Disrupted gonadogenesis and male-to-female sex reversal in Pod1 knockout mice

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Summary

Congenital defects in genital and/or gonadal development occur in 1 in 1000 humans, but the molecular basis for these defects in most cases remains undefined. We show that the basic helix-loop-helix transcription factor Pod1 (capsulin/epicardin/Tcf21) is essential for normal development of the testes and ovaries, and hence for sexual differentiation. The gonads of Pod1 knockout (KO) mice were markedly hypoplastic, and the urogenital tracts of both XX and XY mice remained indistinguishable throughout embryogenesis. Within Pod1 KO gonads, the number of cells expressing the cholesterol side-chain cleavage enzyme (Scc) was increased markedly. Biochemical and genetic approaches demonstrated that Pod1 transcriptionally represses steroidogenic factor 1 (Sf1/Nr5a1/Ad4BP), an orphan nuclear receptor that regulates the expression of multiple genes (including Scc) that mediate sexual differentiation. Our results establish that Pod1 is essential for gonadal development, and place it in a transcriptional network that orchestrates cell fate decisions in gonadal progenitors.

Key words: Pod1, Tcf21, Sf1, Gonadogenesis, Testis development, Sex reversal, Leydig cell

Introduction

Mammalian sexual differentiation is a complex process that begins with the establishment of genetic sex (XX or XY) at the time of fertilization. In mice, the bipotential gonads arise from the coelomic epithelium of the urogenital ridges and initially are indistinguishable in males and females. Between 10.5 and 12.5 days post coitum (dpc), a gene on the Y chromosome, designated Sry, initiates the male developmental pathway (Gubbay et al., 1990; Koopman et al., 1990; Sinclair et al., 1990). By 12.5 dpc, the XY gonads form testicular cords, which contain fetal Sertoli cells and primordial germ cells, surrounded by peritubular myoid cells, steroidogenic Leydig cell precursors, and developing blood vessels in the interstitial region. In the absence of Sry, an ovary develops that contains granulosa and steroidogenic thecal cells. In contrast to the testis, morphogenesis of the ovary occurs postnatally and depends upon the presence of viable XX germ cells (McLaren, 1991).

Further reproductive development of the internal and external genitalia is determined by the presence or absence of a functioning testis. The internal genitalia derive from either the Müllerian (paramesonephric) or Wolffian (mesonephric) ducts, which initially are present in both XX and XY embryos. Sertoli and Leydig cells produce three hormones that mediate male sex differentiation. Sertoli cells produce anti-Müllerian hormone (AMH), which causes regression of the Müllerian ducts. Leydig cells produce testosterone, which induces the formation from the Wolffian ducts of seminal vesicles, epididymis, vas deferens, and the peptide hormone insulin-like 3 (Insl3), which is essential for normal testes descent. In the absence of testicular hormones, the Wolffian ducts regress and the Müllerian ducts form the oviducts, Fallopian tubes, uterus and upper vagina in the female developmental pathway (Byskov and Hoyer, 1994).

Although Sry unequivocally initiates the male developmental pathway, most of the mechanisms that mediate testes development remain to be defined. Gene knockout studies have established essential roles in early gonadal development for several transcription factors, including Wilms tumor suppressor 1 (WT1) (Kreidberg et al., 1993), lim-homeodomain protein (Lhx9) (Birk et al., 2000), and the orphan nuclear receptor steroidogenic factor 1 (Sf1) (Parker et al., 1996), but the precise mechanisms by which these genes contribute to gonadogenesis remain undefined. Even less is known about the transcriptional pathways downstream of these genes that establish specific gonadal cell lineages, and this remains a key area for ongoing investigations.

Transcription factors with the basic helix-loop-helix (bHLH) motif play crucial roles in cell fate determination and differentiation in a variety of tissues, including the gonads. For example, the bHLH factor Hand1 is required for gonadal
development in *C. elegans* (Mathies et al., 2003), whereas the bHLH gene *FIG alpha* (*Figla*) is required for formation of the primordial follicles in the mammalian ovary (Soyal et al., 2000). To date, however, no bHLH factors have been implicated in mammalian testes development or prenatal sex differentiation.

We previously identified a bHLH protein named Pod1 and generated a null *Pod1* allele through homologous recombination in embryonic stem cells (Quaggin et al., 1999; Quaggin et al., 1998). *Pod1* KO mice displayed defects in kidney, facial muscle, and splenic development, and died at birth from respiratory failure due to an absence of alveoli (Lu et al., 2000; Lu et al., 2002; Quaggin et al., 1999). We subsequently noted that the external genitalia were feminized in XY *Pod1* KO pups (data not shown), prompting us to examine the role of *Pod1* in gonadal development. We show here that the absence of *Pod1* in the urogenital ridges leads to ectopic expression of Sf1, aberrantly committing a population of urogenital progenitor cells to a steroidogenic cell fate in both XX and XY gonads, and disrupting normal processes of gonadal development.

**Materials and methods**

**Targeted disruption of *Pod1* and collection of fetal tissues**

Generation of the *Pod1* targeting vector and *Pod1* KO mice has been described in detail (Quaggin et al., 1999). lacZ and neomycin cassettes replace the first exon that encodes the entire bHLH domain generating a null *Pod1* allele. For timed matings, noon of the day when a vaginal plug was detected was counted as 0.5 dpc. Tail or head DNA was purified from embryos at 11.0-18.5 dpc, or from pups from postnatal day 0 (P0) onwards. The *Pod1* genotype was determined by Southern blot analysis or polymerase chain reaction (PCR), as described (Quaggin et al., 1999). Genetic sex was determined by PCR using *Zfy* primers, which generated a 180-bp fragment in XY samples (Gubbay et al., 1992), and *Rapsyn* primers (Colvin et al., 2001), which generated a 589-bp fragment in all samples.

**X-gal staining**

Whole genital ridges containing the mesonephros and gonads from embryos at 11.5 and 12.5 dpc were dissected in phosphate-buffered saline (PBS) and transferred to *lacZ* fixative for 30 minutes at room temperature, as described (Partanen et al., 1996). Samples were then rinsed in wash buffer and incubated in *lacZ* stain at 37°C for 20-30 minutes, and post-fixed in 10% formalin for 2 hours. The gonads from XX and XY embryos at 18.5 dpc were dissected and fixed in *lacZ* fixative for 1 hour at room temperature. After rinsing in *lacZ* wash buffer, the gonad was immersed in 30% sucrose overnight at 4°C, and embedded in OCT. Ten micrometer thick sections were cut with a microtome blade on a Leica CM-3050 cryostat. Samples were rinsed in wash buffer, then incubated in *lacZ* stain for 1-4 hours, post-fixed in 10% formalin and counterstained with nuclear Fast Red.

**Whole-mount double-label immunohistochemistry**

Embryonic genital ridges were dissected and fixed overnight in 4% paraformaldehyde at 4°C. Samples were then washed in PBS and blocked in a solution of 3% BSA, 1% heat-inactivated goat serum, and 0.1% Triton X-100 in PBS for 2-3 hours at room temperature before staining with antibodies. The primary antibodies used were anti-CD31/PECAM (Pharmingen, Ontario, Canada; 1:300 dilution), anti-laminin (1:300 dilution), anti-Sf1 (1:500 dilution), anti-β-galactosidase (Promega, Madison, WI, USA; 1:200 dilution) and anti-GFP (Molecular Probes, Eugene, OR; 1:2000 dilution). Samples were incubated in the primary antibodies and rocked at 4°C overnight. After washing four times for at least 1 hour in PBT, samples were incubated with secondary antibodies for 1 hour. The secondary antibodies used were Cy3-conjugated goat anti-rat IgG (Jackson Laboratories, Ontario, Canada; 1:500 dilution) to detect anti-CD31, Cy3-conjugated donkey anti-mouse IgG (Jackson Laboratories; 1:200 dilution) to detect anti-β-galactosidase and FITC-conjugated goat anti-rabbit IgG (Jackson Laboratories; 1:500) to detect anti-laminin, anti-GFP or anti-Sf1. Samples were finally washed four times for 1 hour in PBT and mounted in DABCO (Sigma) for subsequent confocal microscopy with a Zeiss LSM 410 laser scanning confocal microscope.

**Migration assays**

XY gonads from 12.5 dpc ICR (albino outbred strain; JAX Laboratories, Bar Harbor, ME, USA) or *Pod1*−/− mice were assembled with mesonephroi from 11.5 dpc GFP-positive mice and co-cultured on an agar block for 46 to 72 hours, as described (Martineau et al., 1997). A total of 20 experiments were performed with 10 mice of each genotype. The GFP-positive mice were generated in the laboratory of Dr A. Nagy and express enhanced green fluorescent protein ubiquitously (gift of A. Nagy, Samuel Lunenfeld Research Institute). Organ cultures were collected and fixed, and wholemounts were immunostained for GFP and CD31, and visualized by confocal microscopy as described above.

**In situ hybridization**

In situ hybridization was performed on paraformaldehyde-fixed/OCT-embedded sections, as described (Conlon and Rossant, 1992). Whole-mount in situ hybridization was performed, as previously described (Wilkinson and Nieto, 1993). Probes used for in situ hybridization were the murine *Scc* probe, a 0.5-kb *EcoRI-BamHI* fragment (Martineau et al., 1997), *Sox9* (mouse, pSox9, 0.5-kb *SmaI* fragment) (Wright et al., 1995), mouse 11 *beta-hydroxylase* (Domáčik et al., 1991) (564 bp fragment), *Dhh* (Yao et al., 2002), *Dmel* (a gift from David Page, MIT; which contains bases 602-1245 of the Dmel gene, GenBank NM 010599), *Wnt4* (a gift from Andy McMahon at Harvard; includes the entire coding region), *follistatin* (a gift from Martin Matzuk at Baylor; consists of a 846 bp fragment of the 3’ UTR of the follistatin cDNA). Digoxigenin-labeled probes were prepared according to the Boehringer-Mannheim-Roche protocol.

**Analysis of apoptosis**

Apoptosis analysis was performed on paraffin sections using TUNEL labeling methods. Embryonic genital ridges were dissected and fixed in 10% formaldehyde at 4°C and embedded in paraffin wax. After dewaxing, samples were rehydrated and digested, before being pre-incubated with One-Phor-ALL-buffer (Amersham Pharmacia Biotech, Canada) for 10 minutes and incubated with TdT solution mix, which includes 1 × one-Phor-ALL-buffer; 6 nM Biotin-16-dUTP (Roche Applied Science, Canada), 1 μM dATP; 0.2 U TdT enzyme and 0.01% Triton X-100, for 2 hours at 37°C. Samples were then incubated in ABC solution (VectorStain Kit; Vector Laboratories, Burlingame, CA 94010) and further developed with DAB (Peroxidase Substrate Kit DAB, Vector Laboratories) color staining. Samples were counterstained with Hematoxylin, dehydrated, mounted and photographed.

**Results**

The internal and external genitalia of *Pod1* KO mice develop abnormally

As described previously, *Pod1* KO mice die shortly after birth because of severe lung defects (Quaggin et al., 1999). Although XX and XY *Pod1* KO mice were born in the expected 50:50 ratio, the external genitalia were feminized in XY pups such that all pups were indistinguishable externally (data not shown). To determine the basis for this sex reversal, we
Pod1 is required for sexual differentiation

Pod1 is expressed in both XX and XY gonads during embryogenesis

The dramatic gonadal phenotype in male and female Pod1 KO mice could reflect either intrinsic defects in the gonads or secondary effects due to lack of Pod1 expression in other sites. To investigate Pod1 expression, we took advantage of a lacZ
reporter gene incorporated into the KO allele in Pod1+/– mice. At 11.5 dpc, lacZ staining was observed in both XY and XX urogenital ridges (Fig. 2A,B). Sections taken from the stained urogenital ridges demonstrated that Pod1 expression in both sexes localized primarily to the coelomic epithelium of the gonad, and to the boundary region between the gonad and mesonephros (Fig. 2C,D). At 12.5 dpc, lacZ expression persisted in both XY and XX gonads (Fig. 2E,F), with somewhat higher expression seen in XY gonads (Fig. 2G,H), mostly concentrated in the coelomic epithelium.

At 18.5 dpc, lacZ staining again was observed in both XY and XX gonads (Fig. 2I,J). Again, expression was primarily restricted to the coelomic epithelium and some underlying cells (G,H). At 18.5 dpc, high levels of lacZ expression were observed in the interstitial cells of the testis (I,K) both in fetal Leydig cells (le) and in the peritubular myoid cells (pm) surrounding the testicular cords (tc). lacZ was also expressed throughout the developing ovary (J,L). Expression was concentrated particularly in the ovarian medulla (arrowhead), and in cells surrounding the developing follicles, which may represent theca cell progenitors. The inset (L) shows Pod1 expression in pericytes (pe) associated with a capillary. go, gonad; ce, coelomic epithelium; m, mesonephros; le, Leydig cells; pm, peritubular myoid cells; tc, testicular cords; pe, pericyte; en, endothelial cell.

lacZ-expressing cells were concentrated in the ovarian medulla and in the interstitial spaces between forming follicles. Similar lacZ expression patterns were observed in the adult testis and ovary, and in situ hybridization for Pod1 transcripts confirmed the expression patterns observed with the lacZ reporter (data not shown).

**Early gonad development is disrupted in Pod1 KO mice**

To pinpoint when the Pod1 KO gonads first exhibit abnormalities, we examined earlier stages of gonad development. Gonads are distinguishable from the mesonephros by approximately 10.5 dpc. In males, the Sertoli cells cluster around the primordial germ cells at ~12.0 dpc to initiate testicular cord formation, and by 12.5 dpc, the testes can be grossly distinguished from the ovaries because they are larger and exhibit a male-specific vascular pattern.

At 11.0 dpc, differences were already observed between Pod1 KO and wild-type gonads. Both XY and XX Pod1 KO gonads were slightly shortened in length and had an irregular surface (data not shown). At 12.5 dpc, testes from Pod1 KO embryos lacked the features of normal testes noted above, and instead resembled Pod1 KO ovaries (Fig. 3A,B). Both XY and XX Pod1 KO gonads displayed morphological abnormalities, including a large invagination of the surface epithelium near the anterior end of the gonad (Fig. 3A,B).

Microscopic examination of sections from wild-type testes at 12.5 dpc revealed testicular cords, peritubular myoid cells, and extensive mesenchyme in the interstitium between cords (Fig. 3C), whereas no such histological organization was observed in Pod1 KO testes (Fig. 3E). In genetic females, both wild-type and Pod1 KO ovaries exhibited little morphological differentiation and showed a similar arrangement of germ and somatic cells. The Pod1 KO ovary, however, lacked a distinct mesenchymal zone (Fig. 3D,F).

To further assess testicular cord formation in Pod1 KO testes, we examined expression of laminin and CD31/PECAM. Laminin is a component of the basal lamina deposited by Sertoli cells that delineates testicular cords, whereas PECAM...
is a membrane protein specific to germ cells and vascular cells. Wild-type testes at 12.5 dpc displayed numerous cords that were clearly outlined by the laminin staining (Fig. 4A). The characteristic male-specific coelomic vessel was clearly visible in the mesenchyme just beneath the coelomic epithelium (Fig. 4C). By contrast, the Pod1 KO testes (Fig. 4B) lacked testicular cords and the coelomic vessel. The coelomic epithelium (blue arrowheads) was highly disorganized and invaginated in many locations. In wild-type females (E,G), no clear morphological organization was observed at this stage of development. However, compared with the control, the Pod1 KO XX gonad (F,H) exhibited a very disorganized surface epithelium, similar to that in gonads from the XY mutant. Of note, germ cell numbers did not appear to be affected in either XY or XX Pod1 KO mice.

Fig. 3. Abnormal gonadal morphology in both male and female Pod1 mutants. (A) At 12.5 dpc, gonads from XY Pod1 KO mice (bottom) were smaller than in the wild-type testes (top). (B) Gonads from a Pod1 KO XX embryo at 12.5 dpc also were reduced in size compared with the control. In both XY and XX Pod1 KO embryos, an abnormal invagination of the surface was observed at the anterior region of the gonad (g) (arrowheads). g, gonad; m, mesonephros. (C-F) Semi-thin sections from 13.5 dpc gonads were stained with Toluidine Blue. At 13.5 dpc, the wild-type XY gonad (C) showed organized testicular cords (tc), peritubular myoid cells (pm) and extensive mesenchyme (m). However, no organized testicular cords, peritubular myoid cells or mesenchyme were seen in Pod1 KO XY gonads (E). At 13.5 dpc, Pod1 KO XX gonads (F) showed a similar arrangement of germ (g) and somatic (s) cells as the control (D), but lacked the small but distinct mesenchymal zone near the coelomic epithelium. tc, testicular cord; pm, peritubular myoid cell; m, mesenchyme; ce, coelomic epithelium; g, germ cell; s, somatic cell.

Fig. 4. Structural and vascular defects in Pod1 KO mice. Confocal images are shown of 12.5 dpc gonads double-labeled with antibodies to laminin (green) and CD31/PECAM (red), which labels both germ cells (round) and vascular cells (elongated). In wild-type males at 12.5 dpc (A,C), the green laminin staining delineated numerous testicular cords (tc, arrows). The wild-type testes also displayed the characteristic coelomic vessel, which forms right beneath the coelomic epithelium (C, white arrowheads). In the Pod1 KO testes (B,D), no testicular cords were present and the coelomic vessel was also absent. The coelomic epithelium (blue arrowheads) was highly disorganized and invaginated in many locations. In wild-type females (E,G), no clear morphological organization was observed at this stage of development. However, compared with the control, the Pod1 KO XX gonad (FH) exhibited a very disorganized surface epithelium, similar to that in gonads from the XY mutant. Of note, germ cell numbers did not appear to be affected in either XY or XX Pod1 KO mice.
At 12.5 dpc, germ and somatic cells were intermingled throughout the wild-type ovaries (Fig. 4E,G), which lacked a distinct histological organization. However, obvious differences were observed in the Pod1 KO XX gonads, which closely resembled the Pod1 KO XY gonads (Fig. 4F,H) and displayed an irregular coelomic epithelium with one large invagination and a similar vascular pattern.

Vascular development is abnormal in Pod1 KO gonads because of an intrinsic defect in the gonad

Endothelial cell migration from the mesonephros into the developing gonad is an early event in testis development (Brennan et al., 2002). We therefore used co-culture migration assays to determine whether defective endothelial cell migration contributed to the abnormal development of the coelomic vessel and other vessels in the mutant testes. GFP-expressing wild-type mesonephroi were combined with wild-type or Pod1 KO 12.5 dpc XY gonads, and co-cultured for 48 to 72 hours (Fig. 5A,B). By 48 hours, a GFP-positive vascular network was clearly observed in wild-type gonads but was absent from Pod1 KO gonads. Although this result is interesting and may explain the defects in vascular patterning observed in the mutant gonads, it is not clear whether Pod1 is normally required within the gonad for endothelial cell migration to occur, or if other morphological defects in the mutant gonads are responsible for the block in migration.

Because Pod1 also is expressed in pericytes that surround developing capillaries, we used electron microscopy to determine whether pericytes were affected in mutant Pod1 gonads. At 13.5 dpc (Fig. 5G-J), pericytes were clearly visible around developing capillaries in the wild-type gonads, but were absent in Pod1 KO gonads. These results suggest that the absence of Pod1 impedes the differentiation of pericytes, which in turn may be associated with the impaired vasculogenesis seen in the Pod1 KO gonads.

Sertoli cells can still differentiate in Pod1 KO testes

Sertoli cells are the first somatic lineage to arise in the testes and are believed to play a crucial role in its subsequent differentiation and organization. To determine whether Sertoli cell differentiation was disrupted in Pod1 KO testes, we examined the expression patterns of two Sertoli cell-specific markers, Sox9 and desert hedgehog (Dhh). At 12.5 dpc, both Sox9 and Dhh were highly expressed in the wild-type testes (Fig. 6A,C), but were absent in wild-type ovaries (Fig. 6B,D). Both Sox9 and Dhh were expressed in the Pod1 KO testes, although transcript levels were decreased, particularly in the anterior domain (Fig. 6A,C). Real-time PCR data analysis showed no difference in Sry expression between Pod1 KO and Pod1+/− XY gonads (data not shown). These results suggest that Pod1 is not required for Sertoli cell differentiation (as these cells express Sertoli cell-specific markers), but rather that it may be required for the maintenance or expansion of the Sertoli cell population. As expected, neither Sox9 nor Dhh were expressed in Pod1 KO ovaries. By 18.5 dpc, no Sox9 or Dhh expression was observed in XY Pod1 KO gonads (not shown), although this may reflect the degeneration of the mutant gonads rather than a disruption of later Sertoli cell development.

The steroidogenic cell population is expanded in Pod1 KO gonads

Leydig cells are first observed in the embryonic testes shortly after Sertoli cells arise (e.g. at ~12.5 dpc). The cholesterol side-chain cleavage enzyme (Scc) is an early marker for Leydig cell differentiation and catalyzes the initial reaction in the steroidogenic pathway (Morohashi and Omura, 1996; Rice et al., 1990). Scc is also a marker for the steroidogenic cells of the adrenal glands, which arise adjacent to the gonads. We therefore examined Scc expression to assess steroidogenic cell differentiation and development in Pod1 KO mice. At 12.5 dpc, Scc was expressed in scattered cells throughout the wild-type XY testes, as well as in the adrenal primordium of both XY and XX wild-type embryos (Fig. 6E,F). At the same stage, Pod1 KO
 gonads had dramatically higher levels of Scc expression relative to controls, particularly within the posterior portion of the gonad (Fig. 6E,F). Although the levels of Scc expression were similar in wild-type and Pod1 KO adrenals, the developing adrenal gland in the Pod1 KO mice did not separate cleanly from the anterior portion of the gonad. The region of the mutant gonad that maintained contact with the adrenal primordium was the same region in which decreased levels of Sox9 and Dhh were observed.

Although Scc also is required for steroid hormone synthesis in the postnatal ovary, mouse ovaries normally do not express Scc in utero (Fig. 6F). Pod1 KO ovaries had marked upregulation of Scc relative to wild-type ovaries (Fig. 6F). As in XY Pod1 KO mice, this expression concentrated at the posterior region of the Pod1 KO ovary, whereas the anterior end of the gonad again appeared to be fused with the adrenal primordium (Fig. 6F).

At 11.5 dpc, Scc expression is restricted to the adrenal primordia of wild-type XX and XY embryos, but is precociously expressed throughout the gonads within the urogenital ridges of Pod1 KO XX and XY mice (Fig. 6G,H), demonstrating that the steroidogenic cell lineage is not only expanded but also differentiates prematurely in Pod1 mutants.

To determine whether other cytochrome P450 steroidogenic enzymes also were aberrantly expressed, we performed in situ analysis for the adrenal-specific enzyme, steroid 11β-hydroxylase (11β-OH). In contrast to Scc, this enzyme was appropriately restricted to the adrenal primordia in both wild-type and Pod1 KO embryos, suggesting that the absence of Pod1 does not cause a general dysregulation of steroid hydroxylase expression (Fig. 6I,J). Furthermore, these results show that although no clear morphologic boundary can be seen between the adrenal primordial and the gonad in Pod1 KO embryos, these tissues are distinguishable at the molecular level.

XX markers are expressed in Pod1 KO gonads

To determine how early ovarian development is affected in XX Pod1 mutant gonads, early markers of XX gonad formation were examined (Fig. 7). We performed in situ analysis for Wnt4 and follistatin, both markers of XX somatic cells, and Dmc1, a marker for XX germ cells entering meiosis. Wnt4 is normally expressed within the gonads of XX but not XY mice at 12.5 dpc. Wnt4 was expressed in both mutant and wild-type XX gonads at this stage. Of note, expression of Wnt4 in the mesonephros was increased in both XX and XY mutants, as compared with controls, but the significance of this is not clear. Follistatin (Menke and Page, 2002) was also expressed in both mutant and wild-type XX gonads at this stage. Finally, Dmc1 (Menke et al., 2003) expression was also observed in Pod1 mutant XX gonads. These results demonstrate that both somatic cells and germ cells initiate aspects of normal ovarian development, but this is clearly disrupted by 18.5 dpc, as no meiotic germ cells are observed in Pod1−/− XX gonads at this stage.

The domain of Sf1 expression is expanded in gonads and mesonephroi of Pod1 KO mice

Steroidogenic factor 1 (Sf1) is an orphan nuclear receptor that

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**Fig. 6.** Disruption of male-specific markers in Pod1 KO gonads. Whole-mount in situ hybridization for Sox9 (A,B) and Dhh (C,D) was performed with gonads from 12.5 dpc embryos. Sox9 and Dhh were expressed by Sertoli cells in wild-type testes (A,C, top), but were absent in wild-type XX gonads (B,D, top). In Pod1 XY mutants (A,C, bottom), expression of both Sox9 and Dhh was reduced relative to controls, especially in the anterior domain of the gonad (arrowheads). Neither Sox9 nor Dhh was expressed in gonads from XX mutants (B,D, bottom). Scc, a marker of Leydig and adrenocortical cells, was expressed in the wild-type XY gonad (E), and in the adrenal primordial cells (ap) of both XY (E) and XX (F) wild-type embryos. Pod1 mutant XY and XX gonads (E,F) had greatly increased Scc expression, particularly at the posterior end of the gonad. Of note, the anterior ends of the Pod1 KO gonads did not separate from the adrenal primordium (E,F; arrowheads), although a distinct boundary between the gonads and adrenal glands was present in the controls (E,F, arrowheads). (G,H) At 11.5 dpc, Scc expression was restricted to adrenal primordia (ap) of wild-type XX and XY embryos, but was seen throughout the gonads (go) within the urogenital ridges of Pod1 mutant XX and XY gonads. (I,J) The adrenal-specific steroidogenic marker 11β-hydroxylase was expressed appropriately in the adrenal primordia (ap) of both wild-type and Pod1 KO mice at 12.5 dpc. ap, adrenal primordia; go, gonad.
plays key roles in steroidogenesis and reproduction. Of note, Sf1 KO mice have adrenal and gonadal agenesis, establishing its essential roles in development of the primary steroidogenic tissues (Parker, 1998; Parker et al., 1996; Parker and Schimmer, 1997). Sf1 is first expressed in the urogenital ridge at ~9 dpc and this expression continues in the early gonads. As sex differentiation occurs, Sf1 expression in the ovary decreases at ~12.5-13.5 dpc, whereas expression persists in both Sertoli cells and Leydig cells in the testes. Sf1 has been proposed to be an essential regulator of Scc, prompting us to examine whether the dysregulation of Scc might reflect abnormal expression of Sf1. In wild-type testes at E11.5, Sf1-positive cells were scattered throughout the interior of the gonad (Fig. 7A), and no Sf1-positive cells were observed in either the coelomic epithelium or the boundary area between the gonad and the mesonephros. In both male and female Pod1 KO embryos, Sf1 expression was increased in both the coelomic epithelium and the boundary region between the gonad and mesonephros (Fig. 8A, and data not shown), where Pod1 is normally expressed (Fig. 8A). Furthermore, the number of Sf1-positive cells throughout the gonad was increased considerably, very likely in the same cells that aberrantly express Scc.

To determine whether Sf1 is ectopically expressed in the same cells that normally express Pod1, immunohistochemistry was performed using antibodies to β-galactosidase and Sf1. At 12.5 dpc, Pod1-expressing cells do not express Sf1 in heterozygotes. However, co-expression of both Sf1 and β-galactosidase can be seen in mutant gonads using confocal microscopy and immunostaining for β-galactosidase and Sf1 (Fig. 8B).

**Discussion**

Previous studies have defined essential roles of Pod1 in lung, kidney, facial muscle, and splenic development. We now extend these analyses to the gonads, showing that Pod1 deficiency markedly impaired gonadal development and sex differentiation. We further provide a potential mechanism – the dysregulated expression of Sf1 – to explain the gonadal abnormalities seen in the Pod1 KO mice.

We show here for the first time that Pod1 is expressed in the indifferent gonad at 11.5 dpc, subsequently localizing to the interstitial region as the testes form discrete compartments. By 18.5 dpc, the Pod1-directed lacZ reporter in testes was expressed in peritubular myoid cells, fetal Leydig cells, and pericytes surrounding blood vessels, whereas lacZ-expressing cells in the ovaries were found in the medulla and the interstitial spaces between the primordial follicles. We also noted lacZ expression directed by Pod1 regulatory sequences in the coelomic epithelium of the gonad and mesonephric stromal cells at the boundary between the gonad and mesonephros. Thus, the gonadal abnormalities seen in Pod1 KO mice, which are apparent by the indifferent gonad stage at 11.5 dpc, may reflect intrinsic defects in cells that arise directly in the indifferent gonad. However, Pod1 is also expressed in regions from which progenitor cells migrate into the gonads to generate several somatic lineages in the interstitial region of the testes (Karl and Capel, 1998; Martineau et al., 1997). Although further studies with cell-specific KO of Pod1 are needed, it is likely that both intragonadal and extragonadal expression of Pod1 is required for normal development of the gonads.

One striking defect in Pod1 KO testes is the absence of the characteristic coelomic vessel. Furthermore, vascular abnormalities were observed throughout both XX and XY gonads. Migration assays showed that endothelial cell migration from wild-type GFP-expressing mesonephroi into XY KO gonads was markedly decreased compared with wild-type gonads. This observation most likely explains the absence of the male-specific coelomic vessel and its branches in the testes, as these structures are known to derive from migrating endothelial cells (Brennan et al., 2002). Gonadal pericytes, which are intimately associated with endothelial cells, also express Pod1. Defects in pericyte differentiation have previously been described in Pod1 KO mice (Cui et al., 2003), and pericytes are absent in Pod1 KO gonads. Disrupted pericyte development in Pod1 KO mice may contribute to the observed vascular defects, as previous studies have shown that
Pod1 is required for sexual differentiation

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Fig. 8. Expansion of Sf1 expression in gonads and mesonephroi of Pod1 KO mice. (A) In situ hybridization analyses and immunohistochemistry of transverse sections and whole-mount genital ridges of XY gonads (go) at 11.5 dpc are shown. Gonads were labeled with a riboprobe against Pod1, or double-labeled with antibodies to Sf1 (green) and PECAM (red). Pod1 expression was concentrated in the coelomic epithelium (arrows) and the boundary of the gonad and mesonephros (arrowheads). Sf1-positive cells were evenly scattered in the interior of the control XY gonads. In the Pod1 KO XY gonads, Sf1 expression was increased in both the coelomic epithelium (arrow) and the interior of the gonad. A large population of Sf1-positive cells was seen at the boundary region between the gonad and the mesonephros (arrowhead). Note that the coelomic epithelium and the boundary between the gonad and the mesonephros are domains where Pod1 is expressed. (B) Confocal images of 13 dpc gonads double-labeled with antibodies to Sf1 (green) and β-gal (red). In 13 dpc XX and XY control gonads, Sf1 is not expressed in cells that express the Pod1lacZ reporter gene. By contrast, Sf1 is co-expressed in mutant Pod1lacZ-expressing cells (arrowheads, yellow). (C) Model for Pod1 function in XY gonad development. Pod1 is proposed to repress Sf1 expression in a pluripotent interstitial cell precursor (in the mesonephros and/or coelomic epithelium, ce), thereby permitting differentiation of several interstitial cell lineages, including fetal Leydig cells (Le), peritubular myoid cells (PMC) and pericytes (Pe). Loss of Pod1 leads to ectopic expression of Sf1, and prematurely commits the progenitor cells to a steroidogenic cell lineage.
Consistent with this model, Pod1 repressed Sf1 promoter activity in mouse Y1 and MA-10 steroidogenic cell lines in a dose-dependent manner (data not shown). Moreover, mutation of the E box at −82 to −77 markedly decreased Sf1 promoter activity, as previously described (Tamura et al., 2001). Although previous studies have shown that Pod1 can bind to the E-box in the smooth muscle α-actin and p21 promoters (Funato et al., 2003; Hidai et al., 1998; Lu et al., 1998), the E-box in the Sf1 promoter does not contain the Pod1 consensus sequence determined through binding-site selection (P. Igarashi, unpublished). Furthermore, Pod1 was unable to bind to the Sf1 E-box element in EMSAs, even in the presence of the cofactor E12 (data not shown). Instead, we found that Pod1 can inhibit the binding of Usf1 to the Sf1 E-box in a dose-dependent manner (data not shown), thus preventing the action of this known activator of Sf1 expression (Daggett et al., 2000) although co-immunoprecipitation results failed to show that Pod1 directly interacts with the Usf1 protein. Collectively, our results suggest that Pod1 represses Sf1 expression in an indirect manner.

Although our results do not prove that the ectopic expression of Sf1 causes the impaired gonadogenesis in Pod1 KO mice, they do demonstrate a striking association between Pod1 deficiency and dysregulated Sf1 expression. Based on this association, we propose that Pod1 normally represses Sf1 expression in a pluripotent interstitial progenitor cell population, and that dysregulated expression of Sf1 in Pod1 KO mice commits them to differentiate prematurely or excessively towards the steroidogenic cell lineage (Fig. 5C). Similar ectopic expression of Sf1 in embryonic stem cells forced them to differentiate towards a steroidogenic cell fate, and to express Scc (Crawford et al., 1997). In the XY gonad, we further propose that expansion of the Leydig cell population is associated with the loss of peritubular myoid cells and pericytes, thereby disrupting the organization of testicular structure and vasculature. Although the different cell types in the embryonic ovary are less well defined, a similar increase in the steroidogenic lineage was observed, suggesting that Pod1 plays similar roles in both sexes during the early stages of gonad formation. Regardless of the underlying mechanism, our studies show that Pod1 is essential for testis and ovary development, and establish a novel transcriptional pathway for allocating the somatic cell lineages within the gonad.

Despite the expanded domain of Sf1 and Scc expression, neither XX nor XY pups underwent virilization of internal or external genitalia, and the testes failed to descend. These findings suggest that the biosynthesis of all three mediators of male sex differentiation is impaired in XY Pod1 KO mice. As noted above, ectopic Sf1 expression in embryonic stem cells induced the expression of Scc but did not induce the full complement of steroidogenic enzymes (Crawford et al., 1997). Studies of KO mice and of patients with impaired sex differentiation suggest that multiple genes interact to direct the complex developmental events in gonadogenesis and sex differentiation (Parker et al., 1999); thus, the combined activation of several genes may be needed to induce the biosynthesis of the hormones that mediate male sex differentiation. Alternatively, it remains possible that the impaired virilization in Pod1 KO mice results from degeneration of Leydig cells and/or the vascular defects described above. Nonetheless, our data are consistent with analyses of humans with autosomal dominant and recessive inactivating mutations in Sf1 (Achermann et al., 1999; Achermann et al., 2002), suggesting that precise regulation of Sf1 is required for normal gonadal development.

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