

DEVELOPMENTAL HISTORY OF THE MAMMALIAN OOCYTE: INSIGHT FROM MOUSE MUTATIONS

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1. ABSTRACT

Growth and differentiation of the mammalian oocyte is regulated with the coordinate development of the granulosa cells. The complex signaling pathways that regulate the growth and development of mammalian oocytes are beginning to be elucidated through the use of gene targeting. These technologies have provided new insight into the roles of specific genes during the development of the germ cells and gonads, as well as post-pubertal development of oocytes. In many cases, these studies have resulted in a new understanding of the function of certain genes, in others they have provided new genes and pathways to be studied in mammalian reproductive biology. Ultimately, these studies will shed light on human genetic disease and infertility.

2. INTRODUCTION

It has become clear that the developmental history of the oocyte is regulated by reciprocal interactions with the surrounding somatic cells, especially the granulosa cells of the follicle. Communication between the granulosa cells and the oocyte occurs both through paracrine signaling and directly through gap junctions that form between the oocyte and the surrounding granulosa cells. The oocyte secretes signals that induce granulosa cell proliferation, regulate steroidogenesis, and maintain the architecture of the developing follicle. Similarly,

Signals from granulosa cells regulate meiotic arrest, promote oocyte growth and facilitate the reinitiation of meiosis and oocyte maturation. Understanding the roles of specific genes will provide insight into these regulatory networks and ultimately into the genetic bases of infertility in humans.

Currently, the genetic basis for the regulation of these processes, and the interplay between different signaling pathways, is not well understood. However, the past decade has seen a dramatic increase in the use of genetic approaches in mice to examine the function of individual genes during folliculogenesis and oocyte maturation. Use of these technologies allows for the *in vivo* dissection of the complex interactions required for the successful development and meiotic maturation of the mammalian oocyte. Data gathered from null mutations has already had a profound impact on our understanding of the complex signaling pathways that coordinate the estrous cycle and regulate fertility. The use of molecular genetic techniques to ask questions about gene function has provided new insight into the roles of signaling molecules that regulate oocyte development. In this review, we will discuss insight gained from genetically engineered mice with a focus on phenotypes that directly impact the development of germ cells, or the functional maturation of oocytes.

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3. DEVELOPMENT OF OOCYTES FROM PRIMORDIAL GERM CELLS

The origins of mammalian oocytes lie in primordial germ cells that migrate to the gonad early in fetal development (reviewed in 1). In mice, primordial germ cells (PGCs) arise from the posterior primitive streak around E6.5 to E7.5, and associate with the endodermal cells at the base of the allantoic diverticulum (2-4). Between E9.5 - E10.5, the PGCs migrate through the hindgut mesentery into the genital ridge, where they aggregate with somatic pregranulosa cells (5,6). At this stage, the PGCs (now referred to as oogonia) undergo mitotic division, expanding the germline, until E12.5 when they enter meiosis. Oogonia subsequently arrest in prophase of the first meiotic division, where they remain until ovulation. Granulosa cells of the follicle are derived from epithelial cells invaginating into the urogenital ridge. The pregranulosa cells associate with the oocytes as they enter the gonad. Oocytes enter meiosis between E13.5 and E16.5, and by birth, have progressed synchronously through the stages of meiotic prophase. Oocytes become arrested in diplotene and have an enlarged diploid nucleus, referred to as the germinal vesicle (GV). The oocytes remain arrested at this stage until the mouse reaches sexual maturity (7). In this section, we will review genes that are associated with the prefollicular events of germ cell migration, attrition, and meiosis.

3.1. Migration of Primordial Germ Cells

The migratory path of the PGCs is dependent on interactions between adhesion molecules on the cell surface with extracellular matrix glycoproteins produced by the surrounding somatic cells. Characterizing the substrate requirements for migration has been limited *in vivo*. However, in culture, PGCs are able to adhere to fibronectin, laminin, and collagen IV (8). PGCs isolated before, during, and after, migration display differences in their adhesiveness to these three substrates. For example, migration into the urogenital ridge is dependent on adherence to a long tract of laminin. This suggests that there is a corresponding change in the composition of the adhesion molecules expressed on the surface of the germ cells during migration.

Candidate molecules for mediating PGC migration include the integrins, a family of heterodimeric receptors (alpha and beta subunits). The composition of the receptor determines which extracellular matrix proteins, including fibronectin and laminin, that integrins are able to bind. Four alpha integrin subunits (alpha 3, alpha 5, alpha 6, alpha V) and two beta subunits have been detected in migrating PGCs (1). The importance of integrins to this process has been demonstrated through a chimeric analysis with beta 1 integrin deficient cells. This study demonstrated that beta 1 integrin is required for normal motility of PGCs. The calcium-dependent adhesion molecules, N-, P-, and E-cadherin, are also expressed in a dynamic pattern during PGC migration. P-cadherin is expressed throughout migration, while E-cadherin is expressed in the germ cells after exiting the hindgut. N-cadherin is expressed only after the PGCs have completed migration. It has been shown that

interference with the function of E-cadherin prevents the normal coalescence of the germ cells in the indifferent gonad (9).

These observations underscore the importance of the interactions between the PGCs and cell adhesion molecules expressed on the surrounding somatic cells during migration to the gonad. Changes in the requirement for specific cell adhesion molecules during, and after, migration raises the interesting issue of how the PGCs alter the expression of cell surface receptors in response to changes in the composition of the extracellular matrix along the path and the molecular triggers that regulate this process.

3.2. Attrition of the Oogonia

Germ cells undergo significant expansion in number both before and after their arrival in the developing ovary. At E8.5, approximately 145 PGCs are present, as visualized by alkaline phosphatase expression. The size of the germ cell pool increases to over 1000 by E10.5 and 26,000 by E13.5 (10). However at birth, the female mouse has lost two-thirds of the potential germ cells (11). The attrition in germ cells is due to apoptosis throughout embryogenesis, with the greatest loss at the onset of meiosis (E13- E16) (12,13). Since the size of the pool of primordial follicles is fixed at the time of birth, regulation of germ cell death directly impacts fertility and the reproductive lifespan of the animal.

One of the primary regulatory pathways for germ cell survival functions through KIT, a receptor tyrosine kinase. KIT is expressed on the surface of PGCs beginning at E7.5, the time of migration into the genital ridge. Its ligand, Steel/SCF/kit ligand (KL), is expressed in the somatic cells along the migratory path from the allantois to the genital ridge, starting at E9.0 (14,15). Mutations in either the receptor or ligand result in gonadal dysgenesis and sterility of both male and females (16). The addition of KL to PGCs in culture promotes survival, indicating its role in inhibiting apoptosis (17-21). The restricted expression of the ligand along the migratory path suggests an additional role for KL is to guide the migration of Kit-expressing cells. It is likely that the loss of germ cells in the mutant mice is due to a combination of cell death and a failure to properly migrate.

Other cytokines that influence the proliferation and survival of PGCs have been identified in culture. Factors such as leukemia inhibitory factor (LIF), basic fibroblast growth factor, tumor necrosis factor-alpha (TNF-alpha), insulin-like growth factor I (IGF-I), and interleukin-1 beta (IL1 beta) have been shown to promote PGC and oogonia proliferation in culture (19-26). Of these, only LIF has been demonstrated to have a similar role *in vivo*. Alternatively, cytokines such as transforming growth factor beta1 and beta2 (TGF beta1 and 2) and Fas ligand are able to induce death of the oogonia (27,28). The presence of apoptotic and anti-apoptotic factors in the milieu of the gonads has lead to a model in which germ cell attrition is regulated by subtle changes in the balance of cytokines (29).

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The target of factors that promote or prevent apoptosis is the Bcl-2 gene family in the mitochondria of the PGC and oogonia (13). The Bcl-2 family of mitochondrial genes can be divided into anti-apoptotic (e.g. Bcl-2 and Bcl-XL) and pro-apoptotic genes (e.g. Bax and Bok) (30,31). Activation of *bcl-2* transcription by KL, LIF, and IGF-I occurs through the phosphatidylinositol 3'-kinase-mediated phosphorylation of c-Akt, a serine-threonine kinase (32-35). Other cytokines, such as IL1 beta, are able to induce the Bcl-2 pathway through the generation of sphingomyelinase 1-phosphate by activating the cytoplasmic enzyme, ceramidase. In the absence of IL1beta stimulation, pro-apoptotic factors such as acid sphingomyelinase-generated ceramides accumulate in the cell (25).

Expression of Bcl-2 or Bcl-XL in the mitochondria leads to stabilization of the organelle, and the suppression of cytochrome C. In contrast, Bax or Bok leads to a destabilization of the mitochondria and the release of cytochrome C (36,37). This ultimately leads to the activation of the caspase signaling pathway and apoptosis (36,38,39). Consistent with the predicted role of these genes in regulating germ cell number, mice homozygous for a null *bcl-2* mutation possess a significantly reduced number of oocyte-containing primordial follicles (40). In addition, expression of exogenous Bcl-2, or the inactivation of *bax*, confers resistance to apoptosis in mouse oocytes (40). Conversely, the inactivation of *Bax* in mice leads to an abrogation of apoptosis in the germ cells (42,43).

3.3. Other Genes Required for the Survival of Primordial Germ Cells

The *ataxia-telangiectasia* mutant gene (*ATM*) is associated with the autosomal recessive ataxiatelangiectasia disorder that is characterized by a broad array of maladies including gonadal atrophy (44,45). *ATM* belongs to a family of genes that are involved in the control of cell cycle progression, processing DNA damage, and maintenance of genomic stability (46). In *ATM*-deficient mice, oocytes in the ovaries begin to undergo apoptosis around E16.5, and the ovaries are devoid of oocytes at the time of birth (47). Telomere clustering is aberrant, and the mutant oocytes are disrupted in prophase of meiosis I (47,48). Elevated levels of p53, p21, and Bax, in *ATM*-deficient oogonia suggest that infertility may be due to an activation of the apoptotic pathway (49). Consistent with this hypothesis, compound *ATM*^{-/-}/*p53*^{-/-} and *ATM*^{-/-}/*p21*^{-/-} mutants partially rescue the prophase I defect.

Other genes that have been found to be required for the survival of oocytes in primordial follicles include a putative transcription factor, *Zfx*, and an RNA-binding protein *DAZL1*. With either gene, the role of the gene during oocyte development remains to be determined. *DAZL1* is the autosomal homologue of the Y-chromosomal *DAZ* gene, which is deleted in azoospermic males (50,51). *Dazl1* is broadly expressed in the follicles of prepubertal ovaries and becomes restricted to the periphery of the oocyte cytoplasm in adults (52). A targeted null mutation of *Dazl1* results in a complete loss of male and female germ cells (52). Interestingly, the ovaries from *Dazl1*^{-/-} mice

contained steroidogenically active cells in the absence of any follicular structure (53).

Zfx is a gene found on the X chromosome that has been implicated in Turner syndrome and sex differentiation of the indifferent gonads (54,55). The gene encodes a protein containing 13 zinc fingers and a highly acidic domain that is able to activate transcription (56). Mice homozygous for a null allele of the *Zfx* gene are less fertile than their wild type littermates and have a shortened reproductive lifespan (57). An analysis of the indifferent gonads of E11.5 *Zfx*-null embryos revealed a reduction in the total number of primordial germ cells, implying that this gene is required for the proliferation of primordial germ cells prior to sex determination.

4. INITIATION OF EARLY FOLLICLE DEVELOPMENT AND OOCYTE GROWTH

Once a primordial follicle initiates growth and development, the oocytes are committed to ovulate or the follicles become atretic. Early follicle development is associated with a growth in the size of the oocyte and proliferation of the surrounding granulosa cells. Reciprocal interactions between the oocyte and the granulosa cells play an important role in regulating initiation and development. The rate at which primordial follicles enter the growing pool directly impacts the reproductive lifespan of the female. Hypoinitiation could result in a failure to ovulate, while hyperinitiation could lead to premature reproductive senescence. In this section, we will discuss genes that are required for proper initiation and development of primordial follicles.

4.1. Kit-Kit Ligand Signaling

As discussed earlier, an interaction between Kit and its ligand is critical for the early survival of primordial germ cells. However, there are at least two natural mutations in Kit ligand, *Mgf*^{Sl-t} and *Mgf*^{Sl-pas}, in which follicles are present in reduced numbers (58-59). An analysis of the ovaries from these mutant mice has revealed additional roles for the Kit signaling pathway in follicle development and oocyte maturation.

The patterns of Kit and KL transcription are consistent with their role throughout follicle development. Kit expression ceases in the germ cells at the time at which they enter meiosis. A second wave of Kit transcription begins in oocytes of primordial follicles and expression is maintained in oocytes throughout follicle development (60). In antral follicles, Kit is also expressed in the thecal cell layer that surrounds the granulosa (61). KL transcripts are detectable in the granulosa cells of primary follicles, and increase with the growth of the follicle (62). With the differentiation of multiple granulosa cell types during antral follicle development, KL expression is restricted to the mural granulosa. Two splice variants of KL have been detected; both encode biologically active proteins; KL-1, a soluble form, and KL-2 a membrane bound form (62,63). The significance of the two forms of KL has not been determined. Regulation of KL-1 and KL-2 expression in the granulosa cells is positively regulated by testosterone

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produced by the thecal cells. Expression can be enhanced by follicle stimulating hormone (FSH) produced by the pituitary, and inhibited by signals from the oocyte (63). Recent observations indicate that the oocyte-specific factor growth and differentiation factor 9 (GDF-9) can inhibit KL-1 and KL-2 transcription. In mice that are deficient for *gdf-9*, KL-1 and KL-2 are aberrantly expressed in the cumulus cells (64).

As mentioned above, the ovaries of *Mgf^{Sl-t}* and *Mgf^{Sl-pan}* mice contained follicles that arrest at a very early stage of development postnatally, prior to antrum formation (58,59,65). These follicles have exited the primordial follicle pool, but are blocked at the point at which follicles would normally undergo rapid growth. This predicted a role for Kit in the initiation of follicle growth. Experiments done that inactivated Kit in wild type females by injection of the anti-kit antibody, ACK₂ provided further evidence of a role for Kit in initiation (66). If mice were treated between birth and day 2, the subsequent growth of follicles was completely blocked due to a reduction in granulosa cell proliferation. Further, the addition of KL in culture stimulated primordial follicle development (67). Since Kit is not expressed in the granulosa cells, proliferation of these cells is likely induced by a paracrine factor(s) produced by the oocyte in response to Kit-KL signaling. The mechanism by which this occurs has not been established.

There is evidence that signaling through Kit plays a role in regulating oocyte maturation and the resumption of meiosis. In rat follicles, the addition of KL in culture resulted in a block in the progression of meiosis into metaphase I (MI), while the addition of an antisense oligonucleotide specific to Kit had the opposite effect (68,69). This predicts that KL expressed in granulosa cells around the oocyte in preantral follicles is required to maintain the oocyte in meiotic arrest. The loss of KL expression as cumulus cells differentiate in antral follicles would remove the block. It remains to be determined whether KL has the same effect in mice or humans.

The expression of Kit in the theca cells and KL in mural granulosa cells along the basal lamina predicts a role for these genes in steroidogenesis and thecal cell differentiation. There are a number of observations that support this notion. The production of the testosterone precursor androstenedione by theca cells and follicles in culture is induced by the addition of KL (70-72). KL is also able to stimulate the differentiation of stromal-interstitial cells around preantral follicles in culture. Further, it was demonstrated that KL induced proliferation of stromal and theca cells was dose-dependent (70). In small antral follicles there is higher KL expression in the mural granulosa cells than in large antral follicles (63). Since, Kit - KL signaling blocks aromatase activity in granulosa cells (71), the decrease in signaling in larger follicles would lead to increased estrogen production and expression of LHR. These data indicate the complexity of the signaling interactions that regulate the maturation process, signaling between theca and granulosa and granulosa and oocyte.

4.2. Growth and Differentiation Factor 9

Oocytes express a soluble factor, GDF-9, which acts to promote granulosa cell proliferation. GDF-9 is a member of the TGF beta superfamily of secreted signaling proteins (73). GDF-9 is expressed in oocytes beginning at the early growing follicle stage (74). In mice that are deficient for GDF-9, the follicles are arrest at the type 3b stage; follicles have a growing oocyte surrounded by a single layer of cuboidal granulosa cells. The oocytes of GDF-9-deficient mice continue to grow in size and eventually degenerate. This is followed by luteinization of the granulosa cells (75,76). Using recombinant GDF-9 in a granulosa cell culture system, it was found that this factor induces the expression of cyclooxygenase 2 (cox-2), steroidogenic acute regulator protein (StAR), and increases granulosa cell progesterone synthesis in the absence of FSH. Further, GDF-9 inhibited the expression of urokinase plasminogen activator (uPA) and LHR mRNA. The expression of HAS2 and inhibition of uPA are key events in cumulus expansion and implicated GDF-9 in this process. This was confirmed by the observation that GDF-9 could induce cumulus expansion in oocytectomized follicles (74). Thus, GDF-9 has two roles to play, inducing both the early proliferation of granulosa cells and the later differentiation of the cumulus cells. This is one of many signaling pathways that have pleiotropic functions in folliculogenesis, it will be important to understand what changes in gene expression underlie these different roles.

4.3. Growth and Differentiation Factor 9 b/Bone Morphogenetic Factor 15

Recently, a gene that is expressed exclusively in oocytes with a high degree of homology to *gdf-9* was identified, and is called either *gdf-9b* or *BMP-15*. Expression of this gene is first noted in primary follicles (one layer of cuboidal granulosa cells) and expression levels increase to a peak in antral follicles (73,77,78). *In vitro* studies in rat follicles indicate that GDF-9B/BMP-15 plays an important role in stimulating cell proliferation in the surrounding granulosa cells (78). In addition, this factor was able to selectively inhibit FSH-induced progesterone production, but not FSH-induced estradiol production, due in part to the regulation of FSH receptor transcription (79). The most compelling *in vivo* evidence for a function for GDF-9B comes from the study of a natural mutation occurring in sheep, FecXI, which maps to *gdf-9b/BMP-15* on the X-chromosome (80). Homozygous null females are infertile, due to an arrest in folliculogenesis at the primary stage. In contrast, heterozygous females are displaying an increased fertility. This suggests that fertility is regulated by GDF-9B/BMP-15 in a dosage-sensitive manner.

5. ESTABLISHING DIRECT COMMUNICATION BETWEEN THE OOCYTE AND CUMULUS GRANULOSA CELLS

5.1. Zona Pellucida

The zona pellucida is an extracellular matrix secreted by the oocyte that forms a boundary between the egg and the surrounding somatic cells. Prior to ovulation, the zona is required for the oocyte to achieve competency (81,82). After ovulation, this matrix mediates both initial

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sperm-egg recognition (83) and triggers the acrosome reaction. Once the oocyte has been fertilized, cortical granule N-acetylglucosaminidase from the egg "hardens" the zona (84,85). The hardened zona is impervious to further sperm penetration, effectively preventing polyspermy. The fertilized embryo remains encased in the zona during its passage through the oviduct. Presumably, the zona prevents premature adherence of the embryo to the oviduct wall (86,87).

The mouse zona pellucida is composed of three sulfated glycoproteins, ZP1, ZP2, and ZP3 (88,89), which are 180-200, 120-140, and 83 kDa, respectively. The zona first appears as patches of coalesced extracellular matrix in primary follicles and is completely formed in fully-grown oocytes of early antral follicles (90,91). The zona does not create a complete barrier between the oocyte and the surrounding granulosa cells. Cellular processes from the cumulus granulosa cell layer penetrate the zona to form gap junctions with the oocyte (92). Transcription of the three Zp genes is regulated by the basic helix-loop-helix (bHLH) transcription factor, FIG alpha (93). A bHLH enhancer element (E box) has been identified in the promoter region of Zp1, Zp2, and Zp3, which will bind FIG alpha and direct transcription. Further, mice deficient for *fig alpha* fail to express the Zp genes (94).

The contribution of the individual Zp genes to the formation of the matrix has been examined through targeted null mutations. In the ovaries of mice deficient for *ZP1* a porous zona forms that allows the migration of cumulus cells into the perivitelline space. Early mutant embryos experience precocious hatching, which results in a reduction in survival (95). The oocytes from *Zp2*^{-/-} mice form a thin zona pellucida, which breaks down in follicles prior to ovulation. Fewer early antral follicles are present in the ovaries of *Zp2*^{-/-} females, and fertilized eggs fail to progress beyond the two-cell stage (82). *Zp3*^{-/-} females are also infertile, and the primary follicles fail to form any zona pellucida even though both ZP1 and ZP2 are expressed (81). Similar to the *Zp2*^{-/-} mice, fertilized eggs in the *Zp3*^{-/-} mice fail to develop to the blastula stage. It has been shown that oocytes stripped of their zona can be fertilized and will progress to the blastocyst stage. This therefore indicates that the zona pellucida plays an additional role in regulating the competence of oocytes during folliculogenesis.

5.2. Gap Junctions

Intercellular communication between the oocyte and the surrounding granulosa cells is critical for proper follicle development and meiotic competency. It has been proposed that gap junction channels connecting the oocyte with the granulosa act as primary conduits of communication. Gap junctions are composed of two opposing hexameric hemi-channels consisting of six transmembrane proteins called connexins. To date, 17 members of this family have been characterized and organized into subfamilies, based on sequence homology (96). Ovarian gap junctions mediate (1) the uptake of nutrients from granulosa cells (97); (2) transmission of paracrine endocrine signaling (92,98); (3) the co ordination of steroidogenesis in the granulosa cells (99); (4)

maintenance of oocytes in meiotic arrest (100-102); and (5) LH induced maturation of the oocyte (100).

Immunohistochemical studies in mouse ovaries revealed the differential expression of alpha connexins (alpha 1, -4, -5, and -6) in the granulosa cells and beta connexins (beta 1, -2, -4, and -6) in the oocyte and thecal layer (103). Further, the expression of individual members varied with the developmental stage of the follicle (i.e. primordial, antral, preovulatory, and atretic). Targeted null mutations have begun to elucidate the role of individual connexin genes at discreet points in follicle development. Connexin 43 (alpha1) is expressed in the granulosa cells of primary follicles. The follicles in the ovaries of *connexin 43*-deficient mice are arrested at the primary stage (104). In contrast, mice deficient for *connexin 37* (alpha4), which is initially expressed in granulosa cells of early antral follicles, are ovulation incompetent (105,106), lack antral follicles, and develop numerous inappropriate CL. In addition, oocytes isolated from *connexin 37*-deficient follicles are unable to reinitiate meiosis. These results suggest that differential expression of members of the connexin family is important for the proper progression through folliculogenesis.

6. REGULATORS OF OOCYTE MATURATION

Oocyte maturation is initiated following the surge of LH from the pituitary. Oocytes competent to mature have already completed growth, formed their zona pellucida, and are surrounded by cumulus granulosa cells within an antrum. The first step usually associated with the initiation of oocyte meiotic maturation is breakdown of the GV (GVBD). The events of GVBD include, the disruption of the nuclear envelope of the GV (107), changes in the structural organization of the chromatin (108), and condensation of chromatin into discernable chromosomal bivalents comprised of synapsed homologous chromosomes. Following GVBD, the first meiotic spindle forms and meiotic anaphase follows and segregates individual homologous chromosomes at opposite poles of the spindle. The spindle orientation is accentic at the oocyte cortex, resulting in conserved, limited cytokinesis with the outside spindle pole protruding through the oocyte surface into the perivitelline space. Thus, at the conclusion of the first meiotic division, one set of segregated homologous chromosomes remains within the oocyte and the other set is abstracted in the first polar body. After establishment of the second meiotic spindle, the cell has reached the secondary oocyte stage, is genetically haploid, and has completed meiotic maturation. Ovulation follows, and the mature oocyte is fertilizable. In mammals, the secondary oocyte or mature egg, is arrested at the second meiotic metaphase, or MII, remaining at that stage until the oocyte is penetrated by sperm during fertilization.

Most emphasis in recent research directed at the regulation of maturation has focused on the mechanisms by which the oocyte progresses from the arrested GV stage of meiotic prophase at meiotic G2 to the M-phase to complete the first meiotic division. Intensive studies in *Xenopus* has lead to a model of control of cell cycle progression by the

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MAP kinase cascade and cyclin-B-Cdc2 kinase (maturation promoting factor; MPF)(reviewed in 109). Regulation of the onset of maturation and the subsequent block in MII is dependent on the interplay between MAP kinase and MPF, and their activation through phosphorylation. Studies in other vertebrates, including mice, have revealed some variations in the regulation of critical components of the cell cycle control machinery (109). Here we present genetic evidence reinforcing the importance of cyclin-B, mos, and components of the prostaglandin signaling pathway.

6.1. Cyclin B1 and B2

In mammals, meiotic maturation is regulated by the activation of the cell cycle kinase, MPF, which drives cells into the division or M-phase of the cell cycle. MPF is composed of a catalytic subunit p34cdc2 and a regulatory subunit, cyclin B (110-113). The activity of MPF has been shown to increase early in oocyte maturation up to the first meiotic metaphase, to decrease at anaphase of the first meiotic division, and then to rise again at the transition to second meiotic metaphase (114,115). The modulation of cyclin protein synthesis and degradation is crucial to the control of MPF activity. The mitotic cyclins are synthesized throughout the cell cycle and destroyed during a short period, just before the metaphase-anaphase transition (116,117). In mouse oocytes, synthesis of cyclin B increases progressively during meiotic maturation, it is at its peak levels by the end of the first meiotic M phase, and is degraded at the time of polar body extrusion (118,119). There are somewhat differing reports regarding the relative amounts of p34cdc2 and cyclin B in mammalian oocytes competent to undergo maturation, however, there is general agreement that at the end of oocyte growth relatively high concentrations of p34cdc2 protein and cyclin B protein are present before initiation of GVBD (120-123).

There are two *cyclin B* genes in mammals; *B1* and *B2*, null mutants of both genes have been constructed in mice (124). Interestingly, *cyclin B2*^{-/-} mice are viable and produce normal offspring, although with reduced litter size, but *cyclin B1*^{-/-} mutants die embryonically. The subfertility of the *cyclin B2* mutants has not been studied, but could indicate a role for this gene in oocyte maturation. More recently, Leden *et al.* (125) injected oocytes with cyclin B1 antisense RNA and found two distinct phenotypes. Most of the injected oocytes were blocked in MI, but others extruded the first polar body prematurely and were unable to enter MII. Injection of antisense cyclin B2 had no effect on maturation. It might be interesting in light of this data to study compound mutations, such as *cyclin B2*^{-/-}/*B1*^{+/+}, for possible changes in fertility due to decreased levels of cyclin B. These observations indicate that the regulation of the timing of events during meiotic maturation is tightly tied to the synthesis of cyclin B.

6.2. Mos

The c-mos proto-oncogene product (Mos) is a serine/threonine kinase essential for oocyte maturation. Mos is a component of cytostatic factor (CSF), that was originally described as a regulator of arrest at metaphase II. In *Xenopus*, Mos activates and/or stabilizes the MPF complex through a pathway that involves the MAP kinase

cascade. This results in the resumption of meiosis, extrusion of the first polar body, suppression of DNA synthesis, and arrest in metaphase II. To determine the function of Mos in mice, *c-mos*-deficient mice were generated by gene targeting. MAP kinase failed to be activated in these mice. The female mice were subfertile; producing only a few litters consisting of 1 or 2 pups. Oocytes from *mos*^{-/-} mice progress normally through folliculogenesis and meiotic maturation, but activated parthenogenetically due to a failure to arrest at metaphase II (134,135). During the transition between the two meiotic metaphases, the microtubules and chromosomes evolve towards an interphase-like state in *mos*^{-/-} oocytes, while in wild type oocytes they remained in an M-phase configuration (136). Thus Mos appears to be required for chromatin organization and arrest at metaphase II in the mouse though it is necessary throughout maturation in *Xenopus*.

Mos is a MAPKKK and thus is predicted to activate MAP kinase through an intermediate kinase. However, microinjected constitutively active forms of the MAPKKs, MEK1 and Raf, failed to activate MAP kinase in *mos*^{-/-} oocytes (137). In contrast, MAP kinase could be activated by the phosphatase inhibitor okadaic acid. This suggests that MAP kinase is normally inactivated by phosphatases and that one function of Mos is to inhibit protein phosphatases. Activated MEK1 was able to induce the phosphorylation of a MAP kinase mutant that was resistant to dephosphorylation. This has led to dual paths for Mos during the activation of MAP kinase, inducing phosphorylation and inhibiting phosphatases.

6.3. Prostaglandin signaling pathway

It is known that some functions of gonadotropins are mediated by prostaglandins, these compounds modulate the actions of hormones and can have profound effects on cellular functions. Prostaglandins are synthesized from arachidonic acid; the rate limiting step in prostaglandin synthesis is mediated by the enzyme cyclooxygenase (cox). There are two isoforms of this enzyme (cox-1 and -2), encoded by separate genes (138,139). Cox-1 is expressed in cells constitutively, including cells of ovarian follicles, however, expression of cox-2 is induced in follicles by gonadotropins (140,141). *Cox-1* and *cox-2* deficient mice have been generated (142-144). *Cox-1* null mice are fertile, whereas *cox-2*^{-/-} mutant female mice have multiple reproductive defects (145). The ovarian phenotype of these mice includes a defective ovulatory response to gonadotropins and a lack of proper oocyte maturation. The latter conclusion was based on the observation that the few eggs released by these mutants were not fertilizable and did not extrude a first polar body (145). Interestingly, mice deficient for the prostaglandin E receptor, EP2, exhibit reduced fertility that also was attributed to a fertilization failure. It was noted that the *EP2*^{-/-} follicles did not undergo cumulus expansion, and this was concluded to directly lead to the fertilization defect (146). Interestingly, GDF-9 has been shown to induce signaling through the EP2 receptor, and to directly regulate the expression of *cox-2* (147). These studies further highlight the importance of reciprocal signaling in the eventual release of a fertilizable oocyte.

7. PERSPECTIVE

Fertility in mammals depends upon a tightly coordinated sequence of events that lead to the growth, maturation, and ovulation of the oocyte. These events are regulated by a complex autocrine/paracrine signaling network that includes the brain, ovary, oocyte, and granulosa and theca cells. *In vitro* approaches have been successfully used to examine the role of individual genes during oocyte development. However, the interpretation of these experiments are compromised by the removal of the oocyte or follicle from the entire signaling milieu. Genetic manipulations of the mouse, including targeted null mutations and transgenics, have provided complementary approaches to examine the same gene within the *in vivo* signaling context. This review has concentrated on the advances in our understanding of the development of the oocyte based on genetic mutations in mice.

Embedded in the developmental history of each oocyte are several checkpoints integral to the reproductive success of the animal. Most notably are the cell cycle checkpoints that follow the switch from mitosis to meiosis, that maintain the oocyte in prophase I (prior to maturation), and anaphase II (prior to activation). Other checkpoints include, the initiation of primordial germ cell migration, and the initiation of primordial follicle growth. Though much is known about the genes that regulate the onset of oocyte maturation and activation, little is known about the molecular triggers for earlier checkpoints. Both the loss, or permanent block, of these checkpoints are likely to result in subfertile females through a failure to produce fertilizable eggs or a premature depletion of the primordial follicle pool. The past decade has seen a dramatic increase in the identification of genes involved in regulating follicle and oocyte development. These genes can now be used to design approaches to identify upstream regulators that are proximate to these important developmental checkpoints.

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Key words: Folliculogenesis, Primordial Germ Cells, Oocyte Growth and Maturation, GVBD, Meiotic Arrest, GDF-9, Kit, Review

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