In the past few years, several genome-wide profiling studies have been made to characterize E2-dependent miRNA in breast cancer cell lines and biopsies (223–226). In a recent study to understand the effect of E2 on miRNA expression in both MCF7 and ZR75 cells, 172 miRNA were identified to be up- or down-regulated by ER $\alpha$ , of which 52 are similarly regulated in both of the cell models (225). The most consistently deregulated miRNA on E2 treatment are miR-206, miR-125a/b, miR-17–5p, miR-34a; some members of the let-7 family that act as tumor suppressor genes; and miR-21, miR-155, and miR-10b, which are usually overexpressed in breast cancer and may act as oncogenes (225). The miR-21 expression is found to be higher in ER-positive breast cancer tumors than negative. E2 induced down-regulation of miR-21 in MCF7 cells and concomitantly induced overexpression of miR-21 target genes, bcl2 and PTEN (227). On the contrary, Bhat-Nakshatri *et al.* (228) have reported an increase in miR-21 expression on E2-mediated induction of

MCF7 cells. This discrepancy can be explained by the biphasic regulation of E2, *i.e.*, induction followed by repression of miR-21. A recent study has demonstrated that re-expression of miR-21 results in migration and invasion by activating the EMT process and enhancing the characteristics of cancer stem cells in MCF7 cells (229). Maillot *et al.* (230) identified a set of 23 miRNA (including miR-181a, miR-21, miR-181b, miR-26a, miR-200c, miR-26b, miR-27b, miR-23b) to be down-regulated by E2 in various ER-containing human cell lines. Several pri-miRNA of these miRNA, particularly pri-miRNA-21 and pri-miRNA-181a~b-1, are primary targets of ER $\alpha$  transcriptional repression. miR-26a and miR-181a oppose the E2-dependent increase in cell proliferation through a global deregulation of genes (*e.g.*, PR) involved in the control of cell growth (230). Another study reported that E2 significantly induced B-cell lymphoma 2, cyclin D1, and survivin expression by suppressing the levels of miR-16, miR-143, and miR-203 in MCF7 cells, and these miRNA are highly expressed in triple positive breast cancers (231). In a genome-wide microarray approach, the miRNA that were up-regulated by E2 were identified as members encoded by the paralogous transcripts, pri-mir-17-92 and pri-mir-106a-363a. c-MYC, an ER $\alpha$  transcriptional target, seems to regulate miR-17-92 expression by directly binding to its promoter in response to E2 treatment. However, the miRNA (miR-18a, miR-

19b, and miR-20b) derived from these pri-miRNA are again involved in an inhibitory loop and down-regulate ER $\alpha$  (232). E2 also down-regulates the promoter activity of miR-34b gene through the interaction between ER $\alpha$  and p53 (233). From these studies, one can derive the possible mechanisms by which E2 regulates miRNA expression by directly binding to the regulatory sites of miRNA, by inducing mRNA-encoding genes that harbor miRNA genes in their introns, by regulating transcription factors that in turn regulate miRNA expression, or by regulating miRNA processing machinery, *e.g.*, E2 can induce Dicer (228) and Ago2 (234). In another instance, the human vascular endothelial growth factor transcript bears several target sequences for E2-regulated miRNA like miR-16 in its 3' untranslated region (UTR). In response to E2 treatment, half-lives of the human vascular endothelial growth factor transcripts were stabilized (235). The activated ER $\alpha$  attenuates the processing of primary miRNA into pre-miRNA through E2-dependent association with the Drosha complex, resulting in stabilization of the transcript of an ER $\alpha$  target gene through its 3' UTR. The miRNA that are known to be modulated by E2 are listed in Fig. 3A. In addition to the miRNA listed above, many more miRNA that are yet to be discovered may be targets for E2.

**Figure 3.**

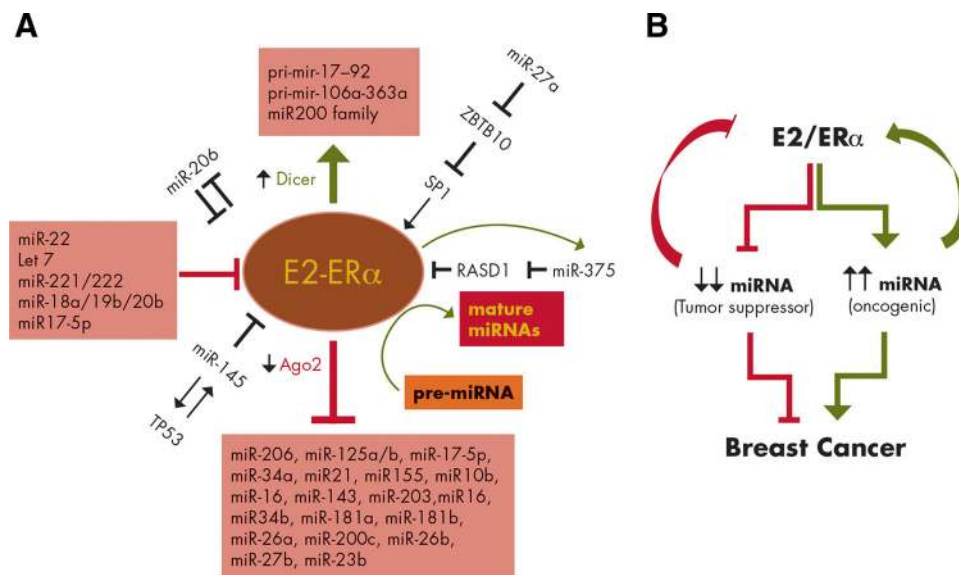


Figure 3. Reciprocal regulation of E2/ER $\alpha$  signaling and miRNA. A, Figure represents the miRNA that are targets of E2-ER $\alpha$  signaling and vice versa in breast cancer cells. E2-ER $\alpha$  signaling also modulates enzymes involved in miRNA processing such as Dicer and Ago2. ER $\alpha$  not only regulates miRNA expression but also controls miRNA maturation. miRNA375, a target of E2-ER $\alpha$  signaling, also regulates ER $\alpha$  levels through a positive feedback mechanism by repressing ER $\alpha$ 's inhibitor, RASD1. miR-206 and ER $\alpha$  mutually repress each other's expression. miR-145 and TP53, which depend on each other for their activation, repress ER $\alpha$  levels. B, Hypothetical model illustrates that E2 may activate oncogenic miRNA while affecting the expression of miRNA that show tumor suppressor activity to ensure breast cancer development.

### B. miRNA that target ER $\alpha$ in breast cancer cells

The ER $\alpha$  mRNA has putative binding sites for several miRNA. These miRNA act by reducing ER $\alpha$  mRNA stability or translation. The miRNA that target ER $\alpha$  are shown in Fig. 3A. Ectopic expression of miR-206 into MCF7 cells has been shown to reduce ER $\alpha$  levels and also the basal expression levels of ER $\alpha$  target genes such as PR, cyclin D1, and pS2, resulting in decreased cell proliferation (236). miR-206 expression was found to be low in ER $\alpha$ -positive human breast cancer tumors and MCF7 cells, whereas there were increased levels in ER-negative MB-MDA-231 cells. This indicates the presence of a negative feedback loop between miR-206 and ER $\alpha$  (236, 237). Recently, a cell-based screen using a cotransfection assay with luciferase reporter plasmid carrying a 4.7-kb 3' UTR of ER $\alpha$  mRNA and a synthetic miRNA expression library has identified miR-22 as a potential ER $\alpha$ -targeting miRNA (238). miR-22 is frequently down-regulated in ER $\alpha$ -positive human breast cancer cell lines, and clinical samples indicating miR-22 could play a pivotal role in the pathogenesis of breast cancer (239). Several reports have shown that the let-7 family of miRNA is down-regulated in breast cancer tissues (240). The let-7 miRNA are down-regulated in breast tumor-initiating cells (BT-IC) and increased during BT-IC differentiation. Restoration of let-7 in BT-IC reduced cell proliferation, mammosphere formation, *in vitro* tumor formation, and metastasis in nonobese diabetic/severe combined immunodeficiency (SCID) mice (241). Introduction of let-7 miRNA in the MCF7 cell line negatively regulated ER $\alpha$  activity, whereas attenuating the ER $\alpha$  signaling by let-7 miRNA inhibited cell proliferation and subsequently triggered apoptosis in MCF7 cells (229). In fact, screening of the entire let-7 family of miRNA by *in situ* hybridization revealed let-7g as a unique member of the let-7 miRNA family, whose nullification can induce metastasis in otherwise nonmetastatic mammary carcinoma cells via preferential targets, Grb2-associated binding protein 2 and fibronectin 1, and consequent activation of p44/42 MAPK and specific matrix metalloproteinases (242). Cochrane *et al.* (243) have reported that Dicer expression is low in ER-negative breast cancers because these cells express high levels of miR-221/222 and miR-29a, which in turn targets and represses Dicer. miRNA-221/222 also targets ER $\alpha$  and confers tamoxifen and fulvestrant resistance in breast cancer cells (244, 245). In another study, mammosphere culture conditions were used to induce EMT in MCF7 cells, an ER-positive breast cancer cell line. This EMT was associated with increased cancer stem cell-like properties and reduced ER $\alpha$  expression, which correlated with suppression of miR-200c, miR-203, and miR-205 and overexpression of miR-222 and miR-221, further suggesting that ER $\alpha$  is the target of

miR-221/222 in breast cancer cells (246). Intriguingly, miR-375 is found to be involved in a positive feedback loop with ER $\alpha$  in breast cancer cells by repressing RASD1, a GTPase activator protein, which inhibits ER $\alpha$  (247). In ER-positive MCF7 cells, ER $\alpha$  is also regulated indirectly by miR-27a through suppression of ZBTB10, a SP repressor (249). Because ER $\alpha$  expression is dependent on SP1 transcription factor, miR-27a-mediated suppression of ZBTB10 results in the expression of SP1 and its target gene such as ER $\alpha$  and subsequently establishing hormone responsiveness in breast cancer cells (249). miR-145, another important tumor suppressor miRNA, down-regulates ER $\alpha$  expression and exerts a proapoptotic effect in breast cancer cells in a TP53-dependent manner. TP53 activation in turn stimulates miR-145 expression, thereby TP53 is involved in a death-promoting loop with miR-145 (248). A novel protein lysate microarray-based study identified miR-18a, miR-18b, miR-193b, miR-206, and miR-302c as ER $\alpha$  repressors. This is further confirmed by the high expression levels of miR-18a and miR-18b in ER-negative as compared with ER-positive clinical tumors (250). Because coregulators modulate ER $\alpha$  functions, miRNA that regulate coregulators also influence ER $\alpha$  functions in breast cancer cells. miR-17-5p, for instance, represses the translation of AIB1 mRNA, whereby it blocks ER $\alpha$ -mediated cell proliferation in MCF7 cells (251). With the above examples, we can understand that E2 may activate oncogenic miRNA, whereas affecting the expression of tumor suppressor miRNA to promote breast cancer development (Fig. 3B). Future research awaits whether these new blossoms (miRNA) in the garden of E2 signaling will serve as potential therapeutic targets for breast cancer treatment.

### VII. Deregulated Expression of ER $\alpha$ in Breast Cancer

It is well documented that the activity of ER $\alpha$  is regulated at multiple levels in breast cancer cells. Extensive research over the last two decades established that various chemicals, hormones, hormone receptor modulators, transcription factors, and epigenetic modulators regulate ER $\alpha$  expression in breast cancer cells (reviewed in Refs. 252 and 253). The human ER $\alpha$  gene is located on chromosome 6 and is extensively methylated in ER-negative breast cancer cell lines and tumors, but not in ER-positive breast cancers, implying that methylation suppresses ER $\alpha$  expression in ER-negative cells (254, 255). This is one of the reasons that ER-negative tumors show poor response to tamoxifen treatment (256). Methylation of promoter by DNA methyltransferases hinders the binding of transcrip-

tion factors and RNA polymerases to reduce the target gene transcription. In association with methyltransferases, HDAC repress ER $\alpha$  promoter activity by deacetylating histones H3 and H4, which further ensures the compact nucleosome structure and suppression of ER $\alpha$  transcription. Therefore, treatment of ER-negative breast cancer cells with trichostatin-A, an HDAC inhibitor, induces ER $\alpha$  re-

expression (257). Furthermore, a synergistic effect on ER $\alpha$  expression is observed in the treatment of cells with both trichostatin A and 5-aza-2-deoxy cytidine, an antimethylating agent, indicating the inactivation of ER $\alpha$  gene expression by both methylation and deacetylation (258). Several other novel modulators of ER $\alpha$  expression are identified. Table 2 summarizes the effects of various mod-

**TABLE 2.** Modulators of ER $\alpha$  expression in breast cancer cells

Agent	Mode of action	Cell type	ER $\alpha$ protein levels	Ref.
<b>Chemicals</b>				
Arsenite	Decreased mRNA expression	MCF7	–	259
Artemisinin	Decreased mRNA expression	MCF7	–	260
Cadmium	Decreased mRNA expression	MCF7	–	261
Celastrol	Decreased mRNA expression	MCF7 and T47D	–	262
Polyamines	Decreased mRNA expression	MCF7 and T47D	–	263
Shikonin	Posttranslational regulation	MCF7	–	264
Taxol	Inhibiting mRNA translation	MCF7	–	265
TPA	Posttranscriptional-destabilization of mRNA	MCF7	–	266
Valproic acid	HDAC inhibition	MDAMB 231	+	267
<b>Epigenetic factors</b>				
5-AZAC	Demethylating agent	MCF7	+	258
LBH589	HDAC inhibition	MDAMB 231	+	269
Trichostatin A	HDAC inhibition	MDAMB 231	+	257
<b>Growth factors</b>				
EGF	Growth factor signaling	MCF7	–	271
IGF-I	Insulin/IGF-I signaling	MCF7	–	272
TGF $\beta$ 2	GSK3 $\beta$ /SNAIL signaling	MCF7 and T47D	–	273
<b>Hormone receptor modulators</b>				
Bazedoxifene	SERM, posttranslational destabilization of protein	MCF7	–	274
EB-1089	Vitamin D agonist	MCF7	–	275
ICI 182 780	Estrogen antagonist	MCF7	–	276
KH-1069	Vitamin D agonist	MCF7	–	275
ORG 2058	Progesterone agonist	T47D	–	277
R5020	Progesterone agonist	T47D and MCF7	–	277
Raloxifene	SERM	MCF7	–	278
Ro 23-7553	Vitamin D agonist	MCF7	–	275
Ro 27-0574	Vitamin D agonist	MCF7	–	275
RU486	Progesterone agonist	T47D	+	277
Tamoxifene	SERM	MCF7	ne	278
<b>Hormones</b>				
1,25(OH) $_2$ D $_3$	Transcriptional regulation	MCF7	–	275
E2	Posttranslational regulation	MCF7	–	279
hCG	Gonadotropin/PKA	MCF7	–	280
Insulin	Insulin/IGF-I	MCF7	+	281
<b>Hypoxia inducers</b>				
Cobalt chloride	Hypoxia/HIF1 $\alpha$	MCF7	–	282
<b>Ligands</b>				
Wnt-5a	Wnt signaling	MCF7 and MDAMB 231	+	283
<b>Pathway blockers</b>				
Celecoxib	PI3K/Akt kinase	MCF7 and ZR75	+	284
Green tea polyphenol-epigallocatechin-3 gallate	PI3K/Akt kinase	MCF7 and ZR75	+	284
Wortmannin	PI3K/Akt kinase	MCF7 and ZR75	+	284
<b>Transcription factors</b>				
FoxM1	ERK 1/2	MCF7 and ZR-75	+	285
FOXO3a	PI3K/Akt kinase	MCF7 and ZR-75	+	284
GATA3	Binding to cis-regulating element	MCF7 and T47D	+	286

FOXO3a, Forkhead box transcription factor 3a; hCG, human chorionic gonadotropin; 1,25(OH) $_2$ D $_3$ , 1,25 dihydroxyvitamin D $_3$ ; ORG2058, 16 $\alpha$ -ethyl-21-hydroxy-19-norpregn-4-ene-3,20-dione; RU486, 17 $\beta$ -hydroxy-11 $\beta$ -(4-dimethylamino-phenyl)-17 $\alpha$ -(1-propynyl)-estra-4,9-dien-3-one; R5020, 17,21-dimethyl-19-norpregna-4,9-dien-3,20-dione; EGF, epidermal growth factor; 5-AZAC, 5-azacytidine; FoxM1, forkhead box protein M1; HIF-1 $\alpha$ , hypoxia-inducible factor 1 $\alpha$ ; TPA, 12-O-tetradecanoylphorbol-13-acetate; +, increase; –, decrease; ne, no effect.

ulators on ER $\alpha$  expression in breast cancer cells (259–286). The reason for the broad interest in studying the ER $\alpha$  reexpression is mainly because ER-positive breast cancers can be treated with selective ER modulator (SERM) therapies.

### VIII. Role of E2 Signaling in Breast Cancer Stem Cells—Beginning of a New Concept

As reviewed in the previous section, the adult mammary gland undergoes massive epithelial tissue remodeling during reproductive cycles. Over recent years, accumulated evidence has shown that mammary epithelium has a hierarchical organization. Using a fluorescence-activated cell sorting-based approach, two groups recently identified a subpopulation of murine mammary cells with  $\text{lin}^- \text{CD}29^{\text{hi}} \text{CD}24^+$  and  $\text{CD}49^{\text{hi}} \text{CD}29^{\text{hi}} \text{CD}24^{+/\text{mod}}$  to have properties of mammary stem cells (MaSC) that could recapitulate into an entire mammary epithelial tree on transplantation into an epithelium-free mammary fat pad (287–289). However, these MaSC show a receptor-negative phenotype for ER $\alpha$ , PR, and ErbB2 (290). Despite the lack of steroid hormone receptors, ovariectomy of mice significantly reduced MaSC number and tumor-forming potential *in vivo*, whereas MaSC activity increased in mice treated with E2 plus progesterone (291). This indicates an increased risk of breast cancer associated with pregnancy; however, the molecular mechanism of such response still remains unclear and requires further investigation.

Because the lobular epithelium in the mammary gland is also the site for most breast tumors, evidence suggests the existence of a hierarchical organization for breast tumorigenesis similar to that of mammary gland development (292). A small population of tumor cells termed cancer stem cells is able to initiate tumor formation and undergo self-renewal. The most accepted model is that adult stem cells which are slow-dividing and long-lived, with a high proliferative capacity, accumulate multiple mutations and undergo transformation to generate these cancer stem cells (292–295). However, few research groups hold the idea that the cell of origin, the normal cell that acquires the first cancer-promoting mutation, need not necessarily be related to the cancer stem cell (296). In that line, Al-Hajj *et al.* (297) engrafted cells obtained from human breast cancer tumors into nonobese diabetic/SCID mice and found only a few to have the potential to generate new tumors. These were identified as a small population of breast cancer-initiating cells based on their cell surface markers ( $\text{CD}44^+ \text{CD}24^{-/\text{low}}$ ) that exclusively retained tumorigenic activity and display stem cell-like properties

(297). In addition, Dontu *et al.* (298) reported that cells expressing high aldehyde dehydrogenase (ALDH) have stem/progenitor properties both in normal and neoplastic human breast epithelium, and expression of ALDH1 is correlated with poor prognosis of breast cancer (294, 298–300). Stem cells expressing high ALDH and  $\text{CD}44^+ \text{CD}24^{-/\text{low}}$  signature showed enhanced malignant and metastatic ability (301). However, the relation between the hormone signaling and the expression of surface markers in mammary cancer stem cells is unknown.

Although the role of E2 signaling in mammary gland development and breast cancer progression is well documented, the role of E2 and ER $\alpha$  status, molecular characteristics, and clinical significance in breast cancer stem cells (BrCSC) are still a matter of debate. Recently, it has been reported that E2 reduces the stem cell population in both normal mammary gland and breast cancer, whereas overexpression of stem cell genes OCT4 (octamer-binding transcription factor 4), SOX2 (sex-determining region Y-box 2), and NANOG reduces ER $\alpha$  expression and increases the number of stem cells and their capacity for invasion, properties that are associated with tumorigenesis and poor prognosis (302). On the contrary, another report reveals that E2 signaling expands the pool of functional BrCSC through a paracrine fibroblast growth factor/fibroblast growth factor receptor/Tbx3 signaling pathway (303). In one investigation, tumor-initiating mammospheres derived from ER-positive breast cancer cell lines show significantly reduced ER $\alpha$  expression and down-regulation of ER $\alpha$  target genes compared with the parent cell line, although ER $\alpha$  mRNA levels were not considerably down-regulated (304). Evidence from a number of investigations supports that  $\text{CD}44^+$  BrCSC are ER-negative, although they were isolated from human ER $^+$  tumors (300, 305, 306). This can justify the failure of ER-targeted endocrine therapy in breast cancer. However, there are other reports of BrCSC derived from ER-positive MCF7 cells that can induce tumors when cells as low as  $10^3$  are injected into the mammary fat pad of an SCID mouse, indicating the existence of distinct ER $^+$  BrCSC (307). The “side population” cells obtained from mammospheres that effluxed Hoechst dye expressed high levels of ER $\alpha$ , p21(CIP1) and Msi1 genes (308). Because the role of ER $\alpha$  in BrCSC and tumor progression remains ambiguous, one fundamental question that still needs to be addressed immediately is whether or not breast cancers with different ER $\alpha$  status are derived from different MaSC. Current opinion is that ER $\alpha$  status of MaSC correlates with the ER $\alpha$  expression of BrCSC, *i.e.*, ER-positive breast cancers arise through ER-positive stem cells, and ER-negative breast cancers arise from the most ER-negative stem

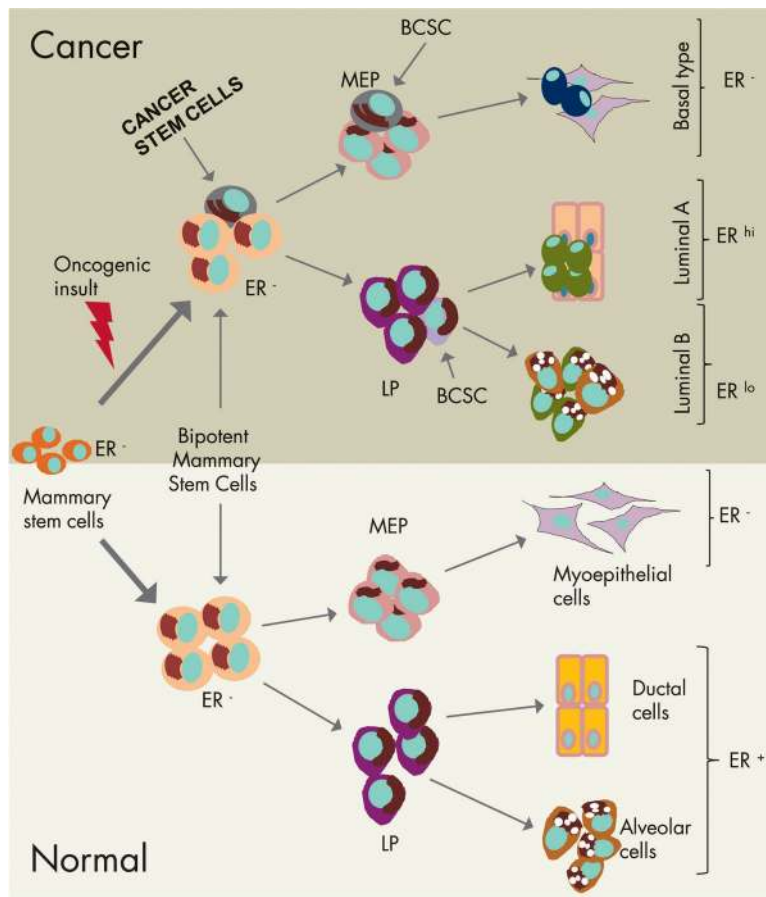
**Figure 4.**

Figure 4. Hypothetical model illustrating the hierarchy of breast normal and cancer stem cells with ER $\alpha$  status. MaSC differentiate into bipotent stem cells that are ER-negative, and the differentiated progeny arising from this population is also ER-negative. Luminal type of mammary tissue that arises from its progenitor shows high ER $\alpha$  status, whereas myoepithelial cells arising from its progeny are ER-negative. In response to an oncogenic insult, rare population of MaSC become cancerous and give rise to three types of breast cancers such as basal type, which are ER $\alpha$ -negative; luminal A, which are high ER $\alpha$ ; and luminal B, which show low ER $\alpha$ . BCSC, Breast cancer stem cells; LP, luminal progenitor; MEP, myoepithelial progenitor.

cells (294, 309) (Fig. 4). Another view about ER $\alpha$  status in BrCSC is that the normal mammary gland contains stem cells with basal phenotype that are ER $\alpha$  negative, so the BrCSC are endocrine-resistant, making the SERM therapy ineffective to treat breast cancers (310). More research in this area is warranted to know the expression status and precise role of ER $\alpha$  in BrCSC.

### IX. Estrogen Receptor Subtypes in Breast Cancer

Until recently, there were two known classical receptors that mediate E2 action, ER $\alpha$  and ER $\beta$ . In the last decade, several isoforms of ER $\alpha$  and other related receptors have

been identified. Of these, the role of ER $\beta$  in mammary gland development and its inverse relation with breast cancer progression is well characterized (311). In contrast to the positive correlation seen between ER $\alpha$  expression and breast cancer risk, various studies have shown that decreased expression of ER $\beta$  mRNA and protein levels in tumors compared with normal tissues (312). The loss of chromosome 14q, which encodes ER $\beta$ , was observed in some breast cancers, indicating the inverse correlation between ER $\beta$  and breast cancer risk (313, 314). It is clear that overexpression of ER $\beta$  in different breast cancer cell lines results in a decrease of proliferation and motility and promotes apoptosis (315, 316). ER $\beta$  appears to reduce the cell proliferation in response to E2 by inhibiting cyclin D1, cyclin E, and cdc25A expression, key factors that control cell division (317). Although ER $\beta$  also palmitoylated and targeted to plasma membrane like ER $\alpha$ , due to the lack of its interaction with PELP1/MNAR and Src kinase, ER $\beta$  does not stimulate the E2 extranuclear signals important for cell cycle progression (*i.e.*, ERK/MAPK and PI3K/AKT) and cyclin D1 transcription (318). ER $\beta$ 2, an isoform of ER $\beta$  (also called ER $\beta$ cx), was found to have no affinity for E2 and cannot activate transcription of ERE-responsive genes, but it was shown to negatively regulate the ER $\alpha$  transactivation in human breast cancer cells (319, 320). These findings suggest a tumor-suppressive function of ER $\beta$ .

Previous observations that E2 modulates the expression of several genes in ER $\alpha$  knockout mice and also specific aberrations in uteri of ER $\beta$  null mice in response to E2 suggested the presence of a novel receptor for E2 (321, 322). A newly identified G protein-coupled receptor (GPR30) was thought to mediate these functions. Indeed, GPR30 was shown to bind E2 both *in vitro* and *in vivo*, and it plays a key role in nongenomic signaling of E2 (323–327). GPR30 mediates E2-induced proliferation of ER-negative breast cancer cells through the rapid activation of MAPK (323, 328, 329). GPR30 signaling by E2 also promotes cell proliferation and migration in ER-negative breast cancer cells via induction of connective tissue growth factor (330). Immunohistochemistry analysis of a large number of breast carcinomas showed that half of these tumors, which are negative for ER $\alpha$ , are GPR30-positive, suggesting that these tumors may respond to E2 through GPR30 (331). Further overexpression of GPR30



is shown to associate with tumor size and Her2 expression, indicating that GPR30 may serve as a prognostic factor for aggressive breast cancers. Although these studies indicate that GPR30 mediates E2 actions in breast cancer cells and GPR30 expression correlates with aggressive breast cancers, controversies about its binding to E2 and E2-mediated GPR30 signaling remain. For instance, unlike ER $\alpha$  null mice, *Gpr30* null mice show no abnormalities in reproductive organs and, therefore GPR30 is dispensable in mediation of E2 effects in organs like the uterus and mammary gland (332). In addition, Levin's group demonstrated that silencing of *GPR30* by *GPR30*-specific siRNA had no effect on E2 nongenomic signaling in MCF7 cells (ER-positive) (333). Despite these controversies, accumulated evidence indicates that GPR30 is involved in breast cancer cell proliferation, tumor formation, migration, metastasis, and drug resistance (334–337). For example, heregulin-induced GPR30 promotes migration and invasion potential of the ER-negative breast cancer cell line SKBR3 through the activation of the ERBB2-ERBB3/MAPK pathway (338). The IGF-I-GPR30 axis was also shown to regulate MCF7 cell migration (339). Together, these studies suggest that GPR30 promotes tumor development through the activation of growth factor signaling independent of ER $\alpha$ .

In addition to the above-mentioned E2-related receptors, recently a number of ER $\alpha$  splice variants have been reported to be important for breast cancer development. The ER $\alpha$  variants such as ER $\alpha$ 36 and ER $\alpha$ 46 initiate their transcription from exon 2 of the ER $\alpha$  gene. ER $\alpha$ 46 lacks the first coding exon of ER $\alpha$  (AF1) and acts as an inhibitor for ER $\alpha$  functions, whereas ER $\alpha$ 36 lacks both transcriptional activation domains (AF1 and AF2) but retains the DNA binding domain and the ligand binding domain (340). ER $\alpha$ 36 is predominantly located in plasma membrane and in the cytoplasm and can be detected in both ER-positive and ER-negative breast cancers (341). Down-regulation of ER $\alpha$ 36 mRNA correlated with local progression, lymph node metastasis, and advanced cancer stages, indicating its involvement in breast cancer progression (342). It appears that ER $\alpha$ 36 mediates extranuclear and mitogenic E2 signaling in ER-negative breast cancer cells like MDA-MB-231 and MDA-MB-436 through the EGFR/Src/ERK signaling pathway, implying that ER $\alpha$ 36 may play an important role in the malignant growth of ER-negative breast cancers (342). ER $\alpha$ 36 is also known to be involved in tamoxifen resistance in breast cancer cells. For instance, rapid phosphorylation of ERK1/2 and AKT was detected in ER $\alpha$ 36-overexpressed MCF7 cells treated with tamoxifen (341, 343). These subtypes of

ER $\alpha$  pose an additional layer of complexity to breast cancer development and require attention for further research.

## X. Therapeutic Targeting of ER $\alpha$ Pathway—A Cure for ER-Positive Breast Cancers

Breast cancer is the fifth leading cause of all cancer deaths worldwide (1). It is well documented that within breast cancers, ER-positive breast cancers account for two thirds of cases (3). To extirpate the ER-sensitive breast cancers, multiple options were explored to target ER $\alpha$  signaling pathways. Endocrine therapy was the first targeted therapy used in the oncology field, long before the therapeutic agents were known (344). After the discovery and characterization of ER $\alpha$  and ER $\beta$ , attention was focused on developing new strategies and drugs that specifically target the ER $\alpha$  pathway. In pursuit of this, many SERM and selective ER down-regulators were developed and are still in use for breast cancer therapy (345). About two thirds of breast tumors that express ER $\alpha$  respond well to tamoxifen, an anti-estrogen; however, prolonged treatment with tamoxifen resulted in resistance to the drug (346). Alternatively, several other related SERM such as arzoxifene and raloxifene are also available to treat breast cancer. Both anastrozole and letrozole, which block E2 synthesis by inhibiting aromatase, are considered as first-line treatment of advanced breast cancer in postmenopausal women with ER-positive breast cancer on par with tamoxifen (347). Fulvestrant, a potent antiestrogen that targets and degrades ER $\alpha$ , was approved for treatment of hormone receptor-positive breast cancer in postmenopausal women with disease relapse after antiestrogen therapy (348).

Although the majority of breast cancers are ER-positive, about 30% of invasive breast cancers are hormone independent because they lack ER $\alpha$  expression due to hypermethylation of ER promoter (254, 255). Attempts were made to re-express ER $\alpha$  in ER-negative breast cancers because ER-positive breast cancers respond to SERM therapies. Indeed, such efforts were successful on cell lines. For instance, treatment with epigenetic modulators such as DNA methyltransferase inhibitors and/or HDAC inhibitors induces ER $\alpha$  expression and restores tamoxifen sensitivity in ER-negative breast cancer cell lines (349, 350). Valproic acid, an HDAC inhibitor, also induces ER $\alpha$  and FoxA1 expression in MDA231 cells (ER-negative breast cancer cell line) and restores E2 sensitivity to these cells (267). Several HDAC inhibitors (*e.g.*, trichostatin A, vorinostat, de-

citabine, *etc.*) either alone or in combination with other drugs were used in phase I or phase II clinical trials (351–355). Although disease stabilization was observed using vorinostat in relapsed or refractory breast cancer patients, no consistent response was seen (351). In a similar phase II trial using vorinostat but in advanced and metastatic tumors, stable disease was observed in a limited number of patients. However, the lack of a complete or partial response led to termination of the study (352). A phase II trial using vorinostat combined with tamoxifen exhibited an encouraging response in reversing hormone therapy-resistant breast cancers (354). Similarly, a good clinical response was also observed in metastatic breast cancer patients when a combination of vorinostat with paclitaxel and bevacizumab was used (353). EZH2, a histone H3 Lys 27 (H3K27) methyltransferase and polycomb group protein, is reported to be down regulated in association with up-regulation of ER $\alpha$  in breast cancer cells. As a result, growth of ER-negative breast cancer requires EZH2 expression. Thus, suppression of EZH2 expression which ensures ER $\alpha$  reexpression, provides an option for better response to antiestrogens in ER-negative breast cancers (356, 357).

Because peptide drugs have more target-specific activity and coregulators influence ER $\alpha$  transcriptional activity through LXXLL motifs, attempts are being made to generate small peptide molecules that mimic these motifs to target ER $\alpha$  (358, 359). A group of linear and cyclic peptides that inhibit interaction between coactivator–steroid receptor were synthesized. Of these, pentapeptide, a short cyclic peptide containing a copy of the LXXLL nuclear receptor box, exhibited strong binding abilities and selectively interacted with ER $\alpha$ , with a  $K_i$  (inhibitory constant) of 25 nM (360). Because dimerization is key for ER $\alpha$  nuclear translocation and activity, “dimer-interface” oligopeptides, called I-box peptides, were synthesized. The I-box peptide exerted ER $\alpha$  inhibitory action by promoting aggregation and precipitation of both ligand bound and unbound receptor (361).

Extensive studies revealed the direct functional interaction of the ER $\alpha$  signaling pathway with several growth factor signaling pathways, which include PI3K/AKT, Src/MAPK, mammalian target of rapamycin, EGFR, *etc.* Previous reports show that E2 activates the PI3K/AKT signaling pathway, and inhibition by its inhibitors such as wortmannin and LY294002 has been shown to suppress cellular proliferation and transforming activity of breast cancer cells (169, 362). Hence, several drugs that target the PI3K/AKT pathway in mul-

tiples are in clinical trials; most of them are competitive inhibitors for ATP or mimetic of ATP. For example, BKM120, XL-147, PX-866, CAL-101, INK-1117, and BYL719 specifically inhibit PI3K, whereas GDC-0068, GSK690693, and MK-2206 specifically inhibit AKT (363). Because E2 also activates Src kinase by extranuclear signaling and kinase activity of Src is linked to E2/ER $\alpha$ -dependent cell proliferation and transformation, Src inhibitors such as dasatinib, bosutinib, and PD180970 were also developed to treat breast cancers and have shown potential in the clinical setting (113, 364). Data from phase II trials with dasatinib have shown limited activity in hormone receptor-positive breast cancer patients (364). Therefore, clinical trials using a combination of dasatinib with other drugs are ongoing.

Because ER $\beta$  exhibits tumor-suppressive actions in breast, in recent years several ER $\beta$  agonists have been synthesized. For example, genistein, a natural compound of the isoflavone family, binds to ER $\beta$  by 26-fold higher affinity over ER $\alpha$  and activates ER $\beta$  by 7-fold greater potency than ER $\alpha$  (127). Structurally modified derivatives of genistein have also exerted better anticancer activity in breast cancer cells (128). Similarly, 2,3-bis(4-hydroxyphenyl)propionitrile (DPN) binds to ER $\beta$  by 72-fold higher affinity over ER $\alpha$  and activates ER $\beta$  by 80-fold greater potency than ER $\alpha$  (207). DPN has shown an antiproliferative effect and also inhibitory action on cellular transformation (268). Recently, in a virtual screening based on a structure optimized through molecular dynamics and bioassay approach, 18 potent ligands of ER $\beta$  were discovered (270). Some of these compounds could be novel SERM of the future that could benefit the therapy of ER-positive breast cancer.

## XI. Conclusions and Future Prospects

ER-positive breast cancer constitutes a major proportion of breast cancer types. Therefore, breathtaking research has been carried out in the last three decades to understand ER $\alpha$  function and its relevance with breast cancer. As a result, many novel mechanisms of E2/ER $\alpha$ -mediated breast cancer development were discovered, including the identification of hundreds of ER $\alpha$  coregulators and their association with breast cancer development. Particularly in the last decade, extensive research on E2 extranuclear signaling led to the discovery of many novel signal transduction pathways associated with breast cancer growth and behavior, which are being explored as therapeutic targets. In addition, many

posttranslational modifications for ER $\alpha$  were identified, and their functional significance in disease progression was well studied. However, cross talk between multiple signaling pathways poses a barrier for such approaches. In such instances, combination therapy involving drugs that target both nongenomic signaling and posttranslational modifications should be developed. Despite all of these advancements, the survival rate has not improved greatly enough. Therefore, a detailed understanding of decoding the mystery behind the E2 signaling and breast tumor growth is important.

Antiestrogens are the current choice of endocrine therapy in the treatment of ER-positive breast cancers. However, drug resistance poses a major hurdle in the usage of antiestrogen therapy. Future studies should be focused on the newly discovered E2 signaling pathways to make use of them in new therapeutics against breast cancers. Especially, many well-characterized coregulators with the potential to influence the ER $\alpha$ -mediated breast cancers should be targeted. To this end, expression profiling data of all coregulators in the form of a “code” should be available for all subtypes of breast cancers. This “coregulator code” eventually may help in patient diagnosis and treatment. In addition, recent studies on the miRNA-ER $\alpha$  axis revealed novel mechanisms of breast cancer development. But more clinical studies are needed to better understand the role of miRNA on ER $\alpha$  actions and breast cancer status. Future research awaits on whether the novel gene therapy of using miRNA in breast cancer treatment will be a powerful tool for breast cancer treatment or just an addition to the existing drugs. The current theories on stem cells indicate that stem cells are important for initiation and maintenance of a tumor; very little is known about E2 signaling in MaSC functions. Therefore, it is certainly no exaggeration that exciting years of research on the role for E2 in mammary/breast stem cell maintenance are coming up to invite a new arena in the E2 signaling.

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Address all correspondence and requests for reprints to: Dr. Bramanandam Manavathi, Assistant Professor, Department of Biochemistry, School of Life Sciences, Gachibowli, Prof. CR Rao Road, University of Hyderabad, Hyderabad 500046, India. E-mail: manavathibsl@uohyd.ernet.in.

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