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Expression of a Dominant Negative Estrogen Receptor Alpha Variant in Transgenic Mice Accelerates Uterine Cancer Induced by the Potent Estrogen Diethylstilbestrol

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Abstract

ER 3 transgenic mice expressing a dominant negative estrogen receptor α (ER α) variant lacking the second zinc finger in the DNA binding domain were developed to examine its potential to inhibit estrogen action *in vivo*. To investigate if ER 3 expression influences uterine carcinogenesis, ER 3 transgenic mice were exposed to diethylstilbestrol (DES) on post-natal days 1–5. Neonatal DES treatment induced uterine adenocarcinomas in 81% of 8-month-old ER 3 mice compared to 49% of wild-type females (p<0.016). ER 3 did not inhibit the expression of the estrogen-responsive progesterone receptor and lactoferrin genes in the presence of ER α or modify their expression in ER α knockout (α ERKO) mice. Higher circulating 17 β -estradiol levels and nonclassical signaling by ER 3 may be related to the earlier incidence of uterine cancer. These

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findings indicate that expression of this $ER\alpha$ variant can influence determining events in uterine cancer development and its natural occurrence in the human uterus would unlikely be protective.

Keywords

diethylstilbestrol; dominant negative receptor; ERa variants; ER 3; lactoferrin; non-classical ER signaling; progesterone receptor; uterine cancer

1. INTRODUCTION

Estrogens are implicated in the initiation and promotion of carcinogenesis in the hormonally responsive tissues of the female reproductive tract [1, 2]. Estrogens stimulate cell proliferation and induce specific cellular responses through direct interaction with the estrogen receptors (ER), ER α and ER β . Both ER subtypes are nuclear receptors that act as ligand-dependent transcription factors. In the presence of an estrogen agonist, ER dimers transactivate or repress estrogen-responsive genes containing one or more estrogen response elements (ERE) [3]. Alternative to this classical pathway, ER also acts through non-classical mechanisms by interacting with other transcription factors, such as the AP-1 family and Sp-1, to influence estrogen responses [4]. In the uterus, ER α is the predominant receptor; the requirement for ER α to elicit a uterotropic response to estrogens or epidermal growth factor (EGF) has been clearly demonstrated in ER α knockout mice (α ERKO), which lack expression of wild-type (WT) ER α [5, 6]. Additionally, both ER α and ER β act through rapid, nongenomic mechanisms [7]; however, a study with a nongenotropic-selective ligand suggests that ER genomic actions are required for uterine stimulation [8].

Exposure to synthetic estrogens, such as diethylstilbestrol (DES), during critical times of development is linked with an increased risk of reproductive tract cancers in women [9] and mice [10]. DES is a potent estrogen, which has high affinity for ER α and ER β [11] and stimulates a uterotropic response at lower doses than the endogenous estrogen, 17 β -estradiol (E₂) [12]. In the late 1940's, DES was approved for the treatment of pregnancy-related complications, including risk of abortion, premature labor, and diabetes. However, after puberty, daughters exposed to DES *in utero* have an increased risk for developing clear-cell adenocarcinoma of the vagina or cervix [9, 13]. The stages of reproductive tract differentiation that occur prenatally in humans include both prenatal and neonatal development in mice [13]. Correspondingly, like women exposed *in utero*, mice exposed prenatally or neonatally to DES also develop reproductive tract cancers, including uterine adenocarcinomas [10].

In women, reproductive tract tumors associated with *in utero* exposure to DES are detected after menarche, usually between the ages of 14–30 years [14, 15]. In mice, removal of the ovaries prior to puberty prevents the formation of DES-induced uterine tumors [16]. Therefore, DES-induced cancer is influenced by estrogens both at the time of treatment, from DES, as well after puberty, from endogenous estrogens. ERα is expressed in uterine epithelial and stromal cells during early stages of reproductive tract development in fetal and neonatal mice as well as in the uterus of sexually mature mice [17, 18]. αERKO mice are resistant to the effects of DES, demonstrating that ERα is required for DES-induced

reproductive tract abnormalities and uterine cancer [19]. In contrast, elevated expression of ER α in MT-mER transgenic mice shortened the latency of uterine tumor development induced by neonatal DES treatment [20]. These data indicate that ER α expression levels and/or activity can influence susceptibility to DES-induced tumor formation. Therefore, neonatal DES treatment provides an effective model for investigating the effects of modified ER expression on hormonally-induced carcinogenesis, such as expression of an ER α variant with the potential to inhibit ER activity.

ERa variants were first detected in breast tumors and cell lines. ER variants arise by alternative splicing of the ERa transcript resulting in the deletion of one or more exons [21]. RNA expression is used to detect the presence of ERa variants in human tissues. A few studies have also verified that the variant RNA is translated into receptor proteins in human tissues and breast cancer cell lines [21–25]. Although the majority of the reports have focused on ER variant expression in breast cancer, ER variant expression has been found in other normal and neoplastic estrogen target tissues [21], including the uterus [26, 27]. The presence of ER variants in normal tissues suggests that these modified receptors may have a role in normal physiology, estrogen responsiveness, and, perhaps, tumor development.

The deletion of exon 3 (ER 3) from the human gene for ER α (ESR1) by alternative splicing was first detected in the T47D breast cancer cell line [28]. The message and protein for ER 3 also occur in MCF-7 cells [24, 25]. The in-frame deletion of exon 3 encodes a receptor protein missing the second zinc finger of the DNA binding domain (DBD). The second zinc finger contains the ligand-independent dimerization domain and may be responsible for discriminating the half-site spacing of DNA response elements [29]. The functional domains outside exon 3, including AF-1 and AF-2, first zinc finger, ligand binding, ligand-dependent dimerization, and nuclear localization domains, remain intact. Despite the loss of the dimerization domain within exon 3, dimerization with WT ERa occurs via its stronger, ligand-dependent dimerization domain [29-31]. In vitro, without the second zinc finger, human ER 3 does not bind to DNA containing the consensus estrogen response element (ERE) or activate transcription of an ERE-reporter gene[28]. However, in transfected HeLa cells, the ER 3 variant displays dominant negative activity; that is, coexpression of the ER 3 variant with WT ERa diminishes the ability of WT ERa to activate an ERE-reporter construct [28]. The postulated mechanism for its dominant negative activity is through the formation of ER 3:ER α and ER 3:ER β heterodimers to prevent DNA binding and, thus, transactivation of ERE-regulated genes [30].

The *in vivo* activities of the ER 3 variant, such as inhibiting the activity of the WT ER, remain untested. Transgenic mouse models expressing other dominant negative receptors have been instructive for investigating the roles of the WT and repressor protein [32–35]. Therefore, our goals were to develop a transgenic mouse model expressing ER 3 and to investigate its actions *in vivo* and its effects on carcinogenesis in estrogen-responsive tissues. The resulting transgenic mice express the mouse ER α variant lacking the second zinc finger, which is encoded by exon 4 in the mouse *Esr1* gene (third coding exon) and corresponds to the human variant lacking exon 3. The amino acid sequence for human exon 3 and mouse exon 4 is 100% conserved in the human and mouse ER α mRNAs, as are the splicing junctions for the message. Based on the reported absence of transactivation function and its

ability to repress ERa activity *in vitro*, we speculated that expression of the ER 3 variant in transgenic mice may provide cancer protection to tissues in which abnormal proliferation has been associated with estrogen exposure. Therefore, in the present study, uterine tumors were induced by neonatal DES treatment in order to investigate the effects of ER 3 expression on the development of hormonally-induced cancer.

2. MATERIALS AND METHODS

2.1. ER 3 Construct and Generation of the Transgenic Mice

For constructing the transgenic mice expressing the mouse ER 3 variant, the sequences for exon 4 of mouse *Esr1* cDNA encoding the second zinc finger were deleted. Due to the late discovery of the first exon in the human *ESR1* gene [36], the numbering for mouse *Esr1* and human *ESR1* exons does not correspond. Exon 4 in the mouse *Esr1* gene is equivalent to exon 3 in the human gene (with first and second exons in human ER α designated 1' and 1, respectively). Therefore, for clarity and comparison with reports on ER α variants in humans, the transgenic model is named to reflect an equivalent deletion in the mouse gene as the naturally-occurring ER 3 variant in humans.

The ER 3 cDNA was generated by PCR to recreate the deletion of exon 3 in human ER α in the mouse ER α cDNA (exon 4 in *Esr1*). Primers P1 (forward),

GCAAGCCCACTGTGTTCAAC, and P2 (reverse),

GCGGATCCCTTGAATGCTTCTCTTAAAG, were used to amplify the region of the mouse ERa cDNA prior to the Not I site through the splice site of the third and fourth exons. At the junction of the third and fifth exons, a BamH I site was included in the primer sequences to aid in the cloning and verification of the variant ER. The PCR generated fragment was digested with Not I and BamH I enzymes and inserted into the Bluescript KS(–) plasmid. Primers P3 (forward), GTTGGATCCGCATACGGAAGACCGCCGA, and P4 (reverse), CATCAGAATCTCCAGCCAGG, were used to amplify the region from the splice site of the fourth and fifth exons to beyond the Xho I site in the mouse ER cDNA. This fragment was digested and inserted into the BamH I and Xho I sites of the vector containing the Not I/BamH I mouse ER fragment. The Not I/Xho I fragment from the mouse ER cDNA from the MOR-100 vector (kindly provided by M. Parker) [37] was replaced with PCR generated sequences containing the deletion. The ER 3 cDNA was removed with EcoR I for insertion into the final vector.

The BamH I-Sal I fragment from the MT-mER construct [38] containing the splicing and polyadenylation signals was inserted into the pUC18 plasmid. Since splicing has been shown to enhance expression of some cDNA transgenes [39, 40], this fragment, which contains the portion of the pKCR2 vector [41] with rabbit β -globin exons and one intron, was included to provide splicing signals for the ER 3 transgene. The β -globin sequences are present only in the untranslated sequences of the ER 3 transcript.

A murine viral enhancer was included in the vector to augment expression of the transgene. The EcoR I-BamH I fragment containing the Harvey murine sarcoma virus (HaMuSV) LTR (kindly provided by M. Ostrowski) [42] was inserted into the vector containing the β -globin sequences. The EcoR I site of the HaMuSV enhancer was converted to a Sal I site using

linkers. The original intent of the ER 3 transgenic mice was to target expression of the variant to osteoblasts using the osteocalcin (*Bglap*) promoter. The promoter regions used for the rat osteocalcin promoter did not confer tissue specificity; therefore, in the ER 3 mice, this promoter region appears to act as a generic basal promoter element. The rat osteocalcin promoter, from sequences –194 to +26, was PCR amplified from DNA isolated from ROS 17/2.8 cells using primers P5 (forward), GCGGATCCGCAGCCTCTGATTGTGTCCT, and P6 (reverse), GCAGATCTCTAGGTCTGCACCGAGTTGC. The primers included the BamH I (5') and Bgl II (3') restriction sites for ligation of the digested PCR fragment into the BamH I site of the vector containing the β -globin and enhancer sequences. The ER 3 cDNA was then inserted into the EcoR I site within the second β -globin exon. The plasmid sequences were removed by Sal I digestion and purified prior to microinjection. The transgene DNA (Fig. 1), was microinjected into the pronuclei of fertilized eggs from FVB/N mice according to standard protocols [43]. This strain of mice has high fecundity as well as clear eggs with large, prominent pronuclei [44].

Seven founders, 4 female and 3 male, were produced by the microinjections, but only 6 generated subsequent progeny. The highest levels of transgene expression were evident in lines D and F. Official designations for lines D and F are FVB/N-TgN(mER_3os)04Eme and FVB/N-TgN(mER_3os)06Eme, respectively.

2.2. Genotyping

Genomic DNA was isolated from tail biopsies [45] and analyzed using PCR [38] as previously described. Southern blots were also performed on the DNA from the founder mice as previously reported [38]. Lines D and F had copy numbers for the transgene of approximately 4 and 8, respectively (data not shown).

2.3. RNase Protection Assay Analyses

Total RNA was prepared using guanidine isothiocyanate-CsCl gradient procedure [46]. The RNase protection assay (RPA) was performed as previously described [38]. The presence of the vector sequences adjoining the ERa cDNA in the RPA probe (see Fig. 1) resulted in a smaller product for the ERa transcript compared to ER 3 mRNA for differentiating the two messages. The antisense cyclophilin probe used for the control was generated from the template pTRI-CYC (Ambion, Austin, TX). Quantitation of the RNA levels was determined with the Phosphoimager and ImageQuant software (Molecular Dynamics, Sunnyvale CA).

2.4. Real-time RT-PCR Analyses

RNA was prepared from mouse tissues using Absolutely RNA RT-PCR Miniprep Kit (Stratagene, La Jolla, CA) according to the kit instructions. The reverse transcriptase (RT) reaction was performed with qScript cDNA Synthesis Kit (Quanta Biosciences, Gaithersburg, MD) prior to the PCR step. An aliquot of the RT reaction was amplified in an iCycler (Bio-Rad, Hercules, CA) with the BR SYBR Green SuperMix for iQ Systems (Quanta Biosciences, Gaithersburg, MD) and the specific primers for each gene using the following cycles: 1 cycle at 95°C for 90 sec followed by 50 cycles at 95°C for 15 sec and at 60°C for 45 sec. Primer sequences are listed in Table 1 for the mouse genes examined, including ER α , ER β , ER 3, progesterone receptor (*Pgr*), and lactoferrin (*Ltf*). Relative

mRNA levels were determined by the 2^{-} ^{Ct} method by normalization to the cyclophilin A (*Ppia*) gene. Amplification of the mRNA was confirmed by comparison to the no RT control and by melting temperature determination. A subset of the RT-PCR samples were run on 2% NuSieve/0.7% agarose gel electrophoresis to verify the proper size product.

2.5. Western Blot Analysis

Total protein homogenates were prepared from uteri from individual WT, line F, and line D female mice at age 3 months in estrus; 10 ug of protein was loaded on a 10% NuPage Bis-Tris mini gel and MOPS buffer (Life Technologies, Grand Island, NY). The gel was run at 200 volts for 2 hours and transferred to nitrocellulose membrane using the iBlot transfer system (Life Technologies, Grand Island, NY). The membrane was incubated overnight with primary antibody for ER α (1:1000; MC-20 Santa Cruz Biotechnology, Santa Cruz, CA) and anti-rabbit IgG secondary (1:5000; Cell Signaling Technology, Danvers, MA). Signal was developed as directed with ECL Prime reagent (GE Healthcare Biosciences, Pittsburgh, PA).

2.6. Animal Care

All procedures involving the mice were performed in accordance with the NIH Guide for the Care and Use of Laboratory Animals with approved protocols by the NIEHS and Duquesne University Animal Care and Use Committees. All mice were housed with 12 h:12 h light:dark cycles in a temperature controlled room with diet and water provided ad libitum.

2.6.1. DES Studies—Wild-type FVB/N female mice (National Cancer Institute Animal Program, Bethesda, MD) were bred with hemizygous ER 3 males. Mice for this study were fed NIH 31 chow. The resulting WT and ER 3 progeny were treated with daily injections of DES (Sigma Chemical Co., St. Louis, MO) dissolved in corn oil at the dose of 2 μ g/pup/day on days 1–5 after birth. Previous studies have shown this dose to be effective at inducing uterine abnormalities and tumors in CD-1 [16] and FVB/N mice [20]. Controls were left untreated. At 3 weeks of age the mice were weaned and genotyped using tail DNA. The mice were housed four or five females per cage. The mice were euthanized at 8 or 12 months of age and subjected to a complete necropsy. Tissues for histological examination were excised and fixed in 10% buffered formalin, embedded in paraffin, and sectioned at 6 μ m. The sections were stained with hematoxylin and eosin and evaluated under a light microscope by the study pathologist (BCB). Some regions of pathological alteration noted initially were serially sectioned for further analysis.

2.6.2. ER 3 and WT (FVB/N) Mice for Examining Estrogen-responsive Gene

Expression—ER 3 line D female and line F mice and FVB/N mice (Jackson Laboratories, Bar Harbor, ME) were euthanized at age 3 months in estrus. Stage of cycle was determined by vaginal smears stained with Dif-stain kit (IMEB Inc., San Marcos, CA) prior to necropsy. Uteri were frozen in liquid nitrogen for later RNA analyses for *Pgr* and *Ltf* RNA levels by real-time RT-PCR. Blood was collected by cardiac puncture in euthanized mice for the hormone assays.

2.6.3. ER 3 and aERKO Crossbred Mice—Dizygous ER 3 mice (FVB/N strain) were bred with heterozygous α ERKO mates (C57BL/6 strain) to generate heterozygous α ERKO/hemizygous ER 3 mice. These progeny were then mated with heterozygous α ERKO mice to ensure all genotypes expressing ER 3 would be hemizygous. This breeding scheme generated littermates expressing ER α (WT), ER α and ER 3 (ER 3), no ER α (α ERKO), and ER 3 without ER α (α ERKO/ER 3) on a mixed background strain (FVB/N and C57BL/6), which were used for RNA analyses by real-time RT-PCR. Genotyping for ER 3 is described in section 2.2 and for the disruption of the ER α gene in the α ERKO mice is previously reported [47]. Female mice with the desired genotypes were euthanized in estrus at age 3 months and the uteri quick frozen for later RNA analysis.

2.7. 17β-estradiol (E₂) and Progesterone (P₄) Serum Levels

Serum E_2 and P_4 were determined with the Double Antibody Estradiol and Coat-a-Count Progesterone kits (Siemens, Los Angeles, CA) on mice in estrus at necropsy.

2.8. Statistical Analyses

Statistics were performed using Graphpad Prism 5.0 software (San Diego, CA). Significance was designated for p values less than 0.05.

3. RESULTS

3.1. Generation of ER 3 transgenic mice

Two of the ER 3 transgenic lines, designated D and F, expressed the transgene in reproductive and non-reproductive tissues by the RNase protection assay (RPA) and realtime reverse transcriptase-polymerase chain reaction (RT-PCR) (Table 2). All organs thus far tested in both lines and genders expressed the transgene (Table 2). For female mice in both lines, similar expression was observed in the adrenal glands, bone, ovary, and uterus; but, line D had higher expression in the liver and mammary gland (Fig. 2A). In line F, the bone, brain, gonads, and liver had similar expression in male and female mice, but the male expressed the ER 3 transgene at higher levels in the kidney (Fig. 2B). As expected, the relative level of the ER 3 transgene expressed in the uterus was considerably less abundant than the endogenous ER α transcript, 1:7 (line D) to 1:9 (line F) ratio. In other tissues which typically express lower levels of ER α , such as the kidney and bone, the levels of the ER 3 transgene message exceeded the levels of the WT ERa. The ovary, which has high expression of ER β [48], is the only organ in both lines in which the levels of ER 3 did not exceed ER^β. However, individual variations likely occur for these levels, as is observed with some tissues from the mice analyzed by RPA versus real-time RT-PCR (see Table 2). A receptor protein that corresponds to the expected size for ER 3 (approximately 61 kDa) was also detected in the uteri of line F and line D mice in addition to the 66 kDa WT ERa (Fig. 2C).

There is no evidence of infertility or diminished reproductive functions in the males or females in lines D and F. In the hemizygous mice, the only evident phenotype occurs in line F females, which develop spontaneous cataracts after puberty [49]. In dizygous mice, the growth of line D male and female mice is stunted, resulting in adult body weights that are

less than half the weight of the WT (FVB/N), hemizygous line D and F, or dizygous line F mice (data not shown). It is unknown if the stunted growth in dizygous line D mice is related to transgene expression or due to the disruption of an unknown gene important for growth at the site of transgene insertion. Thus, only hemizygous mice were studied for DES-induced uterine cancer.

3.2. DES-Induced Uterine Cancer

To investigate the effects of ER 3 expression on DES-induced uterine cancer, DES (2 μ g/ pup) was administered to ER 3 and WT pups daily from birth through post-natal day 5. Both line D and F female mice were examined to ensure that the resulting outcomes would be due to the ER 3 transgene and not related to the site of transgene insertion, which would be random and, thus, unique for each line. The neonatal DES treatment induced strong cataracts in both male and female ER 3 mice from lines D and F, which were evident when the pups first opened their eyes [49]. In the reproductive tract, non-malignant abnormalities, which are common after neonatal DES treatment, were evident in the ER 3 and WT female mice (FVB/N strain). As with other strains [50], no corpora lutea were detected in the ovaries in the DES-treated ER 3 and WT mice, suggesting that normal cycling did not occur. In addition, 89% of the ER 3 females at 8 months of age and all of the ER 3 and WT females at 12 months of age had progressive proliferative lesions of the oviduct. All DES-exposed females also displayed excessive keratinization of the vagina (data not shown). The uteri of the treated mice for both genotypes were hypoplastic with minimal gland development. The glands that were observed were located at the cervical-uterine junction and were often hyperplastic. There were also "gland-like" structures in the cervix. Therefore, due to these similar effects in WT and ER 3 mice, the expression of the ER 3 transgene did not compound or diminish the previously reported effects of DES on reproductive tract development.

Besides the non-malignant phenotypes, neonatal DES exposure in hemizygous ER 3 (lines D and F) and WT littermates also resulted in the appearance of uterine adenocarcinomas. The histological appearance of the tumors in the WT FVB/N mice has been reported previously [20]. The malignant lesions usually arose at the junction of uterine and cervical epithelium in both WT and transgenic DES-treated females. Focal areas of squamous metaplasia were also evident in a few of the tumors. At age 8 months, a significantly higher number of ER 3 females developed uterine tumors compared with WT mice (p< 0.016, Fisher's exact test; Table 3). No significant differences in uterine cancer incidence were noted between the two ER 3 lines, with 9/13 line D and 12/13 line F females having uterine tumors by 8 months of age, and the levels of transgene expression in the uteri of these two lines were comparable (Fig. 2).

At 12 months, the percentage of WT mice with neoplastic uterine lesions increased, but remained lower than the incidence in ER 3 mice at 8 and 12 months of age. However, the difference between the two genotypes was not significant at age 1 year. In addition to a higher incidence at younger ages, the uterine adenocarcinomas detected in the ER 3 females were more locally invasive and involved more of the uterine horn compared to tumors in WT females (data not shown). These data suggest that DES-induced tumor development is

accelerated in the ER 3 transgenic mice. Unexpectedly, two untreated ER 3 females had uterine adenocarcinomas at 12 months of age (Table 3). The presence of this malignant lesion was not observed in the WT FVB/N females in our study or in those previously reported at ages 14 or 24 months [51]. These data indicate that the ER 3 female mice may have a slight predisposition for developing uterine adenocarcinomas, even in absence of DES exposure.

The unexpected higher incidence of uterine adenocarcinomas with neonatal DES treatment in ER 3 mice mimicked the incidence observed in transgenic mice overexpressing mouse ER α (mER α), MT-mER mice [20]. At 8 months of age, both ER 3 and MT-mER mice had significantly higher incidence of DES-induced uterine cancer compared to the WT group, which included WT mice from both studies (Fig. 3). Additionally, the tumor incidence was not significantly different between the two transgenic models. These results suggest ER 3 did not reduce estrogen activity in the uterus.

3.3. Estrogen-Responsive Gene Expression in the Uterus

The accelerated onset of uterine cancer does not coincide with the predicted ability of ER 3 to inhibit ER α action. To test the potential of ER 3 to inhibit uterine estrogen responsive genes in the presence of WT ER α , the expression of progesterone receptor (*Pgr*) and lactoferrin (*Ltf*) was examined in line F ER 3 and WT uteri by real-time RT-PCR. No suppression was observed as their RNA levels were similar for WT and ER 3 mice (FVB/N strain) in estrus (when estrogen levels are high) for both the progesterone receptor (PR) (Fig. 4A) and lactoferrin genes (Fig. 4B).

To determine how ER 3 influences the expression these estrogen-responsive genes in the absence of WT ERa, line F ER 3 mice were crossbred with α ERKO mice (C57BL/6 strain). As observed above in the FVB/N strain (Fig. 4A–B), relative uterine expression of PR (Fig. 4C) and lactoferrin transcripts (Fig. 4D) also were not significantly different between the WT and ER 3 progeny on the mixed strain background (FVB/N and C57BL/6). In the absence of ERa, higher PR expression was detected in α ERKO/ER 3 mice compared to WT mice (3.7 fold; p<0.05, Tukey's test). In contrast, both α ERKO and α ERKO/ER 3 uteri had significantly lower lactoferrin expression compared to uteri from WT (0.04-fold) and/or ER 3 (0.02-fold) littermates (p<0.05, Tukey's test; Fig. 4C–D). However, for both genes, no difference was observed between the α ERKO and α ERKO/ER 3 mice. Collectively, these data demonstrate that ER 3 does not modify uterine expression of these two estrogen-responsive genes compared to mice without ER 3, either in the presence (WT vs. ER 3) or absence of ERa (α ERKO vs. α ERKO/ER 3).

3.4 Circulating Estradiol and Progesterone Levels

A potential mechanism for enhanced estrogen action in ER 3 mice could be due to alterations in circulating hormone levels. ER 3 is expressed at equivalent levels as ERa and ER β in the ovary of both lines and at decreased levels in the pituitary in line F female mice (7:1 ratio for ERa:ER 3). If ER 3 influences estrogen or progesterone synthesis through its expression in the ovaries and/or pituitary or other tissues, the resulting levels could influence tumor development in post-pubertal DES-treated mice. Although progesterone (P₄) levels

were similar in both genotypes, 17β -estradiol (E₂) levels were significantly increased in ER 3 mice (p=0.023, Mann Whitney test) compared to WT mice in estrus (Fig. 5).

4. DISCUSSION

Neonatal exposure to DES resulted in an increased incidence of uterine tumors in 8-monthold ER 3 females compared with WT mice. The similar effect in both lines D and F indicates that the increased tumor incidence is due to ER 3 expression versus modelspecific effects from the site of transgene insertion. The lack of significance at 1 year indicates that DES-induced tumors appear at younger ages in ER 3 mice compared to WT mice. Therefore, contrary to our predicted results of providing cancer protection, these data indicate that expression of the ER 3 variant accelerates the development of hormonallyinduced uterine cancer.

ER α is required for DES to induce the adverse effects on the female reproductive tract as evidenced by the lack of effects in neonatal-treated α ERKO mice [19]. In MT-mER transgenic mice overexpressing ER α (which express both the WT mER α transgene plus the normal, endogenous ER α gene), neonatal DES treatment also induced an earlier onset of uterine adenocarcinomas [20]. The tumor results in MT-mER mice fit with the premise that estrogens acting through ER α are promoting tumor development; however, the similar tumor incidence in ER 3 females does not (Fig. 3). The paradox of both transgenic models accelerating DES-induced uterine tumor development despite expressing ER α receptors with opposite activities suggests that ER 3 expression resulted in increased versus decreased estrogen activity in the uterus.

Before the generation of the ER 3 transgenic mice, the ability of the ER 3 variant to inhibit WT ER α activity had only been tested in transfected mammalian cells. Transfecting a 1:10 ratio of WT ER α to ER 3 vectors into T47D breast cancer cells was found to inhibit approximately 80% of WT receptor activity [28]. Although the actual intracellular ratio of ER α :ER 3 receptors is unknown (since the 1:10 ratio reflects the relative levels of the transfected vectors and not the quantity of each receptor in an individual cell), higher or equal levels of dominant negative receptors are usually required to inhibit the activity of the WT receptor. With the inherently high levels of ER α in the uterus, ER 3 transcript levels do not exceed those of ER α in the uterus of lines D and F ER 3 mice (Table 2). A previous study in transfected breast cancer cells found that the ratio of ER α 3:ER α transcripts also reflected their protein levels [52]. The high ratio of ER α to ER 3 transcripts (7:1) may be one reason that ER 3 did not provide protection against DES-induced uterine cancer and that the transcript levels of the PR and lactoferrin genes are not reduced in the ER 3 versus WT uterus, especially for lactoferrin which contains a palindromic ERE in its promoter [53].

The findings with the tested estrogen-responsive genes indicate ER 3 might not be expected to inhibit uterine cancer development, but would not explain the accelerated onset. Dominant negative activity for ER 3 has only been demonstrated with classical ERE-induced gene expression [30]. In contrast, ERa receptors with DBD mutations or deletions can activate transcription of estrogen-responsive genes by non-classical mechanisms through interactions with other transcription factors, such as the AP-1 family and Sp1 [4]. In

transfected HeLa cells, ER 3 inhibits expression of an ERE-regulated reporter gene, but stimulates expression of a reporter construct regulated by an AP-1/ERE half site [30]. A study in cultured breast cancer cells also provides direct evidence that human ER α and mouse ER α with deletions in the second zinc finger stimulate non-classical pathways in an Sp1-regulated reporter gene [54]. These findings suggest ER 3 could stimulate versus inhibit genes regulated by these transcription factors. Thus, the lack of inhibition for the PR and lactoferrin genes in the ER 3 uteri in estrus may be related to their regulation at Sp1 and AP-1 sites, with and without half-ERE sites, which have been identified in the promoters of the PR [55–58] and lactoferrin genes [53]. Although ER 3 did not significantly increase expression of these two genes, other untested genes regulated by non-classical ER mechanisms, which are involved in promotion of the DES-induced uterine tumors, may be modified by ER 3. Additionally, PR and lactoferrin genes may be modified by ER 3 at other stages of the estrous cycle.

The lactoferrin, but not PR, gene contains a palindromic ERE [53, 58], which may explain why only its expression was significantly reduced in α ERKO and α ERKO/ER 3 mice. The expression of these genes in α ERKO mice (Fig. 4C–D) are in accord with a previous study showing transcript levels for PR are unaffected, but lactoferrin mRNA is substantially repressed in the uteri of α ERKO versus WT mice [59]. Additionally, treatment with estradiol did not modify the expression levels of either gene in ovariectomized α ERKO mice, implicating ER α in regulating their expression [59]. ER 3 did not modify the constitutive levels of PR and lactoferrin transcripts in the uteri of α ERKO/ER 3 mice compared to α ERKO animals, suggesting that ER 3 expression is not sufficient to stimulate the preexisting levels of either gene through the AP-1 and Sp1 sites or that the genes may already be maximally stimulated in the α ERKO mice to prevent further stimulation by ER 3. However, PR expression in the uteri of α ERKO/ER 3 mice was significantly higher than their WT littermates (Fig. 4C), which may suggest ER 3 has a slight influence on PR expression.

The regulation of estrogen responses by non-classical mechanisms has been reported to be important in uterine epithelial proliferation. NERKI transgenic mice were developed that express ER α with a point mutation in first zinc finger of the DBD, which is unable to activate an ERE, does not have dominant negative activity, but retains non-classical ER signaling [60]. In NERKI mice lacking WT ER α (KIKO mice), estrogen did not induce a uterotropic response [61]. These findings demonstrate that non-classical signaling by the NERKI mutant in the absence of WT ER α is not sufficient for estrogen-induced uterine proliferation. However, in intact NERKI female mice expressing WT ER α , the uteri appear hypersensitive to estrogen since they are enlarged with cystic endometrial hyperplasia [60]. Although the NERKI and ER 3 receptors differ in action and structure and the ER 3 mice are fertile, these models have similarities since ER 3 transgenic mice also express WT ER α and a variant that can stimulate non-classical, but not classical, signaling. Therefore, in ER 3 mice, expression of the variant may augment WT ER α -induced endometrial proliferation, especially in the elevated E₂ environment, which could ultimately lead to earlier tumor formation.

Since the ER 3 transgene is expressed in most tissues (Table 2), uterine tumor development may be influenced by ER 3 expression in other estrogen target tissues. This potential is supported by the higher circulating levels of E_2 , which would be due to ER 3 expression outside the uterus, such as in the pituitary gland and/or ovary (Table 2). Due to the known effects of excess estrogen on uterine cancer risk [1, 62], the higher E_2 levels or the resulting imbalance in E_2 to P_4 levels may contribute to the earlier cancer development in the ER 3 mice.

DES-induced uterine cancer is influenced by both the neonatal and post-pubertal stages of development [16]. Consequently, the ER 3 transgene may influence either or both of these developmental stages: 1) during development and differentiation of the immature reproductive tract, when DES exposure occurs, and 2) after the onset of puberty and estrogen cycling. However, since latency is affected, these findings suggest a greater effect of the ER 3 variant on the mature uterus than during developmental DES exposure. Thus, in post-pubertal mice, elevated E_2 levels and/or non-classical signaling may be promoting the growth of tumors initiated in the neonatal uterus to allow their detection at younger ages. Similar post-pubertal ER 3 actions are likely overstimulating uterine proliferation in the untreated adult female mice since two ER 3 females not treated with DES also developed uterine adenocarcinomas (Table 3).

In humans, transcripts for ER 3 [63] and other ER α splicing variants [26, 64, 65] have been detected in the normal human endometrium. No difference in ER 3 endometrial expression was detected between infertile and fertile women and patients with endometriosis. These findings suggest that the ER 3 variant does not influence fertility [63], which agrees with the findings in the ER 3 transgenic mice. Additionally, the ER 3 variant mRNA has been detected in human endometrial hyperplasia, but not in endometrial cancer [66]. Based on the results in the ER 3 transgenic mice, expression of ER 3 in the human uterus would not be expected to be protective. If sufficient levels of this variant were expressed in the human uterus, such as the 11–14% relative to ER α in the untreated mice (Table 3). Whether elevated circulating E₂ levels would also be required to increase uterine cancer risk by ER 3 expression in other tissues, like the pituitary gland, is unknown; but, ER 3 variant transcripts have been reported in human pituitary adenomas and the normal rat pituitary gland [67, 68].

The tumor and gene expression results from this study do not provide direct evidence that ER 3 has dominant negative activity *in vivo*; however, dominant negative effects may be most evident *in vivo* in non-uterine tissues with lower ERα expression, such as the mammary gland. This premise is supported by the significant delay in mammary cancer in female ER 3 transgenic mice (line F) compared to mice not expressing the ER 3 transgene (Davis et al., unpublished results). Thus, ER 3 inhibits mammary tumor development despite the higher circulating estrogen levels. However, besides ERα levels, other tissue-specific characteristics may be related to the contrasting results on cancer onset in the uterus and mammary gland of ER 3 mice. For example, responses that differ between these two tissues include the contrasting actions of the non-classical signaling ERα mutant in NERKI

mice, which have hyperplasia in the uterus and hypoplasia in the mammary gland [60], and the differing regulation of the PR promoter by various estrogenic ligands [55].

4.1. Conclusions

ER variants have been detected in many normal, premalignant, and cancerous tissues in humans and animals and speculated to have a role in normal physiology and cancer development, growth, endocrine responsiveness; however, studies in animal models are needed to understand their *in vivo* actions. Using a transgenic mouse model, this study demonstrates that expression of the ER 3 transgene can alter events important in normal uterine physiology that result in the earlier appearance of malignant lesions. Although ER 3 inhibits transcription from ERE-regulated genes in a dominant negative manner, it also stimulates expression of promoters with AP-1 and Sp1 sites [30, 54]. In addition, E₂ levels were elevated due to ER 3 actions in other tissue(s). Therefore, the variant expression both in and outside the uterus may have a role in uterine cancer development in the ER 3 mice. In women expressing ER 3 mRNA in the uterus, the variant would be unlikely to protect the uterus from estrogen-induced uterine cancer due to its ability to stimulate non-classical signaling. The ER 3 transgenic mice provides a novel model system for future investigations into the roles of this ER α variant in cancer development, progression, and treatment as well as in the normal physiology of estrogen target tissues.

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Abbreviations

aERKO	estrogen receptor alpha knockout		
DES	diethylstilbestrol		
DBD	DNA binding domain		
ERa	estrogen receptor alpha		
ΕRβ	estrogen receptor beta		
ERE	estrogen response element		
PR	progesterone receptor		
WT	wild-type		

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- ER 3 transgenic mice express the mouse ERa variant lacking the second zinc finger
- Many tissues express ER 3; a higher ratio of ERa to ER 3 occurs in the uterus
- Neonatal diethylstilbestrol accelerated uterine cancer in ER 3 versus wild-type mice
- Estrogen-responsive genes (*Pgr*, *Ltf*) are not modified by ER 3 in the uterus
- 17β -estradiol serum levels are higher in ER 3 than wild-type mice



Figure 1. Diagram of the ER 3 construct used to generate the transgenic mice

The exons encoding the mER α are numbered according to the coding exons only. The mouse ER α (mER α) cDNA sequences are designated with white bars and noting the loss of exon 3 (3) sequences which correspond to exon 3 of human ER α . The sequences from the pKCR₂ vector [38] include the two rabbit β -globin exons (black bars) and one intron (first dark gray bar between exons) as well as 3' processing signals (second dark gray bar after mER α sequences). The mER α cDNA sequences were inserted into the second β -globin exon. The rat osteocalcin promoter sequences (Osc) are designated as a light gray bar. The enhancer sequences (en) from the U3 LTR of the Harvey murine sarcoma virus (HaMuSV) are indicated by the medium gray bar. The direction of transcription is noted from within the osteocalcin promoter by the arrow. The SV40 polyadenylation signals are located within the pKCR₂ sequences. The region of the construct used for expression analysis by RPA is also indicated. The forward (F) and reverse (R) primers used for genotyping are noted. The thin bars at each end of the construct represent the plasmid sequences which are removed prior to microinjection into the FVB/N embryos.

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Figure 2. Comparison of transgene expression in multiple tissues of adult ER 3 male and female mice and detection of ERa protein in WT and ER 3 female mice

Total RNA was analyzed for ER 3 transgene transcripts by real-time RT-PCR from tissues dissected from a line D and line F female and line F male mouse. CT value is shown for each tissue based on normalization to the cyclophilin A (*Ppia*) gene. Lower CT values indicate higher expression levels. Expression relative to ER α and ER β for these tissues is shown in Table 2. A. Comparisons between female mice for lines D and F are shown for ER 3 expression levels (n=1). B. Relative expression between male and female line F mice is indicated for the ER 3 transgene (n=1). Gonads represent the ovaries for the female and testes for the male mice. C. A protein in the appropriate size range for the ER 3 variant was detected by western blot analysis in the uteri of line D and F ER 3 mice in estrus using an antibody directed against the carboxy-terminus of ER α (MC-20). The images for the two uteri each from 3-month-old WT (FVB/N), line F, and line D mice were obtained from the same 10% gel and blot. The band for WT ER α is noted by the upper arrow at 66 kDa and the lower arrow corresponds to the smaller size expected for the ER 3 variant (approximately 61–62 kDa). The 70 kDa marker is indicated at the line marked with 70.



Figure 3. Similar increased uterine a denocarcinoma incidence in ER $\,$ 3 and MT-mER transgenic mice compared to wild-type mice

The percent of female mice with uterine adenocarcinoma detected by histopathology is depicted at age 8 months. The number of mice examined for the ER 3 mice (black bar) at 8 mo (n=26, from Table 3) and for the previously reported MT-mER mice (grey bar) at 8 mo (n=26) [20]. Wild-type (WT) mice (open bar) are shown with the combined incidence in WT mice (FVB/N strain) for both studies for 8 mo of age: 47.5% for the combined studies (n=59) compared to 49% for the ER 3 study (see Table 1) and 46% for the MT-mER study [20]. Chi-squared analysis demonstrated statistical significance for the 8 mo age groups (p=0.0054). Comparisons between the genotypes by the Fisher's exact test demonstrated significant increases in uterine cancer incidence for MT-mER (*, p<0.035) and for ER 3 mice (**, p=0.0046) compared to the combined WT group; however, the difference in incidence for the ER 3 vs. MT-mER mice was not significant (p> 0.05, Fisher's exact test).



Figure 4. Estrogen responsive genes in the uterus are not repressed by ER 3 Uterine total RNA obtained from 3-month-old female mice in estrus were analyzed for each genotype. Relative mRNA expression was determined by real-time RT-PCR for the progesterone receptor (*Pgr*), panels A and C, and lactoferrin (*Ltf*) genes, panels B and D, with normalization to the cyclophilin A (*Ppia*) gene. In panels A and B, the average C_T values are displayed for WT (FVB/N, n=8) and ER 3 (line F, FVB/N strain) mice (n=8),

uterine progesterone receptor (Pgr) expression; B. uterine lactoferrin (Ltf) expression.

with the fold difference determined by the 2^{-} Ct method indicated within each bar: A.

Expression levels in the ER 3 mice were not significantly different than in WT uteri (p>0.05, Mann Whitney test). In panels C and D, uteri from intact female mice with a mixed background strain obtained by crossbreeding ER 3 (line F, FVB/N strain) and aERKO (C57BL/6 strain) were analyzed. The average C_T values for the 4 genotypes, including WT (n=4), ER 3 (hemizygous, +/-; n=4), α ERKO (homozygous for the ER α disruption, -/-; n=4), and α ERKO/ER 3 (-/- and +/-, respectively; n=6) are depicted. The fold difference of ER 3 relative to WT mice (1.0) and aERKO/ER 3 relative to aERKO determined by the 2^{-} Ct method are indicated within each bar. C. Uterine progesterone receptor (*Pgr*) expression was significant (p=0.025, 1-way ANOVA) with a significant difference between WT and aERKO/ER 3 mice (Tukey's test). Fold differences relative to WT (1) are 3.1 for α ERKO and 3.7 for α ERKO/ER 3 and relative to ER 3 (1) are 1.9 for α ERKO and 2.3 for aERKO/ER 3. D. Uterine lactoferrin (Ltf) levels were significant (p=0.0042, 1-way ANOVA). The negative C_T levels reflect higher *Ltf* expression compared to the normalizing *Ppia* gene. Fold differences relative to WT (1) are 0.04 for both aERKO and aERKO/ER 3 and to ER 3 (1) are 0.2 for the two aERKO genotypes. Genotype comparisons for panels C and D were analyzed by Tukey's test: a, p<0.05 compared to WT; b, p<0.05 compared to ER 3.

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Serum hormone levels were measured in 3-month-old female mice in estrus. A. 17β estradiol (E₂) serum levels are increased in the ER 3 mice compared to wild-type (WT) mice (FVB/N strain). The 29 ER 3 mice examined includes female mice from lines F (n=16) and D (n=13); sera from 13 WT mice were analyzed. * p=0.023, Mann Whitney test. B. Progesterone (P₄) serum levels analyzed in 14 WT FVB/N female mice and in 27 ER 3 mice (n=16 for line F and n=11 for line D) were not significant (p>0.05, Mann Whitney test).

Table 1

Primers for Real-Time RT-PCR Analysis

Gene	Sequence
ERa (Esr1)	Forward: GTCCAGCTACAAACCAATGC Reverse: ATCTCTCTGACGCTTGTGCT
$\text{ER}\beta$ (<i>Esr2</i>)	Forward: AAATGTGCTATGGCCAACTTC Reverse: TTGGCGCTTGGACTAGTAAC
ER 3	Forward: ATTCAAGGGATCCGCATAC Reverse: ACAAGGCAGGGCTATTCTTC
Lactoferrin (Ltf)	Forward: ACAATGCTGGAGATGTGGCT Reverse: TTGTCATTCGTGCTTCGGGA
PR (Pgr)	Forward: TGGGAGCTGCAAGGTCTTCT Reverse: TGCCAGCCTGACAACACTTT
Cyclophilin A (Ppia)	Forward: TATCTGCACTGCCAAGACTG Reverse: ACAGTCGGAAATGGTGATCT

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Table 2

Relative Transcript Levels of ER 3 to ERa and ERB in Tissues from Lines D and F Adult Transgenic Mice

Line/Sex	Tissue	RNA Detection Method	Relative to ERa	Relative to ERβ
Line D Q	Adrenals	RT-PCR	↑ (3:1)	↑ (1400:1)
	Bone (skull)	RT-PCR	↑(10:1)	↑ (5200:1)
	Kidney	RPA	↑ (9:1)	nd
	Liver	RT-PCR & RPA	↑ (4:1 & 5:1)	\uparrow^a
	Lung	RPA	↑ (18:1)	nd
	Mammary gland	RT-PCR & RPA	↑ (14:1 & 7:1)	↑ (15800:1)
	Ovary	RT-PCR	= (0.7:1)	= (0.7:1)
	Uterus	RT-PCR & RPA	\downarrow (0.1:1 & 0.4:1)	↑ (100:1)
Line F Q	Adipose	RT-PCR	↓ (0.5:1)	↑ (1500:1)
	Adrenals	RT-PCR	↑ (2:1)	↑ (2400:1)
	Aorta	RT-PCR	=(1:1)	\uparrow^a
	Bone (skull)	RT-PCR	↑ (3:1)	\uparrow^a
	Brain	RT-PCR	↑ (23:1)	† (110:1)
	Kidney	RT-PCR & RPA	† (33:1 & 5:1)	↑ (8500:1)
	Liver	RT-PCR & RPA	\downarrow (0.2:1 & 0.2:1)	\uparrow^a
	Lung	RPA	↑ (6:1)	nd
	Mammary gland	RT-PCR & RPA	\downarrow (0.6:1 & 0.6:1)	↑ (4100:1)
	Ovary	RT-PCR	= (0.8:1)	=(1:1)
	Pituitary	RT-PCR	$\downarrow (0.1:1)^b$	nd
	Uterus	RT-PCR & RPA	$\downarrow (0.1:1^{C} \& 0.7:1)$	† (190:1)
Line F 🗗	Bone (skull)	RT-PCR	↑ (3:1)	↑ (1500:1)
	Brain	RT-PCR	↑ (39:1)	↑ (280:1)
	Kidney	RT-PCR	↑ (23:1)	↑ (30100:1)
	Liver	RT-PCR	= (0.9:1)	↑ (2100:1)
	Testes	RT-PCR	↑ (3:1)	† (2300:1)

 a ER β not detected by real-time RT-PCR

 $b_{n=3}$ versus n=1 for other tissues

°n=6

RT-PCR: real-time RT-PCR (reverse transcriptase-polymerase chain reaction); for ER 3, ER α , and ER β RPA: ribonuclease protection assay; for ER 3 and ER α on a different female mouse than for RT-PCR nd: not determined (tissue not examined for ER β expression)

 \uparrow , ER 3 levels higher than ER α /ER β ; =, ER 3 levels are similar to ER α /ER β ; \downarrow , ER 3 levels lower than ER α

Table 3

Incidence of Uterine Adenocarcinomas in Wild-type and ER 3 Transgenic Mice with and without DES Exposure

	UNTREATED		DES-TREATED	
Age	WT	ER 3	WT	ER 3
8 months	0% (0/21)	0% (0/28)	49% (17/35)	81% (21/26)*
12 months	0% (0/17)	10% (2/20)	72% (13/18)	86% (12/14)

* p<0.016, Fisher's Exact Test

DES. Diethylstilbestrol; WT, wild-type (FVB/N strain)