

Review

Genetics of early mammalian folliculogenesis

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Abstract. Early ovarian folliculogenesis begins with the breakdown of germ cell clusters and formation of primordial follicles. Primordial follicles are the smallest ovarian follicle units continuously recruited to grow into primary and more advanced ovarian follicles. Genes expressed in the germ cells such as *Figla*, *Nobox*, *Kit* and *Ntrk2*, as well as genes expressed in the surrounding so-

matic cells such as *Foxl2*, *Kitl* and *Ngf*, play critical functions during early folliculogenesis. Transgenic mice continue to provide important insights into the genetic pathways that regulate early mammalian folliculogenesis. Genes critical in early folliculogenesis are important determinants of reproductive life span and represent candidate genes for human ovarian failure.

Key words. Folliculogenesis; primordial follicle; primary follicle; germ cell clusters.

Introduction

A founder population of approximately 45 primordial germ cells (PGCs) at embryonic day 7 post conception (E7.5) gives rise to the germ cell lineage in the mouse [1, 2]. During mouse embryonic development from E9.5 to E11.5, the primordial germ cells migrate from the proximal epiblast to the urogenital ridge to form germ cell clusters also called cysts [3, 4]. Mitotic division of primordial germ cells, coupled with incomplete cytokinesis, results in clusters of oocytes around E10.5. Circa E13.5, female germ cells begin entry into the prophase I of meiosis and arrest in the diplotene stage of the first meiotic division. Oocytes arrested in meiosis I remain arrested until the time of ovulation. Mouse germ cell clusters, formed in the embryonic gonad, often contain more than 8 oocytes per cluster and break down shortly after birth as primordial follicles form (fig. 1). Primordial follicles consist of oocytes less than 20 μm in diameter individually enveloped by flat somatic cells, sometimes called pre-granulosa cells. Primordial follicles occupy the rim of the ovary with more advanced follicles located cen-

trally. By postnatal day 7, most of oocytes in the mouse ovary are present in the primordial follicles with few germ cell clusters remaining. Around day 3 after birth, primary follicles appear in the mouse and consist of oocytes larger than 20 μm enveloped by somatic cells that are now cuboidal in shape. Primary follicles grow into larger secondary follicles, and ultimately become antral follicles, where oocytes reach a diameter of approximately 70 μm and are surrounded by highly differentiated granulosa cells.

The breakdown of germ cell clusters and formation of primordial follicles represents a critical stage in ovarian development. Transcription of numerous oocyte-specific genes is initiated, genes that are important in folliculogenesis, such as *Gdf9*, as well as maternal effect genes that affect two cell stage embryos such as *Zar1* [5–7]. Oocyte numbers decline after birth, although controversy exists whether the decline begins within the embryonic ovary or after birth [2, 4]. Regardless, not all oocytes within the germ cell clusters are thought to become primordial oocytes, and it is unclear why some become primordial oocytes and others die. The dogma has been that the ovary is endowed with finite number of oocytes, resting in primordial follicles. The primordial oocytes are continu-

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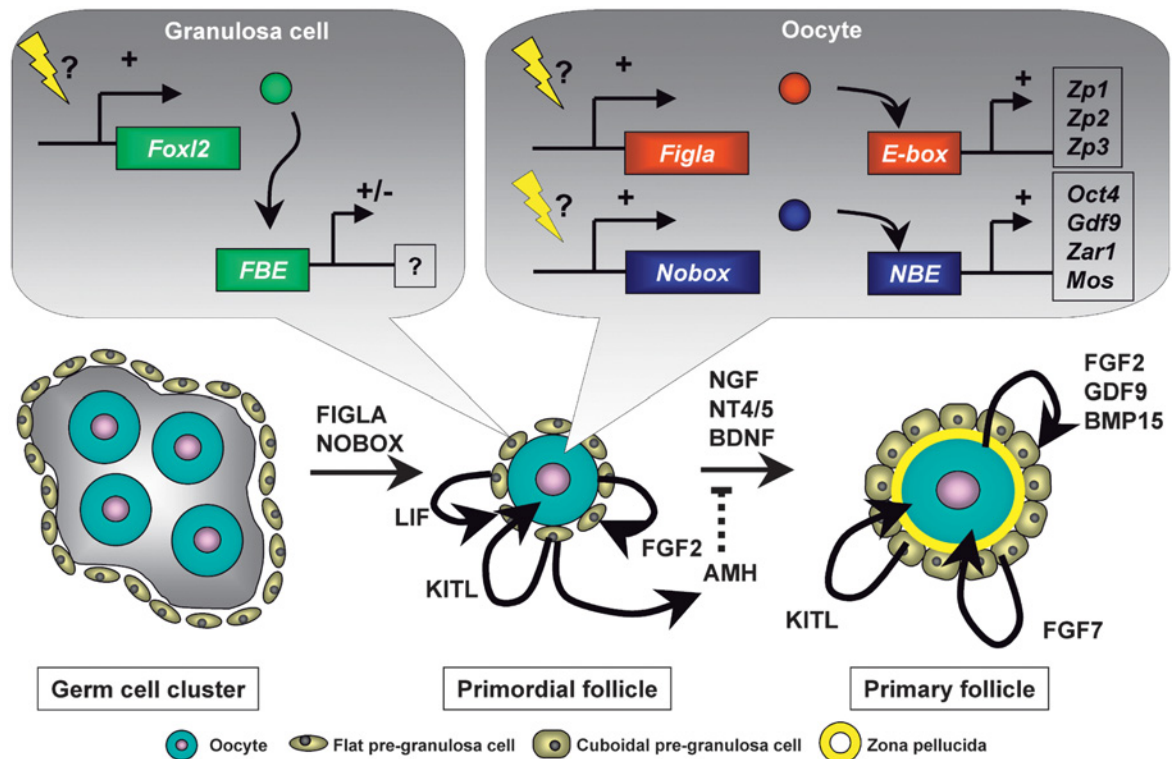


Figure 1. Genes that are important in the formation of primordial and primary follicles. The follicle structures involving the oocyte, zona pellucida, granulosa and theca cells are shown. Cell-to-cell interactions are mediated by KITL, FGF2, FGF7, GDF9, BMP15, NGF, NT4/5, BDNF, AMH and FOXL2. Transcriptional regulations are controlled by FIGLA and NOBOX. NBE is a putative NOBOX binding element. It is unknown whether NOBOX exerts direct or indirect action on *Oct4*, *Gdf9*, *Zar1* and *Mos*. FBE is a putative FOXL2 binding element. *Figla* and *Nobox* are expressed in the oocytes of germ cell clusters, primordial and more advanced follicles.

ously recruited to develop into more advanced follicular types. Since the vast majority of oocytes die during the recruitment, germ cell depletion in the ovary ultimately leads to menopause. Preliminary data suggest the existence of germline stem cells in the ovaries [8, 9]. The location of these germline stem cells is unclear, and more studies are necessary to ascertain their existence and physiologic relevance.

Follicle stimulating hormone beta, follicle stimulating hormone receptor and gonadotropin releasing hormone deficient mice can develop follicles that are beyond the primordial follicle stage, and therefore gonadotropins are not essential for early folliculogenesis [10–15]. Local factors produced by somatic and germ cells appear to play critical roles in early folliculogenesis. We will review here what is known about the molecular mechanisms of early folliculogenesis with an emphasis on knowledge derived from transgenic mouse models.

Factor in the germline alpha (*Figla*)

Factor in the germline alpha (FIGLA) is a basic helix-loop-helix transcription factor discovered in a screen to identify transcription factors that bind zona pellucida (*Zp*)

promoters [16]. Mouse *Figla* is expressed as early as E13.5 in the female gonad, and appears exclusively confined to oocytes of germ cell clusters and throughout folliculogenesis. Although *Figla* is also expressed at low levels in testis, only female *Figla* knockout mice are infertile. The deficiency of *Figla* does not affect germ cell migration or proliferation, and embryonic gonads appeared normal [17]. However, oocytes rapidly disappeared after birth, and primordial follicles did not form. *Figla* was the first germ cell-specific transcription factor shown to affect primordial follicle formation. FIGLA can bind a promoter motif called E-box (CANNTG), located approximately 200 bp upstream of transcription start sites of the zona pellucida (*Zp*) proteins, and interacts with the ubiquitous transcription factor E12 [16]. *Zp1*, *Zp2* and *Zp3* are major components of the extracellular zona matrix that surrounds the developing oocytes, and zona pellucida proteins are required for fertilization. Individually, *Zp1*, *Zp2* and *Zp3* mouse knockouts can form primordial through antral follicles [18–20]. It is not known whether the triple knockout for the *Zp* genes disrupts early folliculogenesis. *Figla* deletion does not affect the transcription of other genes preferentially expressed in the oocyte, including growth differentiation factor 9 (*Gdf9*), bone morphogenetic protein (*Bmp15*), kit receptor (*Kit*), connexin 43

and fibroblast growth factor 8. All these findings suggest that FIGLA likely regulates the expression of other downstream target genes that are critical in early folliculogenesis. Moreover, continual expression of *Figla* throughout folliculogenesis suggests that it is required to sustain transcription of its target genes that may be critical both in folliculogenesis and early embryogenesis.

Newborn ovary homeobox gene (*Nobox*)

Newborn ovary homeobox protein (NOBOX) is another germ cell-specific transcription factor critical in early folliculogenesis. *Nobox* was originally discovered by *in silico* subtraction of expressed sequence tags (ESTs) derived from the newborn ovaries [21, 22]. *Nobox* expression is detectable as early as E13.5, although its expression is significantly higher in E15.5 embryonic ovaries and beyond [23]. *Nobox* RNA and protein are preferentially expressed in oocytes of germ cell clusters and in primordial and growing oocytes throughout different stages of folliculogenesis [21, 23]. *Nobox* deletion causes postnatal oocyte loss and abolishes the transition from primordial to growing follicles in mice [23]. Newborn ovary histology in *Nobox* knockout and wild-type mice is grossly similar, but differs significantly at the molecular level. Numerous genes preferentially expressed in the oocytes, including *Gdf9*, *Bmp15*, *Mos* and *Oct4*, are downregulated in oocytes that lack *Nobox*. *Nobox* therefore directly or indirectly regulates transcription of critical oocyte-specific genes. The onset of molecular changes in the *Nobox* knockout ovaries is likely to occur in the embryonic gonad, and microarray analysis of knockout and wild-type embryonic gonads at different times during the development will be useful. *Nobox* deficiency did not significantly affect expression of all oocyte-specific genes. *Figla*, *Zp1*, *Zp2*, and *Zp3* were similarly expressed in the *Nobox* knockout and wild-type newborn ovaries. Whether FIGLA directly regulates *Nobox* is unknown.

Transcriptional regulators upstream of *Figla* and *Nobox* are currently unknown, but their discovery will help better understand molecular pathways that govern germ cell development in mammals and hopefully shed a light on genes necessary to establish a female germline. It is likely that multiple other, yet unknown, oocyte-specific transcription factors are involved. Moreover, the role of others, such as *Pou5f1* (POU domain, class 5, transcription factor 1, *Oct4*), needs to be clarified. *Pou5f1* is expressed throughout folliculogenesis and is detectable in primordial oocytes, but its role in early and later folliculogenesis is unclear.

Kit-ligand (*Kitl*) and kit receptor (*Kit*)

Kit ligand (KITL) and Kit receptor (KIT) were originally found by studying mutations of the *steel* (*Sl*) and *domi-*

nant white spotting (*W*) loci in mice, respectively. The mutation at both alleles causes various deficiencies in pigmentation, hematogenesis as well as defects in germ cell migration and proliferation [24–29]. The *Sl* locus encodes a growth factor, kit ligand (*Kitl*), and the *W* locus encodes the kit receptor, *Kit* [30–36]. KITL was the first granulosa cell-derived growth factor that can directly stimulate theca cell growth in the bovine ovary [37]. Theca cells in human fetal ovaries do not stain for KIT and the role of KITL in human theca cell growth is therefore unclear [38]. KITL is also known in the literature as steel factor [26], stem cell factor [39], and mast cell factor [40]. Alternative splicing generates two membrane-bound forms of kit ligand, KITL1 and KITL2, and it is not clear whether the two forms have different effects in early folliculogenesis [26]. *Kitl* messenger RNA (mRNA) is present as early as E9.5 in the fetal ovary and continues to be expressed in the ‘pre-granulosa’ and granulosa cells throughout folliculogenesis [41–43]. KITL signals through its receptor, KIT, which is a member of the family of type III transmembrane tyrosine kinase receptors. *Kit* expression becomes detectable in germ cells from E7.5, but is not detectable between E13.5 and E15.5, at the time when female germ cells enter meiosis [44]. *Kit* is expressed in the oocytes of primordial and growing follicles [37, 41–43].

There are 45 phenotypic alleles in the *Kitl* locus, and 87 phenotypic alleles in the *Kit* locus. Phenotypes differ depending on the mutation in the *Kitl* allele. The *Sl^{fl}* allele infertility results from the deficiency of the germ cells in the ovary [45]. The *Sl^{pan}*, *Sl^{con}* and *Sl^l* mutant females have defects in postnatal ovarian follicle development [46–48] that affect early folliculogenesis. KITL addition to *in vitro* culture of the 4-day-old rat ovaries accelerates the transition from the primordial-to-primary follicles [49]. This effect is slight but statistically significant [49]. The importance of the KITL in primordial-to-primary follicle transition was demonstrated by using antibodies (ACK2) against KITL [49, 50]. ACK2 did not affect primordial follicle formation *in vitro* and *in vivo* but blocked primordial-to-primary follicle development [50]. These results implicate KITL in the primordial-to-primary follicle transition, but the role of KITL in the breakdown of germ cell clusters into primordial follicles is not clear.

Anti-Müllerian hormone (*Amh*)

The dimeric glycoprotein anti-Müllerian hormone (AMH) is a member of the transforming growth factor-beta (TGF β) superfamily known also as Müllerian-inhibiting substance (MIS). AMH was originally found in degenerating Müllerian (female) ducts during male sexual differentiation [51]. *Amh* is also expressed in the mesenchymal cells adjacent to the epithelium of somatic and

granulosa cells of the fetal and adult female gonads [52–55]. AMH and its receptor AMHR2 are postnatally present in the granulosa cells of primary and growing follicles of the ovary in mice [51, 53, 56–60]. AMH appears to be the only natural ligand of the AMHR2 receptor, as the phenotype of *Amh* and *Amhr2* null mice are indistinguishable from each other in contrast to the diverse signaling pathways of other TGF β gene family signaling pathways [61]. Female *Amh* null mice are fertile and have normal litter size [52]. However, the ovaries from 4-month-old and 13-month-old *Amh* knockout mice contained significantly less primordial follicles than corresponding wild-type mice [62]. AMH may have an inhibitory effect on follicle growth by attenuating the sensitivity of ovarian follicles to FSH in the sexually mature ovary [63]. *In vitro* experiments with postnatal day 2 mouse ovaries treated with AMH [59] showed fewer growing follicles, and these experiments support claims that AMH inhibits the growth of primordial follicles. The experiments above appear to exclude the possibility that AMH deficiency negatively affects the total number of female germ cell endowment in the embryonic ovary. It is interesting that this is exactly what occurs in mice that overexpress human *Amh* under the control of the mouse metallothionein promoter. *Amh* over-expressing mice are infertile, contain fewer germ cells in the ovary at birth and lose germ cells within 2 weeks of birth [64]. The molecular mechanisms whereby overexpression of *Amh* leads to the rapid loss of germ cells remain unclear. It is possible that overexpression of *Amh* at an inappropriate time during folliculogenesis has a dominant negative effect on other TGF β family members that in turn disrupts folliculogenesis. AMH may have dual functions in folliculogenesis: one that regulates the number of germ cells during embryogenesis, and the other that controls the size of the growing follicle pool by affecting the rate of recruitment.

Forkhead box L2 (*Foxl2*)

Forkhead box L2 (FOXL2) is a member of the forkhead (FKH)/hepatocyte nuclear factor 3 (HNF3) gene family of transcription factors [65]. The FKH/HNF3 family of transcription factors contains a conserved winged helix domain important for DNA binding to a common DNA motif in the promoter of target genes. Forkhead transcription factors bind to a 7-bp DNA binding motif (G/A) (T/C) (C/A) A A (C/T) A [66–70]. Mutations in the *Foxl2* gene cause type I blepharophimosis ptosis epicanthus inversus syndrome (BPES) and type II BPES in humans [65]. Unlike type II BPES, type I BPES women present with premature ovarian failure.

In mice, *Foxl2* is preferentially expressed in the pre-granulosa cells within the ovary [71, 72]. Ovaries of *Foxl2* null mice contain oocytes surrounded by flat granulosa cells

[73, 74], but no advanced follicular structures are present. *Foxl2* deficiency aborts the proliferation of granulosa cells as well as the transition of flat squamous cells that surround primordial oocyte to cuboidal granulosa cells that surround primary oocytes. FOXL2 targets are not known. The deficiency of *Foxl2* has no effect on the expression of other oocyte-specific genes such as *Figla*, *Gdf9* and *Kit*, but the expressions of *Activin* β A and *Amh* were reduced in the ovaries of *Foxl2* null mice [59, 60, 75–77]. FOXL2 binding DNA motif is present upstream of the steroidogenic acute regulatory (*Star*) gene [78]. FOXL2 repressed the activity of the *Star* promoter, and engineered dominant negative mutations within *Foxl2* abolished wild-type FOXL2 repression activity of *Star in vitro*. *Star* may be a direct downstream target for *Foxl2*. *Star* is expressed in steroidogenic tissues, including granulosa and theca cells of the ovary, and plays a role in mobilization and delivery of cholesterol precursors to the inner mitochondrial membrane. However, derepression of STAR activity in *Foxl2* mice probably does not disrupt early follicle formation, and a more comprehensive search for FOXL2 downstream targets that affect early folliculogenesis is necessary.

Neurotrophins and their receptors

Neurotrophins have a wide-ranging role in the development of both the nervous system and the development of non-neuronal systems, including the cardiovascular, endocrine, reproductive and immune systems [79]. Nerve growth factor (NGF) is one of the neurotrophins, and the neurotrophin family includes brain-derived neurotrophic factor (BDNF), neurotrophin 3 (*Ntf3*) and neurotrophin 5 (*Ntf5*). *Ngf* expression in the somatic cells and oocytes of the ovary precedes follicle formation [80–84]. Neurotrophin receptors *Ngfr* (*p75*), *Ntrk1* (*trkA*), *Ntrk2* (*trkB*) and *Ntrk3* (*trkC*) are all expressed in the oocytes as well as the somatic cells of the ovary [81, 85–87]. Ovarian expression of *Ntf5* and its receptor *Ntrk2* was increased, *Ngf* and its receptor *Ntrk1* mRNA expression was reduced, whereas *Ntf3* and *Ntrk3* (*trkC*) mRNAs did not change at the time of early folliculogenesis [81]. These findings suggest that each neurotrophin and its respective receptor play different roles in the proliferation and differentiation of somatic cells as well as early folliculogenesis.

The role of neurotrophins and their receptors has been examined in transgenic knockout mice. *Ngf*-deficient ovaries contain a reduced number of primary and secondary follicles and an increased number of oocytes enclosed within the germ cell clusters in the ovary [88, 89]. In addition, the proliferation of somatic cells was reduced in the ovaries of *Ngf*-deficient mice compared with wild-type mice. These results suggest that NGF plays a role in the formation of follicles by affecting differentiation of

flat squamous cells, which surround primordial oocytes, into cuboidal pre-granulosa cells that surround primary oocytes. The reduction in the number of secondary follicles indicates that GDF9 and KITL may interact with NGF to induce proliferation and differentiation of somatic cells surrounding the oocyte. NGF signals through the tyrosine kinase receptors *Ngfr* and *Ntrk1*. These two receptors are expressed in the ovaries of wild-type and *Ngf* null mice [88]. The lack of *Ngfr* does not affect the formation of primordial, primary or secondary follicles, and *Ngfr* null mice are fertile [90]. *Ntrk1* deficiency causes death at or shortly after birth [91, 92]. The function of these receptors in the ovary remains unclear and conditional, ovary-specific knockout of *Ntrk1*, will be useful to assess *Ntrk1* contribution to early folliculogenesis. It is also possible that NGF signals through receptors other than NGFR and NTRK1.

Ntf5 and BDNF, the other two neurotrophins, preferentially signal through NTRK2 receptors. Mice deficient in both *Ntf5* and *Bdnf* have a significantly lower number of primary and secondary follicles compared with wild-type [89, 91, 93]. *Ntrk2* null mice suffer from neurologic deficits and die within the first week of life. As expected, if *Ntrk2* functions as a preferential receptor for *Ntf5* and *Bdnf*, *Ntrk2*-deficient seven-day-old ovaries contained a reduced number of secondary follicles [93], and the block appeared to be in the transition from primary to secondary follicles, partially reminiscent of *Gdf9* null ovaries [94, 95]. The presence of *Gdf9* and *Kitl* in *Ntrk2* null ovaries suggests that *Ntf5* and *Bdnf* may affect the transition of primary into secondary follicles by a different pathway. Quantitative reverse-transcription polymerase chain reaction (RT-PCR) shows that the expression of follicle-stimulating hormone receptor (FSHR) was significantly reduced in *Ntrk2* null mice as compared with wild-type mice, but this may be just a reflection of the decreased number of secondary follicles in *Ntrk2* null ovaries.

Ntrk2 null ovaries were also transplanted under the kidney capsule to study postnatal ovarian development, and these studies showed rapid loss of oocytes in *Ntrk2* null ovaries. Neurotrophins clearly play an important role in nonneuronal targets, and alongside *Gdf9* and *Kitl*, are critical in early stages of folliculogenesis through unknown molecular mechanisms. Use of conditional, ovary-specific knockouts will be very useful to study the effects of neurotrophins and their receptors in mouse models affected by perinatal lethality.

Growth differentiation factor 9 (*Gdf9*) and bone morphogenetic protein 15 (*Bmp15*)

Growth differentiation factor 9 (GDF9) and bone morphogenetic protein 15 (BMP15, also known as GDF9b) are members of the transforming growth factor- β superfamily

[5, 6, 96, 97]. *Gdf9* and *Bmp15* are preferentially expressed in oocytes [6, 97]. In mice, *Bmp15* null females are subfertile, with decreased ovulation and fertilization rate and normal gross histologic appearance of the ovary [98], while *Gdf9* null female are infertile, and follicle growth arrests at the primary follicle stage [94]. *Gdf9* and *Bmp15* do not appear critical in the formation of primordial follicles, and *Gdf9* in mice is essential for the growth and differentiation of the surrounding granulosa cells [95, 99, 100], antral follicle growth and ovulation [101-104]. The subtle phenotype in *Bmp15* knockout mice was surprising.

However, the importance of BMP15 in ovarian function was shown in the study of Inverdale and Hanna sheep, which carry naturally occurring missense and nonsense mutations in the *Bmp15* coding region [105, 106]. These mutations increase fertility in the heterozygotes but cause infertility in homozygotes [105]. Interestingly, the ovarian phenotype in *Bmp15* sheep mutants is phenotypically similar to that in *Gdf9* null mice, but not in *Bmp15* null mice. The *Bmp15* deletion mutation engineered in mice causes null phenotype and no adverse effects on GDF9 action, while nonsense and missense mutations in sheep are likely to cause dominant negative effects on GDF9 action [107, 108]. It would be of great interest to generate mutant mice that carry sheep mutations and study whether such mutations will disrupt rodent folliculogenesis. The dominant negative role of *Bmp15* mutations in granulosa cell signaling may also account for infertility in humans [109]. Two female siblings of an Italian family had primary amenorrhea, ovaries that lacked follicles, a normal 46 XX karyotype, and no evidence of autoimmune disease or consanguinity. A search for candidate genes revealed a mutation in the human BMP15 that involved an A-to-G transition at nucleotide 704, changing a tyrosine (Y) at position 235 to a cysteine (C). The mutant Y235C protein was unable to stimulate incorporation of ^3H -thymidine into human granulosa cells, and it also inhibited wild-type BMP15 ability to stimulate ^3H -thymidine incorporation into granulosa cells. In sheep, mutated BMP15 likely act in a dominant negative manner to block GDF9. When sheep were immunized with GDF9 peptide, BMP15 peptide or ovine BMP15 mature protein, normal follicular development was arrested at the transitory or primary stage [110]. Above experiments clearly indicate that GDF9 and BMP15 are important in follicular growth in mice, sheep and humans.

Fibroblast growth factor 2 (*Fgf2*)

Fibroblast growth factor 2 (FGF2) is a member of a family of fibroblast growth factors. *Fgf2* is involved in cell differentiation, migration and angiogenesis in many tissues [111, 112]. *Fgf2* is primarily localized in the oocyte of primordial and growing follicles as well as the granulosa cells in the ovary [113-116]. FGF2 receptor is de-

tected in granulosa cells surrounding the ovary [117, 118]. FGF2 can induce an increase in the transition of primordial to growing follicles in FGF2-treated rat ovaries [114], and antibody against FGF2 slightly decreased follicle development. FGF2 can stimulate the growth of theca and stroma cells. Ovaries treated with FGF2 appear to express higher levels of *Kitl* mRNA [119]. These observations suggest that one function of oocyte-derived FGF2 may be to increase granulosa-derived *Kitl* expression, and that both KITL and FGF2 are required to optimally promote primordial-to-primary follicle transition. Furthermore, FGF2 suppresses apoptosis in granulosa cells [120]. Therefore, FGF2 produced by the oocyte in early follicles appears to regulate a variety of ovarian functions, including cell growth, development of the primordial follicles and stabilization of the follicle. *Fgf2* knockout mice are viable and fertile [121], although detailed examination of *Fgf2* knockout ovaries has not been reported.

It would be of interest to examine more closely the reproductive function in *Fgf2* null mice, since subtle fertility defects may be missed. In addition, these mice may be useful to identify which growth factors may compensate *in vivo* for the lack of *Fgf2*.

Fibroblast growth factor 7 (*Fgf7*)

Fibroblast growth factor 7 (FGF7, also known as keratinocyte growth factor, Kgf) is like FGF2, a member of the fibroblast growth factor family. *Fgf7* was originally found as a human mitogen with preferential action in the epithelial cells, and plays an important role in mesenchymal stimulation of normal epithelial cell proliferation [122, 123]. FGF7 mediates mesenchymal-epithelial cell interactions in many tissues including the ovary [124, 125], placenta [126], bladder [127], hair follicle [128], stomach [129], lung [130, 131], ventral prostate [132], and seminal vesicle [133]. *Fgf7* mRNA is detected in thecal cells, and its receptor is expressed in granulosa cells in the ovary [124, 134]. FGF7 produced by thecal cells stimulates proliferation of granulosa cells during follicular development in the ovary [125]. Primordial-to-primary follicle transition was increased from 45% to 65% with the addition of FGF7 to the 4-day-old rat ovary organ culture system [135]. FGF7 may act as a mesenchymal factor that promotes primordial-to-primary follicle development. However, *in vivo* knockout data to support this view is lacking. *Fgf7* knockout mice display abnormal hair development but no mention is made with regards to fertility [128].

Leukemia inhibitory factor (*Lif*)

Leukemia inhibitory factor (LIF) is a multifunctional glycoprotein cytokine. LIF is produced in blastocysts [136]

and several tissues including the uterus [137, 138], thymus and lung [139], hypophysis [140], cardiac muscle [141], kidney [142], and in the skin [143]. LIF signals through its heterodimeric membrane receptor composed of a low-affinity LIF-specific receptor and the gp130 receptor chain [144]. LIF is present in follicular fluid, and its levels rise around the time of ovulation, indicating that LIF may play a role in ovulatory events, embryonic development and implantation [138, 145–149]. LIF protein is detected in the granulosa and somatic cells of primordial and primary follicles in the mouse ovary [150]. Exogenous treatment of the 4-day-old rat ovaries with LIF increased the primordial-to-primary follicle transition relative to the unstimulated controls [150]. Like FGF2, LIF treatment increased expression of *Kitl* mRNA in cultured granulosa cells, but LIF did not affect the proliferation of granulosa cells. These studies suggest that LIF may indirectly play a role in promoting the transition of primordial-to-primary follicles through induction of *Kitl* expression. *Lif* knockout mice are viable and fertile [147, 151], although detailed examination of ovaries lacking LIF has not been done.

In vitro effects observed on the primordial-to-primary follicle transition with LIF and other growth factors may not be relevant *in vivo*. However, functional redundancy may exist whereby deficiency of one growth factor is compensated by other growth factors. *In vivo* effects of FGF2, FGF7 and LIF on the primordial-to-primary follicle transition may require generation of double or triple knockout mice.

Steroids in early folliculogenesis

Steroids may play a role in early folliculogenesis. In mice primordial follicle formation occurs perinatally, when a precipitous drop in estrogen and progesterone occurs. Aromatase knockout mice provides an excellent model to study the effects of complete estrogen deficiency on follicular development. Ovaries that lack aromatase can develop primordial, primary, secondary and antral follicles. Estrogen deficiency is therefore not critical for early folliculogenesis. However, a closer look at aromatase knockouts revealed that the number of primordial follicles was approximately 40% less than in the wild-type ovaries [152, 153]. The number of primary follicles was statistically not significantly different between aromatase knockout and wild-type animals. Germ cell numbers in the newborn and embryonic aromatase knockout ovaries are not known, so the possibility remains that aromatase deficiency disrupts embryonic germ cell development. Primordial follicle numbers were also reduced in the newborns of pregnant baboons treated with an aromatase inhibitor [154]. It is unclear if the aromatase inhibitor effect is due to the direct effect on the developing ovary

Table 1. Mouse models affecting early folliculogenesis.

Gene	Phenotype of transgenic or knockout mouse	References
<i>Figla</i>	knockout; infertile; oocyte loss by postnatal day 2; unable to form primordial follicles	[17]
<i>Nobox</i>	knockout; infertile; most oocytes lost by postnatal day 14; primordial to primary follicles transition disrupted	[23]
<i>Sl^d</i>	spontaneous mutation; infertile; lack of germ cells	[45]
<i>Sl^{t, pan, con}</i>	spontaneous mutation; infertile; defect in folliculogenesis at primordial follicle stage; reduced number of germ cells	[46-48]
<i>MT-Amh</i>	<i>Amh</i> transgenic overexpression; infertile; lack of Müllerian duct derivatives; rapid loss of germ cells by postnatal day 14	[64]
<i>Foxl2</i>	knockout; infertile; block at stage of the primordial and primary follicle	[73, 74]
<i>Ngf</i>	knockout; reduced number of primary and secondary follicles; reduced proliferation of somatic cells;	[88, 89]
<i>Ntf4/5 & Bdnf</i>	double knockout; reduced number of primary and secondary follicles	[91, 93]
<i>Ntrk2</i>	knockout; failed transition from primary to secondary follicle	[93]
<i>Gdf9</i>	knockout; infertile; arrest of follicle growth at the primary follicle stage	[94]
<i>Bmp15</i>	knockout; subfertile; defects in ovulation and fertilization	[98]

or whether aromatase inhibitors exert subtle effects on the embryonic vasculature resulting in the smaller endowment of germ cells.

In vivo and *in vitro* studies on rat ovaries suggest that progesterone may inhibit primordial follicle formation from germ cell clusters [155]. *In vitro* rat studies also suggest that estrogen and progesterone may inhibit primordial-to-primary follicle transition. Progesterone receptor knockout mice have apparently normal follicular development until ovulation [156], and observed progesterone effects in rat ovaries may be artifactual, or progesterone may act via a nonnuclear receptor. The rapid decline in estrogen and progesterone concentrations after birth was hypothesized to be in part responsible for the breakdown of germ cell clusters and formation of primordial follicles in mammals. It is interesting to note, however, that primordial follicle formation occurs in humans during the time of continual rise in estrogen and progesterone levels, around 17–19 weeks of gestation [157–159]. In summary, the effects of estrogen and progesterone on early folliculogenesis are not critical, as shown by mouse knockout models, and further research is necessary to determine whether the observed effects documented by *in vitro* and *in vivo* approaches are physiologically relevant.

Conclusion

The breakdown of germ cell clusters and the formation of primordial follicles is poorly understood. These early steps in folliculogenesis are critical, as primordial folli-

cles are considered the fundamental reproductive units of the ovary that give rise to all dominant follicles. Transcription of numerous genes, essential for both folliculogenesis and embryogenesis, is initiated during early folliculogenesis [23]. Both naturally occurring mutations as in the case of *Kit* and *Kitl*, and targeted disruption of critical genes such as *Figla* and *Nobox*, have helped elucidate genes critical in early folliculogenesis. Recent studies have focused on identifying the molecular and cellular mechanisms whereby follicle formation is regulated. Analysis of mouse newborn ovary and embryonic gonad transcriptomes as well as the use of microarrays will help identify other critical genes in early folliculogenesis [160, 161]. Mouse transgenic and knockout models for growth factors, cytokine, cell surface factors and transcriptional factors that affect early folliculogenesis will allow better functional understanding of genetic networks that are critical in early folliculogenesis (table 1). It is clear that oocyte-specific and somatic genes are critical for early folliculogenesis. Somatic growth factors such as KITL and NGF are clearly important and bind oocyte specific receptors KIT and NTRK2, respectively, to effect primordial follicle formation. In mice, oocytes from secondary follicles accelerate somatic cell differentiation and proliferation [162, 163]. It is possible that germ cell clusters and primordial oocytes manufacture growth factors involved in early signaling with surrounding somatic cells. Such oocyte-specific growth factors may play an important role in the transition from primordial-to-primary follicles, just as GDF9 is essential for primary-to-secondary follicle transition. Oocyte-specific transcription factors

such as *FIGLA* and *NOBOX* do not appear to affect primordial germ cell migration and proliferation, but the precise onset of molecular pathology is unclear. It is likely that *Figla* and *Nobox* deficiencies disrupt genetic pathways in the embryonic gonad, probably after germ cells enter meiosis. Transcriptome differences between knockout and wild-type embryonic ovaries may exist, and these differences should be assessed with microarray technologies.

The integration of genomic technologies into reproductive biology assisted and will continue to assist in uncovering critical genetic components in early folliculogenesis. Similarly, new developments in the stem cell biology field may affect our view about the earliest stages of follicle development. Recently, it has been proposed that germline stem cells exist within mouse ovaries [9] or bone marrow [8] and give rise to new oocytes in the adult ovaries. The existence of mammalian germline stem cells challenges the dogma that the initial primordial follicle pool gives rise to all mature eggs. However, data supporting ovarian germline stem cells in mammals is relatively new and warrants further investigation. The definitive experiment for adult ovarian germline stem cells (i.e. birth of offspring carrying the genetic markers of the bone marrow donor) has not been accomplished as of yet. Even so, it is possible that oocyte regeneration during adulthood is a rare event, but as such, it may be physiologically irrelevant to overall reproductive success. Whatever the outcome, a re-examination of primordial follicle physiology is likely to reveal additional important mechanisms in follicle development.

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