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## Epigenetic effects of endocrine-disrupting chemicals on female reproduction: An ovarian perspective

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### Abstract

The link between *in utero* and neonatal exposure to environmental toxicants, such as endocrine-disrupting chemicals (EDCs) and adult female reproductive disorders is well established in both epidemiological and animal studies. Recent studies examining the epigenetic mechanisms involved in mediating the effects of EDCs on female reproduction are gathering momentum. In this review, we describe the developmental processes that are susceptible to EDC exposures in female reproductive system, with a special emphasis on the ovary. We discuss studies with select EDCs that have been shown to have physiological and correlated epigenetic effects in the ovary, neuroendocrine system, and uterus. Importantly, EDCs that can directly target the ovary can alter epigenetic mechanisms in the oocyte, leading to transgenerational epigenetic effects. The potential mechanisms involved in such effects are also discussed.

### Keywords

epigenetics; techniques; DNA methylation; ovary; transgenerational epigenetic effects; EDC; DES; BPA; genistein; methoxychlor

## 1. Introduction

Female fertility disorders are becoming increasingly prevalent and an emerging women's health concern [1;2;3]. These disease outcomes reflect the interplay between individual genetic composition and the environment. Since the genetic composition at the population level is relatively slow to change, the significant role of our dramatically changed environment, in the last century, has to be considered. The impact of the environment, especially during development is highly relevant to adult health and is highlighted by the Barker hypothesis, also known as the developmental origins of health and disease (DoHAD) [4;5;6]. Although the Barker hypothesis was originally based on nutritional deprivation *in utero* and cardiovascular or metabolic disorders in adulthood, its perspective can be applied to developmental exposure to environmental endocrine-disrupting chemicals (EDCs) and fertility disorders in females during adulthood [3].

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EDCs are synthetic and natural compounds in the environment that interfere with (i.e., mimic and/or antagonize) the actions of endogenous hormones and disrupt the functions of the endocrine system. The United States Environmental Protection Agency (EPA) has identified hundreds of EDCs that have estrogenic, anti-estrogenic, or anti-androgenic activities [2;7;8]. Potentially there are many compounds that either already exist in the environment or are newly introduced, whose effects have not yet been studied in the female reproductive system. EDCs include several groups of chemicals such as insecticides, herbicides and fungicides; plastics and plasticizers; surfactants; industrial chemicals such as polychloro biphenyls (PCBs), polybrominated biphenyls (PBBs), and dioxins; flame retardants; pharmaceuticals; and phytoestrogens such as genistein and coumestrol. There are numerous ways in which exposures to EDCs can occur. While a few compounds are for medicinal use, exposures to the vast majority of these EDCs are through unintended exposure. For example, DDT, which was banned in 1972, was intended for use as a pesticide against disease-bearing insects. It was heavily used for many years and eventually it was found that wildlife, especially bird populations were drastically diminished due to consumption of DDT tainted fish [9].

The overall fertility rate of women aged 15–44 years in the United States dropped 44% between 1960 and 2002 [10]. Lifestyle choices may have been a major contributor of this decline as this study included all women in this age group. However, according to the data from the *National Survey for Family Growth*, the ‘impaired fecundity rate’ was increased from 11% to 15% between 1982 and 2002 [11]. Furthermore, the incidence of female reproductive disorders such as early puberty, irregular menstrual cycles, endometriosis, premature ovarian failure, and polycystic ovarian disorder is increasing in parallel with the increasing number of EDCs in the environment [1].

Human epidemiological studies suggest that there is a clear association between developmental EDC exposure and adverse health outcomes in females. For example, high maternal serum concentration of p'p'-DDT significantly reduces the probability of pregnancy for their daughters [12]. In addition, there is an association between potential exposure to other EDCs, such as bisphenol A (BPA) and genistein and female reproductive problems. Levels of BPA in blood are associated with a variety of conditions in women including endometrial hyperplasia, recurrent miscarriages, sterility, and polycystic ovary syndrome (PCOS) [13;14;15]. An example is that of the inverse correlation between the levels of BPA in urine of women undergoing infertility treatment with the number of eggs recovered in *in vitro* fertilization (IVF) clinics and serum estradiol levels [16]. High BPA exposure is also associated with chromosomal abnormalities [17]. More alarming recent evidence suggests that there is an association between intrauterine and early life exposure to soy formula and uterine fibroids in adulthood [18]. The same study also showed a similar association between *in utero* diethylstilbestrol (DES) exposure and fibroids.

Direct evidence from unintentional human exposure to EDCs and observations with wildlife species or lab animals shows that developmental exposure to EDCs singly or in mixtures can cause similar types of consequences as described above [19;20;21;22;23;24]. Further evidence from lab animal studies for the effects of developmental exposure to EDCs on the female reproductive system is provided in section 4. The importance of epigenetics (*vs* genetics) in disease susceptibility and phenotypic differences are becoming very clear [25;26;27;28]. Epigenetic mechanisms that play a role in the delayed effects of developmental exposure to EDCs are also presented in section 4 and Table 1. From a public health perspective, the most serious concern emerging from these studies is that developmental exposure to adverse environmental EDCs may lead to effects in subsequent generation(s) via epigenetic mechanisms, broadly termed transgenerational epigenetic effects (see Section 5 for more details).

## 2. Epigenetics

The term “epigenetics” was first introduced in the 1940s by Conrad H. Waddington to describe the developmental program where genes determine the individual’s phenotype and internal and external environmental cues are also taken into consideration [29;30]. Although the word epigenetic was originally derived from an older terminology “epigenesis” – referring to an embryological concept, it literally means “beyond or above genetics” [31]. However, the current use of the term is somewhat restricted and describes the study of mitotically and meiotically heritable changes in the gene function (i.e., expression) without changing the DNA sequence [32;33]. These changes are effected by several molecular mechanisms now commonly known as epigenetic mechanisms. These include DNA methylation and post-translational modifications of histone proteins, which bring about changes in chromatin structure and function. The important role of non-coding RNAs as an additional epigenetic mechanism in this process is being recognized. Figure 1 describes the variety of techniques that can be employed to study epigenetic mechanisms. For further details on this topic refer to Supplemental Material.

### 2.1. Epigenetic mechanisms

**2.1.1. DNA methylation**—Methylation of DNA occurs at cytosine residues in CpG dinucleotides and was first implicated in the control of gene regulation and X-chromosome inactivation in a heritable manner, in the mid-1970s [34;35]. Since then it has been well established that DNA methylation is essential for processes such as genomic imprinting, suppression of retrotransposons, and X-chromosome inactivation [36]. CpGs are underrepresented in the genome except in segments of DNA called CpG islands (CGIs), where the CG content is markedly increased compared to the AT content [37]. Approximately 60–70% of human genes contain CGIs in their promoter regions [38]. CpG sites that are not located in CGIs, such as in repeat sequences and retrotransposons, are usually methylated [39] as are those involved in X-chromosome inactivation and genomic imprinting processes (see Section 6, [40]). In general, DNA methylation is associated with the interference of transcription factor binding, resulting in a down-regulation of gene expression [41], while demethylation allows access of transcription factors and upregulation of gene expression [42;43]. The methylation status of CpGs that are not part of CGIs, but are associated with the promoter region of the genes, does not usually affect the gene regulation. Such genes are primarily regulated by availability of transcription machinery such as TATA binding protein (TBP) and by histone modifications (see below, [37;44]). Increased CGI methylation is normally associated with aging and can silence genes. Furthermore, the silencing of tumor suppressor genes can lead to cancer and other serious pathologies [39;40;44]. Exposure to EDCs can also induce such changes in CGIs, which can turn on/off critical genes in various organs, leading to organ dysfunction (see section 4).

Normal mammalian development requires the action of DNA methyltransferases (DNMTs) for the establishment (DNMT3A and 3B) and maintenance (DNMT1) of DNA methylation within the genome [39;45]. DNMT3L (DNMT3-like) is similar in sequence to DNMT3A and B but lacks enzymatic activity and functions as a regulator of DNMT3A and B. DNMT1 $\alpha$  is oocyte specific, accumulates in oocytes, and maintains the imprinted genes in the embryo [45]. Deletion of any of these enzymes leads to DNA methylation abnormalities and causes mutant mice to die either embryonically [*Dnmt1*, *Dnmt3b*, and *Dnmt3a* and *Dnmt3b* double knock out (KO) mice] or in the early postnatal period (*Dnmt3a*). When *Dnmt3l* or *Dnmt1 $\alpha$*  are deleted, the mutant animals are viable but their heterozygous mutant offspring die embryonically [45;46]. The function of DNMT2 is not known since the mice lacking *Dnmt2* are normal [39;45]. The expression level of these enzymes is highly regulated and peaks during the establishment of imprinting during postnatal oocyte

development [47;48;49;50]. In male germ cells, the levels are upregulated before birth [embryonic day (E) 15.5-18.5] roughly corresponding to the time of establishment of imprinting [47;51].

**2.1.2. Histone modifications**—Histones are proteins of the nucleosome core. The core consists of two copies of each of the following four histones: H2A, H2B, H3 and H4. The DNA is wrapped around this core complex [52]. The function of the nucleosome core proteins goes beyond the packaging of DNA and includes the highly elaborate post-translational modifications of the amino acids at N termini, which play a significant role in gene expression and is named the “histone code” [37;53]. The modifications are on specific amino acid residues and include acetylation of lysine, methylation of lysine and arginine, and phosphorylation of serine and threonine on the various histone proteins.

In general, acetylation of lysine residues, which takes place in the N terminal of all four histone proteins, is associated with relaxation of chromatin, allowing access to transcription factors and active transcription – euchromatin. Similarly, methylation of lysine 4 of histone 3 (H3K4) and H3K79 is also associated with euchromatin [37;54;55]. In contrast, along with deacetylation, various levels of methylation (one to three) of H3K9, H3K27, and H4K20 leads to compaction of the chromatin, disallowing the access of transcription factors and causing the silencing of the loci (heterochromatin). This silencing can be reversible or irreversible, depending on further modification [37;54;55;56]. For example, some histone methylation events (e.g., H3K9me3) work in conjunction with DNA methylation to stably silence genes [39].

The enzymes that add acetyl and methyl groups to lysine residues include various histone acetyl transferases (HAT) and lysine methyltransferases (HMT), respectively. In contrast, the enzymes that remove acetyl and methyl groups are histone deacetylase (HDAC) and various lysine demethylases [39;57]. The effects of environmental EDCs on histone modifications are relatively less known, but evidence is accumulating regarding histone modifications that are altered by EDC exposures in the reproductive tract [56]. It is expected that more research will be directed to understanding the effects of EDCs on histone modifications.

**2.1.3. Non-coding RNA**—The importance of non-coding RNAs (ncRNA) in biological processes has been recognized more recently [58]. Non-coding RNAs are transcripts without a clear open reading frame. Their size can range from 15-21 nucleotides (nt; miRNAs), 100–200 nt (small RNAs), or over 10,000 nt (large RNAs) [59]. The major role of ncRNAs is in gene silencing. The varying mechanisms include X-chromosome inactivation (e.g., *Xist* and *Tsix*), chromatin structure regulation (e.g., RNA-induced initiation of transcriptional silencing and RNAi mediated heterochromatin formation), genomic imprinting (e.g., *H19* and *Air*), and RNA directed DNA methylation. ncRNAs alter many cellular activities related to differentiation and development, abnormalities of which can lead to cancer, neurological diseases, and imprinting disorders (e.g., Beckwith-Wiedmann syndrome and Prader-Willi/Angelman syndrome) [60;61]. It is likely that EDCs can affect these important epigenetic regulators, but little data is available at this time.

## 2.2. Interaction between different epigenetic mechanisms

The three epigenetic mechanisms described above work in an interactive cooperation during the establishment and maintenance of epigenetic marks on the DNA, to regulate cellular development, differentiation, and function [46;62;63]. In general, during the establishment of the marks, histone modifications lead to DNA methylation, while in maintenance or inheritance of the marks, DNA methylation plays a primary role. For example, the

protection of CGIs from methylation during development is primarily mediated by histone modifications. Specifically, RNA polymerase II is recruited to CpG islands in a sequence-specific manner, which in turn recruits specific methyltransferases that methylate H3K4. Methylated H3K4 inhibits the contact of *de novo* DNMTs with DNA, leaving the CpG islands unmethylated while the rest of the CpG sites are methylated [37;64]. Similarly, during the targeted *de novo* methylation of the CpG islands during later stages of development, histone modifications guide the *de novo* DNMTs to the CpG islands following recruitment of the repressors to these sites [30;37;64]. In contrast, for inheritance of epigenetic marks following cell division, maintenance of DNA methylation by DNMT1 provides the initial silencing conferring mitotic heritability, which is further enhanced by a series of histone modifications that are conducive to gene silencing [30]. Specifically, methylated DNA (i) recruits a methyl cytosine binding protein (e.g., MECP2 or MDB2) that in turn recruits a HDAC to deacetylate DNA, (ii) directs H3K9 methylation, and (iii) inhibits H3K4 methylation [41;64;65]. In other cases, the sites that are actively regulated have bimodal modifications including trimethylation of H3K4 and H3K27 at CGIs in promoter regions, which can lead to silencing or activation depending on the other factors affecting gene regulation [56;57;64]]. There is also clear but emerging evidence that an ncRNA is a part of these interactions [66]. In plants, ncRNA-directed chromatin modifications such as histone modifications, and DNA methylation, are well known [67]. In addition, ncRNAs, histone modification and DNA methylation work cooperatively in X-chromosome inactivation [68], allele-specific gene silencing [59;69], and silencing of retrotransposons [70].

### 3. Development of female reproductive system

Successful female reproductive function requires three components that work in close communication with each other: the ovary, the neuroendocrine system or hypothalamus pituitary gonadal (HPG) axis, and the reproductive tract, including the uterus and oviduct. Therefore, EDC exposure that can affect any one these components can impact the others as well. A recent review provides in-depth information on ovarian development and function and on the factors that play a role in these processes [71]. In this section, we summarize ovarian development and emphasize the stages that are likely to be affected by EDCs (see Figure 2). We reviewed the actions of steroid hormones (e.g., estrogens, androgens), including their receptors as well as select transcription and paracrine factors. Even though relatively little is known of the epigenetic regulation of these factors, we focused on those that are regulated by steroid hormones. In the last part of this section, the most vulnerable processes in neuroendocrine and uterine development are highlighted. We refer primarily to research studies using mice and rats because data from a large body of developmental studies with transgenic mice and extensive toxicological studies with these species are available.

#### 3.1. Ovary development and function

**3.1.1. Primordial germ cells and gonadal differentiation**—The mammalian ovary consists of two general cell populations: somatic cells and germ cells. The sexually undifferentiated primordial germ cells originate from extragonadal tissues at around embryonic day (E) 7.0-7.5 [72] and begin their migration into the indifferent gonad at E9.0-9.5 [73], where they rapidly proliferate. In the male (XY) gonad, proliferating germ cells are enclosed in the seminiferous cord and enter mitotic arrest at approximately E14 [74]. In the female (XX) gonad, proliferating germ cells form oocyte nests, enter meiosis, and arrest at meiosis I by E17.5 [75].

The indifferent gonad is derived from the cells of the genital ridge and gives rise to the embryonic testis or ovary. The key factor that initiates testis differentiation is SRY (sex-

determining region of the Y chromosome). When *Sry/SRY* gene is deleted or mutates, an ovary forms in an XY embryo instead of a testis [76]. Conversely, if *Sry* is expressed in an XX embryo, a testis forms instead of an ovary [77]. Progression of the gonadal differentiation farther along the male pathway requires multiple additional factors that are downstream of SRY (see for review [78;79;80]).

Since testis development requires SRY and in its absence, an indifferent gonad differentiates into an ovary, ovarian developmental pathway had initially been considered to be a “default” or “passive” pathway [80]. However, accumulating experimental evidence, suggests the contrary. Many genes are differentially upregulated in the ovary during the period of gonadal differentiation [81;82;83;84]. Some of these factors are essential in ovary differentiation, and in their absence an XX gonad displays testis-like features such as coelemic vessel formation (reviewed elsewhere [85]).

One of the major differences between male and female germ cell differentiation pathways is the timing of the establishment of genomic imprinting, or epigenetic programming through DNA methylation (see Figure 2, [86]), a process that is considered to be vulnerable to the effects of EDCs [87;88]. In rodents, the germ cell genome that is normally methylated prior to migrating to the genital ridge [86] is unmethylated, including at imprinted loci, after the migration. Subsequently, re-methylation, which is mediated through an interaction between somatic and germ cells, occurs in a sex-specific manner at different developmental stages [89]. Therefore, the effects of EDCs on this event also can be sex-specific. In mice, while male germ cell re-methylation starts at E14 and is mostly completed by E16-17 [51;90], female germ cell re-methylation is initiated during the postnatal period PND 1-5 and continues throughout oocyte growth until the preantral follicle stage [91;92].

**3.1.2. Oocyte nest breakdown and early folliculogenesis**—Meiotic female germ cells, which are referred to as oocytes, are arrested at the early diplotene phase of meiotic prophase I and enclosed in oocyte nests that are surrounded by somatic pregranulosa cells. Starting at E16.5, most of these germ cells are eliminated via apoptosis [93]. Accordingly, deletion of the pro-apoptotic molecule *Bax* increases the number of primordial follicles in the ovary [94]. The remaining oocytes are surrounded by a single layer of flattened pregranulosa cells and form the primordial follicles. Primordial follicles start appearing postnatally, and this process is mostly completed by PND3-4. Most of the primordial follicles remain quiescent, but some begin growing and transition to the next stage, primary follicles. Both of these early processes, primordial follicle formation and primordial to primary follicle transition are tightly regulated by interactions between paracrine factors, transcription factors, and steroid hormones. However, importantly, since these processes determine the success of female reproduction their disturbances can lead to early depletion of follicles and therefore may result in early reproductive senescence [95].

**3.1.3. Primordial follicle formation**—The oocyte plays a central role in primordial follicle formation, supported by the data that in the absence of oocytes, primordial follicles fail to form [96]. One such oocyte-derived factor is the basic helix-loop-helix family member factor in germline-alpha (FIGLA). *Figla*-deficient female mice do not form primordial follicles, thus highlighting its critical role in that process [97]. Several growth factors and cytokines including tumor necrosis factor- $\alpha$  (TNF $\alpha$ ), neurotrophins (NTs), inhibins, and activins have been shown to play roles in primordial follicle formation [98;99;100;101].

In both mice and rats, progesterone has been shown to inhibit primordial follicle formation by inhibiting apoptosis [102;103]. Later it was shown that the inhibitory action of progesterone could be reversed by pro-apoptotic TNF $\alpha$  [98;104]. In mice, estradiol also

blocks primordial follicle formation [103]. The inhibitory action of estradiol and other estrogenic compounds (e.g., DES) may involve the inhibition of pro-apoptotic molecules, such as Fas ligand [105]. Inhibition of apoptosis by progesterone or estradiol leads to multioocyte follicles (MOFs) [103].

Activins have a stimulatory role on primordial follicle formation. Neonatal activin treatment increased the number of postnatal primordial follicle by 30% in mice. However, the excessive number of follicles was not maintained at puberty or beyond [101]. There is interplay between the inhibitory activity of estradiol and the stimulatory role of activins in follicular formation. Neonatal estradiol or DES induces MOFs but also inhibits activin levels in the ovary [106]. These results suggest that the paracrine systems that control the primordial follicle formation process can be influenced by estrogenic EDCs.

**3.1.4. Primordial to primary follicle transition**—Primordial to primary follicle transition is also described as “initial recruitment” (as opposed to “cyclic recruitment”, which takes place at the peri-antral stage during each cycle under the influence of gonadotropins after puberty [107]). Once follicular growth is initiated, folliculogenesis has to continue through one of two developmental pathways: ovulation or death by follicular atresia. Therefore, a close regulation of the initial recruitment is critical for reproductive success in order to not deplete the follicular reserve too rapidly.

The factors that are critical for this process include KIT ligand (KL) and its receptor, KIT; anti-Mullerian hormone (AMH); Forkhead box O3 (FOXO3) and FOXL2 transcription factors. Granulosa cells express KL, while oocytes and theca cells express its receptor KIT [108;109]. KIT and KL are important in ovarian follicle development and are encoded by *Steel (Sl)* and white spotting (*W*) loci of the mouse, respectively. Initiation and maintenance of ovarian follicle development are adversely affected and follicles arrest at the primary follicle stage in mice homozygous for certain *Sl* alleles, such as *Sl<sup>pan</sup>* and *Sl<sup>con</sup>* [110;111]. Using *in vitro* culture systems, the stimulatory roles of KL in oocyte growth [112] and primordial to primary follicle transition were shown (reviewed in [95]). Interestingly, KL regulates trafficking of DNMTs between oocyte nucleus and cytoplasm during epigenetic reprogramming [113].

Another paracrine factor AMH, has an inhibitory effect on early follicle development, in contrast to KL. In *Amh*-null mice, primordial follicle recruitment is increased, so, the reserve is rapidly depleted [114]. In ovary organ culture experiments, AMH inhibits the initiation of primordial follicle growth, supporting the *in vivo* observation [115]. AMH starts being expressed in primary follicles, and remains detectable through the early antral stage. However, AMH expression is reduced in large antral follicles [116;117]. It can thus be proposed that growing follicles produce AMH in order to down-regulate the number of follicles that are recruited during each cycle [116]. In addition, *Amh* has estrogen responsive elements in its promoter [118] suggesting that estrogenic or anti-estrogenic compounds, including EDCs can affect AMH expression and, in turn, the process of initial recruitment [117;119;120].

It is clear that estradiol and progesterone have inhibitory roles in the initial recruitment [102]. In a rat neonatal organ culture system, it was shown that the initial recruitment rate in the absence of estradiol is three times greater than the normal *in vivo* rate, suggesting an inhibitory role for estradiol *in vivo*. However, when estradiol was added to the ovary cultures, the rate of transition was dramatically reduced [102]. *In vivo*, when newborn rats were injected with estradiol benzoate (EB), the ovary had more primordial follicles [119]. It is interesting that the neonatal exposure to EB, while impairing follicular development, concomitantly elevates expression of inhibitory growth factor AMH [120]. In contrast, P450

aromatase KO (CYP19A1, ArKO) mice, which lack endogenous estradiol, have fewer primordial and primary follicles [121]. Collectively, these data suggest that while estradiol is needed for early folliculogenesis, excessive estradiol inhibits follicular progression.

The oocyte-derived FOXO3 was shown to be a major suppressor of primordial to primary follicle transition [122]. When it is deleted in mice, although the initial primordial follicle pool is established normally, primordial follicles are massively activated, leading to early elimination of follicular reserve and reproductive senescence. Androgens, which have dual roles in folliculogenesis, acting as a ligand for androgen receptor (AR) and as a substrate for aromatase enzyme may play a stimulatory role in the recruitment by inhibiting FOXO3. In neonatal mouse ovary organ culture, testosterone or dihydrotestosterone (non-aromatizable androgen) increased the number of primary follicles, but reduced secondary follicle numbers, suggesting that androgens stimulate primordial to primary follicle transition, but inhibit follicle growth beyond the primary stage [123]. Androgens may accomplish these roles by inhibiting FOXO3 activity and also suppressing the expression of growth differentiation factor-9 (GDF9), a well-known stimulator of follicle development beyond the primary stage (see Section 3.1.5). As a result, exposure to androgens causes an accumulation of preantral-stage follicles. Overall, estrogens may inhibit the initial recruitment by stimulating inhibitory paracrine factors (e.g., AMH) while androgens may stimulate the initial recruitment by inhibiting suppressive factors (e.g., FOXO3).

**3.1.5. Preantral follicle development**—Preantral follicle development includes the proliferation of granulosa cells to multiple layers, the growth of the oocyte in size, and the establishment of a second layer of somatic cells, the theca cells. However, the exact timing of this recruitment is debated and it may be species-specific [124]. Preantral growth is mediated primarily by oocyte-derived factors, most notably GDF9 and bone morphogenic protein-15 (BMP-15). Additional factors that are involved in the regulation of preantral follicle development include inhibins, KL, and NTs [95].

One of the essential paracrine factors that stimulate follicular growth beyond the primary follicle stage is GDF9, which is present in the oocyte from the primary follicle stage through ovulation [125;126]. In addition, KL plays a role in theca cell recruitment [127;128]. Evidence from studies with juvenile rats suggests that gonadotropins, luteinizing hormone (LH) and follicle stimulating hormone (FSH), have some role during preantral follicle growth [91;129], and their receptors are expressed starting at PND7 [130]). Although gonadotropins stimulate growth and differentiation of preantral follicles, follicles can develop up to the antral stage in the absence of gonadotropins [131].

**3.1.6. Follicle selection, antral follicle development, and ovulation**—In monoovulators, one follicle within the recruited cohort is selected to complete the full course of folliculogenesis and ovulation. This selection takes place around the antral stage of folliculogenesis. The selected follicle has relatively high levels of estradiol secretion. Estradiol production is accomplished by cooperation of theca cells and granulosa cells under the regulation of LH and FSH, respectively, which forms the basis of the “two-cell two-gonadotropin” hypothesis (see [132;133;134] for details). Fine-tuning of this process is mediated by local growth factors such as insulin-like growth factors (IGF), activins, transforming growth factor (TGF)  $\alpha$  and  $\beta$ , hepatocyte growth factor, and FGF7 [135].

IGFs are considered to be highly important for follicular maturation and therefore considered to be “co-gonadotropins” [136]. *Igf1*-deficient mice show a very similar ovarian phenotype as FSH-KO mice [71]. IGF-I stimulates cell proliferation and steroidogenesis in granulosa cells of various species [137;138]. In contrast, IGF binding proteins (IGFBPs) can suppress FSH-induced follicular growth and differentiation, which leads to atresia, possibly

by sequestering IGF-I protein and inhibiting its activity [139;140]. FSH reduces IGFBP activity by stimulating proteolytic mechanisms that degrade IGFBPs. One such protease is pregnancy-associated plasma protein-A (PAPP-A), which degrades IGFBP and increases the bioavailability of IGFs for stimulation of the follicles. PAPP-A has been considered a marker of selected follicles [141]. Recently, it has been shown that *Pappa* KO mice have compromised fertility due to reduced ovulation and steroidogenic capacity [142]. Epigenetic regulation of *PAPP-A* by EDCs in the ovary was shown (see [143] and Section 4.1).

In the pre-ovulatory stage of folliculogenesis, estradiol production is markedly elevated, which exerts a positive-feedback effect on gonadotropin secretion. The rise in FSH and LH supports further increase in steroidogenesis by the selected follicle and initiates the luteinization, whereby granulosa cells switch from the almost exclusive production of estradiol to the production of both estradiol and progesterone. This process upregulates multiple genes, including the LH receptor (LHR) in the granulosa cell to prepare for upcoming ovulation. The feedback dynamics within the HPG axis continue and culminate with the pre-ovulatory LH that stimulates ovulation [144]. Elevated LH, and to a lesser extent FSH, stimulate the terminal differentiation of granulosa cells leading to their further luteinization. Multiple genes play roles in ovulation, including estrogen receptor (ER)  $\beta$ , progesterone receptor, proteases, epidermal growth factor-like proteins, and prostaglandin synthase-2 (see [144] for review). Following ovulation, the remnants of the ovulated follicle are stimulated by LH to terminally differentiate into the corpus luteum (CL). The CL, as a primary source of progesterone, is essential for enabling the initiation and maintenance of pregnancy (reviewed in [145;146]).

As presented here, the ovary is a hormone-responsive tissue and contains follicles at every stage of their development and CL. The events described above are highly dynamic and require time- and cell-specific and stage-dependent regulation of numerous genes, which could be controlled by epigenetic mechanisms, and can be affected by the developmental exposure to EDCs. Therefore, the ovary provides a unique target for EDCs for epigenetic modulation.

### 3.2. Expression patterns and roles of ERs and androgen receptor in the ovary

Actions of EDCs in the ovary can be mediated by ERs (ER $\alpha$  and ER $\beta$ ) and AR. ER $\alpha$  and ER $\beta$  are expressed during early folliculogenesis in the ovary in cell- and stage- specific manner in several species, including primates [147], cattle [148], rats [149](Zama and Uzumcu unpublished), and mice [150]. ER $\alpha$  is expressed primarily in theca cells, and ER $\beta$  is expressed in granulosa cells. Gene-deletion studies in mice show that ER $\beta$  is essential for FSH-directed granulosa cell differentiation as well as for LH responsiveness [151;152]. Data also show that ER $\beta$  can facilitate mechanisms that promote follicle maturation from the early antral to the pre-ovulatory stages [153;154]. ER $\beta$  may also play a major role in primordial follicle formation in the ovary [154;155;156;157;158]. In contrast, although ER $\alpha$  plays a role in the regulation of theca cell steroidogenesis in the ovary, its main function is to mediate estrogen-regulated feedback in the hypothalamus and pituitary [159;160].

Androgen receptor is expressed in the ovaries of several species, including rats [161], marmosets [162], humans [163], and sheep [164]. The expression occurs in granulosa cell, oocyte, and to a lesser extent thecal/interstitial cells [165;166]. The expression starts with primordial stage follicles and its level is elevated in preantral stage and starts declining as the folliculogenesis progresses [167]. Although androgens modulate follicular development, they may not be essential for female fertility since testicular feminized mice (Tfm), in which the AR is dysfunctional, remain fertile with a reduced fecundity [168]. Similarly, *Ar*-null (ARKO) mice, although initially fertile with a similar ovarian histology as the wild-type, reach reproductive senescence earlier due to progressive follicular loss [169]. Interestingly,

estradiol regulates androgen production through ER $\alpha$  primarily expressed in theca cells [170].

### 3.3. The establishment of the HPG axis and the development of the reproductive tract

The main hormones of the HPG axis are the hypothalamus-released gonadotropin releasing hormone (GnRH), pituitary gonadotropins, and gonadal steroid hormones. The establishment of the hypothalamic neural networks composed of multiple neuronal inputs (nuclei, or cell types) is essential for the pulsatile release of GnRH and pre-ovulatory surge of GnRH/LH in females. The brain is sexually-dimorphic [171], in both morphology and function. In female embryos, androgen production is low, and the small amount of estrogen produced is sequestered by  $\alpha$ -fetoprotein, thus making it unavailable in the brain. However, in male embryos, the T produced from the testis is not sequestered by  $\alpha$ -fetoprotein and is aromatized to estrogens in the brain, which masculinizes the brain [172]. EDC actions can alter this process since estrogenic EDCs are normally not sequestered by the  $\alpha$ -fetoprotein, thereby providing an early estrogenic activity in the brain that potentially alters the sexually dimorphic development of the brain [14;173]. There are two main sexually dimorphic nuclei in the hypothalamic region of the brain that are established in early neonatal stages in rats: the anteroventral periventricular nucleus (AVPV) of the pre-optic area (POA) and the sexually dimorphic nucleus of the POA (SDN-POA). The AVPV is larger in females while the SDN-POA is larger in the males. The AVPV innervations into the GnRH perikarya in the hypothalamus are among the multiple neuron inputs necessary for the normal secretion of GnRH [174]. The SDN-POA has a known role in normal sexual behavior, but the complete gamut of its functions is not known. Both these nuclei express steroid hormone receptors in abundance (albeit in sex-specific amounts), thereby making them susceptible to EDC actions. Several classes of EDCs have been shown to affect the AVPV, SDN-POA volume, and cellular phenotype depending on the timing of exposure and the dosage [175;176;177;178].

The uterus differentiates from the Mullerian ducts along with the oviduct, cervix, and upper vagina [179]. Most stages of differentiation of the uterus occur postnatally in rodents, starting at PND1-3 [180], which matches human uterine development at around gestational week 14 [181]. Mesenchymal cells in close proximity to the epithelium differentiate into the endometrium, while the distal cells differentiate into the myometrium [182]. Subsequently, the secretory glands develop (adenogenesis) from luminal epithelium [183]. This latter process is completed by PND7 and involves many endocrine and paracrine inputs in mice.

The uterus has varied roles depending on the reproductive stage: implantation, maintenance of pregnancy, and parturition. Estrogens can induce target gene expression in the uterus for cellular functions such as organ growth and proliferation. ERs are actively expressed during Mullerian duct development and are seen as early as E13 in the mesenchyme, while the uterine epithelium expresses ERs soon after birth [184]. The main ER receptor in the uterus is ER $\alpha$ ; using KO studies, it has been demonstrated that ER $\alpha$  disruption cause hypoplastic uterine and vaginal tissues [151;185].

## 4. EDCs and their effects on the female reproductive system

In this section, we focus on selected EDCs, methoxychlor (MXC), DES, genistein, and BPA that have been shown in recent animal studies to adversely affect the female reproductive system, especially through epigenetic mechanisms (Table 1). Some of these effects are transgenerational, as well (see Section 5). Each EDC section was organized in the following order: brief description of the EDC, human epidemiological studies, experimental animal studies, physiological effects on the ovary, HPG, and uterus, and any associated epigenetic studies discussed along side the physiological effects in the specific tissue.

#### 4.1. Methoxychlor (MXC)

MXC is an organochlorine pesticide that is used as a replacement for DDT and is a well-studied EDC. MXC is an estrogenic compound that demonstrates low-affinity binding for the ER [186]. The major MXC metabolites, HPTE [2, 2-bis-(*p*-hydroxyphenyl)-1, 1, 1-trichloroethane] and mono-OH MXC can function as estrogenic, anti-estrogenic, or anti-androgenic compounds [187;188], and therefore constitute model compounds for similar EDCs common in the environment [132;186].

Human epidemiological studies have shown that there is a strong association between occupational or nutritional exposure to organochlorine pesticides and female fertility. These include a two to threefold increase in risk of prolonged time-to-pregnancy and spontaneous abortion, among female greenhouse workers [189;190] and increased infertility in women with agricultural work histories [191]. Adverse effects that were observed in these association studies are reminiscent of the effects observed in experimental animals exposed to MXC during adulthood. Exposure to MXC (2500 or 5000 ppm) interfered with the normal estrous cycle, reduced mating rate and litter size [192]. However, when the exposure was withdrawn, these animals reverted to regular estrous cycles. In general, this observation applies to MXC exposure in adulthood and is probably applicable to most other estrogenic EDCs. Further studies demonstrated that adult mice or rats that were exposed to MXC showed persistent vaginal estrus [193], direct inhibition of embryonic growth, implantation failure [194], pregnancy loss [195], and ovarian atrophy due to inhibition of folliculogenesis leading to atretic follicles and reduced ovulation and decreased numbers of CL [193;196;197]. It was shown that exposure to MXC in adult mice selectively affects the antral follicles and induces atresia using the Bcl2/Bax signaling pathway, without affecting the HPG axis [198].

In contrast, when the exposure periods included *in utero* and early postnatal development period, the effects lasted into adulthood with more severe outcomes on reproductive parameters in rats. These included acceleration of the vaginal opening (a sign of puberty), acceleration of the onset of the first estrus, irregular cycles with persistent vaginal estrus, reduced pregnancy rate and litter size despite apparent mating, and early reproductive senescence [199;200;201]. Serum estradiol and progesterone levels were altered with increased FSH levels [200]. The effects on the ovary were dramatic, with both folliculogenesis and ovulation being inhibited.

In a more recent study, female rats were treated during fetal and neonatal development (E19-PND7) with a dose of MXC that is comparable to the dose used in the above studies (100 mg/kg/day) the exposed females displayed similar abnormalities in reproductive parameters as well as in ovarian morphology by adulthood [202]. A close examination of follicle composition showed that developmental MXC treatment did not affect the total number of follicles or follicles at primary and secondary stages in adult females. However, the number of preantral and early antral follicles was increased and the number of CL was reduced, with numerous large cystic follicles. Immunohistochemical staining and quantification of expression patterns of important regulators of ovarian functions revealed that while LHR, CYP11A1, and CYP19A1 levels were reduced, levels of AMH and AR were increased, and levels of StAR and ER $\alpha$  were unchanged [202]. Especially noteworthy was that ER $\beta$  level was unchanged in primary and secondary follicles, yet decreased dramatically in peri-antral stage follicles, which are responsive to gonadotropins. These observations suggest that hormone-responsive follicles are most affected by EDC exposure. These data are also supported by a recent *in vitro* study examining the effect of HPTE on global gene expression in immature rat granulosa cell culture [203]. Treatment with HPTE either upregulates or down-regulates approximately 3–10 times more genes in FSH-stimulated than in unstimulated granulosa cells.

Epigenetic analyses using bisulfite-sequencing PCR and methylation-specific PCR showed that MXC caused hyper-methylation in multiple CpGs in two CGIs in ER $\beta$  promoter sequences while it had no effect on DNA methylation levels in the ER $\alpha$  promoter at PND60 [143]. This finding correlates with the lack of significant effects on the levels of ER $\alpha$  protein in the adult ovary [143;202]. Further analysis has shown that the DNA methylation levels in the promoter regions of these genes were unchanged in neonatal ovaries (PND7) immediately after the exposure (Zama and Uzumcu, unpublished). These data demonstrate the age-dependence/hormone responsiveness of the epigenetic changes, which has also been shown in other tissues (e.g., uteri) with other compounds (e.g., DES, genistein) (see Section 4.3 [204]). The global DNA methylation analysis using AP-PCR showed that there were multiple loci that were hypermethylated in MXC-treated ovaries [143]. The majority of candidates were those encoding transcription factors or ribosomal proteins. One candidate that was shown to be hypermethylated in multiple MXC-treated samples was an endopeptidase encoded by *Pappa* locus (see Section 3.1.6 [143]). Reduced *Pappa* activity due to increased methylation could limit its availability in follicles and thus increase IGFBP content and sequester IGF-1. This could lead to the observed defect in follicle selection and maturation [202]. Interestingly, in the same set of studies, exposure to a low dose of MXC (20  $\mu\text{g}/\text{kg}/\text{day}$ ) caused a significant increase in the expression of AMH [202] and multiple methylation events both in the ER $\beta$  promoter sequences and the *Pappa* locus [143]. There was a significant upregulation in ER $\beta$  expression in the granulosa cells of multiple stages of follicles at PND7, similar to high-dose MXC-treated follicles (Zama and Uzumcu, unpublished). While these epigenetic alterations did not cause any functional defects in the low dose-MXC treated females, the high dose-MXC treated animals had the characteristic ovarian dysfunction.

While the above-mentioned epigenetic analyses and additional *in vivo* studies showing reduced ovulation rate in response to exogenous gonadotropin stimulation in developmentally MXC-treated prepubertal females, suggesting that there are direct effects on the ovary [202], some effects on the HPG axis have also been demonstrated. For example, developmental exposure to MXC alters behaviors in hamster [205] and eliminates or reduces sexually-dimorphic behaviors in mice [206;207]. Although some studies show that treatment with MXC alters GnRH mRNA levels in the POA in adult female rats [208], oral exposure to 1200 ppm MXC during fetal and neonatal periods, did not affect the size of the SDN-POA in the hypothalamus [209]. In contrast, similar oral developmental exposure caused an increase in PR in the POA of adult female rats [210] and altered the number of gonadotropes and lactotropes in the pituitary [211]. More recently, it was shown that MXC exposure during fetal and neonatal periods altered ER $\alpha$  gene expression in the POA in aged (17–18 months) female rats [212]. Importantly, these long-lasting effects suggest an epigenetic mechanism of regulation in the brain as well and warrant further investigation [212].

Uterotrophic effects of MXC are well established [213]. MXC increases uterine wet weight, proliferation and protein secretion [214;215]; these effects have been attributed to its estrogenic actions [117;194;205;216;217;218]. In some cases, MXC can interfere with or differ from the actions of estradiol [193]; this was also reported in other experimental systems [219;220;221]. More recently, it was shown that *in vivo*, neonatal MXC exposure inhibits *Hoxa-10* expression in the adult uterus in mice and interferes with the binding of estradiol to ERE of *Hoxa-10* [222]. Although a potential epigenetic mechanism was suggested, confirmation of this possibility awaits future studies [223].

#### 4.2. Diethylstilbestrol (DES)

DES is a nonsteroidal synthetic estrogen that was prescribed to pregnant women at doses of 5–150 mg/day to prevent miscarriages from 1940s to 1970s [224]). Even though early on

DES was shown to be an ineffective drug, it was continued in use till the 1970s [225]. Numerous abnormalities in the reproductive, cardiovascular, and immune systems have since been reported in both male and female offspring of women treated with DES, and validated in animal models [19;226;227]. There are limited reports that these effects are being observed in the granddaughters of DES-treated women as well [228]. While DES caused vaginal clear cell adenocarcinoma in only 0.1% of the female offspring, over 95 % reported reproductive tract dysfunction and poor pregnancy outcomes [229;230]. Since there is evidence of multi-generational effects, epigenetic mechanisms could play an important role and were therefore investigated: see Section 5 [231;232;233;234].

Mice injected with a single dose of 10 µg/kg DES on E15 and examined at 7 months of age had no CL and numerous atretic follicles [235]. They were also found to have vacuolated interstitial tissue with lipid droplet inclusions. Other studies with varying doses of DES (5 µg/kg to 100 µg/kg) administered either *in utero* (E9-E16) [236], or neonatally (PND1-PND5) [237], demonstrated that adult DES ovaries developed similar hypertrophy and vacuolation of interstitial tissue, hemorrhagic cysts and lack of corpora lutea. These animals also had high levels of testosterone [236]. There was a dose-dependent reduction in the number of the litters as well as the number of oocytes ovulated after stimulation with exogenous gonadotropins [238]. The oocytes derived from such treated ovaries and used in IVF showed lower levels of fertilizability, suggesting reduced oocyte quality [239;240;241]. However, 5 µg/day DES-treated ovaries transplanted into untreated ovariectomized host mice were able to give rise to normal female offspring that in turn gave birth to normal size litters and had normal uterine morphology, suggesting that the DES treatment effects were not mediated via germ cells [242]. However, the age at which these animals were sacrificed was 8–12 weeks, and other studies have shown that DES-treated animals do develop epithelial cancers of the uterus by 18 months of age [233].

DES can bind to both ERs with many fold higher affinity than estradiol [155]. Multiple studies from Iguchi and colleagues showed that *in utero* (E15–18) and neonatally (PND1-5) DES-treated mice had ovaries containing excessive number of MOFs by adulthood [243;244]. MOFs were also observed in ovaries that were treated *in vitro* at PND1-5, following their transplantation to untreated mice, suggesting a direct effect of DES in the ovary [244]. Recent studies showed that neonatal exposure to 3 µg/kg DES induced MOFs, a process mediated by ERβ and not ERα [158]. DES exposure was shown to reduce oocyte apoptosis (potentially suppressing oocyte nest breakdown) via ERβ signaling mechanisms. Furthermore, it was hypothesized that such alterations in the germ cell and somatic cell populations may affect the invasion of pregranulosa cells and basement membrane remodeling during primordial follicle formation [105]. Interestingly, the incidence of MOFs has been reported with other EDC exposures as well (see below, [157]).

The effects of DES on the sexual dimorphism of the brain have been documented. *In utero* and postnatal exposures increased the size of SDN-POA in females thereby defeminizing the region [245]. It was also found that PND1-10 treatment led to a significant reduction in the levels of LH secreted although a similar effect was not found when the exposure was prenatal (E16-20), highlighting the importance of DES actions on the neuroendocrine circuits [246].

It is well known that DES caused T-shaped uteri and clear cell adenocarcinoma of the uterus, cervix, and vagina in women whose mothers were exposed to DES during pregnancy [227]. There are numerous animal studies validating these human reports. For example, progeny of DES-treated mice have shown malformations of the uterus, squamous metaplasia of the luminal and glandular epithelium, endometrial hyperplasia and leiomyomas, and oviductal proliferative lesions [247;248]. Ovariectomized animals when supplemented with

estradiol are able to respond by a transient increase in gene expression and concomitant uterine proliferation and growth [249;250;251]. When such a stimulus is removed, the uterus returns to its unstimulated state. However, when DES or estradiol is administered during neonatal development, expression of immediate early genes such as *lactoferrin*, *EGF*, and proto-oncogenes such as *c-fos*, *c-jun*, and *c-myc* is upregulated even into adulthood [249;252;253]. Inversely, expression of genes that are necessary for uterine development, such as the *Abdominal B (AbdB) Hox* gene, *Hoxa-10*, (known to be controlled by estradiol and progesterone, [254]), *Wnt7a* as well as *Msx2* are repressed leading to structural abnormalities of the reproductive tract [255;256;257;258]. Numerous studies have been conducted to assess the methylation patterns of promoters of several of these estrogen-responsive genes associated with uterine development (see Table 1 for details).

Neonatal DES exposure in mice caused nearly 90% incidence of epithelial cancers of the uterus by 18 months of age [259]. In mice similarly treated with DES, the promoter region of the *lactoferrin* gene was found to be hypomethylated in the adult uterus. However, if the animals were exposed for the same length of time during adulthood, no such methylation or expression defects were observed [260]. Subsequently, it was also found that *exon 4* of the *c-fos* gene was extensively hypomethylated while the promoter region and intron 1 was unaffected, thereby potentially allowing for the upregulation of *c-fos* expression [261]. QPCR studies performed by Sato and colleagues examining the expression of *Dnmts* in neonatally DES exposed C57BL/6 mice, revealed that expression of *Dnmt1* and *Dnmt3b* was decreased at PND5 in DES-treated mice, and the pattern continued until PND14 [262]. Interestingly, it was found that human leiomyoma samples had alterations in the levels of *Dnmts* as well, with concomitant global hypomethylation [263].

As mentioned above, DES down-regulates *Hoxa* gene expression. These effects are akin to those associated with uterine abnormalities found in *Hoxa* KO mice. The predominant phenotype is the loss of boundary between the oviduct and uterus. It has been shown that the anterior to posterior specific pattern of *Hoxa-9* is essential for the normal development and function of the uterus and that DES causes a posterior shift of *Hoxa-9* and *Hoxa-10* expression and homeotic anterior transformations [255]. A recent report by Bromer and colleagues has shown that after *in utero* (E9-16) exposure to 10 µg/kg DES, there is hypermethylation in the promoter and *intron 1* regions of *Hoxa-10* gene, in the caudal part of the uterus with a concomitant increase in the *Hoxa-10* expression in the same region [264]. While these data are interesting from the point of epigenetic regulation of the regionalization of the uterus, the authors suggest that the apparently conflicting data i.e., increased methylation vs increased gene expression might be due to differential binding to transcriptional repressors. Since previous studies have shown that no epigenetic changes were detected in the promoters of *Hoxa-10* and *Hoxa-11* genes [265], continuation of these studies is warranted.

Alworth and colleagues showed that *in utero* exposure (E12-18) of CD-1 mice to DES doses of 0.1–100 µg/kg followed by estradiol administration at 7–8 months of age caused opposite responses between low and high doses. The lower dose enhanced the response to exogenous estrogens, resulting in an increase in uterine weight, while the high dose dampened the response resulting in lighter uteri. A global methylation assay was conducted employing DMH (see Supplemental Material, Section 2.1, Table 1 and Figure 1), which was suitable to detect hypermethylation events. Over 300 CpG island loci were examined and five candidates were identified in 18S rDNA and 45S pre-rDNA methylation, suggesting a role for ribosomal assembly and protein synthesis in the mediation of DES effects [266].

Couse and colleagues have shown that ER $\alpha$  is essential for the mediation of DES effects in the uterus:  $\alpha$ ERKO female mice exhibited a complete resistance to the effects of DES while

$\beta$ ERKO mice did not [267]. Additionally, as mentioned earlier, ER $\alpha$  induction is necessary for activation of estrogen responsive gene expression including that of the *lactoferrin* and *c-fos* genes [249;252;253;268]. Since these genes are all downstream of ER $\alpha$  signaling, it is imperative to thoroughly examine the potential role of epigenetic mechanisms in the regulation of ER $\alpha$  expression after EDC exposure. Interesting new studies by Bredfeldt and colleagues have now provided a link between ER signaling and regulation of histone modifications. It was found that rapid PI3K/Akt signaling downstream of membrane-associated ER, in response to estradiol as well as DES, caused reduction in trimethylation of H3K27 (see Section 2.1.2). More interestingly, activation of this non-genomic signaling caused reprogramming of the uterine gene expression profile [56]. Whether such altered epigenetic mechanisms are transgenerational would be of great interest to the field [269].

### 4.3. Genistein

Genistein is a well-studied isoflavonoid phytoestrogen that is derived from soy products. Phytoestrogens were originally shown to have endocrine disrupting-potential in domestic species: newborn lambs born to ewes fed clover had reproductive abnormalities (in the late 1940s [270]). Soy products are popular since they are a lactose-free substitute for dairy products. Recent reports of low incidence of breast cancer in Asian women and other positive effects on breast cancer risks [271] have further spurred the use and study of soy products. United States FDA has approved 25 g/day soy consumption, approximately equivalent to 75 mg of isoflavones/day (1 mg/kg/day), as being beneficial against coronary artery disease (FDA, 1999). However, a cause for concern is that babies who are fed soy formula consume on average of 6–9 mg/kg body weight, which would result in babies being exposed to 4–7 times higher amounts of soy as compared to adults that are on a soy-rich diet or as per FDA guidelines [272;273]. *In utero* or neonatal genistein exposure has been shown to cause specific reproductive effects in mice. It has also been demonstrated that the estrogenic action of genistein is mediated via ER mediated pathways [154;274].

Neonatal administration of 0.5–50 mg/kg genistein (PND1-5) caused an increase in anogenital distance (masculinization), accelerated puberty, and irregular estrous cycles in adult CD-1 mice [23]. In this context, genistein-treated (50 mg/kg/d) mice exhibited defects in the ovary such as the MOF phenotype, which correlated with a reduction in the number of apoptotic oocytes, previously shown to involve ER $\beta$  mediated actions [103;156;157]. This was also associated with fewer pups born to these females over their shortened reproductive lifespan [275;276]. Genistein and other phytoestrogens have been shown to readily cross the placenta [277] and exposure *in utero* between E15 and E19 has shown similar effects as mentioned above [278]. A most recent report on the oral administration of genistin (the glycosylated form of genistein) revealed that exposure between PND 1 and PND 5 also resulted in ovaries with MOFs, delayed puberty, irregular estrous cycles and reduced litter sizes [279].

Phytoestrogen administration during development has been shown to diminish the size differences of the SDN-POA between males and females [280]. Bateman and Patisaul have reported that a short 2-day neonatal exposure to a 10 mg/kg genistein dose caused an advancement in pubertal age and abnormal estrous cyclicity. Additionally, they showed that there is an impaired ability to stimulate GnRH neuronal activity, suggesting that genistein could cause defeminization of the female HPG axis. It is well documented that neuronal inputs from the Kisspeptin system are able to regulate the GnRH neuronal activity and the coordination of puberty and steroid feedback. AVPV Kisspeptin neurons are more numerous in females than males, and genistein exposure significantly reduced their density in females, thus defeminizing the AVPV [281].

Protection against apoptosis is necessary, since the numbers of neurons are critical for the normal regionalization and function of the nuclei and ERs have been shown to be involved. ER $\beta$  expression is usually down-regulated by estradiol in the PVN; however, it is increased by phytoestrogens [280]. Furthermore, it has been reported that a short neonatal exposure to genistein resulted in ER $\alpha$  and tyrosine hydroxylase (TH) expression changes in the AVPV at PND19. Females had larger AVPV and higher number of TH expressing cells and three times more ER $\alpha$  expressing cells than in males [282]. Overall, studies on the effects of genistein on the expression of various genes involved in the HPG axis have varied depending on the treatment dose and animal species examined, but females generally appear to be more susceptible to its effects [283].

Numerous uterine defects have been documented in CD-1 mice that were neonatally exposed (PND1-5) to genistein (50 mg/kg/day) [23;284;285] supporting epidemiological data from women who were soy-fed as babies that had irregular menstrual cycle lengths and pain during cycles or uterine fibroids [18;286]. A recent paper showed that the oocytes are themselves competent for fertilization and early embryonic development, but the uteri are unable to produce viable implantations: the sites were smaller and fewer in number [287].

Tang and colleagues recently investigated whether neonatal DES/genistein exposure could cause epigenetic changes and alter gene expression in adult uteri and whether there are interactions between adult ovarian hormones and such epigenetic reprogramming. CD-1 mice were exposed to DES (1  $\mu$ g and 1000  $\mu$ g/kg) or genistein (50 mg/kg) from PND1-5. Subsequently, some animals were sacrificed at PND19 while others were aged to 6 and 18 months with or without ovariectomies. Genome-wide methylation analysis was conducted with MSRF and candidate genes were identified. Of interest was the *nucleosomal binding protein 1 (Nsbp1)*, which was shown to be hypomethylated at PND19 and hyper-methylated by puberty, in the control. Low-dose DES- and genistein- treated vs high-dose DES-treated animals had opposing methylation patterns. Furthermore, it was shown that in the aged animals, both DES and genistein caused hyper-methylation in the ovariectomized animals but remained hypomethylated in non-ovariectomized animals. These data suggest that *Nsbp1* is hyper-methylated in intact mice with age and that DES and genistein have opposing effects on the methylation patterns in intact vs ovariectomized aging animals (hypomethylation vs hyper-methylation), respectively. These studies highlighted the age-dependent aspect of epigenetic reprogramming and also its interaction with steroid hormones [204].

#### 4.4. Bisphenol A (BPA)

BPA is a plasticizer used in the manufacture of polycarbonate plastics, to make them clear and hardened and also in the manufacture of epoxy resins (reviewed in [14]). Total worldwide production of BPA exceeds 6 million tons per year. Nearly 95 % of adults that were tested had detectable levels of BPA in their urine (CDC report, [288]). Daily exposure occurs via plastic food containers (especially when heated or microwaved), lining inside cans, baby formula cans, carbonless print paper, and numerous other sources. Infants in neonatal intensive care units have particularly high exposure to BPA, presumably from its use in medical devices and from the migration of BPA into infant formula from the container. It has also been found in detectable amounts in dust [289;290;291;292]. Early studies with BPA showed that it had estrogenic properties and that it is transferred both lactationally as well as transplacentally [13;14]. BPA has a lower binding affinity to ERs than estradiol or DES [155;293]. The “safe” exposure limit for BPA is 50  $\mu$ g/kg/day but studies with lower doses than the “safe” dose demonstrated numerous detrimental defects in the female reproductive system [14].

Perinatal exposure to low environmentally relevant BPA doses (25–250 ng/kg) caused accelerated puberty, altered estrous cyclicity and disrupted ovarian morphology associated with changes in body weight and LH levels [294;295;296]. An increased occurrence of ovarian cysts with blood filled bursae, abnormal numbers of antral follicles, and decreased CL was found in aged mice that were neonatally exposed to a 100 µg/kg dose of BPA [297]. Another study by Adewale and Patisaul [298], demonstrated that exposure of rats to 50 µg/kg and 50 mg/kg doses during the period of hypothalamic neuronal establishment (PND0-3), resulted in a reduction in CL and increase in numbers of MOF and hemorrhagic follicles confirming that BPA has direct effects on the ovary that are independent of GnRH neuronal activity. MOFs were also observed in studies with neonatal BPA exposure (150 µg/kg dose), in mice [299].

Another effect of BPA is exerted at the level of oogenesis and is of very high concern [16]. Studies from Hunt and colleagues demonstrated that BPA released from damaged animal cages and water bottles, which were inadvertently treated with harsh alkaline detergent, induced defects in the meiotic prophase stage of oocyte development in mice: oocytes had increased levels of meiotic aneuploidy due to congression failure. This effect was mimicked when cages were intentionally damaged, or when 20 to 22 day old mice were exposed to a similar dose of BPA (20 ng/g body weight) for as few as 7 days [300]. Further studies demonstrated that BPA caused defects in synapsis and recombination in the homologous chromosomes in the fetal ovary. Interestingly, βERKO animals exhibited very similar meiotic defects in the pachytene oocytes of their fetal gonads. *In utero* treatment of ERKO females with low doses of BPA did not enhance the oocyte defects, suggesting that BPA could act via the ERβ signaling pathway alongside other non-genomic mechanisms [301].

In ArKO mice that were given BPA (0.1 or 1.0% w/w in chow), the ovarian expression of IGF-I, IGF-I receptor, GDF9, and BMP-15 were increased to normal levels, an effect resembling that of ArKO mice given estradiol replacement [302]. These authors further reported that BPA exerted “little effect” within ovarian and other estradiol-dependent tissues of wild-type mice.

BPA (50 µg/kg or lower) had similar effects on the HPG axis as genistein, with AVPV sexual dimorphism being disrupted after a 2-day neonatal exposure to 500 µg BPA [303]. Rubin and colleagues also showed that environmentally relevant doses do indeed have an effect on AVPV neuronal numbers [304]. Other studies showed that BPA exposure altered the HPG axis by precocious hypothalamic–pituitary maturation leading to precocious puberty, altered GnRH pulsatility in neonates and adults, and severe effects on GnRH signaling in the adult pituitary [305]. Interestingly, as mentioned above, Adewale and colleagues [298] have shown that the ovary can be impacted independent of GnRH activity.

In the uterus, neonatal BPA exposure has been shown to cause long-term adverse effects, including cystic endometrial hyperplasia, as well as the occurrence of more serious uterine pathologies such as adenomyosis, leiomyomas (fibroids), atypical hyperplasia, and stromal polyps [297]. Furthermore, paraovarian cysts, progressive proliferative lesions of the oviduct, and cystic mesonephric (Wolffian) duct remnants in the uterus were found in the BPA-treated mice after *in utero* exposure [306].

Similar defects were shown in *in utero* BPA-exposed mice (25 to 250 ng/kg), using Alzet osmotic pumps [296]. Vaginal wet weight was decreased and lamina propria of the endometrium was decreased as well, with concomitant increase in glandular epithelial proliferation at 3 months of age. BPA caused an increase in ERα and PR expression in the lumina typifying a hyper estrogenic response of the uterus. It would be of interest to examine if hypomethylation is associated with such an increase in gene expression. A recent

study by Varayoud and colleagues showed that in an ovariectomized, neonatally BPA or DES exposed mouse model, progesterone priming followed by estradiol treatment caused an impaired proliferative response and altered PR and ER $\alpha$  expression in the sub-epithelial stroma of the uterus suggesting that the uteri were unable to respond to ovarian steroids [307]. In addition, *Hoxa-10* expression was decreased even though methylation of its promoter was unaffected. Furthermore, an abnormal overexpression of the corepressor, silencing mediator for retinoic acid and thyroid hormone receptor (SMRT), was found in the same stromal cells in which *Hoxa-10* expression was reduced. Further epigenetic analyses on BPA-treated uteri are warranted to obtain further clarifications of these interesting studies.

## 5. Transgenerational epigenetic effects of EDCs

Transgenerational epigenetic effects, including those that are induced by EDCs have been discussed in recent reviews [308;309]. Epidemiological studies have suggested that transgenerational epigenetic effects occur in humans. In the Dutch famine of the 1944, not only did the fetuses that were exposed to under-nutrition in utero suffer from cardiovascular or metabolic disorders during their adulthood, but the grand-children also showed a lower birth weight [310]. In an independent study, an association between paternal grandfathers access to excessive food during prepuberty and the occurrence of cardiac disease or diabetes in their grandsons was shown [311]. Although molecular mechanisms remain to be detailed, these observations suggest that effects of environment are transmitted between generations via epigenetic (non-Mendelian) inheritance [312].

For over two decades, scientists have considered the possibility that epigenetic changes in the germline induced by exogenous factors can be inherited [313;314]. Mitotic inheritance of the epigenetic marks was discussed in Section 2.1.1, and meiotic inheritance is described as follows. The epigenetic marks that are transmitted between generations and are described loosely as transgenerational epigenetic effects do not necessarily qualify as 'transgenerational epigenetic inheritance' [308]. The latter involves epigenetic modifications that are transmitted via germline. This distinction is important because the epigenetic marks are cleared between generations with some exception, such as imprinted genes (see below). In order for an transgenerational epigenetic effect to be considered inherited, the germline that gave rise to the affected offspring should not have been exposed to the environmental factors directly [315;316]. When deciding whether a transgenerational epigenetic effect is inherited, the following criteria have to be fulfilled: the exposure specifically targets the germline, and if it does not, the exposure should occur before or during germ cell lineage specification [317] It was proposed that epigenetic inheritance is less commonly observed in mammals as compared to other organisms (e.g., plants) because the germ cells are specified much earlier in mammalian development. Thus, an event that may affect the embryo may not necessarily affect the germline [317].

### 5.1. General observations of transgenerational epigenetic effects

There are well-established examples of transgenerational inheritance of epigenetic patterns in some animal models [318] and plants [319]. In mice, results from studies at loci with metastable epialleles, such as viable yellow agouti ( $A^{vy}$ ) and axin fused ( $Axin^{fu}$ ) [318;320;321], show epigenetic transgenerational inheritance. The  $A^{vy}$ , which is one of the best-studied examples of metastable epialleles and is at agouti (A) locus. *Agouti* gene is normally expressed in skin and gives the normal coat color of agouti mice. In the  $A^{vy}$  allele, a transposon, intracisternal A particle (IAP) is inserted into the regulatory region of the gene, whose methylation status determines the expression level of the gene and gives variation of coat color ranging from complete agouti (pseudo-agouti) to yellow coat color [318]. The methylation of IAP silences the gene leading to pseudo-agouti and the lack of

methylation leads to expression, and in turn yellow coat color. These alterations in the coat color are also associated with the overall health of the animals with pseudo-agouti being healthy and yellow being obese, diabetic, and susceptible to tumor development. Recent experiments have shown that both nutrients and EDCs (i.e., genistein or BPA) that these animals are exposed to during their development *in utero* affect the methylation status of IAP and hence the health of the mice [322;323]. The relevant feature of these isogenic mouse strains to transgenerational epigenetic effect is that the epigenetic phenotype of the mother is a determinant of the epigenetic phenotype of the offspring. Thus, the epigenetic marks on the IAP are not erased during meiosis in the female germ cells but are inherited [318]. In plants, a similar type of inheritance has been observed for numerous loci for multiple generations [308]).

In humans, increased familial risk of colorectal cancer was linked to epimutations of tumor suppressor genes (see [324] for details). In addition, the abundance of transposons in the genome, lead one to speculate similar transgenerational epigenetic inheritance in humans [325]. However, given the outbred nature of humans, it would be nearly impossible to rule out the role of genetics in such transgenerational effects [326].

## 5.2. Transgenerational epigenetic effects associated with EDC exposures

Documentation of the transgenerational epigenetic effects of EDCs has been accumulating such as the case of transgenerational effects of DES exposure reported in humans [228]. Exposure to DES while *in utero* was shown to affect the female F2 generation but not males in mice [231]. Later studies with DES exposure showed that it leads to reproductive tract tumors in both F2 generation males and female mice [232;233]. Exposure to vinclozolin and MXC during *in utero* testis development (E8-15) was shown to affect sperm parameters and testis function; these effects were transmitted through the male germline up to the four generations and were associated with DNA methylation alterations in the F2 and F3 generations [87]. Additional pathologies in other organ systems (e.g., kidney and prostate) were observed in 17–50% of the males [327]. Furthermore, F3 males displayed reproductive behavior and anxiety problems [328;329]. However, milder pathologies (e.g., uterine bleeding and anemia) with a much weaker occurrence rate (6.5–8.6%) were observed in F1-F3 females when both parents were exposed to the EDC, but not when only one parent was exposed [330]. The reasons for lower penetrance and a requirement for both parents exposure in females can be because the timing of the exposure and establishment of genomic imprinting varies between males and females (see Section 3.1.1). To be most effective, the treatment for females should include *in utero* as well as early postnatal life, when the epigenetic reprogramming of female germ cells takes place (Figure 2). Alternatively, if the demethylation process could be influenced by EDCs, an exposure during this period should affect both males and females.

More recently, two research groups reported a failure to observe transgenerational effects of vinclozolin [331;332]. However, another study demonstrated the transgenerational (F2 and F3 generation) effects of vinclozolin on imprinted genes in sperm (see below, [333]). The discrepancy between these studies can be due to differences in the route of exposure or in sub-strains of animals used in the studies [309]. Other EDCs were also reported to cause transgenerational epigenetic effects. For example, perinatal exposure to BPA can induce gene expression alterations in testicular steroid receptor co-regulators [334]. More recently, transgenerational epigenetic effects of phthalates in the gonad and dioxins in the uterus were also reported [335;336].

### 5.3. Potential mechanisms of transgenerational epigenetic effects

In mammals, transgenerational epigenetic effects of EDCs can be potentially transmitted via multiple mechanisms, including histone proteins [269], and RNA [348] as well as DNA methylation. Here, we focus on DNA methylation.

DNA methylation alterations in different DNA sequences can be transmitted via (1) imprinted genes, (2) parasitic DNA sequences, and (3) imprinted-like sequences.

1. **Imprinted genes.** In the mammalian genome, approximately 1% of the autosomal genes are imprinted (i.e., expressed from only one parental allele). Genomic imprinting refers to the epigenetic form of gene regulation that involves DNA methylation in an allele-specific manner established in the gametes [28]. Genomic imprinting plays an important role in normal development and growth, and a disturbance of the genomic imprinting has been shown in developmental disorders such as Beckwith-Wiedemann and Prader-Willi/Angelman syndromes [337], and cancer [338]. One of the well-studied imprinted gene sets is *Igf2* and *H19*, located on mouse chromosome 7 [339]. *Igf2* is expressed from the paternal allele, and *H19* is expressed from the maternal allele. This expression pattern is regulated by differential methylation that is established in a gender-specific development period (see Section 3.1.1); the methylation status of the differentially methylated region is shared between these two genes [340]. A disturbance during the imprinting process can affect the germ cells of F1 individual in a sex-specific manner, and the effect can be transmitted to the F2. Due to the epigenetic reprogramming of the germline, DNA methylation changes are less likely to be transmitted beyond F2. However, in the recent vinclozolin study, the effects of vinclozolin are reported on several imprinted genes, including *H19*, through the F3 generation [333]. Although effects on imprinted genes are reduced in F3, they did not completely disappear [333], suggesting a mechanism that makes EDC-induced changes are resistant to the germline epigenetic reprogramming and requires further investigation.
2. **Parasitic DNA sequences.** During the erasure and establishment of methylation patterns in imprinted genes [341], parasitic DNA sequences such as retrotransposons (e.g., LINE-1 and IAP) remain mostly methylated [89;342]. Even a minor disruption of methylation patterns of these sequences can lead to a broad spectrum of abnormalities ranging from metabolic disorders to cancer [325;343;344]. As in the case of viable yellow agouti mice, these sites can be altered by estrogenic EDCs such as BPA [323] or genistein [345]. Since these sites remain altered during epigenetic reprogramming, the changes can be transmitted to the next generation.
3. **Imprinted-like DNA sequences.** It was proposed that EDC exposure could generate imprinted-like DNA sequences [346]. Since these sequences are not normally set for reprogramming, the changes on them may not be corrected between generations and thus may be transmitted to the F3 generation and beyond, but further studies are needed to test this hypothesis.

## 6. Conclusions and future directions

Data from the reviewed studies collectively suggest that perinatal EDC exposure affects adult ovaries and female reproductive tissues, leading to reproductive dysfunction, supporting the DoHAD concept. In addition, these effects are mediated primarily by steroid hormone receptors, especially the ERs: via ER $\beta$  in the ovary and ER $\alpha$  in the uterus and perhaps both in the hypothalamus and pituitary [143;156;157;202;267]. Furthermore, most of the EDCs discussed in this article lead to MOF (a potential precursor to premature

ovarian failure), with the process being mediated by ER $\beta$  agonistic actions [158]. On the other hand, EDCs with ER $\beta$  antagonistic actions showed inhibitory effects on follicular maturation, and also lead to reduced fertility in females.

An emerging theme from these animal studies is that perinatal EDC exposure can cause epigenetic alterations, and these can be modified by later hormone stimulation. Studies have confirmed that the proliferative response to can be modulated by endogenous hormones. Furthermore, hypomethylation of ER-responsive genes are closely tied to the process of overexpression of proto-oncogenes and thereby carcinogenesis [349]. Some studies suggest that ERs are themselves epigenetically modified after EDC exposure [143]. Cancer epigenomic studies have already demonstrated a role for ERs in the proliferation and progression of tumors in human cancers. For example, increased ER $\beta$  gene expression and decreased DNA methylation were observed in endometriotic tissues as compared to normal endometrial tissues [350]. Hyper-methylation and reduced gene expression of ER $\beta$  were also observed in breast and prostate cancers [351;352;353;354].

It is also clear that low doses of EDCs have effects on the epigenetic signature of a tissue, which may not necessarily translate into physiological changes in the exposed animals [143]. Studies using mixtures of EDCs show that while the dose of a given EDC may not have any obvious effects when used alone, it becomes effective when in mixtures [24]. Humans are exposed to mixtures of EDCs over their lifetime, and it is quite possible that they may accumulate numerous patterns of epigenetic alterations and yet be asymptomatic until an additional stressor is applied, at which time the symptoms become apparent. Validating such a hypothesis in a biologically relevant model system is critical.

Current epigenetic analysis methods used for discovering new genes in this area include MSRF and AP-PCR which have relatively low coverage (Table 1). Although results from these methods provided valuable “proof-of-principle” type of information, more comprehensive methods of analysis are needed for a better understanding of the broader effects of EDCs. For example, Tang and colleagues showed that neonatal DES and genistein exposures with or without ovarian steroid exposure caused vastly different epigenotypes of the *Nsbp1* gene, which in turn resulted in alterations in its gene expression in aged animals [204]. These authors used MSRF to identify the targets. Earlier studies by Li and coworkers used the bisulfite-sequencing technique for examining individual uterine genes after DES exposure [349]. The genes examined in the latter studies, *c-fos* and *lactoferrin*, were not identified as candidates using the MSRF technique. Similarly, bisulfite-sequencing of the ER $\beta$  promoter in MXC-treated ovaries showed that it was hypermethylated. However, ER $\beta$  was not among the candidates discovered by AP-PCR analysis [143]. Distribution of RE-digestion sites may be a limiting factor since they may not be ubiquitous. Therefore, use of targeted array-based technologies to identify entire pathways is warranted. Now, with a combination of deep sequencing after ChIP (ChIP-seq) or bisulfite treated DNA on targeted arrays or immunoprecipitated DNA on targeted arrays, we can identify the exact methylation changes within a resolution of 2–3 bases. These new approaches can be used to determine epigenetic alterations across time (neonatal to pubertal to aged animals) and across dose (ranging from environmentally relevant low doses to high doses). Once pathways are identified, comparisons can be drawn across estrogenic EDCs as to whether they are relative in terms of estrogenic effects or specific to the particular EDC. A case in point are data from microarray analyses that show that different doses of estrogens result in completely different sets of genes that were up- or down-regulated, suggesting a non-monotonic effect [266;355;356]. To further test such a hypothesis, for example, that all ER responsive gene pathways are epigenetically modified by a particular EDC, collaborative multi- lab, multi-platform, and multi-tissue studies would have to be conducted. Biobanking of samples that are appropriate for purposes of various analyses from multiple tissues would be necessary.

Biomarker panels can be developed for diagnosis of past exposures at perinatal and pubertal periods so that potential risks can be assessed for preventative and therapeutic purposes. The demonstration that epigenetic changes can be reversed with nutrient supplementation, such as with the *A<sup>vy</sup>* mice, has been an important step in the field. However, can this be applicable to reversing or preventing epigenetic alterations induced by developmental EDC exposure?

There are a few reports as to the effects of EDCs transmitted to subsequent generations by the male germline, however very little is known about the female germline in such instances. In addition, the role of epigenetic mechanisms that are affected by the EDC exposures and importantly, the quality of the oocytes from such exposures need to be closely examined. If such effects do exist, the public health risk would be enormous. Future studies are likely to bring fruitful discoveries with an ultimate goal of using the obtained information for improving public health.

## Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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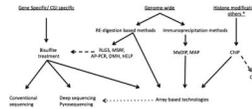
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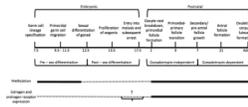


### Figure 1. Techniques available to examine epigenetic mechanisms

Bisulfite treatment and conventional sequencing is the most common approach to obtain gene-specific CpG methylation status. Genome-wide analyses are necessary for identification of networks/pathways that are potentially altered. Combinations of restriction enzyme (RE) digestions at methylation sensitive sites or the immunoprecipitation of methyl cytosine residues followed by genomic arrays or high throughput sequencing alongside chromatin immunoprecipitation (ChIP) assays have given rise to a wide range of choices. See Supplemental Material online for details.

Abbreviations: RLGS, restriction landmark genomic scanning; MSRF, methylation sensitive restriction fingerprinting; AP-PCR, methylation sensitive arbitrarily-primed PCR; HELP, HpaII tiny fragment enrichment by ligation-mediated PCR; DMH, differential methylation hybridization; MedIP, methylated DNA immunoprecipitation; MAP, methyl binding domain affinity purification, and QPCR, quantitative real-time PCR. \* See [357] for details of techniques used in microRNA analysis.

Validation methods: broken lines; Optional steps: dotted line.



**Figure 2. Timeline of ovarian development in mice**

The main stages of ovary development and function are shown. See text for details. After early embryonic lineage specification, germ cells proliferate and become sexually differentiated in mid-gestation. During these stages, the germ cell genome is methylated (thick line), with demethylation (dotted line) occurring after migration. Epigenetic reprogramming is sex-specific and remethylation events (thick line) occur postnatally in the ovary. The expression of estrogen and androgen receptors is at low levels or absent (dotted line) embryonically and increases (thick line) from early postnatal stages. ? - further studies are needed. Timeline is not to scale.

Table 1

ic analyses of effects of EDC exposures

Dose	Species	Treatment period	Age and tissue examined for epigenetic alterations	Loci analyzed	Techniques used	Observed epigenetic effect	Gene expression changes	Reference(s)
20 µg/kg/day or 100 mg/kg/day	Rat	E 19 – PND 7	PND 60, ovary	Whole genome, ERα and ERβ	AP-PCR, bisulfite sequencing	Hypermethylation of multiple loci, promoter region of ERβ, no alterations in methylation of ERα	Reduced expression of ERβ, no change in ERα	[143]
1 mg/kg/day	Rat	PND 5 and PND 10-12	1, 6, 12 hrs after treatment, uterus	EZH2*	Immunoprecipitations, immunohistochemistry	Increase in PI3K/Akt signaling and EZH2 levels	Reduced H3K27Me3 trimethylation	[56]
1 or 1000 µg/kg/day	Mouse	PND 1-5	PND 19 and 6 and 18 months, uterus	Whole genome, <i>Nsbpl1</i> *	MSRF, Bisulfite sequencing	<i>Nsbpl1</i> hypermethylation at puberty, hypomethylation in DES-exposed older animals	Reduced expression of <i>Nsbpl1</i> at puberty, persistent overexpression in DES- exposed older animals	[204]
2 µg/pup/day	Mouse	PND 1-5	PND 17, 21, 30, uterus and DES-induced uterine tumors, at 6 months	<i>lactoferrin</i>	Bisulfite sequencing	Hypomethylation of promoter	Persistent overexpression of <i>lactoferrin</i>	[260]
1–100 µg/kg/day	Mouse	E 12-18	7–8 months, uterus	Whole genome	DMH	Hypermethylation of ribosomal DNA	Increase in uterine weight	[266]
2 µg/pup/day	Mouse	PND 1-5	PND 17- 60, uterus	<i>c-fos</i>	Bisulfite sequencing	Hypomethylation of <i>exon-4</i>	Persistent overexpression of <i>c-fos</i>	[261]
3 µg/pup/day	Mouse	PND 1-5	PND 5, 14, 30	<i>Dnmt3</i>	QPCR, RLGS	Lower levels of <i>Dnmt3</i> at PND 5 and 14, aberrant DNA methylation at PND 30	Both hypo and hyper methylation observed in 10 genomic loci	[262]
2 µg/pup/day	Mouse	PND 1-5	PND 5, 30 and 18 months, uterus	<i>Hoxa-10</i> <i>Hoxa-11</i>	Bisulfite sequencing	No change at PND 5 or 30. Significant hypermethylation only at 18 months in DES-induced uterine carcinomas	Repression of <i>Hoxa-10</i> and <i>Hoxa-11</i> expression	[265]
10 µg/kg/day	Mouse	E 9- 16	PND 14	<i>Hoxa-10</i>	Bisulfite sequencing	Regionalized hypermethylation in the uterus	Decreased expression in the cranial uterus and increase in the caudal region	[264]
50 mg/kg/day	Mouse	PND 1-5	PND 19 and 6 and 18 months, uterus	Whole genome, <i>Nsbpl1</i> *	MSRF, Bisulfite sequencing	<i>Nsbpl1</i> hypermethylation at puberty, hypomethylation in genistein- exposed older animals, reversal by ovariectomy	Reduced expression of <i>Nsbpl1</i> at puberty, persistent overexpression in genistein- exposed older animals	[204]
0.05 mg/kg/day, 20 mg/kg/day	Mouse	PND 1, 3, 5, and 7	PND 60	<i>Hoxa-10</i>	Bisulfite sequencing	No change	Decreased <i>Hoxa-10</i> expression and increased SMRT*	[307]

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\* EZH2- histone methyl transferase enhancer of Zeste homolog 2; *Nsfp1*- nucleosomal binding protein 1; SMRT- silencing mediator for retinoic acid and thyroid hormone receptor. See Figure 1 for detailed abbreviations of techniques used.