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## What's New in Estrogen Receptor Action in the Female Reproductive Tract:

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### Abstract

Estrogen receptor alpha (ER $\alpha$ ) is a critical player in development and function of the female reproductive system. Perturbations in ER $\alpha$  response can affect wide-ranging aspects of health in humans as well as in livestock and wildlife. Because of its long-known and broad impact, ER $\alpha$  mechanisms of action continue to be the focus on cutting-edge research efforts. Consequently, novel insights have greatly advanced understanding of every aspect of estrogen signaling. In this review, we attempt to briefly outline the current understanding of ER $\alpha$  mediated mechanisms in the context of the female reproductive system.

### Estrogen Receptor

The vast majority of estrogen's activities are mediated by the estrogen receptor (ER), a member of the nuclear receptor family of hormone activated transcription factors. Our understanding of the physiological role of estrogen action has been greatly advanced by the generation of experimental mouse and rat models with knockout of receptors or co-activators either globally or in specific tissues and cells, or with knock-in expression of mutated forms of these molecules. These models, used in combination with microarray, RNA next generation sequencing (RNA-seq), and chromatin immunoprecipitation next generation sequencing (ChIP-seq) methods, allow comprehensive mapping of interaction of ERs with the chromatin landscape to impact genomic response. Together, these models and techniques have led to better understanding of the molecular details of estrogen receptor roles in biological processes.

Estrogen receptor  $\alpha$  (ER $\alpha$ ) cDNA was the first described and cloned estrogen receptor (termed *ESR1* ER $\alpha$ ) (Walter, et al. 1985). A second ER gene, termed *ESR2* (ER $\beta$ ), was discovered in 1996 (Kuiper, et al. 1996). ER $\alpha$  and ER $\beta$  are not isoforms but rather distinct receptors encoded by two separate genes on different chromosomes. ER $\alpha$  is found on chromosome 6 in humans, and chromosome 10 in mice. ER $\beta$  is found on chromosome 14 in humans and chromosome 12 in mice. The ER $\alpha$  proteins are 595 and 599 amino acids in

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length in humans and mice, respectively, with an approximate molecular weight of 66 kDa (Fig. 1) ([Gibson and Saunders 2012](#); [Heldring, et al. 2007](#); [Le Romancer, et al. 2011](#)).

The *ESR2* encodes a receptor of 549 amino acids in rodents and 530 amino acids in humans, each with an approximate molecular weight of 60–63 kDa (Fig. 1) ([Gibson and Saunders 2012](#)). Therefore, ER $\beta$  is slightly smaller than ER $\alpha$ , and most of this difference lies within the smaller N-terminus.

## Receptor Structure

The estrogen receptors are composed of five functional domains (Fig. 1), an N-terminal domain (NTD) or A/B domain, the DNA-binding (DBD or C) domain, a hinge (D) region, LBD (LBD or E), and a C-terminal F domain ([Aagaard, et al. 2011](#); [Brelivet, et al. 2012](#); [Helsen, et al. 2012](#); [Hilser and Thompson 2011](#); [Laudet and Gronemeyer 2001](#)).

### NTD or A/B Domain

Crystallography of the ER NTD or A/B domain has been largely unsuccessful because this portion of the receptor is unstructured and fluctuates in aqueous solutions. However, evidence suggests that intramolecular interactions between the A/B and other receptor domains are likely to induce a more structured NTD ([Aagaard et al. 2011](#); [Hilser and Thompson 2011](#); [McEwan 2004](#)), as evidenced from recent cryogenic Electron Microscopy (cryo-EM) studies ([Yi, et al. 2015](#)). Current models of ER signaling incorporate the flexibility of intrinsically disordered (ID) regions of the receptor, including the NTD, into a mechanism of allosteric interaction and co-ordination of ligand, DNA motif and ER domain functions ([Aagaard et al. 2011](#); [Hilser and Thompson 2011](#)). The NTD contains the transcriptional activation function-1 (AF-1) domain and provides for cell and promoter-specific activity of the receptor as well as a site for interaction with co-receptor proteins (Table 1). More recent description of full-length ER $\alpha$  structure derived using cryo-EM indicates A/B domain is positioned near the LBD, and facilitates recruitment of the steroid receptor transcriptional co-activator, SRC-3 ([Yi et al. 2015](#)). Posttranslational modifications, such as phosphorylation, of the A/B domain can dramatically affect the overall behavior of the receptor and are thought to be an important mechanism for the modulation of AF-1 functions ([Le Romancer et al. 2011](#)).

### DNA-Binding or C Domain

The C domain of the ER recognizes and binds to the *cis*-acting enhancer sequences, called estrogen responsive elements (EREs) ([Helsen et al. 2012](#)). The C domain contains two zinc fingers, each composed of four cysteine residues that chelate a single Zn<sup>2</sup> ion.

Crystallography studies indicate a highly conserved structure consisting of dual  $\alpha$ -helices positioned perpendicular to each other ([Aagaard et al. 2011](#); [Helsen et al. 2012](#); [Hilser and Thompson 2011](#)). Amino acids in the C-terminal “knuckle” of the first zinc finger form the “P-box” (proximal box) of the DNA binding domain and confer DNA sequence recognition specificity to the receptor for binding DNA sequences; hence, the proximal zinc finger is often referred as forming the “recognition helix”. Amino acids at the N-terminal “knuckle” of the second zinc finger form the “D-box” (distal box) and are more specifically involved in

differentiating the “spacer” sequence within the ERE as well as providing a secondary interface for receptor dimerization.

The consensus motif (estrogen response element or ERE) that ER binds is composed of a 6-base pair (bp) palindromic sequence arranged as an inverted repeat and separated by a 3-bp spacer, GGTCAnnnTGACC. The inverted-repeat arrangement of the ERE dictates that the ER homodimerizes in a “head-to-head” position when bound to DNA. Structural analysis has revealed the importance of the 10-30 amino acid carboxy terminal extension (CTE) of the DBD in DNA interaction ([Aagaard et al. 2011](#); [Helsen et al. 2012](#); [Hilser and Thompson 2011](#)). Although this CTE region is variable between steroid receptors, it is crucial for DNA binding, particularly for sequence selectivity of DNA binding, by extending the interaction surfaces between the receptor and the DNA.

### Hinge Region or D Domain

The above described CTE extends into the hinge region, which also contains a nuclear localization signal, and influences cellular compartmentalization of ER, as well as sites of post-translation modifications ([Kim, et al. 2006](#)). Current mechanisms suggest this non-conserved and intrinsically disordered (ID) domain is important for intra-molecular allosteric interactions involving the N-terminal and LBD. This type of flexible structural interaction works to allow rapid response to diverse modulators governing changes in biological environments ([Kumar and McEwan 2012](#)).

### LBD or E Domain

The LBD or E domain of the ER is a highly structured multifunctional region that primarily serves to specifically bind estrogen and provide for hormone-dependent transcriptional activity through an activation function 2 (AF-2) domain located close to the C-terminus of the E domain. A strong receptor dimerization interface, sites for interaction with heat shock proteins, and nuclear localization signals are also within the E domain ([Kumar and McEwan 2012](#); [Laudet and Gronemeyer 2001](#)). Structural studies indicate that the LBD is composed of 11  $\alpha$ -helices (H1, and H3 through H12) arranged in a three-layer  $\alpha$ -helical sandwich to create a hydrophobic ligand-binding pocket near the C-terminus of the receptor ([Huang, et al. 2010](#)). Receptor binding to an estrogen agonist leads to rearrangement of the LBD such that H11 is repositioned and H12 rotates back toward the core of the domain to form a “lid” over the binding pocket. This agonist-induced repositioning of H12 leads to the formation of a hydrophobic cleft, or “NR box”, by helices 3, 4, and 5 on the receptor surface, constituting the AF2, which serves to recruit coactivators (Table 1) to the receptor complex. In contrast, estrogen antagonists are unable to induce a similar repositioning of H12, leading to a receptor formation that is incompatible with co-activator recruitment and is therefore less likely to activate transcription. The LBDs of ER $\alpha$  and ER $\beta$  exhibit approximately 60% homology (Fig. 1) but bind the endogenous estrogen, estradiol (E2), with similar affinity (ER $\alpha$ , 0.1 nM; ER $\beta$ , 0.4 nM) ([Gibson and Saunders 2012](#); [Le Romancer et al. 2011](#)) indicating only a small portion of the LBD sequence governs the specificity of ligand binding. However, given the divergence in homology, it is not surprising that ER $\alpha$  and ER $\beta$  exhibit measurable differences in their affinity for other endogenous steroids and xenoestrogens ([Gibson and Saunders 2012](#); [Le Romancer et al. 2011](#)). Natural and synthetic

steroidal and non-steroidal ER agonists and antagonists have been described, some of which show specificity or preference for one or the other ER subtype, illustrating differences between the LBDs of ER $\alpha$  and ER $\beta$  and provide for conceptual pharmacological tools to discern the overall function of each ER. The most widely used ER sub-type selective ligands currently in use are propylpyrazole (PPT), an ER $\alpha$  selective agonist, and diarylpropionitrile (DPN), an agonist showing preference, but not exclusive selectivity, towards ER $\beta$  (Meyers, et al. 2001; Stauffer, et al. 2000).

## F Domain

Among the sex steroid receptors, only ERs possess a well-defined F domain (Fig. 1). This region is relatively unstructured with little known function, although some data indicate a role in co-activator recruitment, dimerization and receptor stability (Arao, et al. 2013; Katzenellenbogen, et al. 2000; Koide, et al. 2007; Kumar, et al. 2011; Yang, et al. 2008).

## Co-Regulatory Complexes

All steroid receptors interact with co-regulatory molecules, co-activators and co-repressors (George, et al. 2011; Hsia, et al. 2010). The primary co-activator interaction for steroid receptors is with a family of p160/SRC (Steroid Receptor Coactivator) 1, 2 and 3 coactivators (Bulyenko and O'Malley 2011; Johnson and O'Malley 2012; Lonard and O'Malley 2005). SRC1 (NCOA1), SRC2 (GRIP1, TIF2) and SRC3 (pCIP, RAC3, ACTR, TRAM, AIB1) interact with helix 12 of ERs via "LXXLL" motifs in their nuclear receptor interacting domain, which are leucine rich regions with "X" designating any amino acid (Johnson and O'Malley 2012). SRCs also contain activation domains that recruit secondary molecules such as p300, and a bHLH-PAS motif within the N-terminal region, which can interact with other transcription factors (Johnson and O'Malley 2012). ERs and SRCs function as a nexus interacting with massive multimeric complexes, including the SWI/SNF chromatin remodeler, mediator complex, or proteasomes (Table 1) (Bulyenko and O'Malley 2011). These interactions coordinate the specific functions necessary to allow appropriate gene and cell selective access to chromatin, via modifications of histones or members of co-regulatory complexes (O'Malley, et al. 2012). In this way, co-activators dynamically mediate and coordinate processes necessary to accomplish transcription, including initiation, elongation, termination, and clearing or turnover of the transcriptional modulators.

## Mechanisms of Estrogen Response

Our understanding of the mechanisms by which estrogens influence cell function and behavior has expanded profoundly since initial models of ligand-dependent activation, which is now referred to as the "classical" or ligand dependent direct DNA binding model of receptor function (Fig. 2). In the years since, numerous discoveries primarily in cell-based systems have been made that illuminate the complexity of ER signaling in cells and tissues. The entrée into the "omics" era has facilitated massive expansion for the study of transcriptional regulation and chromatin remodeling. In addition, several alternative receptor signaling mechanisms that diverge from the classic model have become apparent, including "tethering" of the ER to heterologous DNA-bound transcription factors to provide for regulation of genes that lack ERE sequences (Fig. 2); plasma membrane estrogen signaling,

often referred to as “nongenomic” steroid actions and ligand-independent “cross-talk” with intracellular and second messenger systems that provide for ER activation in the absence of the cognate steroid ligand (Fig. 2). These modes of ER responses as currently understood are discussed below.

### Ligand-Dependent Actions: Direct or Classical

In the classic model of estrogen response (Fig. 2 and 3) estrogen ligands diffuse across the plasma and nuclear membranes to bind ER, primarily localized to the nucleus, resulting in a conformational change in the receptor, transforming it to an “activated” state that interacts with chromatin via ERE motifs and transcriptional mediators. ERs seem to be preferentially recruited to open regions of chromatin (Biddie, et al. 2010). Studies using MCF7 breast cancer cells indicate that FoxA1 acts as a pioneering factor, providing accessible regions in the chromatin that recruit ER $\alpha$  (Fig.3) (Carroll and Brown 2006; Carroll, et al. 2005; Fu, et al. 2011; Zaret and Carroll 2011). The ligand-ERE-bound receptor complex then engages coactivator molecules as described above (Johnson and O'Malley 2012) leading to modulation of transcription rates of responding genes. This classic steroid receptor mechanism is dependent on the functions of both AF-1 and AF-2 domains of the receptor, which synergize via the recruitment of coactivator proteins, most notably the p160 family members (Johnson and O'Malley 2012). Depending on the cell and target gene promoter context, the DNA-bound receptor complex may positively or negatively affect expression of the downstream target gene. Initially, study of ER mediated gene regulation was carried out on a gene-by gene basis using a handful of known hormone regulated transcripts. Now, after numerous comprehensive analyses of hormonally regulated transcriptional profiles, using microarray and more recently RNA-seq, thousands of ER targets have been found in various cell lines and tissues.

### Indirect/Tethered Actions (ERE Independent)

In *in vitro* reporter gene systems, ligand-activated ER can modulate the expression of genes that lack a conspicuous ERE within their promoter (Kushner, et al. 2000; Safe and Kim 2004, 2008). This mechanism of ERE-independent steroid receptor activation is postulated to involve a “tethering” of the ligand-activated receptor to transcription factors that are directly bound to DNA via their respective response elements (Fig. 2). However, the ER $\alpha$ <sup>EAAE/EAAE</sup> mouse, which is mutated in the ER $\alpha$  DBD and lacks ERE binding, does not exhibit estrogen response *in vivo*, indicating the tethering mechanism, at least on its own, is unable to mediate hormonal responses (Ahlborn-Dieker, et al. 2009; Hewitt, et al. 2014) and is likely complimentary to the direct DNA stimulated responses.

### Non-Genomic Actions

Rapid effects of E2 have been described, including a rapid activation of endothelial nitric oxide synthase in endothelial cells (Levin 2011) and potentiation of nerve conductance (Kim, et al. 2011; Takeo and Sakuma 1995). Because these estrogen effects occur within minutes, they have been thought to not involve direct estrogen receptor activation of gene transcription, they are often collectively referred to as representing “non-genomic” pathways of estrogen action. Questions remain concerning whether the membrane-associated receptors

mediating these events are identical or variant forms of the ER or instead distinct receptors altogether.

One potential mediator of rapid membrane localized hormone response is the G protein coupled estrogen receptor (GPER; originally referred to as GPR30), which is activated by E2 (Prossnitz and Barton 2011). *Gper* null mice lack reproductive phenotypes (Langer, et al. 2010), although effects on the degrees of uterine responses elicited by E2 have been observed with G15, a GPER selective antagonist, suggesting a potential role for GPER in modulating ER $\alpha$  mediated responsiveness (Gao, et al. 2011).

### Ligand Independent Actions: Membrane Receptor Cross-Talk

Peptide growth factors are able to activate ER $\alpha$ -mediated gene expression via mitogen-activated protein kinase activation of ER $\alpha$  in the absence of E2 (Fig. 2). Likewise, growth factors are able to mimic the effects of E2 in the rodent uterus via E2 independent activation of ER $\alpha$  (Curtis and Korach 1999; Fox, et al. 2009). In some cases, the MAP kinase protein ERK is co-recruited to chromatin with ER $\alpha$  (Madak-Erdogan, et al. 2011). Ligand-independent activation of estrogen receptors is believed to rely largely on cellular kinase pathways that alter the phosphorylation state of the receptor and/or its associated proteins (e.g., coactivators, heat shock proteins) (Fig. 2).

### Uterine Response to Estradiol

Utilizing animal models to follow and manipulate estrogen responsiveness is one way to understand and describe mechanisms of estrogen responses. The reproductive function of the mouse has been especially well studied and characterized in this manner. Treatment of ovariectomized mice with estrogens (e.g., E2 or diethylstilbestrol - DES) has long served as an experimental model to mimic the uterine events that occur during the estrous phase of the rodent cycle or immediately after the preovulatory E2 surge. Morphological and biochemical changes occur in the rodent uterus after estrogen stimulation following an established biphasic temporal pattern (Hewitt, et al. 2003). Estrogen-stimulated changes in the rodent uterus that occur early, within the first 6 hours after treatment, include increases in nuclear ER occupancy, water imbibition, vascular permeability and hyperemia, prostaglandin release, glucose metabolism, eosinophil infiltration, gene expression (e.g., *c-fos*), lipid and protein synthesis. ER $\alpha$  ChIP-Seq profiles from *in vivo* studies of uterine tissues show that in the unstimulated state the receptor pre-occupies chromatin sites in the absence of hormone and that E2 treatment increases ER $\alpha$  recruitment (Hewitt, et al. 2012). The above processes are followed by responses that peak after 24–72 hours and include dramatic increases in RNA and DNA synthesis, epithelial proliferation, and differentiation of epithelial cells toward a more columnar secretory phenotype, dramatic increases in uterine weight, and continued gene expression.

### Changes in Uterine Gene Expression

The dramatic physiological changes that occur in the uterus in response to steroid hormones are presumably the ultimate effects of equally dramatic changes in gene expression among the uterine cells. It is unlikely that the E2-ER complex is directly involved in mediating the



whole genomic response in the uterus but more plausibly serves to stimulate a cascade of downstream signaling pathways that act to amplify the estrogen action. However, early investigations of the genomic response to estrogens in the rodent uterus discovered a handful of genes that are directly regulated via the classic ER mode of action, including progesterone receptor (*Pgr*) and lactoferrin or lactotransferrin (*Ltf*). Microarray analysis has significantly advanced understanding of genomic response of the rodent uterus to E2. Numerous studies have used microarray techniques to map the global gene expression patterns after estrogen exposure in the uterus and largely demonstrate that the biphasic uterine response to estrogens, so well characterized by physiological indicators above, is mirrored by the global changes in gene expression ([Andrade, et al. 2002](#); [Fertuck, et al. 2003](#); [Hewitt, et al. 2005](#); [Hewitt et al. 2003](#); [Ho Hong, et al. 2004](#); [Hong, et al. 2006](#); [Moggs, et al. 2004](#); [Watanabe, et al. 2003](#)). The clearly defined patterns of early and late response genes found in mouse uterine tissues are completely lacking in ER $\alpha$ -null ( $\alpha$ ERKO, Ex3 $\alpha$ ERKO) uteri ([Hewitt et al. 2003](#); [Hewitt, et al. 2010a](#)). The identified genes fall into functional groups, including signal transduction, gene transcription, metabolism, protein synthesis and processing, immune function, and cell cycle. The expression levels of a striking number of genes are actively repressed by estrogen in the mouse uterus, and these effects were absent in ER $\alpha$ -null uteri or are relieved by co-treatment with ER antagonists in the presence of ER $\alpha$ , indicating that ER $\alpha$  is also actively involved in transcriptional repression as part of mediating the physiological responses ([Hewitt et al. 2003](#); [Hewitt et al. 2010a](#)).

Whole transcriptome analyses are now routinely incorporated into studies of disruptions in signaling pathways underlying uterine phenotypes of mouse models such as those described in Table 2. Thus, microarray comparisons have now become just one of many tools employed for investigation of uterine functions.

### Chip-seq

Evaluation of sites of transcription factor interaction with chromatin, by enriching a DNA binding protein, such as ER $\alpha$ , that has been crosslinked *in situ* to chromatin, with immunoprecipitation (Chromatin Immunoprecipitation or ChIP), followed by hybridizing the associated DNA to a chip tiled with promoter region sequences (ChIP-Chip) or by “next generation” massively parallel sequencing (ChIP-seq), have been developed and widely utilized to study sites of ER interaction ([Biddie et al. 2010](#); [Farnham 2009](#); [Green and Han 2011](#); [Martens, et al. 2011](#); [Meyer, et al. 2012](#); [Park 2009](#)). Initial studies focused on ER $\alpha$  binding in MCF7 breast cancer cells, and several similar studies followed, which are summarized and compared in several review articles ([Cheung and Kraus 2010](#); [Deblois and Giguere 2008](#); [Gao and Dahlman-Wright 2011](#); [Gilfillan, et al. 2012](#); [Tang, et al. 2011](#)). These reported that most sites were distal from transcriptional start sites (TSS), or were in intronic regions, rather than adjacent to TSS, as models of ER regulation of target transcripts had hypothesized. These comprehensive maps of cis-acting transcriptional regulators have been dubbed “Cistromes”. The initial ER $\alpha$  cistrome-associated sequences were evaluated for enrichment of transcription factor motifs, and confirmed binding to the experimentally defined “ERE” sequence. In the case of the MCF7 tumor cells, enrichment of motifs for forkhead binding factors (Fox) was apparent as mentioned in the earlier section. Owing to the abundant expression of the FoxA1 member of the Fox family, a potential role for FoxA1

in estrogen response was pursued with an arsenal of bioinformatic, Next Gen sequencing and biological studies that demonstrated FoxA1's role as “pioneer”, creating accessible regions of the chromatin that were subsequently targeted by ER $\alpha$  ([Lupien, et al. 2009](#)) ([Zaret and Carroll 2011](#)).

ChIP-seq analysis examining the ER $\alpha$  binding sites in mouse uterine tissue indicated that, much like the MCF7 breast cancer study, most ER $\alpha$  sites were not proximal to TSS ([Hewitt et al. 2012](#)). ERs bind to thousands of sites within the cellular chromatin, and not all potential EREs in every cell bind ER. Rather, it is apparent that chromatin exhibits “pre-opened” regions destined to recruit ER ([Grontved and Hager 2012](#)). For ER in MCF7, FoxA1 can establish ER accessible regions. The accessible chromatin regions are co-localized within nuclear “hubs”, which seem to optimize frequency of interaction with ER ([Grontved and Hager 2012](#)). ChIP seq is also used to locate other molecules involved in chromatin remodeling and transcriptional regulation, and to examine activating or repressive histone modifications or “marks”. These maps of relative locations and dynamics of ER and chromatin components greatly enhance our understanding of hormone response mechanisms ([Deblois and Giguere 2008](#); [Gilfillan et al. 2012](#); [Green and Han 2011](#); [Martens et al. 2011](#); [Meyer et al. 2012](#)).

### Uterine Phenotypes in Mouse Models of Disrupted Estrogen Signaling

Mouse models of disrupted estrogen receptor signaling have proven invaluable to experimental investigation of estrogen actions and the contribution of each ER form to these functions (Table 2). In addition to the ER-null models are lines of mice that lack the capacity to synthesize E2 due to disruption of the *Cyp19* gene ([Fisher, et al. 1998](#); [Toda, et al. 2001](#)). Below we will describe how these different mouse models have helped to delineate the biological role of ER mechanisms in estrogen hormone action.

### ER $\alpha$ null patients and mice

Only one male patient and one female patient with ER $\alpha$  mutation have been described ([Quaynor, et al. 2013](#); [Smith, et al. 1994](#)). The male patient's mutation is a true null since no ER $\alpha$  protein is expressed due to the mutation generating a premature stop codon in the A/B domain. The female patient has a single point mutation in her ER $\alpha$  LBD that results in decreased activity by reducing the receptor's affinity for coactivator proteins more than 200 fold.

There are currently numerous reported lines of ER $\alpha$ -null mice and additional lines of mice with mutations in functional domains of ER $\alpha$ . Three separate lines of ER $\alpha$ -null mice were generated: the  $\alpha$ ERKO, first described by Lubahn *et al.* in 1993 ([Lubahn, et al. 1993](#)), the ER $\alpha$ KO (or Ex3 $\alpha$ ERKO), described by Dupont *et al.* in 2000 ([Dupont, et al. 2000](#)) and by Hewitt in 2010 ([Hewitt et al. 2010a](#)), and ER $\alpha^{-/-}$  described by Antonson *et al.* in 2012 ([Antonson, et al. 2012](#)). Homologous recombination was employed to disrupt ER $\alpha$  ( $\alpha$ ERKO), or cre-mediated recombination was used to completely excise exon 3, which encodes the ER DNA binding domain ([Antonson et al. 2012](#); [Dupont et al. 2000](#); [Hewitt et al. 2010a](#)) of the murine *Esr1* (ER $\alpha$ ) gene (ER $\alpha$ KO, Ex3 $\alpha$ ERKO and ER $\alpha^{-/-}$ ). The uterine estrogenic response in  $\alpha$ ERKO females differs from the latter two lines, but the overall



spectrum of phenotypes are the same, as  $\alpha$ ERKO animals have minimal level of truncated ER $\alpha$  protein produced from a splice variant, which preserves some residual biological functions (Couse, et al. 1995), but all ER $\alpha$  null female mice are infertile. Recently, an ER $\alpha$  null rat has been derived using zinc finger nuclease (ZFN) genome editing. All phenotypes in the ER $\alpha$  null rats examined thus far were previously seen in the ER $\alpha$  null mice, including infertility due to hypoplastic uteri, polycystic ovaries, and ovulation defects (Rumi, et al. 2014). The female patient with homozygous ER $\alpha$  mutation also has cystic ovaries and a small uterus despite elevated circulating serum E2 (Quaynor et al. 2013).

The essential role of ER $\alpha$  in uterine response to estrogen is indicated by the loss of early phase effects of water imbibition and hyperemia as well as the late-phase effects of increased DNA synthesis and epithelial proliferation in ER $\alpha$ -null uteri (Couse et al. 1995; Hewitt et al. 2010a; Korach, et al. 1996). The  $\alpha$ ERKO model was the first test of a prevailing hypothesis that early uterine effects were non-receptor mediated (Lubahn et al. 1993). Lack of these early responses of water imbibition, hyperemia and eosinophil infiltration in  $\alpha$ ERKO indicated that ER $\alpha$  was involved in some manner and these responses clearly require the estrogen receptor. Additionally, ovariectomized mice normally exhibit a three- to four-fold increase in uterine weight after three daily treatments with E2 or DES, whereas no such response is observed in the uteri of ER $\alpha$ -null females (Hewitt et al. 2010a; Korach 1994; Lubahn et al. 1993). Uteri of mice that lack ER $\alpha$  just in uterine epithelial cells (*Wnt7a<sup>Cre+</sup>;Esr1<sup>f/f</sup>*, called *ER $\alpha$  Epi-cKO*) have an initial proliferative response to estrogen, but full uterine response is impaired, as the growth after 3 days of estrogen treatment is significantly less than expected (Winuthayanon, et al. 2010). The total lack of response to estrogens in ER $\alpha$ -null uteri as well as a lack of late biological response in epithelial ER $\alpha$  knockout uteri provide strong evidence that ER $\alpha$  is required to mediate the full biochemical and biological uterine response to estrogens (Hewitt et al. 2010a; Winuthayanon, et al. 2014; Winuthayanon et al. 2010).

Numerous studies have demonstrated some of the molecular mechanisms of E2-induced uterine epithelial cell proliferative responses in animal models. The transcription factor CCAAT Enhancer Binding Protein Beta (C/EBP $\beta$ ) is involved in hormone-induced uterine proliferation (Mantena, et al. 2006). Maximum uterine expression of C/EBP $\beta$  is induced 1 h after E2 treatment in both epithelial and stromal cells (Mantena et al. 2006; Ramathal, et al. 2010). ICI 182,786 (ER antagonist) strongly inhibited E2-induced *Cebpb* transcript in the uterus suggesting an ER-dependent expression of C/EBP $\beta$  (Bagchi, et al. 2006). In addition, loss of epithelial ER $\alpha$  in the uterus did not alter E2-induced *Cebpb* expression, indicating that *Cebpb* expression is independent of epithelial ER (Winuthayanon et al. 2010), and suggesting the stimulation was through a paracrine mechanism via stromal ER $\alpha$ . This points to the action of estrogen through ER $\alpha$  as the major mediator of C/EBP $\beta$  expression in the uterus. Indeed, the deletion of C/EBP $\beta$  (C/EBP $\beta$ <sup>-/-</sup>) leads to a lack of the E-induced uterine proliferative response (Mantena et al. 2006) as reflected by the absence of mitotic activity, S-phase activity and an increase in apoptotic activity in the uterine epithelial cells (Ramathal et al. 2010). In addition to a blunted uterine growth response to hormones, the C/EBP $\beta$ <sup>-/-</sup> females also exhibit complete infertility (Bagchi et al. 2006), due to implantation and decidualization defects (Mantena et al. 2006).

Pan *et al.* demonstrated that the uterine expression of minichromosome maintenance proteins (MCMs), a complex required for DNA synthesis initiation, is induced after E2 treatment, specifically MCM2 and MCM3 (Pan, et al. 2006). MCM2 activity is crucial and required for DNA synthesis in uterine epithelial cells (Ray and Pollard 2012). Further study demonstrated E2-mediated induction of the transcription factor KLF4, which then targets the *Mcm2* promoter (Ray and Pollard 2012).

### Mice lacking ER $\beta$

ER $\beta$ -null mice have provided insight into the importance of ER $\beta$  to female fertility and studies to date indicate ER $\beta$  plays a particularly important role in ovarian function. Four different lines of ER $\beta$ -null mice have been described. The  $\beta$ ERKO mouse, made using homologous recombination, was first described by Krege *et al.* in 1998 (Krege, et al. 1998), and the ER $\beta$ KO or Ex3 $\beta$ ERKO, was described by Dupont *et al.* in 2000. (Dupont et al. 2000), and by Binder et al, 2013 (Binder, et al. 2013). Cre mediated recombination was employed in both lines to disrupt exon 3 (Binder et al. 2013; Dupont et al. 2000) of the murine *Esr2* (ER $\beta$ ) gene. As described to date, the reproductive, endocrine and ovarian phenotypes of both lines are indistinguishable, with both exhibiting female subfertility. In 2002, Shughrue *et al.* reported the third line of ER $\beta$ KO animals, however, no uterine or ovarian phenotypes were reported (Shughrue, et al. 2002). Recently, ER $\beta$ KO<sub>ST</sub><sup>L-/L-</sup> animals, which contain *LoxP* sites flanking exon 3 of *Esr2*, were generated using the *Cre/loxP* recombination system (Antal, et al. 2008). Interestingly, female mice from this recently described ER $\beta$ KO<sub>ST</sub><sup>L-/L-</sup> colony were reported to be sterile due to an ovarian defect while Ex3 $\beta$ ERKO (Binder et al. 2013) are subfertile, due to ovulatory defects.

### Mice lacking ER $\alpha$ and $\beta$

The two reported lines of compound ER-null mice are the  $\alpha\beta$ ERKO, described by Couse *et al.* in 1999 (Couse, et al. 1999), and the ER $\alpha\beta$ KO, described by Dupont *et al.* in 2000 (Dupont et al. 2000). Both were generated by cross breeding animals heterozygous for the respective individual ER-null mice and as described to date, exhibit comparable reproductive, endocrine and ovarian phenotypes. The most striking phenotype is the unique trans-differentiation of the ovarian granulosa cells to sertoli-like cells in follicles of  $\alpha\beta$ ERKO females which is age dependent. To date, no manipulation of the individual  $\alpha$ ERKO or  $\beta$ ERKO mouse lines can reproduce this novel phenotype. This model clearly uncovered that both ER signaling systems are required to maintain the proper differentiation state of the adult granulosa cells.

### Mice lacking Cyp19

Estrogens are produced by aromatase cytochrome P450, the product of *Cyp19* gene. Female mice with disruption of circulating estrogen production exhibit altered reproduction (Fisher et al. 1998; Honda, et al. 1998; Toda et al. 2001). There are 3 animal models of Cyp19-null mice (called ArKO). Fisher *et al.* reported the first mouse line in 1998, which disrupted exon 9 of *Cyp19* gene, as the region is highly conserved (Fisher et al. 1998). Later in 1998, Honda *et al.* reported a mouse line with targeted disruption of exons 1 and 2 of the *Cyp19* gene (Honda et al. 1998). Subsequently, Toda *et al.* generated the most recent mouse line of

Cyp19-null in 2001 with a targeted disruption of exon 9 of the *Cyp19* gene (Toda et al. 2001). These ArKO female phenotypes are indistinguishable (Fisher et al. 1998; Honda et al. 1998; Toda et al. 2001), with similarity to the  $\alpha\beta$ ERKO mice with a clear metabolic syndrome (Couse et al, 1999) and infertility due to ovarian dysfunction marked by cystic follicles and a failure to respond to exogenous gonadotropins. Interestingly, the phenotype of the original ArKO mice (Fisher et al. 1998) were also shown to exhibit the same age related ovarian phenotype (Britt et al, 2002) as the  $\alpha\beta$ ERKO mice, indicating that hormone mediated ER action is required.

### Female reproductive phenotypes in mice with disrupted estrogen signaling

Females within each respective model exhibit a similar phenotypic syndrome. Female mice lacking ER $\alpha$  or aromatase are infertile due to dysfunction of numerous physiological systems, including the ovary and uterus, whereas ER $\beta$ -null females exhibit reduction or loss of fecundity that is largely attributable to ovarian dysfunction. A level of caution is warranted when making phenotypic comparisons between the ER-null and Cyp19-null models because sensitivity to maternally derived estrogens may provide a more normal developmental environment during gestation in Cyp19-null mice and sensitivity to dietary estrogens during adulthood is able to abate several phenotypes in Cyp19-null mice (Britt, et al. 2002).

The reported uterine phenotypes of these models are summarized in Table 2. All lines of ER-null females exhibit uteri that possess the expected tissue compartments, myometrium, endometrial stroma, and epithelium (Couse 1999; Couse and Korach 1999; Hewitt et al. 2010a). However, in females lacking functional ER $\alpha$  or Cyp19, uteri are overtly hypoplastic and exhibit severely reduced weights relative to wild-type littermates (Britt, et al. 2001; Couse and Korach 1999; Fisher et al. 1998; Toda et al. 2001), whereas ER $\beta$ -null uteri are grossly normal and normally responsive to ovarian-derived steroids (Couse and Korach 1999). The uterus of ER $\alpha$ -null females is severely hypotrophic, poorly organized, and possesses a paucity of glandular structures (Hewitt et al. 2010a; Korach et al. 1996). The luminal and glandular epithelial cells in ER $\alpha$ -null uteri are severely immature with fewer glands present in the adults (Nanjappa, et al. 2015) and consistently exhibit a cuboidal morphology, versus the tall columnar morphology and basal location of the nucleus of an “estrogenized” epithelium in WT uteri. Therefore, fetal, neonatal and perinatal development of the female reproductive tract in mice is largely independent of ER $\alpha$  – and ER $\beta$ -mediated actions, but estrogen responsiveness and sexual maturation of the adult uterus are ablated after the loss of functional ER $\alpha$ . The totality of the ER $\alpha$ -null phenotype and lack of any overt uterine abnormalities in ER $\beta$ -null females suggest that ER $\beta$  has little meaningful function in mediating estrogen actions in the uterus. Moreover, ER $\alpha\beta$ -null also demonstrated a similar uterine phenotype as ER $\alpha$ -null (Walker and Korach 2004). Weihua *et al.* reported that ER $\beta$ -null females exhibited a slightly aberrant uterine growth response after estrogen replacement; however, the uterine bioassay was conducted in immature intact, not ovariectomized adult, animals (Weihua, et al. 2000). In addition, Wada-Hiraike *et al* showed that in immature females, loss of ER $\beta$  leads to increased uterine epithelial proliferation induced by E2 compared to Wild Type uteri (Wada-Hiraike, et al. 2006). Although ER $\beta$ -null females are subfertile, when pregnancies are established they are sustained to term (Krege et

al. 1998), indicating uterine competence. More recent findings suggest that loss of ER $\beta$  leads to complete sterility due to a defect in ovarian function (Antal et al. 2008; Dupont et al. 2000).

### Mice with uterine specific deletion of ER $\alpha$ .

Selectively deleting ER $\alpha$  in the uterus postpubertally, using the *Cre/LoxP* recombination system, by crossing *Pgr*<sup>Cre+</sup> with *Esr1*<sup>f/f</sup> animals (*Esr1*<sup>d/d</sup>), leads to a hypoplastic uterus that lacks a decidual response (Pawar, et al. 2015). Our laboratory has described uterine epithelial cell selective deletion of ER $\alpha$ , using the *Cre/LoxP* recombination system, by crossing *Wnt7a*<sup>Cre+</sup> (Huang, et al. 2012) with *Esr1*<sup>f/f</sup> animals (Hewitt et al. 2010a) (*ER $\alpha$  Epi-cKO*). The expression of ER $\alpha$  in the uterine luminal and glandular epithelium of these animals was ablated, while the ER $\alpha$  expression in the stromal cells and other uterine cells remains intact (Winuthayanon et al. 2010). The epithelial ER $\alpha$  was ablated not only in the uterus in this mouse line (Winuthayanon et al. 2010), but also in the oviduct (Winuthayanon, in press, eLife). As expected, based on findings in the global ER $\alpha$  knockouts, loss of uterine epithelial ER $\alpha$  has no effect on female reproductive tract development. Uterine histological analysis showed a similar uterine morphology as wild type control (Winuthayanon et al. 2010). The *ER $\alpha$  Epi-cKO* uteri are sensitive to 24 h treatment of E2, as the uterine epithelial proliferation is preserved. However, *ER $\alpha$  Epi-cKO* uteri lack a complete uterine response to E2, following a three-day uterine bioassay, which demonstrated a blunted growth response and increased apoptotic activity in *ER $\alpha$  Epi-cKO* compared to the control uteri.

Additionally, a lack of ER $\alpha$  expression in the uterine epithelial cells contributes to complete infertility, due to oviduct, and uterine implantation and decidulization defects (Pawar et al. 2015; Winuthayanon et al. 2010) (Winuthayanon, in press, eLife). This suggests that uterine epithelial ER $\alpha$  is dispensable for early uterine proliferative responses but crucial for a complete adult biological response induced by E2, as well as for establishing pregnancy.

### Mice with mutated DNA binding domains of ER $\alpha$ .

To date, there are two mouse lines with mutations that are designed to disrupt the DNA binding function of the ER $\alpha$  that have been “knocked-in” (KI) at the ER $\alpha$  gene locus. The first line was generated by replacing critical P-box amino acids E207 and G208 with alanines (ER $\alpha$ <sup>AA</sup>). This line was named “Non-genomic ER knock-in” (NERKI), as these mutations were intended to restrict ER $\alpha$  signaling to the non-genomic and tethered mechanisms. Female NERKI<sup>+/-</sup> animals that have one mutated allele and one WT allele (Jakacka, et al. 2002) were infertile, exhibiting a highly novel hyperplastic uterine phenotype, so NERKI<sup>+/-</sup> males were crossed with ER $\alpha$  null heterozygous (WT/KO) females to produce mice with one NERKI mutated allele and one deleted *Esr1* allele, called ER $\alpha$  KIKO or ER $\alpha$ <sup>AA/-</sup> as described by O’Brien et al. in 2006 (O’Brien, et al. 2006). The second line of DNA-binding domain knock-in animals were created through mutation of four amino acids in the first zinc finger of the *Esr1* gene, substituting Y at position 201 with E, and in the critical P box, K at position 210 with A, K at position 214 with A, and R at position 215 with E as described by Ahlbory-Dieker et al. in 2009 (called ER $\alpha$ <sup>EAAE/EAAE</sup>) (Ahlbory-Dieker et al. 2009).

The  $NERKI^{+/-}$  females have normal uterine development but exhibit hyperplastic uteri, and are hypersensitive to estrogen (Jakacka et al. 2002). These  $NERKI^{+/-}$  are infertile and exhibit a uterine abnormality of enlarged hyperplastic endometrial glands despite possessing normal levels of circulating sex steroids (Jakacka et al. 2002).

$ER\alpha^{AA/-}$  females have normal uterine development. Initially, O'Brien *et al.* reported that  $ER\alpha^{AA/-}$  females, with mutation of the DNA binding domain, maintained proliferative responses induced by E2 (O'Brien et al. 2006). However, in subsequent studies, no uterine proliferation was observed (Hewitt, et al. 2010b; Hewitt, et al. 2009). Ahlbory-Dieker *et al.* showed that, unlike the  $NERKI^{+/-}$ , females heterozygous for the  $ER\alpha^{EAAE}$  mutation are fertile. The homozygous  $ER\alpha^{EAAE/EAAE}$  females have normal reproductive tract development but uteri are severely hypoplastic, similar to global  $ER\alpha$ -null uteri. Additionally,  $ER\alpha^{EAAE/EAAE}$  uteri do not respond to E treatment, as normally estrogen-responsive uterine and liver genes are not regulated in  $ER\alpha^{EAAE/EAAE}$  (Ahlbory-Dieker et al. 2009; Hewitt et al. 2014). The females from these two mouse lines with point mutations in the DNA binding domain of  $ER\alpha$  are infertile. Thus the physiological function of the DNA binding domain of  $ER\alpha$  is crucial for female reproduction.  $ER\alpha$  ChIP-seq analysis of the  $ER\alpha^{AA/-}$  uterus revealed that the DBD mutation, rather than completely disrupting DNA binding instead altered the motif specificity, so that  $ER\alpha^{AA}$  could bind HRE motifs normally occupied by progesterone receptor (Pgr or PR). Additionally, this HRE binding lead to E2 regulation of uterine transcripts that are normally progesterone responsive (Hewitt et al. 2014). This novel  $ER\alpha^{AA}$  binding activity may also explain the hyperplastic phenotype of the heterozygous  $ER\alpha^{AA/+}$  females where the normally activated uterine HRE sites are occupied by the mutant  $ER\alpha^{AA}$  and thus blocking the dampening activity of uterine PR at those sites. Adding to this abnormal regulation is the expression of  $ER\alpha^{AA}$  in all uterine cells at all times, whereas, the PR is restricted to epithelial cells and is dynamically induced in the stromal cells during the estrous cycle. Additionally, the phenotype also indicates the specificity of the action at the HRE requires the proper activity of the PR to elicit the dampening action.

### Mice with mutated AF-1 or AF-2 domains of $ER\alpha$

As discussed in the Receptor Structure section, AF-1 and AF-2 are important for ER transcriptional activity (Fig.1). Amino acids 2-128 were deleted from exon 1 of *Esr1*, which removes the AF-1 domain, and knocked into a mouse line (called  $ER\alpha^{AF-1^0}$ ) (Billon-Gales, et al. 2009). There are three reported mouse lines with mutation in the AF-2 domain of  $ER\alpha$ . One with a single point mutation in  $ER\alpha$  of G at position 525 to L in the ligand binding domain (LBD), called "Estrogen-nonresponsive  $ER\alpha$  Knock-in or ENERKI" ( $ER\alpha^{G525L}$ ) (Sinkevicius, et al. 2008). Amino acids 543-549 were deleted from the LBD of  $ER\alpha$ , removing helix 12 and thus AF-2 functionality, to create a second mouse line (called  $ER\alpha^{AF-2^0}$ ) (Billon-Gales, et al. 2011). Two point mutations in the AF-2 of the LBD of  $ER\alpha$  were knocked into a mouse (L543A and L544A; called  $AF2ER^{KI/KI}$  animals) (Arao, et al. 2011).  $ER\alpha^{AF-1^0}$ ,  $ER\alpha^{G525L}$ ,  $ER\alpha^{AF-2^0}$  and  $AF2ER^{KI/KI}$  females are all sterile (Arao et al. 2011; Billon-Gales et al. 2009; Billon-Gales et al. 2011; Sinkevicius et al. 2008).

ER $\alpha$ AF-1<sup>0</sup> females exhibited minimal uterine wet weight gain compared to ER<sup>+/+</sup> uteri after treatment with E2 pellets for 2 consecutive weeks, while ER $\alpha$ AF-2<sup>0</sup> females did not respond (Abot, et al. 2013; Billon-Gales et al. 2009; Billon-Gales et al. 2011). This indicates that the ER $\alpha$  AF-2 functional domain contributes to minimal uterine weight increase induced by E2 in the absence of AF-1. Both lines of AF-2 mutated animals (ER $\alpha$ <sup>G525L</sup> and AF2ER<sup>KI/KI</sup>) display severely hypoplastic uteri, and lack uterine growth response to E2 treatment (Arao et al. 2011; Billon-Gales et al. 2011; Sinkevicius et al. 2008). Interestingly, uterine wet weight can be increased by using the synthetic ER $\alpha$  agonist PPT in ER $\alpha$ <sup>G525L</sup> or by using the ER antagonists ICI 182,780 or tamoxifen in AF2ER<sup>KI/KI</sup> females (Arao et al. 2011; Sinkevicius et al. 2008). The ability of the antagonists to mediate responses seems to be due to a unique conformation of the LBD of the AF2ER that leads to AF-1-dependent transcriptional activity (Arao et al. 2013; Arao et al. 2011). Arao et al. also demonstrated that the uterine response to ICI or tamoxifen includes increased DNA synthesis in the uterine epithelial cells of AF2ER<sup>KI/KI</sup> (Arao et al. 2011). The growth factor IGF-1 induced minimal uterine epithelial proliferation in ER $\alpha$ <sup>G525L</sup>, and was not seen in AF2ER<sup>KI/KI</sup> uteri (Arao et al. 2011; Sinkevicius et al. 2008). Together, these findings indicated that both AF-1 and AF-2 activation domains of ER $\alpha$  contribute to a normal regulation of the complete biological response of uterine growth and reproductive functions. As the AF domains mediate ER-co-regulator interaction (Table 1), this emphasizes the importance of effective ER $\alpha$  co-activator protein recruitment for successful uterine E2 response. Similarly, mice lacking sufficient SRC-1 co-activator (SRC1<sup>-/-</sup>), exhibit measurably diminished uterine response to E2 (Xu, et al. 1998).

### Mice with altered localization of ER $\alpha$

A mutated mouse ER $\alpha$  that remains sequestered outside the nucleus (ER $\alpha$ H2NES), is unable to mediate transcriptional responses in a cell based assay, but maintains estrogen induced MAPK phosphorylation (Burns, et al. 2011). Targeting steroid receptors to the membrane involves palmitoylation, which is facilitated by HSP27 (Levin 2011). The palmitoylation promotes interaction with caveolin-1, which then results in localization of the receptor in membrane caveolin rafts. Two laboratories have mutated the palmitoylation site of the mouse ER $\alpha$ , and created knock in mouse models to study the effect of disabling this mechanism *in vivo* (Adlanmerini, et al. 2014; Pedram, et al. 2014). Both mouse lines have ovarian defects, but differ in several aspects (Table 2). Both involved knocking in an ER $\alpha$  with the same mutation of cysteine 451 to alanine. The first, C451A-ER $\alpha$ , exhibits normal uterine development and E2 induced growth response (Adlanmerini et al. 2014), whereas the nuclear-only ER $\alpha$  [NOER] has a hypoplastic ER $\alpha$ -null like uterus that fails to respond to E2 (Pedram et al. 2014). Both models have elevation in LH, but only the NOER has elevated E2. These mixed results remain to be reconciled to definitively illustrate the role of membrane associated ER $\alpha$  in these physiological systems.

### Conclusions

Female reproduction is a complex staged series of physiological responses occurring in multiple organ systems activated by estrogen and estrogen receptors. Cell based studies have uncovered that cellular signaling mechanisms for ER are multifaceted regarding gene



regulation. Because of the complexity with what is known about female reproduction and fertility, the mechanisms and activities cannot be clearly studied or tested in cell based systems. The development of gene targeting has allowed the evaluation of the physiological roles of estrogen action and estrogen receptor functionality under natural biological conditions. It is now apparent from the experimental and clinical reports outlined in this review that the primary mediator of female reproduction is ER $\alpha$ . What functional aspects of the ER $\alpha$  action are required will be forthcoming with the continued use of new technologies and experimental approaches, which will lead to a better understanding for the potential origins of infertility, reproductive tract disease and development of reproductive therapeutics.

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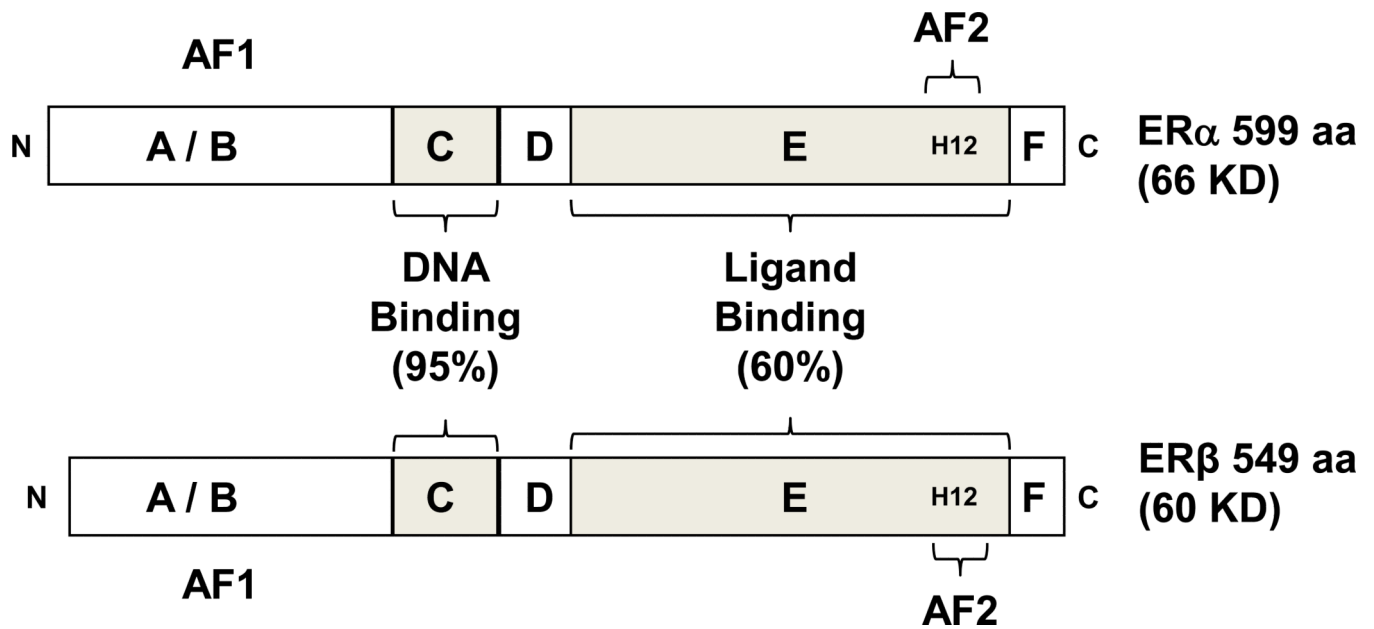
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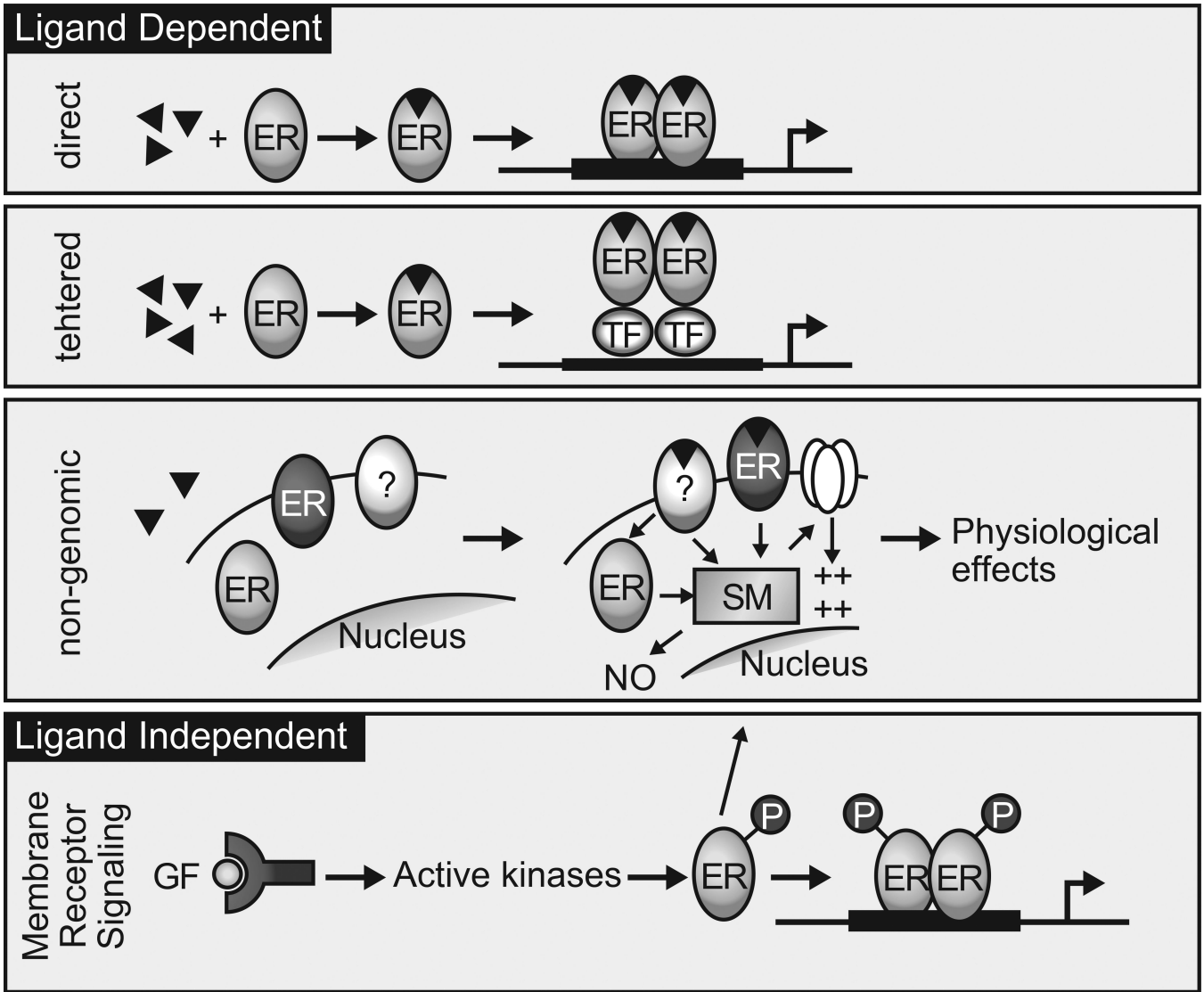
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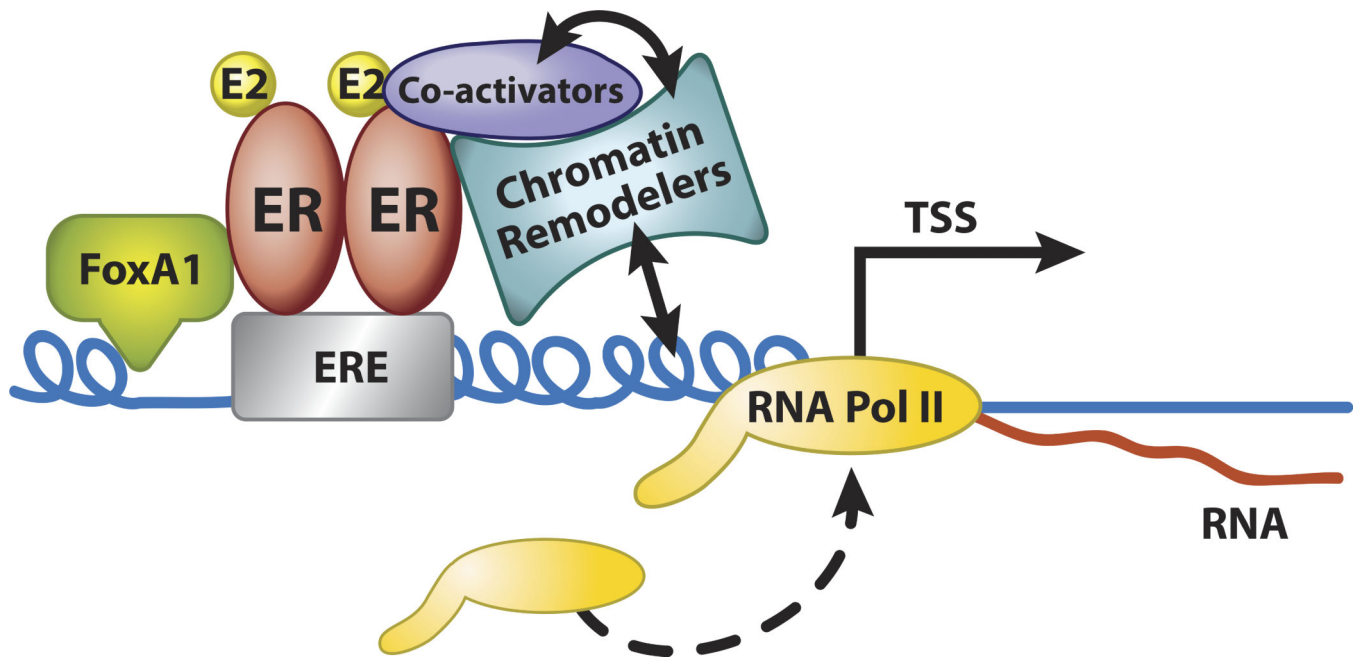


**Figure 1.**

Structures of ER $\alpha$  and ER $\beta$  protein with functional domains. Estrogen receptors ER $\alpha$  and ER $\beta$  share a conserved domain structure. The A/B domain, at the amino terminus (N) of the protein contains activation function 1 (AF1). The C domain binds to DNA motifs called estrogen responsive elements (EREs). The D domain is called the hinge region, and contributes to DNA binding specificity and nuclear localization of the ERs. The E domain is called the ligand binding domain because it interacts with estrogen, through an arrangement of 11  $\alpha$  helices (H1, and H3 through H12). H12 in this region of the receptor is critical to mediating transcriptional activation via activation function 2 (AF2). At the carboxy terminus (C) is the F domain. The % homology shared between ER $\alpha$  and ER $\beta$  in the C and E domains is shown.



**Figure 2.** Ligand-dependent and ligand-independent nuclear receptor mechanisms. The direct “classic” model of estrogen receptor (ER) action involves direct interaction between ER bound to estrogen (triangles) and ERE; the tethered pathway utilizes indirect “tethering” of ER to genes via interactions with other transcription factors (TF). “Nongenomic” signaling is initiated by membrane-localized receptors modulating extranuclear second messenger (SM) signaling pathways. Ligand-independent responses occur as a result of transduction of membrane receptor signaling, such as growth factors (GF), to nuclear ER. Reproduced, with permission, from Binder AK, Winuthayanon W, Hewitt SC, Couse JF & Korach KS (2015) Steroid receptors in the uterus and ovary. In *Knobil and Neill's Physiology of Reproduction*, 4<sup>th</sup> Edn, pp 1099–1193. Eds TM Plant & AJ Zeleznik. Elsevier.



**Figure 3.**

Model of chromatin dynamics in ER mediated transcription. FoxA1 interacts with chromatin, providing access for ER to nearby EREs. ER then interacts with transcriptional co-activators and chromatin modifying enzymes to open up transcription start sites (TSS) for RNA polymerase II (PolII), allowing initiation of transcription. Reproduced, with permission, from Wall EH, Hewitt SC, Case LK, Lin CY, Korach KS & Teuscher C (2014) The role of genetics in estrogen responses: a critical piece of an intricate puzzle. *FASEB Journal* **28** 5042–5054.



**Table 1**

## Estrogen Receptor Co-Regulator Complexes.

Complex	Functions	Comments	References
Src1, Src2, Src3	interact with Helix12 of agonist bound ER, interact with SWI/SNF, histone modifiers		(Hsia, et al. 2010; Johnson and O'Malley 2012)
Mediator	"bridges" ER and transcriptional "machinery" (RNA Pol II) to control transcription	made up of >20 subunits, MED 1-31, arranged in 3 modules (head, middle, tail)	(Conaway and Conaway 2011; Malik and Roeder 2010)
SWI/SNF	regulate access to enhancer sequences via chromatin remodeling, ATPase activity,	Made up of 9+ subunits, examples include BRG1, BRM, BAF subunits	(Roberts and Orkin 2004)
Histone Modifiers	Modify histones to increase or decrease transcription	Acetyltransferase (HAT;eg.p300/CBP), deacetylase (HDAC;eg.NCoR), Methyl transferase (eg.PMRT/CARM), demethylase	(Barnes, et al. 2005; Wu and Zhang 2009)
26S Proteasome	"clears" transcriptional modulatory proteins to facilitate subsequent transcription, transcriptional termination	Structure made up of 20S catalytic core particles (CP), 19S regulatory particles (RP)	(Keppler, et al. 2011; Kim, et al. 2011)

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Table 2

Uterine Phenotypes in Mice Null or Mutated for Estrogen Receptors or Estrogen Signaling.

Mutated or null for sex steroid receptors and signaling	Uterine phenotypes	References
<i>Esr1</i> <sup>-/-</sup> (Homozygous null alleles for ER $\alpha$ : $\alpha$ ERKO and Ex3 $\alpha$ ERKO)	Normal uterine development but exhibits hypoplastic uteri. Insensitive to the proliferative and differentiating effects of endogenous, growth factors and exogenous E2. Implantation defect. * lack decidualization. Infertile.	(Antonson, et al. 2012; Curtis Hewitt, et al. 2002; Curtis, et al. 1999; Dupont, et al. 2000; Hewitt, et al. 2010a; Lubahn, et al. 1993)
<i>NERKI</i> <sup>+/-</sup> (One mutated allele of two-point mutation in ER $\alpha$ DBD and one WT allele)	Normal uterine development but exhibits hyperplastic uteri. Hypersensitive to estrogen. Infertile.	(Jakacka, et al. 2002)
<i>KIKO</i> ( <i>ER</i> <sup>AA/-</sup> ) (One mutated allele of two-point mutation in DNA binding domain of ER $\alpha$ and one ER $\alpha$ KO allele)	Normal uterine development. Insensitive to the proliferative effects of exogenous E2 treatment. ER <sup>AA</sup> binds HRE and induces genes that are normally progesterone responsive Infertile.	(Hewitt, et al. 2010b; O'Brien, et al. 2006)
<i>ER<math>\alpha</math></i> <sup>EAAE/EAAE</sup> (Homozygous animal of 4-point mutation of DBD ER $\alpha$ )	Normal uterine development but exhibits hypoplastic uteri. Loss of E2-induced uterine transcripts. Infertile.	(Ahlbory-Dieker, et al. 2009)
<i>ER<math>\alpha</math></i> AF-1 <sup>0</sup> (Deletion of amino acids 2-128 on ER $\alpha$ )	Normal uterine development and architecture. Blunted E2 response. Infertile.	(Abot, et al. 2013; Billon-Gales, et al. 2009)
<i>ER<math>\alpha</math></i> AF-2 <sup>0</sup> (Deletion of amino acids 543-549 on ER $\alpha$ )	Normal uterine development but exhibits hypoplastic uteri. Insensitive to E2 treatment. Infertile.	(Billon-Gales, et al. 2011)
<i>ENERKI</i> ( <i>ER<math>\alpha</math></i> <sup>G525L</sup> ) (Homozygous animal of one point mutation in LBD of ER $\alpha$ )	Normal uterine development but exhibits hypoplastic uteri. Insensitive to E2 treatment. IGF-1 induced slight uterine epithelial proliferation compared to control littermates (nonhomogenous pattern). Infertile.	(Sinkevicius, et al. 2008)
<i>AF2ER<sup>KIKI</sup></i> (Homozygous knock-in of two-point mutation in LBD of ER $\alpha$ )	Normal uterine development but exhibits hypoplastic uteri. Insensitive to E2 treatment. ER antagonists and partial agonist (ICI 182,780 and TAM) induced uterine epithelial proliferation. Growth factor did not induce the uterine epithelial cell proliferation. Infertile.	(Arao, et al. 2011)
<i>ER<math>\alpha</math></i> Epi-cKO (epithelial cell specific deletion of ER $\alpha$ using <i>Wnt7a</i> <sup>Cre+</sup> ; <i>Esr1</i> <sup>fl/fl</sup> mouse model)	Normal uterine development. Sensitive to E2- and growth factor-induced epithelial cell proliferation. Lack full uterine growth response to E2. Selective loss of E2-target gene response. Implantation and decidualization defects. Infertile.	(Pawar, et al. 2015; Winuthayanon, et al. 2014; Winuthayanon, et al. 2010)
<i>Esr1</i> <sup>del/del</sup> (Uterine deletion of ER $\alpha$ using <i>Pgr</i> <sup>Cre+</sup> ; <i>Esr1</i> <sup>fl/fl</sup> mouse model)	Normal uterine development. Hypoplastic uteri. Defective decidual response.	(Pawar et al. 2015)
<i>Esr2</i> <sup>-/-</sup> (Homozygous null alleles for ER $\beta$ : $\beta$ ERKO, Ex3 $\beta$ ERKO, and ** ER $\beta$ <sub>ST</sub> <sup>L-L</sup> )	Exhibit grossly normal uterine development and function. Sensitive to E2 treatment. Some <i>Esr2</i> <sup>-/-</sup> lines reported elevated uterine epithelial proliferation after E treatment compared to WT Some are complete sterile (due to ovarian phenotype).	(Antal, et al. 2008; Dupont et al. 2000; Krege, et al. 1998; Wada-Hiraike, et al. 2006)
$\alpha$ $\beta$ ERKO (Homozygous null for both ER $\alpha$ and ER $\beta$ )	Normal uterine development but exhibit hypoplastic uteri, similar to those of <i>Esr1</i> <sup>-/-</sup> . Insensitive to E2, infertile	(Couse, et al. 1999; Dupont et al. 2000)
<i>Cyp19a1</i> <sup>-/-</sup> (Homozygous null aromatase: ArKO)	Normal uterine development but exhibits hypoplastic uteri. Sensitive to E2-induced epithelial cell proliferation.	(Fisher, et al. 1998; Toda, et al. 2001)

Mutated or null for sex steroid receptors and signaling	Uterine phenotypes	References
	Infertile.	
<i>Esr1</i> C541A palmitoylation deficient mutants	C451A-ER $\alpha$ normal uterine development, E2 growth response Nuclear-only ER $\alpha$ [NOER] hypoplastic ER $\alpha$ -null like uterus	(Adlanmerini, et al. 2014) (Pedram, et al. 2014)

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\*  $\alpha$ ERKO females have a similar uterine phenotype to the newer Ex3 $\alpha$ ERKO except for maintaining decidualization response, which may due to the splice variants in the original  $\alpha$ ERKO that retains ER activities.

\*\* ER $\beta$ <sup>ST</sup><sup>L-/L-</sup> females are the only line of ER $\beta$  knockout animals that reported to be completely sterile.