

Molecular biology of beta-estradiol-estrogen receptor complex binding to estrogen response element and the effect on cell proliferation

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Abstract

Group of estrogen pollutants, where the highest estrogen activity is reported at estradiol, is characterized by the fact that even at very low concentrations have potential to cause xenoestrogenic effects. During exposure of excessive amounts of estradiols may be produced undesirable effects resulting in the feminization of males of water organisms. The presence of estradiols in drinking water implies also a risk for the human population in the form of cancers of endocrine systems, abnormalities in reproduction or dysfunctions of neuronal and immune system. Currently, the research is focused mainly to uncover the relationship between the estrogen receptors binding affinity with an estrogen response element and estradiol. In this review we summarized facts about molecular biological principles of β estradiol-estrogen receptor complex binding with estrogen response element and its successive effect on cancer genes expression.

Abbreviations:

E2 - β estradiol
EDC - Endocrine disrupting compounds
ER - Estrogen receptor
ERE - Estrogen response element
HSP 90 - Heat shock protein 90
RA - Retinoic acid
LBD - Ligand binding domain
DBD - DNA binding domain

AF1 - Hormone-independent transcriptional activation function domain
AF2 - Ligand-dependent transcriptional activation domain
MAPK - Mitogen-activated protein-kinase
SRC - Steroid receptor coactivator
LSD1 - Lysine-specific demethylase 1
CCAR1 - Cell cycle apoptosis regulator 1
DBC1 - Deleted in breast cancer 1
CARM1 - Coactivator-associated arginine methyltransferase 1
SERMs - Selective estrogen receptor modulator

INTRODUCTION

Estrogenic compounds related to Endocrine Disrupting Compounds (EDC) belong to pollutants gaining the increasing environmental and social concerns in recent years because of their endocrine-disrupting property and other serious side effects on human health (Liu *et al.* 2004; Ballesteros-Gomez *et al.* 2009; Swedenborg *et al.* 2009). With the rapid economy development, a variety of EDCs have been discharged into the aquatic environment (Jeffries *et al.* 2011), received in large amounts in the urine and excreta of livestock (Tang *et al.* 2013) but also in the urine of people that contains residues of contraceptives, whose consumption increases every year (Preda *et al.* 2012; Qiang *et al.* 2013). Estrogenic pollutants, among which the highest activity was reported at β estradiol (E2) (Boulay & Perdiz, 2005; Heldring *et al.* 2007) are characterized by the fact that even at very low concentrations, the long-term exposure can cause xenoestrogenic effects (Lange *et al.* 2012; Qin *et al.* 2013b).

Sewage treatment plants currently do not have a way how to effectively break down these substances from the water. Although a certain amount of these substances remains bound in the sludge (Gagne *et al.* 2013), the rest is released into the receiving waters of the sewage treatment plant (Nie *et al.* 2012). Their adverse effects are caused through the endocrine system by mimicking the action of natural hormones (Bovet *et al.* 2009). As EDCs disrupt the actions of endogenous hormones, they may induce abnormal reproduction, stimulation of cancer growth, dysfunction of neuronal and immune systems (Howdeshell *et al.* 2008; Jenkins *et al.* 2012; Macon & Fenton, 2013; Lee *et al.* 2013; Tang *et al.* 2013). Estrogens provide gene transcription and signaling of plenty processes in cell in a variety of tissues, the bone, breast, and endometrium, through binding and activation of estrogen receptors (ERs) (Ceylan *et al.* 2012; Wolinska-Witort *et al.* 2012; Komm & Mirkin, 2013). Because breast cancer is the most common cancer in women, both in developed and developing countries

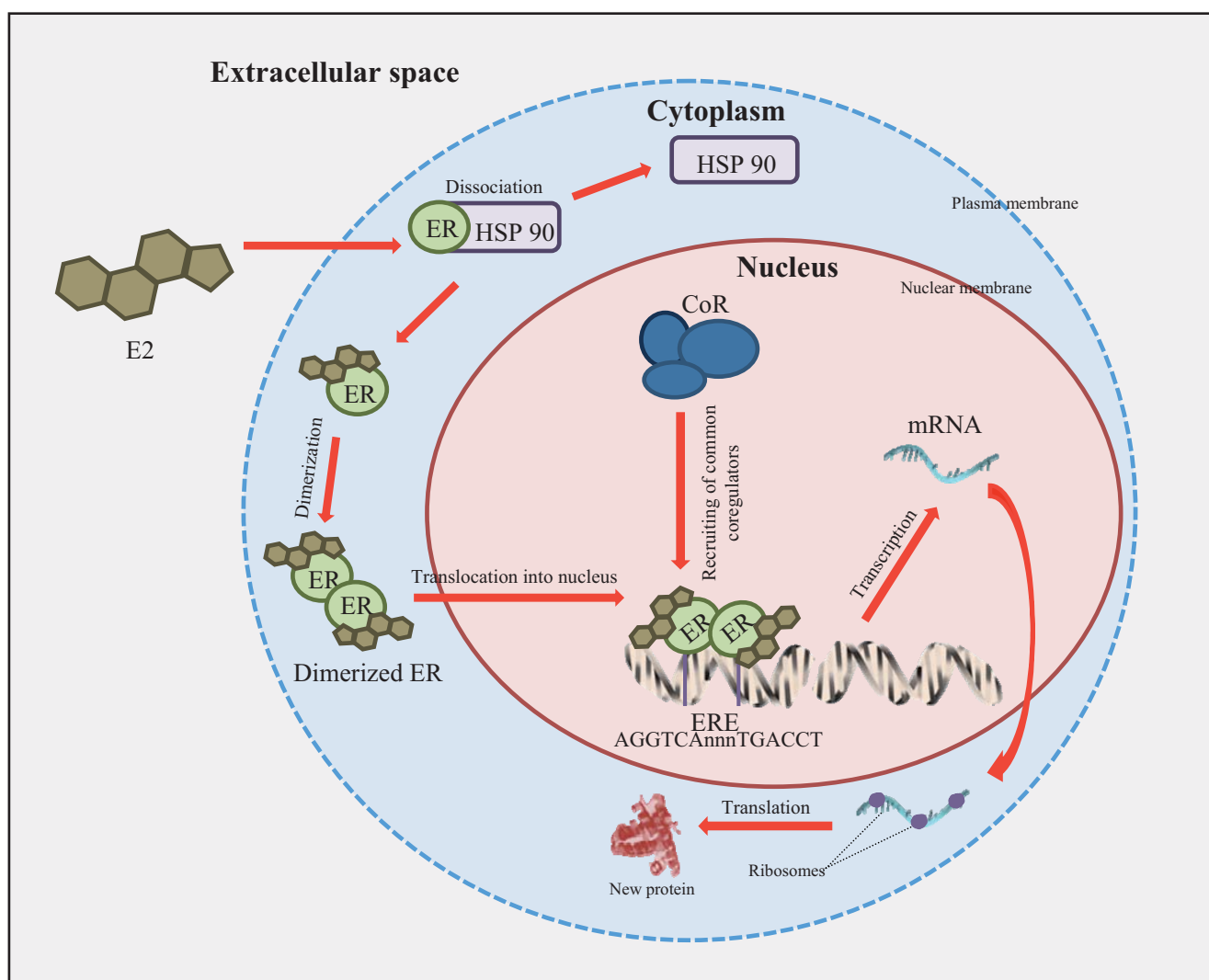


Fig. 1. Scheme of basic molecular biological way of estradiol physiological function, where E2 stays for estradiol, ER for estrogen receptor, HSP 90 for heat shock protein 90, CoR for coregulators and ERE for estrogen response element.

(van Duursen *et al.* 2013), the issue of reproductive toxicants is a major scientific challenge for human health (Bechi *et al.* 2013). The aims of this review are to summarize the facts about the molecular biological principles of estradiol pathways in complex with estrogen receptor, its binding with estrogen response element and its effect on target genes involved in cell proliferation.

MOLECULAR BIOLOGY OF ESTRADIOL

Currently, research covering this issue is applied especially to clarify the relationship between estradiol (Figure 1), estrogen response element (ERE) and estrogen receptor (ER), a member of hormone receptors of the nuclear receptor family (Gronemeyer *et al.* 2004; Srinivasan *et al.* 2013). There are known two subtypes of estrogen receptors ER α and ER β (Muyan *et al.* 2012; Chieffi & Chieffi, 2013; Oh & Chung, 2013) encoded by distinct genes, *Esr1* and *Esr2*, respectively (Billon-Gales *et al.* 2011). These steroid transcription factors remain nowadays the most informative biomarker in breast cancer diagnosis (Patani *et al.* 2013), because more than three quarters of breast tumors are ER α -positive (Dunnwald *et al.* 2007). ERs are composed of the polypeptide chain and located in the cell cytoplasm in multiprotein complex containing the molecular chaperone HSP 90 (heat shock protein 90, Figure 1) (Cheng *et al.* 2012). Ligand binding triggers the conformational changes that lead to dissociation and receptor dimerization (Jeong *et al.* 2012). The proliferative or pro-survival action of estrogens is antagonized in most cases by retinoic acid (RA) (Ombra *et al.* 2013). Activated receptor-ligand complex is replaced into the nucleus of cell, where interactions with coactivators (CoA) or corepressors (CoR) of transcription are undergoing (McDonnell & Wardell, 2010; Coughlan *et al.* 2013).

PRINCIPLES OF E2-ER-ERE BINDING

Because of steroidal hormone properties, estrogens can pass through the phospholipid membranes of the cell to realize the binding with ER (Oh & Chung, 2013; Qin *et al.* 2013a). ER proteins are composed of six functional domains labeled as A through F (Ascenzi *et al.* 2006; Han *et al.* 2007). The E ligand-binding domain (LBD) provides ligand specificity to the receptor and contains ligand-dependent transcriptional activation function (AF2) (MacPherson *et al.* 2009; Jiang *et al.* 2010), localized in its conformationally dynamic region (Figure 2). It was found that ERs conformation changes are leading to a helix 12 realignment with helices 3, 5–6 and 11 and thereby forming a lid on the LBD for the surrounded E2 (Figure 2) (Endler *et al.* 2012). Agonist ligands stabilize a receptor conformation that is optimal for efficient interaction with coactivators and the direct (or indirect) binding to *cis*-acting elements and thereby triggering of a transcriptional activation (Heldring *et al.* 2007; Chen

et al. 2009; Billon-Gales *et al.* 2011). The C domain responsible for targeting the receptor to DNA possesses two zinc fingers forming a helix-loop-helix motif and primarily functions in binding of the receptor to the hormone response elements. Zinc finger contains a P box for identification of the specific DNA sequence. Second zinc finger includes at its base a D box. Its main role is the recognition of the distance between hexamers constituting the ERE in the promoter of the target gene (Puzianowska-Kuznicka *et al.* 2013). In the N-terminus, ER contains a hormone-independent transcriptional activation function domain (AF1) (Alimirah *et al.* 2012), regulated by growth factors acting through the MAPK signaling pathway (Kato *et al.* 1995). Both AF domains recruit a range of coregulatory protein complexes to the DNA-bound receptor, altering the chromatin structure and facilitate recruitment of the RNA polymerase II transcription system (Heldring *et al.* 2007).

ER COREGULATORS

Transcription inhibition or enhancement is achieved by ligand-regulated coactivators and corepressors (Aust *et al.* 2013). Hundreds of potential coregulators with diverse functions, from histone modification and chromatin remodeling to RNA polymerase II recruitment and mRNA splicing, have been identified (Lonard & O'Malley, 2006). Corepressors are crucial regulators of ER α -mediated action, and that their loss could promote breast cancer development and resistance to endocrine therapy (Dobrzycka *et al.* 2003). To the novel coregulators with a multitude functions belongs proline-, glutamic acid-, and leucine-rich protein (PELP1) which expression is deregulated in hormonal tumors, and functions as a proto-oncogene, however, the mechanism by which PELP1 promotes oncogenesis remains unclear (Gonugunta *et al.* 2011). In study by Kim *et al.* (2013) it was reported first evidence about protein CAC1, associated with LSD1, working as an ER α corepressor, implicating a potential antitumor target like Paclitaxel in ER α -positive breast cancer. Jeong *et al.* (2011) demonstrated that interactions with the protein acetyltransferase (TIP 60) are also one of the required coregulators for estrogen-induced transcription of a subset of ER α target genes in human cells. Coactivators, where among the best-characterized belong the steroid receptor coactivators (SRC) or p160 family (SRC-1, SRC-2, SRC-3), work as a scaffold proteins for other coregulators (Jeong *et al.* 2012). Data published by Karmakar *et al.* (2009) indicate that the closely related p160 coactivators are not functionally redundant in breast cancer cells because they play gene-specific roles in regulating mRNA and protein expression, and they therefore are likely making unique contributions to breast tumor genesis. Among important coactivators belong also cell cycle and apoptosis regulator 1 (CCAR1), deleted in breast cancer 1 (DBC1) (Yu *et al.*

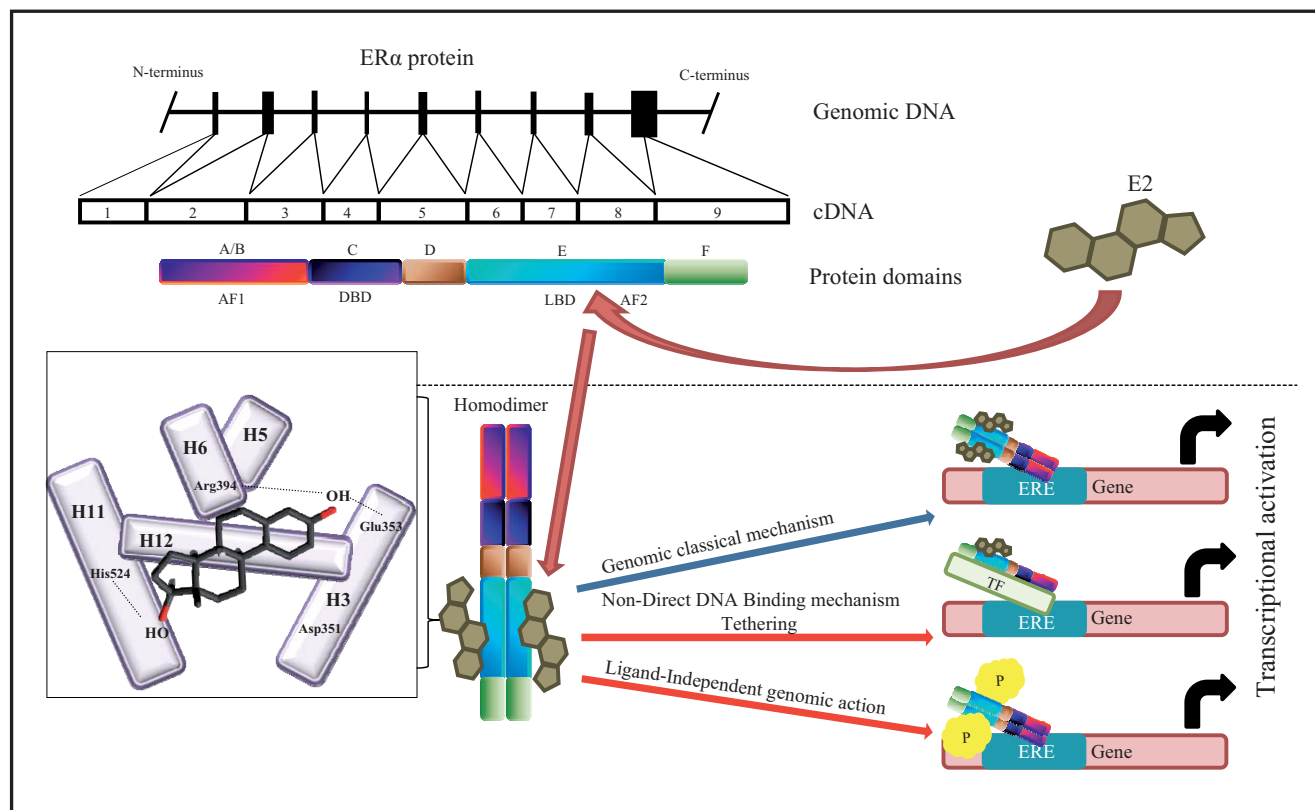


Fig. 2. Scheme of ER protein, its cDNA, gene and its binding mechanisms. DBD stands for DNA binding domain, LBD for ligand binding domain, TF for another protein – transcription factor, interacting with ER during Non-Direct DNA binding mechanism, P for phosphorylation induced by various kinases, AF1 for hormone-independent transcriptional activation function domain and AF2 for ligand-dependent transcriptional activation domain.

al. 2011) and coactivator-associated arginine methyltransferase 1 (CARM1) (Coughlan *et al.* 2013; Zeng *et al.* 2013) important co-activators for estrogen-induced gene expression and estrogen-dependent growth of breast cancer cells.

MOLECULAR PATHWAYS INVOLVING E2-ER COMPLEX BINDING TO ERE

The proliferative effect of estrogens is exerted via genomic and non-genomic pathways (Abbondanza *et al.* 2012). Non-genomic pathway is not as well understood as the genomic mechanism, but has been observed in many tissues. Probably signaling cascades are initiated via second messengers affecting ion channels or increasing nitric oxide levels in the cytoplasm, leading to a physiological responses without involving gene regulation (Heldring *et al.* 2007). In the genomic pathways in the endocrine glands as a mammary gland, proliferating cells express low levels of ER α , which is down regulated through a ubiquitin proteasome pathway, in the presence of β estradiol by direct binding to ERE (Cirillo *et al.* 2013). ERs can also be recruited to genomic DNA by indirect by tethering through other DNA-bound transcription factors, including members of the activating protein-1 (AP-1) and cAMP response element-binding protein family members creating a

heterodimers (Heldring *et al.* 2011). The last of genomic pathways works through ER phosphorylation. Mitogen activated protein kinase (MAPK) is known to directly phosphorylate ER alpha at serine 118 in a ligand-independent manner (McGlynn *et al.* 2013). As a crucial target or ligand-independent pathway is AF1 region that forms the target for receptor phosphorylation. In addition the AF1 and AF2 regions can interact with different coactivators and corepressors, triggering gene transcription separately or synergistically (Acconcia & Kumar, 2006).

GENES EXPRESSED IN CONNECTION WITH ER-INDUCED CANCER

Tumor development occurs when a buildup of genetic mutations in genes, mostly controlling cell growth and division or the damaged DNA repairment, allows cells to grow and divide uncontrollably and to form a tumorous tissue subsequently. For example tumor suppressive p53 gene encodes a same name protein stopping tumor growth. Mutations in p53 gene cause a disorders with potential to develop soft tissue cancers like breast cancer (Chang *et al.* 2013). Many genes involved in cell growth, growth factor signaling, and cell cycle control are estrogen responsive (e.g. *fos*, *myc*, *myb*, *cdc25a*, *A2*, *p53* and *stk15*). Inappropriate expression or activ-

ity of a number of these genes has been implicated in breast cancer (Hodges *et al.* 2003). At *in vitro* study by Shahmoradgoli *et al.* (2013) significantly higher levels of *PPP1R15B* mRNA expression in luminal (ER α -positive) and normal-like subtypes of breast tumors were observed. High levels of *Runx2* expressed in some invasive breast cancer cell lines were observed by Ferrari and colleagues, but intriguingly, *Runx2* was also expressed in the ER negative population (Ferrari *et al.* 2013). Genetic alterations in the *TopBP1* gene influencing the risk of breast cancer were also observed (Forma *et al.* 2013). *ROS1* mRNA expression connection with decreased ER expression was confirmed by Eom *et al.* (2013). Their real-time PCR results showed that *ROS1* expression was decreased in patients with the increased histologic grade and increased mitotic counts. Among genes that are commonly a part of a ER α -positive breast tumor signature belong *GATA-3* (Wilson & Giguere, 2008; Gaynor *et al.* 2013), *FOXA-1* (Schneider *et al.* 2006), *XBP-1* (van't Veer *et al.* 2002) and *TFF3* (Chen *et al.* 2011). In study of Lattrich *et al.* (2013) it was mentioned also the connection between luminal breast tumors exerted by unspecific activation of ER α and proliferative effects accompanied by overexpression of *cyclin B1*, *PR* and *PS2* genes. E2-induced *Bcl-2* transcription effects on demethylation of lysine driven by the LSD1 demethylase, producing reactive oxygen species (ROS) with consequent influence on DNA strands were observed (Perillo *et al.* 2008). Estradiol was proved as a downregulator of *ST8SIA1* mRNA expression as well as *ST8SIA1* core promoter activity linked with luminal breast cancer (Bobowski *et al.* 2013). There exist far more genes involved in progression of cancers, connected with ER observed by different methods, but nowadays the largest discussion arises according to genes *BRCA1* and *BRCA2*, whose mutations are highly linked with different types of breast tumors (Meric-Bernstam *et al.* 2013). The absence of ER in *BRCA1/2* (69.1/19 % of patients, according to (Meric-Bernstam *et al.* 2013)) often induced breast tumors deteriorates the benefits from hormonal therapy, but still sensitivity to cytotoxic treatment regimens remains (Brunello *et al.* 2013).

CONCLUSION

β -estradiol as the most potent estrogen pollutant represents currently significant scientific challenge due to its endocrine-disrupting properties and other serious undesirable effects on health. Although the classical pathway of estradiol-ER direct binding to ERE has been known for quite long period of time, recently there were showed additional possible bindings in the interaction with proteins or after phosphorylation. Knowledge of the molecular pathways of estradiol may help to develop increasingly efficient antitumor drugs, such as SERMs granting the possibility to selectively inhibit or stimulate estrogen-like actions in different tissues.

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