



Published in final edited form as:

J Androl. 2010 ; 31(1): 11–15. doi:10.2164/jandrol.109.008318.

Fetal Leydig Cells: Progenitor Cell Review Maintenance and Differentiation

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Abstract

In most eutherian mammals, sexually dimorphic masculinization is established by androgen-producing fetal Leydig cells in the embryonic testis. Fetal Leydig cells, which lack expression of the testis-determining gene *SRY*, arise after the appearance of *SRY*-expressing Sertoli cells. Therefore, the appearance and differentiation of fetal Leydig cells are probably regulated by factors derived from Sertoli cells. Results from mouse genetic models have revealed that maintenance and differentiation of fetal Leydig cell population depends upon a balance between differentiation-promoting and differentiation-suppressing mechanisms. Although paracrine signaling via Sertoli cell-derived Hedgehog ligands is necessary and sufficient for fetal Leydig cell formation, cell-cell interaction via Notch signaling and intracellular transcription factors such as *POD1* are implicated as suppressors of fetal Leydig cell differentiation. This review provides a model that summarizes the recent findings in fetal Leydig cell development.

Keywords

Reproductive genetics; testis; Hedgehog; Notch; steroidogenic factor 1

The *SRY* gene (sex-determining region of the Y chromosome) determines the sex of the gonad in most mammalian species; however, masculinization of the embryo is controlled by hormones and can be accomplished independent of genetic components (Jost, 1947, 1953). Products of fetal Leydig cells, a testis-specific cell type, are responsible for masculinization of the embryo. Through the action of Leydig cell-produced androgens and insulin-like factor 3 (*INSL3*), the male reproductive tract (or Wolffian duct) is maintained, male secondary sexual characteristics are established, and testicular descent is induced (Haider, 2004; Barsoum and Yao, 2006; Park et al, 2007). Without functional fetal Leydig cells, the male embryos develop the appearance of a female despite the presence of testes. To understand where fetal Leydig cells arise and how they differentiate, researchers have developed various transgenic and knockout mouse models that shed lights on these processes. Before the formation of fetal mouse testis (embryonic day [E]11.5–E12.5), gonadal primordium is composed of a mixture of immigrating primordial germ cells and undefined somatic progenitor cells (Swain and Lovell-Badge, 1999; McLaren, 2000; Brennan and Capel, 2004). These somatic progenitor cells in the gonads express various transcription factors, including steroidogenic factor 1 (*Sf1*, also known as nuclear receptor

5A1), Wilms tumor 1 (*Wtl*), GATA transcription factor 4 (*Gata4*), and Lim homeobox gene 9 (*Lhx9*) (Luo et al, 1994; Hatano et al, 1996; Birk et al, 2000; Mazaud et al, 2002). These progenitor cells (referred to as SF1-positive cells hereafter) are the sources of at least 2 somatic cell lineages in the testis: the supporting-cell lineage (Sertoli cells) that nourishes the germ cells and the steroidogenic lineage fetal Leydig cells.

At E10.5, a subpopulation of the SF1-positive somatic cells starts to express *Sry* and differentiate into Sertoli cells (Gubbay et al, 1990; Koopman et al, 1990; Lovell-Badge and Robertson, 1990; Hacker et al, 1995; Albrecht and Eicher, 2001). Via interaction with SF1, SRY triggers expression of SRY-box-containing gene 9 (*Sox9*), which itself is sufficient to induce testis formation (Sekido et al, 2004; Bullejos and Koopman, 2005; Kanai et al, 2005; Sekido and Lovell-Badge, 2008). The SOX9-positive Sertoli cell population then expands via the action of fibroblast factor 9 signaling and prostaglandin D2 (Schmahl et al, 2000; Wilhelm et al, 2005, 2007). By inducing endothelial cell migration and peritubular myoid cell differentiation, Sertoli cells orchestrate the formation of the testis cords (Wilhelm et al, 2007; Cool et al, 2008; Combes et al, 2009), the physical structures that separate germ cells and Sertoli cells from the testis interstitium.

Steroidogenically active fetal Leydig cells appear in the testis interstitium about 24 hours after Sertoli cell differentiation (Habert et al, 2001; Yao et al, 2002; Barsoum and Yao, 2006). Numbers of fetal Leydig cells increase dramatically from E12.5 to E15.5; however, fetal Leydig cells are mitotically inactive during this period (Orth, 1982; Byskov, 1986; Migrenne et al, 2001). Expansion of fetal Leydig cell population could result from transformation of SF1-positive progenitor cells and/or from addition of cells from sources such as the neighboring mesonephros (Merchant-Larios and Moreno-Mendoza, 1998), neural crest (Mayerhofer et al, 1996), and coelomic epithelium (Karl and Capel, 1998; Schmahl et al, 2000). Regardless of their origins, fetal Leydig cells lack expression of *Sry* or *Sox9*, indicating that their differentiation is dependent upon cues from the *Sry/Sox9*-expressing Sertoli cells. Desert hedgehog (*Dhh*) and platelet-derived growth factor A (*Pdgfa*), 2 Sertoli cell-derived signaling molecules, have been implicated in differentiation of fetal Leydig cells (Clark et al, 2000; Pierucci-Alves et al, 2001; Yao and Capel, 2002; Yao et al, 2002; Walterhouse et al, 2003; Brennan and Capel, 2004; Ross and Capel, 2005; Barsoum and Yao, 2006). In mice, *Dhh* mRNA is expressed in differentiating Sertoli cells at E11.5 and its receptor *Ptch1* is localized to the testis interstitium (Yao et al, 2002). Testes of *Dhh* knockout embryos develop fewer fetal Leydig cells and abnormal testis cord organization. In the prepubertal and adult stages, *Dhh* knockout mice have spermatogenesis defects and lack adult Leydig cells (Bitgood et al, 1996; Clark et al, 2000; Pierucci-Alves et al, 2001; Yao et al, 2002; Yao and Capel, 2002). *Pdgfa*, on the other hand, is also expressed in Sertoli cells, whereas one of its receptors, PDGF receptor α (*Pdgfra*), is present in the testis interstitium (Brennan et al, 2003). In *Pdgfra* knockout male embryos, Sertoli cell proliferation, mesonephric cell migration, and fetal Leydig cell differentiation are all reduced (Brennan et al, 2003). Consequently, the Leydig cell defects in *Pdgfra* knockout testes are likely secondary to defects in Sertoli cell differentiation and progenitor cell migration/proliferation. Sphingosine phosphate lyase 1 (*Sgpl1*) and pleckstrin homology domain-containing family A1 (*Plekha1*), 2 putative downstream targets of PDGF signaling, are recently identified as important for male fertility (Schmahl et al, 2008). However, in both *Sgpl1*^{-/-} and *Plekha1*^{-/-} mice, the testicular morphology and subsequent male development appear normal before postnatal day 20 (Schmahl et al, 2008). This indicates that these 2 genes are unlikely to be involved in fetal Leydig cell development.

We recently developed a transgenic model in which the Hedgehog (Hh) pathway was ectopically activated in the SF1-positive progenitor cells of the fetal ovary (Barsoum et al, 2009). Under normal circumstances, the Hh pathway is inert in the fetal ovary because of

lack of Hh ligands (Bitgood et al, 1996; Clark et al, 2000; Pierucci-Alves et al, 2001; Yao et al, 2002; Yao and Capel, 2002). We used the Cre/loxP system to activate the Hh pathway in the SF1-positive somatic cells of the fetal ovary by targeting Smoothened (SMO), a transmembrane protein responsible for transducing the intracellular signaling pathway induced by Hh ligands. When the SF1-cre transgenic line was crossed to the *Smo^{YFP}* (*Smo^{YFP}*) line, Cre recombinase under the control of the *Sf1* promoter removed the STOP sequence upstream of the *Smo^{YFP}* transgene. Removal of the STOP sequence allowed the transcription of a constitutively active form of mutated *Drosophila* Smoothened (*smo*) fused with a yellow fluorescent protein gene (*YFP*) (Jeong et al, 2004). The *Smo^{YFP}* transgene thus activated the Hh pathway regardless of the presence or absence of the Hh ligands. Ectopic activation of the Hh pathway in fetal ovaries transformed SF1-positive somatic cells into functional fetal Leydig cells. These ectopic fetal Leydig cells produced androgens and INSL3 that caused virilization of female embryos and descent of the ovaries. Sertoli cells and other testicular components were not found in the affected ovaries, indicating that the appearance of fetal Leydig cells was a direct consequence of Hh activation. Along with the findings in *Dhh* knockout models, these results demonstrate that the Hh pathway is necessary and sufficient for the induction of fetal Leydig cell differentiation (Barsoum et al, 2009). In addition, the ability of SF1-positive progenitor cells in the fetal ovary to differentiate into fetal Leydig cells supports that the SF1-positive somatic cells are bona fide progenitor cells for fetal Leydig cells.

In contrast to the Hh pathway, which promotes fetal Leydig cell differentiation, the Notch pathway suppresses fetal Leydig cell differentiation. When the Notch pathway was inhibited in the fetal testis either by treatment with a chemical inhibitor or by inactivation of *Hes1* (hairy and enhancer of split 1), a key intracellular component downstream of Notch receptor, numbers of fetal Leydig cells were significantly increased (Tang et al, 2008). Conversely, constitutive activation of the Notch pathway in the SF1-positive progenitor cells inhibited Leydig cell differentiation. The Notch pathway controls cell fate determination via interaction between membrane-bound ligands and Notch receptor in adjacent cells. We therefore speculate that a subpopulation of SF1-positive progenitor cells in the testis interstitium is set aside as the pool of undifferentiated stem cells. These putative stem cells are prevented from entering the differentiation mode via Notch receptor and its downstream signaling (see model in Figure).

Increasing numbers of fetal Leydig cells were also reported in embryos lacking *Pod1* (Tcf21/capsulin/ epicardin), a basic helix-loop-helix transcription factor (Cui et al, 2004). Similar to our Hh activation model, *Pod1* knockout ovary had ectopic appearance of steroidogenic cells (presumably fetal Leydig cells). Interestingly, the Hh pathway was not activated in the *Pod1* knockout ovaries. However in the absence of *Pod1*, *Sf1* expression was elevated, implying that POD1 may suppress fetal Leydig cell differentiation by counteracting *Sf1* transcription in the progenitor cells (Figure). SF1, a transcription factor that controls expression of steroidogenic enzymes, is critical for establishment of both Sertoli and Leydig cell lineages (Luo et al, 1994). *Sf1* is present in the gonadal primordium of both sexes but later becomes testis-specific after the onset of sex determination (Luo et al, 1994). In the fetal testis, *Sf1* expression was down-regulated in Sertoli cells, whereas it was up-regulated in fetal Leydig cells (Ikeda et al, 1994; Parker and Schimmer, 1997; Parker et al, 2002; Yao et al, 2002). This increased *Sf1* expression in fetal Leydig cells was partially linked to DHH derived from Sertoli cells (Yao et al, 2002; Park et al, 2007). In addition, when the Hh pathway was ectopically activated in the ovary, *Sf1* expression was up-regulated, followed by appearance of fetal Leydig cells (Barsoum et al, 2009). It has been shown that without *Sf1*, Leydig cell differentiation does not occur (Morohashi et al, 1992; Leers-Sucheta et al, 1997; Reinhart et al, 1999; Koskimies et al, 2002; Val et al, 2003). In gonad-specific *Sf1* knockout mice, expression of 2 fetal Leydig cell markers, cytochrome

P450 side chain cleavage (*Scx*) and the steroidogenic acute regulatory protein (StAR), were decreased (Jeyasuria et al, 2004). Also, in *Sfl* heterozygous embryos, fetal Leydig cell markers such as cytochrome P450, subfamily XVII (*Cyp17*) and *Scx* were reduced at E13.5 (Park et al, 2005). Decreases in steroidogenic enzyme expression in the fetal testis were also reported in mouse embryos lacking the transcriptional factor X-linked aristaless-related homeobox gene (*Arx*; Kitamura et al, 2002). *Arx* is strongly expressed in peritubular myoid cells, endothelium, and fibroblasts, but not in Leydig cells. This suggests that *Arx* could play a role in either establishment of fetal Leydig cell population or regulation of steroidogenesis.

The SF1-positive cells represent an undifferentiated progenitor cell pool for both adrenals and gonads that originate from a common adrenogonadal primordium (Ikeda et al, 1994; Hatano et al, 1996). When adrenals and gonads separate, a fetal adrenal enhancer controls *Sfl* expression in SF1-positive cells of adrenal gland (Zubair et al, 2006). At E11.5, the gonadal pool of SF1-positive cells acquires their own enhancer activity within *Sfl* gene (from -589 to +85) that contains WT1 and LHX9 binding sites essential for *Sfl* gene transcription (Wilhelm and Englert, 2002). Under the effect of SRY/ SOX9 and other transcriptional factors (Barsoum and Yao, 2006), some gonadal SF1-positive cells become Sertoli cells. The remaining SF1-positive cells in the interstitium begin their path to steroidogenesis in response to activation of the Hh pathway (Figure). Using double immunohistochemistry for SF1 and steroidogenic enzyme 3 β HSD, we characterized the transition of SF1-positive progenitor cells into steroidogenic fetal Leydig cells. Before E13.0, fetal testes contained only SF1-positive/ 3 β HSD-negative (SF1+/3 β HSD-) progenitor cells in the interstitium. Twelve hours later (E13.5), SF1+/3 β HSD+ (fetal Leydig cells) started to appear, intermingling with the SF1+/3 β HSD- progenitor cells. By E16.5, some of the SF1+/3 β HSD+ cells turned off SF1 expression and became only 3 β HSD+ (SF1-/3 β HSD+; terminally differentiated fetal Leydig cells). The proportion of these 3 populations (SF1+/3 β HSD- progenitor, SF1+/3 β HSD+ fetal Leydig cells, and SF1-/3 β HSD+ terminal differentiated cells) was changed dramatically in response to ectopic activation of the Hh pathway. Ectopic activation of the Hh pathway in the SF1-positive cells resulted in a decrease in the progenitor population and an increase in fetal Leydig cell population compared to the control (unpublished data). This observation further confirms that the SF1-positive progenitor cells are transformed into fetal Leydig cells in response to Hh stimulation.

In this review, we present the hypothesis that establishment of fetal Leydig cell population is balanced by differentiation-promoting factors such as Hh and differentiation-inhibiting factors such as Notch and POD1. It remains to be determined how Hh and Notch pathways interact to maintain a progenitor cell population. If the progenitor cells are indeed present in fetal life, what will they become in the adult testis? We are currently using inducible transgenic approaches and lineage-tracing models to address these questions.

Acknowledgments

We thank Drs Buck Hales and Ken-Ichirou Morohashi for supplying antibodies. We also appreciate the technical help of Lou Ann Miller and Denise Archambeault for proofreading the manuscript at University of Illinois at Urbana-Champaign.

Supported by US National Institutes of Health grant NIH-HD046861 and HD059961 (H.H.Y.), the March of Dimes Birth Defects Foundation (H.H.Y.), and UIUC College of Veterinary Medicine's Billie Field Graduate Fellowship (I.B.B.).

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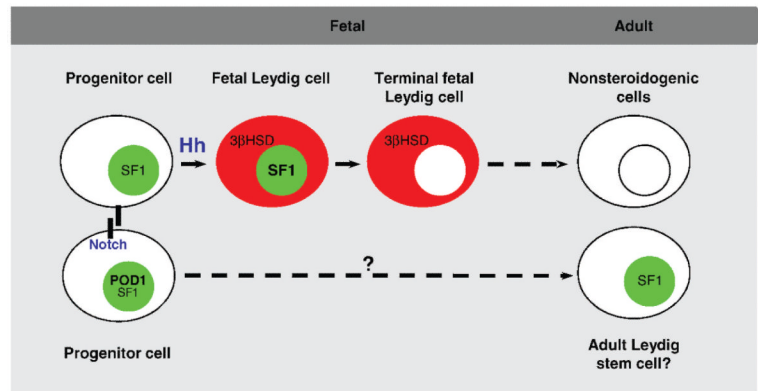


Figure. Model for maintenance and differentiation of fetal Leydig cells in mice: SF1+/3βHSD⁻ progenitor cells are transformed into fetal Leydig cells (SF+/3βHSD⁺) in response to Sertoli cell-derived Hedgehog ligands (Hh). The fetal Leydig cells eventually lose SF1 expression in fetal life and then steroidogenic ability in adulthood. A subpopulation of the progenitor cells is prevented from entering differentiation model via the Notch pathway. The progenitor cell status is putatively maintained as a result of POD1, which down-regulates SF1 expression. Color figure available online at www.andrologyjournal.org.