56:2

# 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.

#### Keywords

- estrogen receptors
- gene expression
- ▶ gene regulation
- hormone action
- uterus/endometrium

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

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 & Saunders 2012). Therefore, ER $\beta$  is slightly smaller than ER $\alpha$ , and most of these differences lie within the smaller N-terminus.

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What's new in estrogen receptor action 56:2



#### 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 AF-1. The C domain binds to DNA motifs called 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 AF-2. 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.

# **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 (Laudet & Gronemeyer 2001, Aagaard *et al.* 2011, Hilser & Thompson 2011, Brelivet *et al.* 2012, Helsen *et al.* 2012).

### 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 (McEwan 2004, Aagaard et al. 2011, Hilser & Thompson 2011), 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 coordination of ligand, DNA motif and ER domain functions (Aagaard et al. 2011, Hilser & 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 coreceptor 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 coactivator, 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 cisacting 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, Hilser & Thompson 2011, Helsen et al. 2012). Amino acids in the C-terminal 'knuckle' of the first zinc finger form the proximal box ('P-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 distal box ('D-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 (ERE) that ER binds is composed of a six-base pair (bp) palindromic sequence arranged as an inverted repeat and separated by a three-bp spacer, GGTCAnnnTGACC. The inverted-repeat arrangement of the ERE dictates that the ER homodimerizes in a 'headto-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, Hilser & Thompson 2011, Helsen *et al.* 2012). 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

**Table 1** ER coregulator complexes. Adapted, 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*, 4th Edn, pp 1099–1193.Eds TM Plant & AJ Zeleznik. Elsevier

Complex	Functions	Comments	References
Src1, Src2, Src3	Interact with Helix12 of agonist bound ER, interact with SWI/SNF, histone modifiers		Hsia et al. (2010) and Johnson & 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 three modules (head, middle, tail)	Malik & Roeder (2010) and Conaway & Conaway (2011)
SWI/SNF	Regulate access to enhancer sequences via chromatin remodeling, ATPase activity	Made up of 9+ subunits, examples include BRG1, BRM, BAF subunits	Roberts & Orkin (2004)
Histone modifiers	Modify histones to increase or decrease transcription	Acetyl transferase (HAT; e.g., p300/CBP), deacetyase (HDAC; e.g., NCoR), methyl transferase (e.g., PMRT/CARM), de-methylase	Barnes e <i>t al.</i> (2005) and Wu & Zhang (2009)
26S proteasome	'Clears' transcriptional modulatory proteins to facilitate subsequent tran- scription, transcriptional termination	Structure made up of 20S catalytic core particles (CP), 19S regulatory particles (RP)	Keppler <i>et al</i> . (2011) and Kim <i>et al</i> . (2011 <i>a,b</i> )

sites of post-translation modifications (Kim *et al.* 2006). Current mechanisms suggest this non-conserved and 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 & 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 (Laudet & Gronemeyer 2001, Kumar & McEwan 2012). Structural studies indicate that the LBD is composed of 11 α-helices (H1, and H3 through H12) arranged in a three-layer α-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 AF-2, 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 coactivator recruitment and is therefore less likely to activate transcription. The LBDs of ER $\alpha$  and ER $\beta$  exhibit ~60% homology (Fig. 1) but bind the endogenous estrogen, estradiol (E<sub>2</sub>), with similar affinity (ERa, 0.1 nM; ERb, 0.4 nM) (Le Romancer et al. 2011, Gibson & Saunders 2012) 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 (Le Romancer et al. 2011, Gibson & Saunders 2012). 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 ERa selective agonist, and diarylpropionitrate (DPN), an agonist showing preference, but not exclusive selectivity, towards ERβ (Stauffer *et al.* 2000, Meyers *et al.* 2001).

### F domain

Among the sex steroid receptors, only ERs possess a welldefined F domain (Fig. 1). This region is relatively unstructured with little known function, although some data indicate a role in coactivator recruitment,

dimerization and receptor stability (Katzenellenbogen *et al.* 2000, Koide *et al.* 2007, Yang *et al.* 2008, Kumar *et al.* 2011, Arao *et al.* 2013).

### **Coregulatory complexes**

All steroid receptors interact with coregulatory molecules, coactivators, and corepressors (Hsia et al. 2010, George et al. 2011). The primary coactivator interaction for steroid receptors is with a family of p160/SRC (steroid receptor coactivator) 1, 2, and 3 coactivators (Lonard & O'Malley 2005, Bulynko & O'Malley 2011, Johnson & O'Malley 2012). SRC1 (NCOA1), SRC2 (GRIP1 and TIF2), and SRC3 (pCIP, RAC3, ACTR, TRAM, and A1B1) interact with helix 12 of ERs via 'LXXLL' motifs in their nuclear receptor interacting domains, which are leucine rich regions with 'X' designating any amino acid (Johnson & 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 & 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) (Bulynko & 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 coregulatory complexes (O'Malley et al. 2012). In this way, coactivators 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

### Ligand-dependent actions: direct or classical

understood are discussed below.

In the classic model of estrogen response (Figs 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 ERa (Fig. 3) (Carroll et al. 2005, Carroll & Brown 2006, Fu et al. 2011, Zaret & Carroll 2011). The ligand-ERE-bound receptor complex then engages coactivator molecules as described above (Johnson & 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 & 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 & 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



## Figure 2

Ligand-dependent and ligand-independent nuclear receptor mechanisms. The direct 'classic' model of 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

elements (Fig. 2). However, the  $\text{ER}\alpha^{EAAE/EAAE}$  mouse, which is mutated in the  $\text{ER}\alpha$  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 (Ahlbory-Dieker *et al.* 2009, Hewitt *et al.* 2014) and is likely complimentary to the direct DNA stimulated responses.

### Non-genomic actions

Rapid effects of  $E_2$  have been described, including a rapid activation of endothelial nitric oxide synthase in endothelial cells (Levin 2011) and potentiation of nerve conductance (Takeo & Sakuma 1995, Kim *et al.* 2011*a*,*b*).

of membrane receptor signaling, such as growth factors (GF), to nuclear ER.

Matthews J, Cheng G, Hartman J, Tujague M, Ström A, Treuter E, Warner M

what are their targets. Physiological Reviews 87 905-931. Copyright 2007

Because these estrogen effects occur within minutes, they

have been thought not to involve direct ER 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

hormone response is the G protein coupled ER (GPER,

tive phenotypes (Langer et al. 2010), although effects on

the degrees of uterine responses elicited by E<sub>2</sub> have been

One potential mediator of rapid membrane localized

Adapted, with permission, from Heldring N, Pike A, Andersson S,

& Gustafsson JA (2007) Estrogen receptors: how do they signal and

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receptors altogether.

56:2



### 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 coactivators and chromatin modifying enzymes to open up transcription start sites (TSS) for RNA polymerase II (PoIII), allowing

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 E<sub>2</sub> (Fig. 2). Likewise, growth factors are able to mimic the effects of E<sub>2</sub> in the rodent uterus via E<sub>2</sub> independent activation of ER $\alpha$  (Curtis & Korach 1999, Fox *et al.* 2009). In some cases, the MAP kinase protein ERK is corecruited 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 E<sub>2</sub>

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.,  $E_2$  or diethylstilbestrol – DES) has long served as an

initiation of transcription. Adapted, 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.

experimental model to mimic the uterine events that occur during the estrous phase of the rodent cycle or immediately after the preovulatory E<sub>2</sub> surge. Morphological and biochemical changes occur in the rodent uterus after estrogen stimulation following an established biphasic temporal pattern (Hewitt et al. 2003). Estrogenstimulated changes in the rodent uterus that occur early, within the first 6 h 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. ERa 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 ERa recruitment (Hewitt et al. 2012). The above processes are followed by responses that peak after 24-72 h 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

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56:2

E<sub>2</sub>–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. 2003, Watanabe et al. 2003, Ho Hong et al. 2004, Moggs et al. 2004, Hewitt et al. 2005, Hong et al. 2006). The clearly defined patterns of early and late response genes found in mouse uterine tissues are completely lacking in ERa-null (aERKO, Ex3aERKO) uteri (Hewitt et al. 2003, 2010*a*,*b*). 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 ERa-null uteri or are relieved by cotreatment with ER antagonists in the presence of ERa, indicating that ERa is also actively involved in transcriptional repression as part of mediating the physiological responses (Hewitt et al. 2003, 2010a,b).

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 (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 (Farnham 2009, Park 2009, Biddie *et al.* 2010, Green & Han 2011,

http://jme.endocrinology-journals.org DOI: 10.1530/JME-15-0254 Martens et al. 2011, Meyer et al. 2012). Initial studies focused on ERa binding in MCF7 breast cancer cells, and several similar studies followed, which are summarized and compared in several review articles (Deblois & Giguere 2008, Cheung & Kraus 2010, Gao & Dahlman-Wright 2011, Tang et al. 2011, Gilfillan et al. 2012). These articles 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 ERa 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 ERa (Lupien et al. 2009, Zaret & Carroll 2011).

ChIP-seq analysis is examining the ERa binding sites in mouse uterine tissue indicated that, much like the MCF7 breast cancer study, most ERa 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 & Hager 2012). For ER in MCF7 and FoxA1 can establish ER accessible regions. The accessible chromatin regions are colocalized within nuclear 'hubs,' which seem to optimize frequency of interaction with ER (Grontved & 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 & Giguere 2008, Green & Han 2011, Martens et al. 2011, Gilfillan et al. 2012, Meyer et al. 2012).

# Uterine phenotypes in mouse models of disrupted estrogen signaling

Mouse models of disrupted ER signaling have proven invaluable to experimental investigation of estrogen

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Table 2 Uterine phenotypes in mice null or mutated for estrogen receptors or estrogen signaling. Adapted, 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, 4th Edn, pp 1099–1193. Eds TM Plant & AJ Zeleznik. Elsevier

Mutated or null for sex steroid receptors and signaling	Uterine phenotypes	References
<i>Esr1<sup>-/-</sup></i> (homozygous null alleles for ERα: αERKO and Ex3αERKO)	Normal uterine development but exhibits hypoplastic uteri Insensitive to the proliferative and differentiating effects of endogenous, growth factors and exogenous E <sub>2</sub> Implantation defect <sup>a</sup> Lack decidualization Infertile	Lubahn <i>et al.</i> (1993), Curtis <i>et al.</i> (1999), Dupont <i>et al.</i> (2000), Curtis Hewitt <i>et al.</i> (2002), Hewitt <i>et al.</i> (2010 <i>a,b</i> ), Antonson <i>et al.</i> (2012)
<i>NERKI</i> <sup>+/-</sup> (one mutated allele of two- point mutation in ER <sup>a</sup> DBD and one WT allele)	Normal uterine development but exhibits hyperplastic uteri Hypersensitive to estrogen Infertile	Jakacka et al. (2002)
KIKO (ER <sup>AA/-</sup> ) (one mutated allele of two-point mutation in DNA binding domain of ERa and one ERaKO allele)	Normal uterine development Insensitive to the proliferative effects of exogenous $E_2$ treatment $ER^{AA}$ binds HRE and induces genes that are normally progesterone responsive Infertile	O'Brien <i>et al</i> . (2006) and Hewitt <i>et al</i> . (2010 <i>a,b</i> )
$ER\alpha^{EAAE/EAAE}$ (homozygous animal of four-point mutation of DBD ER $\alpha$ )	Normal uterine development but exhibits hypoplastic uteri Loss of E <sub>2</sub> -induced uterine transcripts Infertile	Ahlbory-Dieker <i>et al</i> . (2009)
<i>ERαAF-1</i> ° (deletion of amino acids 2–128 on ERα)	Normal uterine development and architecture Blunted $E_2$ response Infertile	Billon-Gales <i>et al</i> . (2009) and Abot <i>et al</i> . (2013)
$ER\alpha AF-2^{\circ}$ (deletion of amino acids 543–549 on $ER\alpha$ )	Normal uterine development but exhibits hypoplastic uteri Insensitive to $E_2$ treatment Infertile	Billon-Gales <i>et al</i> . (2011)
<i>ENERKI (ERa<sup>G525L</sup>)</i> (homozygous animal of one point mutation in LBD of ERa)	Normal uterine development but exhibits hypoplastic uteri Insensitive to E <sub>2</sub> treatment IGF1 induced slight uterine epithelial proliferation compared to control littermates (non-homogenous pattern) Infertile	Sinkevicius <i>et al.</i> (2008)
<i>AF2ER<sup>KIIKI</sup></i> (homozygous knock-in of two-point mutation in LBD of ER«)	Normal uterine development but exhibits hypoplastic uteri Insensitive to E <sub>2</sub> 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 <i>al.</i> (2011)
<i>ERα Epi-cKO</i> (epithelial cell specific deletion of ERα using <i>Wnt7a<sup>Cre+</sup>;</i> <i>Esr1<sup>t/f</sup></i> mouse model)	Normal uterine development Sensitive to $E_{2}$ - and growth factor-induced epithelial cell proliferation Lack full uterine growth response to $E_2$ Selective loss of $E_2$ -target gene response Implantation and decidualization defects Infertile	Winuthayanon <i>et al</i> . (2010 2014) and Pawar <i>et al</i> . (2015)
<i>Esr1<sup>d/d</sup></i> (uterine deletion of ER $\alpha$ using <i>Pgr<sup>Cre+</sup>; Esr1<sup>f/f</sup></i> mouse model)	Normal uterine development Hypoplastic uteri Defective decidual response	Pawar et al. (2015)
Esr2 <sup>-/-</sup> (homozygous null alleles for ER $\beta$ : $\beta$ ERKO, Ex3 $\beta$ ERKO, and ${}^{b}$ ER $\beta_{ST}^{L-/L-}$ )	Exhibit grossly normal uterine development and function Sensitive to $E_2$ treatment Some $Esr2^{-/-}$ lines reported elevated uterine epithelial proliferation after E treatment compared with WT Some are complete sterile (due to ovarian phenotype)	Krege et al. (1998), Dupont et al. (2000), Wada-Hiraike et al. (2006) and Antal et al. (2008)
αβERKO (homozygous null for both ERα and Erβ) <i>Cyp19a1<sup>-/-</sup></i> (homozygous null aromatase: ArKO)	Normal uterine development but exhibit hypoplastic uteri, similar to those of Esr1 <sup>-/-</sup> . Insensitive to E <sub>2</sub> , infertile Normal uterine development but exhibits hypoplastic uteri Sensitive to E <sub>2</sub> -induced epithelial cell proliferation Infertile	Couse <i>et al.</i> (1999) and Dupont <i>et al.</i> (2000) Fisher <i>et al.</i> (1998) and Toda <i>et al.</i> (2001)
Esr1C541A palmitoylation deficient mutants	C451A-ER $\alpha$ normal uterine development, E <sub>2</sub> growth response Nuclear-only ER $\alpha$ [NOER] hypoplastic ER $\alpha$ -null like uterus	Adlanmerini <i>et al.</i> (2014) and Pedram <i>et al.</i> (2014)

<sup>a</sup>«ERKO females have a similar uterine phenotype to the newer Ex3«ERKO except for maintaining decidualization response, which may due to the splice variants in the original a RKO that retains ER activities. <sup>b</sup>ER $\beta_{ST}^{L-L-}$  females are the only line of ER $\beta$  knockout animals that reported to be completely sterile.

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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  $E_2$  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.

### ERa null patients and mice

Only one male patient and one female patient with ER $\alpha$  mutation have been described (Smith *et al.* 1994, Quaynor *et al.* 2013). 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 receptors affinity for coactivator proteins more than 200-fold.

There are currently numerous reported lines of ERanull mice and additional lines of mice with mutations in functional domains of ERa. Three separate lines of ERanull mice were generated: the aERKO, first described by Lubahn et al. (1993), the ERaKO (or Ex3aERKO), described by Dupont et al. (2000) and by Hewitt et al. (2010a,b), and  $ER\alpha^{-/-}$  described by Antonson *et al.* (2012). Homologous recombination was employed to disrupt ERa (aERKO), or cre-mediated recombination was used to completely excise exon 3, which encodes the ER DNA binding domain (Dupont et al. 2000, Hewitt et al. 2010a,b, Antonson et al. 2012) of the murine Esr1 (ERa) gene (ERaKO, Ex3aERKO, and  $\text{ER}\alpha^{-/-}$ ). The uterine estrogenic response in  $\alpha$ ERKO females differs from the latter two lines, but the overall spectrum of phenotypes are the same, as a ERKO animals have minimal level of truncated ERa protein produced from a splice variant, which preserves some residual biological functions (Couse et al. 1995), but all ERa null female mice are infertile. Recently, an ERa null rat has been derived using zinc finger nuclease (ZFN) genome editing. All phenotypes in the ERa null rats examined thus far were previously seen in the ERa null mice, including infertility due to hypoplastic uteri, polycystic ovaries, and ovulation defects (Rumi et al. 2014). The female patient with homozygous ERa mutation also has cystic ovaries and a small uterus despite elevated circulating serum E<sub>2</sub> (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, Korach *et al.* 

http://jme.endocrinology-journals.org DOI: 10.1530/JME-15-0254 1996, Hewitt et al. 2010a,b). The aERKO 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 a ERKO indicated that ERa 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 E<sub>2</sub> or DES, whereas no such response is observed in the uteri of ERa-null females (Lubahn et al. 1993, Korach 1994, Hewitt et al. 2010a,b). Uteri of mice that lack ERa 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 ERa-null uteri as well as a lack of late biological response in epithelial ERa knockout uteri provide strong evidence that ERa is required to mediate the full biochemical and biological uterine response to estrogens (Hewitt et al. 2010a,b, Winuthayanon et al. 2010. 2014).

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/EBPβ) is involved in hormone-induced uterine proliferation (Mantena et al. 2006). Maximum uterine expression of C/EBP $\beta$  is induced 1 h after E<sub>2</sub> treatment in both epithelial and stromal cells (Mantena et al. 2006, Ramathal et al. 2010). ICI 182,786 (ER antagonist) strongly inhibited E<sub>2</sub>-induced *Cebpb* transcript in the uterus suggesting an ER-dependent expression of C/EBP<sub>β</sub> (Bagchi et al. 2006). In addition, loss of epithelial  $ER\alpha$  in the uterus did not alter E<sub>2</sub>-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 ERa. This points to the action of estrogen through ERa as the major mediator of C/EBP<sub>β</sub> expression in the uterus. Indeed, the deletion of C/EBP $\beta$  (C/EBP $\beta^{-/-}$ ) 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  $C/EBP\beta^{-/-}$  females also exhibit complete infertility (Bagchi et al. 2006), due to implantation and decidualization defects (Mantena et al. 2006).

Pan *et al.* (2006) demonstrated that the uterine expression of minichromosome maintenance proteins (MCMs), a complex required for DNA synthesis initiation, is induced after  $E_2$  treatment, specifically MCM2 and MCM3. MCM2 activity is crucial and required for DNA synthesis in uterine epithelial cells (Ray & Pollard 2012). Further study demonstrated  $E_2$ -mediated induction of the transcription factor KLF4, which then targets the *Mcm2* promoter (Ray & Pollard 2012).

# Mice lacking ER $\beta$

ERβ-null mice have provided insight into the importance of ERB to female fertility and studies to date indicate ERB plays a particularly important role in ovarian function. Four different lines of ERβ-null mice have been described. The BERKO mouse, made using homologous recombination was first described by Krege et al. (1998), and the ERβKO or Ex3βERKO, was described by Dupont et al. (2000), and by Binder et al. (2013). Cre-mediated recombination was employed in both lines to disrupt exon 3 (Dupont et al. 2000, Binder et al. 2013) 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. Shughrue et al. (2002) reported the third line of ERBKO animals, however, no uterine or ovarian phenotypes were reported (Shughrue et al. 2002). Recently,  $ER\beta KO_{ST}^{L-/L-}$  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  $ER\beta KO_{ST}^{L-/L-}$ colony were reported to be sterile due to an ovarian defect while Ex3ßERKO (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.* (1999), and the ER $\alpha\beta$ KO, described by 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

http://jme.endocrinology-journals.org DOI: 10.1530/JME-15-0254 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 three animal models of Cyp19-null mice (called ArKO). Fisher et al. (1998) reported the first mouse line in 1998, which disrupted exon 9 of Cyp19 gene, as the region is highly conserved. Later, Honda et al. (1998) reported a mouse line with targeted disruption of exons 1 and 2 of the Cyp19 gene. Subsequently, Toda et al. (2001) generated the most recent mouse line of Cyp19-null in 2001 with a targeted disruption of exon 9 of the Cvp19 gene. These ArKO female phenotypes are indistinguishable (Fisher et al. 1998, Honda et al. 1998, Toda et al. 2001), with similarity to the *a*βERKO 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 aßERKO 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

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56:2

females lacking functional ERa or Cyp19, uteri are overtly hypoplastic and exhibit severely reduced weights relative to wild-type littermates (Fisher et al. 1998, Couse & Korach 1999, Britt et al. 2001, Toda et al. 2001), whereas ERβ-null uteri are grossly normal and normally responsive to ovarian-derived steroids (Couse & Korach 1999). The uterus of ERα-null females is severely hypotrophic, poorly organized, and possesses a paucity of glandular structures (Korach et al. 1996, Hewitt et al. 2010a,b). The luminal and glandular epithelial cells in ERa-null uteri are severely immature with fewer glands present in the adults (Nanjappa et al. 2015) and consistently exhibit a cuboidal morphology, vs 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 ERa. The totality of the ERa-null phenotype and lack of any overt uterine abnormalities in ER<sub>β</sub>-null females suggest that  $ER\beta$  has little meaningful function in mediating estrogen actions in the uterus. Moreover, ERαβ-null also demonstrated a similar uterine phenotype as ERa-null (Walker & Korach 2004). Weihua et al. (2000) reported that ERβ-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. In addition, Wada-Hiraike et al. (2006) showed that in immature females, loss of ERß leads to increased uterine epithelial proliferation induced by E<sub>2</sub> compared with WT uteri. Although ERβ-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 ERB leads to complete sterility due to a defect in ovarian function (Dupont et al. 2000, Antal et al. 2008).

(Couse & Korach 1999, Hewitt et al. 2010a,b). However, in

# Mice with uterine specific deletion of $\text{ER}\alpha$

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.* 2010*a,b*) (*ER\alpha Epi-cKO*). The expression of ER $\alpha$  in the uterine luminal and glandular epithelium of these animals was ablated, while the ERa expression in the stromal cells and other uterine cells remains intact (Winuthavanon et al. 2010). The epithelial ERa was ablated not only in the uterus in this mouse line (Winuthayanon et al. 2010), but also in the oviduct (Winuthayanon et al. 2015). As expected, based on findings in the global ER $\alpha$ knockouts, loss of uterine epithelial ERa has no effect on female reproductive tract development. Uterine histological analysis showed a similar uterine morphology as WT control (Winuthayanon *et al.* 2010). The *ER*α *Epi-cKO* uteri are sensitive to 24 h treatment of E<sub>2</sub>, as the uterine epithelial proliferation is preserved. However, ERα Epi-cKO uteri lack a complete uterine response to  $E_{2}$ , following a 3-day uterine bioassay, which demonstrated a blunted growth response and increased apoptotic activity in ERα Epi-cKO compared with 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 decidulaization defects (Winuthayanon et al. 2010, Pawar et al. 2015, Winuthayanon et al. 2015). This suggests that uterine epithelial  $ER\alpha$  is dispensable for early uterine proliferative responses but crucial for a complete adult biological response induced by E<sub>2</sub>, as well as for establishing pregnancy.

## Mice with mutated DNA binding domains of $\text{ER}\alpha$

To date, there are two mouse lines with mutations that are designed to disrupt the DNA binding function of the ERa that have been 'knocked-in' (KI) at the ERa gene locus. The first line was generated by replacing critical P-box amino acids E207 and G208 with alanines (ER $\alpha^{AA}$ ). This line was named 'non-genomic ER knock-in' (NERKI), as these mutations were intended to restrict ERa 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 $^{+/-}$  males were crossed with ERa null heterozygous (WT/KO) females to produce mice with one NERKI mutated allele and one deleted *Esr1* allele, called ER $\alpha$  KIKO or ER $\alpha^{AA/-}$  as described by 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. (2009; called  $ER\alpha^{EAAE/EAAE}$ ).

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

 $ER\alpha^{AA/-}$  females have normal uterine development. Initially, O'Brien *et al.* (2006) reported that  $ER\alpha^{AA/-}$ females, with mutation of the DNA binding domain, maintained proliferative responses induced by E<sub>2</sub>. However, in subsequent studies, no uterine proliferation was observed (Hewitt et al. 2009, 2010). Ahlbory-Dieker et al. (2009) showed that, unlike the NERKI<sup>+/-</sup>, 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 ERa-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 ERa<sup>EAAE/EAAE</sup> (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 ERa are infertile. Thus the physiological function of the DNA binding domain of ERa 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 E<sub>2</sub> 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 at times, 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 ERa

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*,

http://jme.endocrinology-journals.org DOI: 10.1530/JME-15-0254 which removes the AF-1 domain, and knocked into a mouse line (called ERaAF-1°) (Billon-Gales et al. 2009). There are three reported mouse lines with mutation in the AF-2 domain of ERa. One with a single point mutation in ERa of G at position 525 to L in the ligand binding domain (LBD), called 'estrogen-nonresponsive ERa knock-in or ENERKI' (ER $\alpha^{G525L}$ ) (Sinkevicius *et al.* 2008). Amino acids 543-549 were deleted from the LBD of ERa, removing helix 12 and thus AF-2 functionality, to create a second mouse line (called ERaAF-2°) (Billon-Gales et al. 2011). Two point mutations in the AF-2 of the LBD of ERa were knocked into a mouse (L543A and L544A, called AF2ER<sup>KI/KI</sup> animals) (Arao *et al.* 2011). ERaAF-1°. ERa<sup>G525L</sup>, ERaAF-2°, and AF2ER<sup>KI/KI</sup> females are all sterile (Sinkevicius et al. 2008, Billon-Gales et al. 2009, Arao et al. 2011, Billon-Gales et al. 2011).

ERaAF-1° females exhibited minimal uterine wet weight gain compared with  $ER^{+/+}$  uteri after treatment with E<sub>2</sub> pellets for two consecutive weeks, while ERaAF-2° females did not respond (Billon-Gales et al. 2009, 2011, Abot et al. 2013). This indicates that the ERa AF-2 functional domain contributes to minimal uterine weight increase induced by E<sub>2</sub> in the absence of AF-1. Both lines of AF-2 mutated animals (ER $\alpha^{G525L}$  and AF2ER<sup>KI/KI</sup>) display severely hypoplastic uteri, and lack uterine growth response to E<sub>2</sub> treatment (Sinkevicius et al. 2008, Arao et al. 2011, Billon-Gales et al. 2011). Interestingly, uterine wet weight can be increased by using the synthetic ERa agonist PPT in ERa<sup>G525L</sup> or by using the ER antagonists ICI 182,780 or tamoxifen in AF2ER<sup>KI/KI</sup> females (Sinkevicius et al. 2008, Arao et al. 2011). 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. 2011, 2013). Arao et al. (2011) 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>. The growth factor IGF-1 induced minimal uterine epithelial proliferation in  $ER\alpha^{G525L}$ , and was not seen in AF2ER<sup>KI/KI</sup> uteri (Sinkevicius et al. 2008, Arao et al. 2011). Together, these findings indicated that both AF-1 and AF-2 activation domains of ERa contribute to a normal regulation of the complete biological response of uterine growth and reproductive functions. As the AF domains mediate ER-coregulator interaction (Table 1), this emphasizes the importance of effective ERa coactivator protein recruitment for successful uterine E<sub>2</sub> response. Similarly, mice lacking sufficient SRC-1 coactivator (SRC1 $^{-/-}$ ), exhibit measurably diminished uterine response to E<sub>2</sub> (Xu et al. 1998).

### Mice with altered localization of ERa

A mutated mouse ERa that remains sequestered outside the nucleus (ERaH2NES), 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 ERa, 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 ERa with the same mutation of cysteine 451 to alanine. The first, C451A-ERa, exhibits normal uterine development and E2 induced growth response (Adlanmerini et al. 2014), whereas the nuclearonly ERa (NOER) has a hypoplastic ERa-null like uterus that fails to respond to E<sub>2</sub> (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 ERa in these physiological systems.

## Conclusion

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 ER 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 ERa. What functional aspects of the ERa 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.

Declaration of interest

The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of this review.

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