

## Development of the Mammalian Female Reproductive Tract

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**The female reproductive tract (FRT), which includes the oviduct, uterus, cervix and vagina, is critical for mammalian reproduction. Recent research using genetic knockout mice has contributed substantially to our understanding of the molecular mechanisms governing FRT development. Aside from satisfying our curiosities about the origin of life, these studies have provided us with a better understanding of FRT disorders and ways to improve female fertility. Here we review genes that are involved in various stages of sexual duct formation and development in mammals. In addition, the effect of exogenous estrogen such as DES on FRT development is also discussed.**

**Key words:** DES, Müllerian duct, uterine adenogenesis, uterus, Wolffian duct.

### Müllerian and Wolffian duct formation

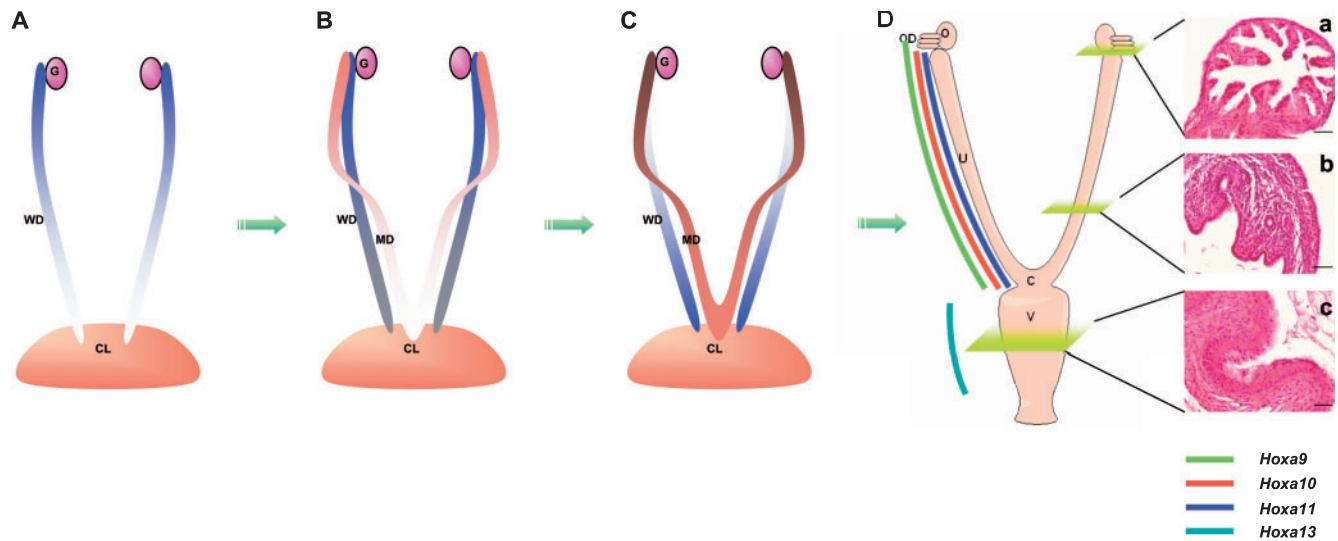
The mammalian sex is determined genetically. Individuals with an X and a Y chromosome normally develop as males, whereas those with two X chromosomes develop as females. However, up to a specific stage during embryonic development, embryos of either sex are indistinguishable. In mammals, the urogenital system originates from the intermediate mesoderm. In the mouse, the male reproductive tract develops from the mesonephric duct (a.k.a. the Wolffian duct) by embryonic day 9.5 (E9.5), and can be distinguished from the surrounding mesonephroi as a solid rod. It grows caudally and fuses with the ventrolateral cloacal wall, which gives rise to the future bladder. The paramesonephric duct (a.k.a. the Müllerian duct), giving rise to the majority of FRT, develops in parallel to the Wolffian duct around E11.5 and reaches the cloaca by E13.5 (1). This stage is the aforementioned sexually indifferent stage, as embryos possess both male and female reproductive duct primordials. Subsequently, in male embryos, the Müllerian duct degenerates, whereas the Wolffian duct differentiates into epididymis, vas deferens, seminal vesicles and ejaculatory ducts. In female embryos, however, the Wolffian duct regresses and the Müllerian duct differentiates into oviduct, uterus, cervix and upper one-third of vagina (Fig. 1).

A number of genes have been identified to be essential for FRT development. Among them, *Lim1*, *Pax2*, *Emx2* and *Wnt4* are indispensable for the early steps of Müllerian duct development. *Lim1* (*Lhx1*), encoding a LIM-domain containing transcription factor, plays an essential role in mouse head and urogenital system development (2, 3). *Lim1* has a dynamic expression pattern in the Müllerian duct as early as E11.5, suggesting that *Lim1* function is crucial for the initial formation of the Müllerian duct. Although most *Lim1*-null embryos die at mid-gestation due to defects in allantois differentiation, some do survive to birth. Analysis of *Lim1*-null neonates revealed that Müllerian duct derivatives were completely

absent. Furthermore, no Wolffian duct derivatives were ever observed in *Lim1*-null neonatal males, demonstrating that *Lim1* is required for the formation of both sexual ducts (3). *Pax2*, a member of the *Pax* gene family, possesses a highly conserved paired box which encodes a 128 amino acid DNA binding domain at the N-terminus, termed the Paired domain (4). Nine *Pax* genes have been identified in both mouse and human, and knockout of each gene in the mouse resulted in developmental abnormalities (for review, see Ref. 5). In addition to defects in ear, eye, and brain, *Pax2*-null neonates also lack kidneys, ureters and genital tracts in both males and females (6–8). Unlike in *Lim1*-null embryos, both the Wolffian and the Müllerian ducts initially form in *Pax2*-null mutants, but later degenerate. This phenotype correlates with *Pax2* expression at this stage in both reproductive tracts on E13.5, indicating a cell-autonomous role for *Pax2* in the developing Wolffian and Müllerian ducts (8). Another homeobox gene, *Emx2*, a mammalian homologue of the *Drosophila empty spiracles*, is also expressed in the epithelial component of the intermediate mesoderm. *Emx2*-/- mutants completely lack the urogenital system, including kidneys, ureters, gonads and genital tracts (9). The Wolffian duct forms in *Emx2* mutant embryos on E10.5, but subsequently degenerates on E11.5. In contrast, the Müllerian duct never forms in these mutants. *Emx2* expression is only detected during early stages of Wolffian and Müllerian duct formation (9). These results suggest that this gene is only required in a specific time period during development of the intermediate mesoderm, possibly providing a survival signal.

The mammalian *Wnt* genes are homologues of the *Drosophila* segment polarity gene *Wingless*. They encode secreted signaling glycoproteins that influence multiple processes during development (for review, see Ref. 10). *Wnt4*-null females exhibit a complete loss of FRTs, whereas male mutants appear normal (11). This phenotype is simply due to failure of Müllerian duct formation in both sexes. Up to E11, *Wnt4* expression is detected in the mesenchyme of gonad and mesonephros in both sexes. Subsequently, its expression is downregulated in male gonads but maintained in female gonads. Similarly,

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**Fig. 1. A schematic representation of FRT development in the mouse.** A, on E9.5, Wolffian ducts are readily distinguishable from the surrounding mesonephroi and are growing caudally. B, Müllerian ducts grow in parallel to Wolffian ducts at around E11.5 and reach the cloaca by E13.5. At this time, the embryo possesses both the male and female reproductive tract primordials regardless of its genetic sex. C, in females, Wolffian ducts start to degenerate in the absence of androgen, while Müllerian ducts develop in the absence of

anti-Müllerian hormone. D, eventually Müllerian ducts differentiate into oviduct, uterus, cervix and upper part of vagina. *AbdB* like *Hox* genes have a nested expression pattern along the A-P axis of the FRT, as illustrated in D. Panels a–c in D, H&E staining of oviductal, uterine and vaginal sections showing morphological differences among the epithelia. G, gonad; WD, Wolffian duct; CL, cloaca; MD, Müllerian duct; OD, oviduct; U, uterus; C, cervix; V, vagina. Scale bars = 50  $\mu$ m.

its expression was no longer detected in the developing Wolffian duct, but continues to be strongly expressed in the mesenchyme of the newly formed Müllerian duct, indicating a requirement for *Wnt4* during the initial stages of FRT morphogenesis (11). Despite these recent exciting discoveries, we still know very little about the nature of the signal(s) that triggers the formation of both sexual ducts from the mesonephric mesenchyme. Future research building on existing mutants may shed light onto this process if upstream regulators and downstream targets of these genes can be identified. Meanwhile, in *Emx2* mutant intermediate mesoderm, *Lim1*, *Pax2* and *Wnt4* are abnormally expressed, whereas *Pax2* expression is abolished in that of *Lim1* mutants, demonstrating the emergence of a genetic pathway in the formation of sexual ducts (9, 12).

### Regression of the Müllerian duct in males

As mentioned earlier, mammalian embryos undergo a sexual indifferent stage in which both male and female reproductive tract primordials are present. Since the degeneration of the Müllerian duct requires the presence of male hormones, it is widely accepted that female development is the default pathway. In male embryos, the sex determining region Y gene (*Sry*) is sufficient to induce testis differentiation and subsequent male reproductive tract development (13). *Sry* is an HMG box containing transcription factor (14). It is believed that *Sry* functions by inducing the expression of Müllerian Inhibiting Substance (MIS, a.k.a. anti-Müllerian hormone, AMH), secreted by the sertoli cells in the testis (15). *MIS* mutant males exhibit normal testis morphology and function. Nevertheless, ovaries as well as the FRTs persist in these mutants which perturb sperm transfer leading to male infertility (16). Molecularly *MIS* expression is regulated

by an array of transcription factors, including GATA factors, nuclear receptor subfamily 0 group B member 1 (Nr0b1, a.k.a. *Dax1*), nuclear receptor subfamily 5 group A member 1 (Nr5a1, a.k.a. *Sf1*), SRY-box containing protein 9 (*Sox9*) and Wilms tumour homologue (*WT1*) (for review, see Ref. 17). *MIS* encodes a glycoprotein that shows homology to the transforming growth factor beta (TGF $\beta$ ) superfamily members. Like most other members of the TGF $\beta$  superfamily, full activation of *MIS* requires a proteolytic cleavage near its C-terminus.

TGF $\beta$  superfamily ligands transmit their signals by binding to a heterodimeric receptor complex consisted of a type I and a type II TGF $\beta$  receptors. Upon ligand binding, the type II receptor, like other serine/ threonine kinase receptors, recruits and phosphorylates the type I receptor which in turn phosphorylates downstream targets (18). The *MIS*-specific type II receptor (*Misr2*) has been identified and cloned in many species (19–22). Its expression was detected in the mesenchyme surrounding the Müllerian duct at E13.5 when regression of the Müllerian duct begins. *Misr2*-deficient males exhibit the same phenotype as *MIS* mutant males, indicating that *MIS* uses *Misr2* exclusively for its signal transduction (22). Natural mutations in *MIS* and *MISR2* genes have also been reported in patients of Persistent Müllerian Duct Syndrome, a rare form of male pseudohermaphroditism (23, 24). In the case of the type I receptor for *MIS*, recent studies showed that activin A receptor type 1 (*Acvr1*, a.k.a. *Alk2*) has a spatial and temporal expression pattern overlapping with that of *Misr2* perfectly in the developing Müllerian duct mesenchyme. Furthermore, *in vitro* cell culture experiments confirmed that *Acvr1* is required for *MIS* signaling, suggesting that it could be one of the type I receptors for *MIS* (25). However, this has not been proven in knockout mice due to early

lethality of *Acr1*-null embryos (25). Generation of an *Acr1* conditional knockout mouse in the Müllerian duct mesenchyme should be able to demonstrate its *in vivo* relevance in MIS signal transduction. Meanwhile, conditional ablation of bone morphogenetic protein receptor type 1A (*Bmpr1a*, a.k.a. *Alk3*) in the developing Müllerian duct mesenchyme using the *cre/lox* system revealed that it could also serve as the type I receptor for MIS (26). In *Bmpr1a* conditional knockout male embryos, *MIS* and *Misr2* expressions are preserved. However, these mutant male neonates still possess oviduct and uterus, indicating that *Bmpr1a* is required in the MIS signaling pathway (26).

Although little is known about the downstream targets of MIS signaling cascades, a few candidates have been proposed. The most promising one is matrix metalloproteinase 2 (*Mmp2*) (27). *Mmp2* has a sexually dimorphic expression pattern during embryogenesis, which is no longer maintained in *MIS*-deficient mice. Inhibition of *Mmp2* in organ culture blocked Müllerian duct regression. On the other hand, activation of *Mmp2* led to Müllerian duct regression in a ligand-independent manner (27). Taken together, *Mmp2*, and may be other members of the *Mmp* family, possibly functions downstream of MIS signaling pathway to mediate Müllerian duct degeneration.

One of the upstream signals regulating *Misr2* expression is *Wnt7a*, which is critically required for the development of reproductive tracts in both sexes. *Wnt7a*-null mice of either sex are infertile, due to persisted Müllerian duct in mutant males and abnormal differentiation of the oviduct and uterus in mutant females (28). The direct cause of persisted Müllerian duct in *Wnt7a*-deficient males is the absence of *Misr2* expression in these mutants. The regulation of *Misr2* expression by *Wnt7a* is thought to be mediated through the canonical *Wnt* pathway and requires the presence of functional  $\beta$ -catenin (29). Transcriptionally, *Misr2* is directly regulated by *Sf1*, suggesting multiple roles played by *Sf1* during male sex differentiation (30). In addition,  $\beta$ -catenin and transcription factor 4 (TCF4) are also required for regulation of *Misr2* by *Sf1* (29).

### Patterning and cytodifferentiation of the Müllerian duct

In female mice, the Wolffian duct regresses due to the absence of male hormones which are necessary for its maintenance. The Müllerian duct proliferates and differentiates rostral-caudally, forming the oviduct, uterus, cervix and upper part of vagina, which is completed by two weeks after birth. During this time, the single-layered Müllerian duct epithelium differentiates into distinct morphologies along the anterior-posterior (A-P) axis of the FRT. For example, the uterine epithelium is composed of simple columnar epithelial cells, whereas stratified squamous cells make up epithelia of posterior cervix and vagina. Classical tissue recombination experiments demonstrated that this differential cell fate determination along the A-P axis requires reciprocal interactions between the epithelium and the underlying mesenchyme (31). The fate of FRT epithelial cells is determined between postnatal days 5 to 7 by cues from the underlying

mesenchyme while some developmental plasticity remains in a subset of epithelial cells for even longer (32).

Homeobox genes encode a family of transcription factors sharing a highly conserved 61 amino acid helix-turn-helix domain, termed the homeodomain. In mammals, *Hox* genes are expressed in a temporally and spatially colinear pattern during organogenesis which provides positional information along several body axes (for review, see Ref. 33). In the developing Müllerian duct, a number of posterior *AbdominalB Hox* genes were found to be expressed in nested patterns along the A-P axis (34, 35). In the case of *AbdB Hoxa* genes, anterior limit of *Hoxa9* expression was detected in the future isthmus region of the oviduct, with that of *Hoxa10* at the uterotubal junction. *Hoxa11* is strongly expressed in the uterus and less intensively in the cervix, whereas *Hoxa13* is expressed only in the cervix and upper vagina (35). Targeted mutagenesis of these genes results in region-specific defects along the FRT. *Hoxa10* deficiency causes homeotic transformation of the anterior part of the uterus into oviduct-like structure and reduced fertility in females (36). Homeotic transformation of the reproductive tract also exists in male *Hoxa10* mutants (36). *Hoxa13* null embryos show agenesis of the posterior portion of the Müllerian duct (37). As mentioned earlier, the molecular cues from the mesenchyme induce the differentiation of Müllerian duct epithelium. While the nature of these stromal signals is not clear at present, swapping the homeodomain of *Hoxa-11* with that of *Hoxa-13* resulted in the expression of a hybrid *Hox* protein in the uterine stroma and subsequent stratification of the uterine epithelium, suggesting that the stromal signals are likely controlled by *Hox* proteins (38). In response to such stromal signals from the cervix and vagina, epithelial expression of *p63*, a homologue of the *p53* tumor suppressor gene, is induced and is thought to be an identity switch in the differentiation of Müllerian duct epithelium (39).

*Wnt7a*, which has been shown to influence Müllerian duct regression, also plays an important role at later stages of FRT cytodifferentiation (28, 40). *Wnt7a*-deficient females show dramatic posterior transformation of the reproductive tract, in which oviducts are absent and uterus exhibits a cytoarchitecture typical of vagina. Molecular analysis showed that expression of *Hoxa10* and *Hoxa11* was reduced in the mutant uterine stroma, suggesting that *Wnt7a* is required to maintain uterine-specific *Hox* gene expression (40). In addition, *Wnt7a* may also be involved in radial axial patterning since *Wnt7a* mutant myometrium is highly disorganized (40). *Wnt5a*, another member of this growth factor family, is also critical for FRT development (41). *Wnt5a*-deficient females have coiled and shortened uterus and poorly defined cervix and vagina. Genetic analyses revealed that *Wnt5a* resides in an genetic pathway with *Wnt7a* and *AbdB Hoxa* genes during FRT development (41).

### Gland formation in the uterus

Endometrial glands are present in the uterus of all mammals. The main biological function of uterine glands is thought to secrete and transport nutrients, termed histotroph, important for embryo implantation and fetal development. In most mammals, uterine gland develop-

ment (also termed uterine adenogenesis) occurs postnatally and the timing is highly species-specific. In rodents, epithelial invagination is first seen on P5, and mature glands can be detected by P15 (42), whereas in ungulates, the process begins right after birth (P0) and is completed by P56 in sheep and by P120 in pigs, respectively. In humans and other primates, however, this process begins *in utero*, continues after birth and glands reach histological maturity at puberty. Typical uterine adenogenesis includes epithelial invagination, bud formation and tubulogenesis, followed by further branching morphogenesis. Unlike primates and ungulates, rodent uterine glands do not undergo extensive coiling and branching morphogenesis, resulting in a simpler, less coiled and branched structure (42, 43). In rodents, at least two known critical proteins, leukemia inhibitory factor (*Lif*) and calcitonin, are exclusively produced by uterine glands. Perturbation of rat uterine calcitonin expression by antisense oligonucleotides during early pregnancy severely affected implantation, resulting in a reduced number of implanted embryos (44). *Lif* is a downstream target of the endogenous estrogen, 17 $\beta$ -estradiol (E2), during pregnancy. *Lif*-null female mice are infertile due to failure of blastocyst invasion and stromal decidualization (45). These results indicate that endometrial glands are essential for successful pregnancy in mammals. The cellular and molecular mechanisms governing uterine adenogenesis are not fully understood. However, several lines of evidence implicate that epithelial-mesenchymal interactions, tissue remodeling factors, steroid hormones and their receptors, and prolactin are involved in this process.

Again, Wnt signaling is important in uterine gland formation. *Wnt7a* is expressed exclusively in the uterine luminal epithelium (LE) and in invaginated LE but not in glandular epithelium (GE), suggesting that *Wnt7a* may play a role in uterine adenogenesis. In contrast, *Wnt5a* is mainly expressed in the uterine stroma during postnatal development. Both *Wnt7a* and *Wnt5a* mutant uteri fail to form uterine glands indicating that Wnt signaling is essential for uterine gland formation. Moreover, recombinant grafts of wild-type stroma and *Wnt5a* mutant epithelium successfully formed glands whereas the reverse recombination failed, indicating that *Wnt5a* is required in the stroma for gland development (40, 41).

Uterine gland development also involves endometrial tissue remodeling. MMPs and their tissue inhibitors (TIMPs) have been shown to be key regulators of branching morphogenesis in various organs (46–48). Consistently, three TIMPs (TIMP-1, -2, and -3) are expressed in the uterus and TIMP-1 knockout mouse exhibits accelerated endometrial gland formation (46, 49). In addition, MMP-2, -10, -11, -14, and -23 are all expressed at high levels in the developing uterus with MMP-9 at a lower level. However, other TIMP and MMP knockout mice do not exhibit impaired uterine gland formation, which may be the result of functional redundancy (50). Future experiment examining uterine adenogenesis in compound genetic mutants is necessary to reveal the function of these proteins in uterine gland formation.

Insulin-like growth factors (IGFs) are multifunctional regulators involved in various biological processes (51). The temporal and spatial expression of IGF1 and several members of IGF-binding proteins have been character-

ized in the developing rat uterus (52). Loss of IGF1 in mice leads to a dramatic hypoplastic uterine phenotype demonstrating its critical role in uterine growth and differentiation (53). Studies in ovine uterus revealed that the highest level of IGF1 and IGF2 mRNA is present in the area surrounding the nascent and proliferating glandular epithelium, whereas IGF1R mRNA is most abundant in luminal and glandular epithelium, suggesting that IGF-mediated epithelial-mesenchymal interactions might be critical for uterine gland development (54).

Numerous studies in lab rodents and ungulates have shown that postnatal development of uterine glands does not depend on ovary and hormones. Yet abnormal exposure to steroid hormones during critical period of postnatal uterine development can severely affect uterine adenogenesis (55–57). In ewe lambs, a distinct uterine gland knockout (UGKO) model was generated by neonatal exposure to a synthetic progestin for as short as eight weeks from birth, which completely abolished uterine adenogenesis (42, 58, 59). The mechanism for this phenotype may involve suppression of estrogen receptor- $\alpha$  (ER- $\alpha$ ) expression, as treatment with an ER- $\alpha$  antagonist also inhibited adenogenesis in neonatal pig uterus (42, 59, 60). However, ER- $\alpha$  knockout mouse uterus develops glands albeit at a reduced number, suggesting that ER- $\alpha$  may not be required for the initiation of uterine adenogenesis but is probably required for GE differentiation (42, 61, 62). Prolactin (PRL) is another important player in uterine adenogenesis. In ewes, PRL is present in the serum from P1, peaks on P14, and declines thereafter until the whole process is complete. Expression of PRL receptor (PRL-R) is restricted to nascent glandular epithelium on P7 and to proliferating GE (63, 64). Treatment with PRL from P0 to P56 increased uterine gland number, whereas treatment with a PRL inhibitor bromocriptin decreased gland number in ewe lambs (64). These results support the idea that PRL positively regulates uterine gland development. However, the molecular mechanism whereby PRL regulates uterine adenogenesis is still not fully understood. A couple of studies indicated that MAPK signaling cascade and JAK/STAT signaling cascade may be involved in this event (65, 66).

### DES-induced reproductive tract phenotypes

Diethylstilbestrol (DES) is the first synthetic estrogenic compound orally administered to pregnant women from 1947 to 1971 in an effort to preserve pregnancy. Despite controlled studies in the 1950s showing no protective effect of DES towards pregnancy, this drug was continually prescribed to pregnant women in the United States and elsewhere in the world for another two decades. During that time at least four million pregnant women and their fetuses were exposed to DES in the United States alone (for review, see Ref. 67). In the late 1960s, eight young women 15–22 years of age were treated in Boston for clear cell adenocarcinoma of the vagina, a rare tumor usually occurring in women over 50 years old (68). Since then, *in utero* exposure to DES has been associated with reproductive tract anomalies such as T-shaped uterus, vaginal adenosis, extensive ectropion, annular cervical rings and clear cell adenocarcinoma in female humans (69, 70). In males who were exposed to DES in utero, cryptorchidism, hypospadias,

Table 1. Genes involved in FRT development and phenotype of the reproductive tract in their mutants.

Gene	Knockout phenotype in reproductive tract	Reference
<i>Lim1</i>	Absence of derivatives of Müllerian duct	(3)
<i>Pax2</i>	Absence of entire FRT	(8)
<i>Emx2</i>	Absence of derivatives of Müllerian duct	(9)
<i>Wnt4</i>	Absence of derivatives of Müllerian duct	(11)
<i>MIS</i>	Persistence of Müllerian duct derivatives in male mutants	(16)
<i>Misr2</i>	Same as MIS-null mice	(22)
<i>Alk3</i>	Oviduct and uterus in male mutants	(26)
<i>Hoxa10</i>	Homeotic transformation of the anterior part of the uterus into oviduct-like structure	(36, 37)
<i>Hoxa11</i>	Hypoplastic uterus, reduced gland number	(74, 75)
<i>Hoxa13</i>	Agenesis of the posterior portion of the Müllerian ducts	(37)
<i>P63</i>	Persistence of columnar epithelium at lower genital tract sites that normally undergo squamous and urothelial differentiation.	(76)
<i>Wnt7a</i>	Absence of oviducts and uteri exhibiting a cytoarchitecture typical of vagina; failure to form uterine glands	(28, 40)
<i>Wnt5a</i>	Coiled and shortened uterus and poorly-defined cervix and vagina; failure to form uterine glands	(41)
<i>Lif1</i>	Failure of blastocyst invasion and stromal decidualization	(45)
<i>IGF</i>	Dramatic hypoplasia of the uterus	(53)
<i>TIMP1</i>	Accelerated endometrial gland formation	(46)
<i>ER<math>\alpha</math></i>	Hypoplastic uteri, nonovulatory ovaries and reduced gland number	(61, 62)

microphallus, testicular hypoplasia and epididymal cysts were found to be associated with DES exposure. DES has a binding affinity for ER- $\alpha$  that is much higher than that of 17 $\beta$ -estradiol (71). Thus it is believed that DES is not readily metabolized in the placenta and therefore can function as a strong estrogen. The establishment of a mouse model for DES-induced reproductive tract defects has made substantial contributions to study the teratogenicity of DES (72). DES also induces pleiotropic defects along the developing mouse FRT. Oviductal malformations include loss of the uterotubal junction, paraovarian cysts, and developmental arrest of the oviduct. Uterine malformations include stratification of the uterine epithelium, delayed adenogenesis, reduced gland formation and stromal layer, and disorganized muscle layers. Defects in cervix and vagina include abnormal presence of glands in the vaginal fornix (vaginal adenosis), abnormal uterine openings in the vagina (persistent urogenital sinus), and failure of distal Müllerian ducts to form a common cervical canal (72). These phenotypes resemble those observed in various *Hoxa* single and compound mutant and *Wnt7a* mutant FRTs. Indeed, *Hoxa-10*, *Hoxa-11* and *Wnt7a* are all repressed by DES in the developing uterus during critical developmental period of FRT patterning offering a possible molecular basis for DES teratogenicity. Our recent studies showed that developmental DES exposure alters uterine epithelial cell fate and induces abnormal epithelial differentiation. A number of stratified epithelial markers were found ectopically expressed in the uterine epithelium (73). Moreover, several additional developmental control genes were also identified.

In summary, although investigations into reproductive tract development began centuries ago, it is not until recent decades that more molecular mechanisms underlying this process have been uncovered owing to the rapid development of modern molecular genetics. This article has reviewed some of the most important factors in this process. Table 1 lists a subset of these genes knockout of which produces defects in reproductive tract development. However, we are still not certain how these genes

assemble into a genetic pathway to orchestrate a complicated and highly organized reproductive tract developmental process. Future research should be concentrated on identifying additional players and elucidating cross-talks between different genetic pathways.

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