NODAL in the Uterus Is Necessary for Proper Placental Development and Maintenance of Pregnancy

Authors: Craig B. Park, Francesco J. DeMayo, John P. Lydon, and Daniel Dufort
Source: Biology of Reproduction, 86(6)
Published By: Society for the Study of Reproduction
URL: https://doi.org/10.1095/biolreprod.111.098277
NODAL in the Uterus Is Necessary for Proper Placental Development and Maintenance of Pregnancy

Craig B. Park, Francesco J. DeMayo, John P. Lydon, and Daniel Dufort

 Division of Experimental Medicine, Royal Victoria Hospital, McGill University Health Centre, Montreal, Quebec, Canada
 Centre for the Study of Reproduction at McGill, Royal Victoria Hospital, McGill University Health Centre, Montreal, Quebec, Canada
 Department of Obstetrics and Gynecology, Royal Victoria Hospital, McGill University Health Centre, Montreal, Quebec, Canada
 Department of Molecular and Cellular Biology, Baylor College of Medicine, Houston, Texas

ABSTRACT

Preterm birth is the single leading cause of perinatal mortality in developed countries, affecting approximately 12% of pregnancies and accounting for 75% of neonatal loss in the United States. Despite the prevalence and severity of premature delivery, the causes and mechanisms that underlie spontaneous and idiopathic preterm birth remain unknown. Our inability to elucidate these fundamental causes has been attributed to a poor understanding of the signaling pathways associated with the premature induction of parturition and a lack of suitable animal models available for preterm birth research. In this study, we describe the generation and analysis of a novel conditional knockout of the transforming growth factor beta (TGFβ) superfamily member, Nodal, from the maternal reproductive tract of mice. Strikingly, uterine Nodal knockout females exhibited a severe malformation of the maternal decidua basalis during placentation, leading to significant intraterine growth restriction, and ultimately preterm birth and fetal loss on Day 17.5 of gestation. Using several approaches, we characterized aberrant placental development and demonstrated that reduced proliferation combined with increased apoptosis resulted in a diminished decidual basalis and compromised maternal-fetal interface. Last, we evaluated various components of the established parturition cascade and determined that preterm birth derived from the maternal Nodal knockout occurs prior to PTGS2 (COX-2) upregulation at the placental interface. Taken together, the results presented in this study highlight an in vivo role for maternal NODAL during placentation, present an interesting link between disrupted decidual basalis formation and premature parturition, and describe a potentially valuable model toward elucidating the complex processes that underlie preterm birth.

NODAL, placenta, preterm birth, transforming growth factor beta, uterus

INTRODUCTION

Successful mammalian reproduction culminates with the induction of parturition and delivery of the fully developed fetus. Term delivery ensures adequate time for embryonic growth and development of the biological systems required for the neonate to survive outside of the nurturing maternal environment. As a result, preterm delivery of immature offspring is a serious complication of pregnancy and is the leading cause of perinatal mortality in developed countries, accounting for approximately 75% of all neonatal deaths [1–3]. Furthermore, premature babies that survive are at an increased risk of developing neurodegenerative disorders, such as cerebral palsy, learning disabilities, impaired vision, or issues associated with psychological development, including behavioral or emotional problems [4, 5]. In addition to the long-term health and social consequences associated with preterm birth, the monetary impact on developed societies is substantial when one considers the services required to assist those who develop disabilities. It is estimated that preterm birth costs the healthcare system a minimum of $26.2 billion annually in the United States alone [6].

NODAL, a morphogen in the transforming growth factor beta (TGFβ) superfamily, plays critical roles during embryonic development by inducing mesoderm formation and patterning the left-right axis [7, 8]. Like other members of the TGFβ superfamily, signaling is achieved when diffusible NODAL ligand binds to a cell surface complex comprising type I (ALK4/ALK7) and type II (ActRIIA/ActRIIB) serine/threonine kinase receptors and an EGF-CFC coreceptor (cripto/cryptic). Activation of the receptor complex results in the downstream phosphorylation of SMAD2/3 and subsequent binding of SMAD4 prior to nuclear translocation and regulation of gene expression. NODAL signaling is regulated by complex autoregulatory interactions that propagate and restrict activity as NODAL binding results in the production of more NODAL ligand and its diffusible inhibitor, Lefty (for detailed reviews see Shen [9] and Schier [10]). Although NODAL is best known for its roles during mammalian development, components of the NODAL signaling pathway have also been implicated in many events associated with mammalian reproduction [11]. Recently, our laboratory [12] and others [13] have been characterizing the expression pattern and potential roles of NODAL signaling in the adult uterus of mice and humans, respectively. Interestingly, NODAL is expressed throughout the mouse uterus during early pregnancy and generates a banding pattern along the proximal-distal axis of the uterine horn at the time of implantation that directly correlates with the
interimplantation nodes. Furthermore, NODAL from a uterine source contributes to the maternal-fetal interface of the placenta during the later stages of pregnancy [12].

In order to further investigate the potential role of NODAL signaling during mammalian reproduction, we report here the generation of a tissue-specific conditional knockout of Nodal in the mouse maternal reproductive tract. In addition to highlighting potential roles during early pregnancy, uterine Nodal deletion promotes preterm birth and fetal loss by disrupting the maternal-fetal interface during placentation. Despite the prevalence and severity of preterm birth, our current understanding of parturition remains relatively unclear [3]. Moreover, the most significant impediment in our efforts to decrease the occurrence of premature birth has been directly attributed to our lack of understanding of the signal transduction pathways that are associated with premature parturition [14]. This is compounded by a lack of suitable animal models available for preterm birth research [15]. The results presented in this study advance our knowledge of parturition by (1) providing evidence that the NODAL signaling pathway is required to ensure successful delivery at term and (2) presenting an interesting link between disrupted placentation and preterm birth.

MATERIALS AND METHODS

Generation of Uterine NodalCre/A Mice

All animal care and experimental procedures were approved by the Animal Care Committee of the Royal Victoria Hospital and were in accordance with the regulations established by the Canadian Council on Animal Care. Mice with loxP sites flanking exons 2 and 3 of the Nodal gene (NodalloxP/loxP) on a mixed background were previously generated and kindly donated by E. J. Robertson (University of Oxford) [16]. Progesterone receptor (PgR)-Cre mice (PgRCre/+ on a C57BL/129 background were generously provided by J. F. DeMayo and J. P. Lydon (Baylor College of Medicine) [17]. Both strains have previously been reported to demonstrate normal fertility, and PgRCre/+ mice have been used in numerous studies to investigate uterine-specific gene function [18, 19]. NodalloxP/loxP mice and NodalloxP/loxP strains were crossed, and the offspring were genotyped by tail nip digestion and PCR. The NodalloxP (200 bp) and Nodal+ (220 bp) alleles were amplified by touchdown PCR (94°C, 58°C, 72°C [30 sec] for seven cycles; decreasing 0.5°C per cycle; 30 cycles at 94°C, 55°C, 72°C [30 sec]; 5'-ATCCACGATCCGAGCAATG-3', 5'-GCTATGCCACG-3'). Ten-micrometer sections were cut with a Leica RM2145 microtome at 8°C in 4% paraformaldehyde. The tissue was placed in melted paraffin wax (Tissue Tek) and xylenes 8°C, followed by pure paraffin overnight under a vacuum. Sections were placed in room temperature and the blocks were solidified at 8°C overnight. Decidua swellings were cut with a Leica RM2145 microtome and dried overnight. Slides were then washed in xylene, rehydrated with a decreasing ethanol gradient (100%, 95%, 85%, 75%, 50%, 20%; 2 min each), and counterstained with Nuclear Fast Red (Sigma) or hematoxylin & eosin (Surgipath). The stained sections were dehydrated with increasing ethanol concentrations, cleared in xylene, and mounted with paraffin glue.

Immunohistochemistry

Day 10.5 paraffin-embedded uterine sections were rehydrated as described above, treated with 3% hydrogen peroxide in methanol (20 min), boiled in 10 mM sodium citrate, pH 6.0 (15 min), and allowed to cool at room temperature. Slides were then washed with 0.5% Triton X, 0.2% bovine serum albumin/PBS (2%, 5 min), and blocked with 1.35% heat-inactivated goat serum diluted in wash buffer for 30 min at 37°C within a humidified chamber. The sections were then rinsed with 0.1% Tween 2000/PBS (3%, 5 min) and incubated overnight at 4°C with 1:100 rabbit-anti-proliferating cell nuclear antigen (anti-PCNA; sc-7907; 0.2 mg/ml; Santa Cruz Biotechnology) or goat anti-MIK167 (sc-7846; 0.2 mg/ml; Santa Cruz Biotechnology) diluted in 1% bovine serum albumin/PBS. Slides were then rinsed, probed with 1:500 goat-anti-rabbit horseradish peroxidase (HRP; sc-2004; 0.4 mg/ml; Santa Cruz Biotechnology) or donkey anti-goat HRP (sc-2020; 0.4 mg/ml; Santa Cruz Biotechnology) for 1 h at room temperature, and visualized using a 3.3-diaminobenzidine kit (Sigma). Uterine sections were counterstained with hematoxylin, dehydrated, cleared in xylene, and mounted with paraffin glue. All tissue section-based experiments (immunohistochemistry, in situ hybridization, etc.) used at least three placentae per category.

Cyroembedding and Immunofluorescence

Uteri and placentae used for immunofluorescence or in situ hybridization were dissected in cold PBS and fixed overnight at 4°C in 4% PFA/PBS. Uteri were treated with 15% sucrose for 3 h and 25% sucrose overnight at 4°C before embedding in Shandon Cryostat (Thermo Scientific) at −80°C. Ten-micrometer sections were cut with a cryotome, mounted on Super Frost Plus slides (VWR), and stored at −80°C. Immunofluorescence was performed as previously described [12]. Slides were probed with rabbit anti-NODAL (sc-2020; 0.4 mg/ml; Santa Cruz Biotechnology), 10 µg/ml; Santa Cruz Biotechnology) or goat anti-HRP (sc-2020; 0.4 mg/ml; Santa Cruz Biotechnology) for 1 h at room temperature, and visualized using a 3,3'-diaminobenzidine kit (Sigma). Uterine sections were counterstained with hematoxylin, dehydrated, cleared in xylene, and mounted with paraffin glue. All full-length cDNA used to generate the hybridization probes were kindly provided by J. Cross (University of Calgary). Tissue samples were cyroembedded, sectioned, and stored as described above. In situ hybridization was performed with the aid of the J. Cross Laboratory using the protocol developed and detailed in Simmons et al. [20]. Briefly, slides were rehydrated in PBS, postfixed with 4% PFA/PBS (10 min, 4°C), and treated with proteinase K (30 µg/ml; 12 min; Roche). Sections were acetylated (0.25% acetic anhydride, 10 min) and hybridized with digoxigenin (DIG)-labeled probes overnight at 65°C. DIG-labeled probes were generated following the manufacturer’s protocol (Roche) and were used at a concentration of 1:2000 with a 1-µg starting template DNA. Following washes in SSC (150 mM sodium chloride, 15 mM sodium citrate)/50% formalin/0.1% Tween 20 (2%) and MABT (100 mM maleic acid, 150 mM sodium chloride, and 0.1% Tween 20; 2%), slides were treated with RNAse A (20 µg/ml; Roche), blocked (2% Blocking Reagent [Roche], 20% heat-inactivated goat serum in MABT), and incubated overnight at 4°C with anti-DIG antibody diluted 1:2500 in block solution. Following MABT washes (4×), the sections were rinsed in NTMT...
(100 mM NaCl; 100 mM Tris, pH 9.5; 50 mM MgCl₂; and 0.1% Tween 20) and developed using an NBT/BCIP kit (Promega). Developed sections were counterstained in Nuclear Fast Red, dehydrated with an ethanol gradient, and mounted in Mowiol 4–88.

**Western Blot Analysis**

Indicated tissue samples (0.5 g) were isolated, rinsed in PBS, and homogenized in extraction buffer (50 mM Tris-HCl, pH 7.2; 10 mM dithiothreitol; 1% Nonidet P-40; 1 mM CaCl₂; 5 mM MgCl₂; 100 U/ml DNase I; 50 μg/ml RNase A; and 75 μg/ml protease inhibitor cocktail [P2714; Sigma]). Homogenate was centrifuged (10000 rpm, 10 min, 4°C), and supernatant was resolved on a 12% SDS-PAGE gel. Protein was transferred to polyvinylidene fluoride membrane membrane (GE Healthcare), blocked with 5% skim milk, and probed with rabbit anti-NODAL or rabbit anti-PGDS2 (COX-2; 160106; 0.1 mg/ml; Cayman Chemical) antibodies diluted 1:500 in block solution. Protein was detected with anti-rabbit HRP diluted 1:4000 and the ECL Plus kit (GE Healthcare). Membranes were subsequently stripped, probed with anti-α-tubulin loading control antibody, and developed. Relative protein concentrations were obtained with the Image J quantification software (National Institutes of Health).

**TUNEL Assay**

Apoptosis was assessed directly on paraffin-embedded sections of Day 10.5 placental tissue with the in situ cell death assay kit (Roche) following the manufacturer’s protocol. Sections were pretreated using the proteinase K option (30 μg/ml in 10 mM Tris-HCl, pH 7.5; 20 min), and positive controls were generated by incubation with 2000 U/ml DNase I for 10 min.

**Progesterone Quantification**

Progesterone concentration in maternal blood serum was quantified by radioimmunoassay with the aid of the B. Murphy laboratory (Université de Montréal; as described in Duggavathi et al. [21]).

**Statistics**

Figure data are presented as mean ± SEM of independent samples. Statistical analysis comparing two groups was performed using the standard Student two-sided t-test. Calculations were confirmed using the GraphPad software. P values less than 0.05 were considered statistically significant.

**RESULTS**

**Nodal Is Efficiently Deleted in the Uteri of NodalΔ/Δ Female Mice**

Mice in which the Nodal gene is conditionally deleted in the reproductive tract of adult females were generated by mating the floxed Nodal (NodelloxP/loxP) and Pgr-Cre (PgrCre/Cre) mouse strains (detailed in Materials and Methods) [16, 17]. In order to verify the targeted deletion of Nodal in the newly generated NodelloxP/loxP, PgrCre/+ mouse strain (denoted NodelΔ/A), genomic DNA isolated from adult uterine tissue was confirmed to have complete excision of the floxed sequence, whereas several untargeted tissues (i.e., kidney, lung, tail snip) contained the full-length Nodal gene (data not shown).

Previous studies of Nodal expression conducted in our laboratory have demonstrated that Nodal is not present in the uterus prior to coitus; however, robust Nodal expression and protein localization was observed in the uterine glandular epithelium during the early peri-implantation period (Days 0.5–3.5 postcoitum) [12]. Although NODAL protein was easily detectable by Western blotting of uterine tissue isolated from double-heterozygous control mice (NodalΔ/+), protein from the glandular epithelium of Day 3.5 NodalΔ/A uteri that were confirmed to be pregnant by embryo flushing of the contralateral uterine horn (Fig. 1, b–g). Taken together, these results verify that NODAL protein production has been effectively eliminated from the uteri of adult NodalΔ/A females.

**NodalΔ/A Females Exhibit a Reduced Rate of Fertility**

In order to assess the reproductive capabilities of NodalΔ/A mice, adult females were mated with CD1 males overnight, and successful copulation was determined by the presence of a vaginal plug the following morning (Day 0.5). Interestingly, plugged NodalΔ/A females demonstrated a reduced ability to establish pregnancy, because mice examined after implantation (on or after Day 5.5) rarely contained decidua swellings or developing embryos (26.3%; n = 19; Fig. 2a and Supplemental Table S1). Full supplemental materials are available online at (www.bioleprod.org)). Preliminary analysis suggests this reduced fertility occurs during early reproduction but is not due to a defect in ovulation, because the number of corporal lutea remains unaffected in floxed control (NodelloxP/loxP, PgrCre/+), double-heterozygous control (NodalΔ/Δ), and Nodal-deleted females (NodelΔ/A, data not shown). The precise role of uterine NODAL in facilitating early reproduction is currently under investigation but beyond the primary focus of this study.

**NodalΔ/A Females Experience Preterm Birth and Fetal Loss**

Strikingly, pregnant NodalΔ/A females that overcome the reduced fertility associated with early reproduction ultimately experienced spontaneous preterm birth on Day 17.5 of gestation, a phenotype very rarely observed in mice [15]. A total of 14 pregnant NodalΔ/A mice were monitored several times daily (0900–2000 h) from Day 15.5 postcoitum until delivery. A total of 9 of the 14 NodalΔ/A females gave birth prematurely on Day 17.5, 2 days prior to normal term gestation of 19.5 days (Table 1). Two additional NodalΔ/A females gave birth moderately preterm on Day 18.5, with the remaining pregnancies going to term (11 of 14 preterm; Fig. 2b). Conversely, 17 of 18 pregnant NodalΔ/+ control females gave birth on Day 19.5, with a single premature delivery observed on Day 18.5 (1 of 18 preterm). As a result, pregnant NodalΔ/A mice experienced spontaneous preterm birth at a significantly higher rate compared with the double-heterozygous females. Despite the early delivery, we did not observe any occurrence of dystocia (abnormally long, difficult delivery) in the experimental NodalΔ/A females.

In addition to premature parturition, most offspring delivered by NodalΔ/A females were stillborn or died shortly after birth. Whereas NodalΔ/+ control females averaged 5.4 live and 1.0 dead pups per dam, the experimental NodalΔ/A mice produced 2.2 live and 3.8 dead pups per dam (Fig. 2c and Table 1). It is important to note, however, most of the live pups obtained from the experimental NodalΔ/A group were contributed by females that experienced moderately premature (Day 18.5) or term deliveries. Taken together, this suggests the fetal loss is primarily due to premature birth, because pups born to pregnant NodalΔ/A females that successfully reached term had a greater likelihood of survival.

**Whole-Mount Decidualization Appears Normal During Midgestation in Pregnant NodalΔ/A Mice**

In order to investigate the underlying source of preterm birth and fetal loss in NodalΔ/A females, whole-mount uteri from pregnant mice were first isolated throughout midpregnancy (Days 6.5–12.5), and the conceptus site number, size, and weight were assessed on Day 8.5. In general, there were no observable differences between whole-mount uteri isolated from the experimental NodalΔ/A or NodalΔ/+ control females.
No significant difference was detected in the number of implantation sites recorded on Day 8.5, and the average conceptus site weight was nearly identical (Nodal$^{+/+}$, 280.4 mg; Nodal$^{+/D}$, 280.7 mg; Fig. 3, b and c, and Supplemental Table S2). Therefore, at the whole-mount level, it appears decidualization and conceptus site growth are unaffected if plugged Nodal$^{+/D}$ females overcome the early reproductive phenotype and successfully establish pregnancy.

Fetuses Developing in Pregnant Nodal$^{+/D}$ Females Experience IUGR During Late Pregnancy

Fetuses were isolated from Nodal$^{+/D}$ knockout and Nodal$^{+/+}$ control females and weighed at several time points throughout pregnancy prior to the onset of premature birth (Days 10.5–16.5). Fetuses isolated from Nodal$^{+/D}$ females were of comparable size when measured during midpregnancy, with no significant difference observed on Day 10.5 and Nodal$^{+/+}$-derived fetuses slightly larger on Day 12.5 (Fig. 4a). However, fetuses obtained from the pregnant Nodal$^{+/D}$ females exhibited significant IUGR during the later stages of pregnancy when observed on Days 15.5 and 16.5 ($P < 0.0001$ on Day 15.5/16.5). By Day 16.5, uterine Nodal deleted mice contained fetuses that were on average 32.0% smaller than those from the heterozygous control females (Nodal$^{+/+}$, 0.609 g; Nodal$^{+/D}$, 0.414 g; Fig. 4b and Supplemental Table S3). Examination of the fetuses suggested this restriction is due to inadequate intrauterine growth rather than a developmental defect or delay, because numerous Day 16.5 markers were observed in the Nodal$^{+/D}$-derived litters (i.e., asperous skin texture, defined upper lip, paralleled digits). As a result, Nodal$^{+/D}$ mothers are unable to support adequate fetal growth during mid to late gestation before the onset of preterm birth.

Placentation in Nodal$^{+/D}$ Females Is Disrupted

The timing and severity of IUGR suggest inadequate placenta development might underlie the observed phenotype. Therefore, an extensive histological examination of the extraembryonic tissues during midpregnancy was conducted. Following implantation, no observable differences were discovered in uteri isolated from Day 6.5 Nodal$^{+/D}$ and Nodal$^{+/+}$ females (Fig. 5, a and b). Embryos appeared morphologically normal, and the area of decidualization (dotted line) was equivalent. On Day 8.5, Nodal$^{+/D}$ uterine sections exhibited a slightly larger area of decidualization, with differentiated stromal cells extending further into the lateral and mesometrial endometrium (Fig. 5, c and d).

Interestingly, Day 10.5 uterine sections displayed abnormal trophoblast giant cell layer morphology around the invasive...
NODAL AND PRETERM BIRTH

FIG. 2. Nodal<sup>+/+</sup> mice exhibit reduced fertility in addition to preterm birth and fetal loss. Graphical illustration of the results presented in Table 1 and Supplemental Table S1. Nodal<sup>+/+</sup> mice mated with wildtype males displayed a low rate of establishing pregnancy (a) due to an early reproductive phenotype (26.3%; n = 19) and experience an increased rate of preterm birth (78.6%; n = 14; b) when compared with double-heterozygous Nodal<sup>+/-</sup> control mice. c) Nodal<sup>+/+</sup> litters also exhibited increased fetal wastage occurring at or shortly after parturition. Box columns display live pups per dam (bottom, colored) and dead pups per dam (top, gray) for both Nodal<sup>+/+</sup> and Nodal<sup>+/+</sup> litters. Values are mean ± SEM. SEM of dead pups per dam is positioned above the column, and SEM of live pups per dam is positioned within the column.

The Fetal Layers of the Nodal<sup>AA</sup> Placenta Remain Distinguishable with Moderate Abnormalities

In order to thoroughly characterize the observed phenotype, Day 12.5 Nodal<sup>AA</sup> and Nodal<sup>+/+</sup> control placentae were probed by in situ hybridization with numerous fetal layer markers. Prolactin family 3, subfamily d, member 1 (Prl3dl); prolactin family 3, subfamily b, member 1 (Prl3bl1); and prolactin family 2, subfamily c (Prl2c) were used to collectively identify parietal (P-), canal (C-), sinusoidal (S-), and spiral artery (SpA-) trophoblast giant cells (TGCs). Using Prl3dl, P-TGCs appear, as expected, in a defined layer along the mesometrial aspect of the fetal compartment (Fig. 6, a and b). Prl3bl1, which in addition to P-TGCs also marks C-TGCs, S-TGCs, and spongiotrophoblasts, displayed moderate disorganization in Nodal<sup>AA</sup> placentae, because staining appeared to be more robust on the mesometrial surface and extended deeper into the fetal labyrinth (Fig. 6, c and d). However, expression of Prl2c, which marks P-TGCs, C-TGCs, SpA-TGCs, and spongiotrophoblasts, remained relatively unaltered, although expression of the Prl2c marker is known to diminish considerably by Day 12.5 (Fig. 6, e and f).

Using prolactin family 8, subfamily a, member 8 (Prl8a8) and trophoblast-specific protein alpha (Tpha), two independent probes were used to mark the fetal spongiotrophoblast layer. Interestingly, Prl8a8 provided minimal staining of the spongiotrophoblast, with no observable differences between the Nodal<sup>AA</sup> and Nodal<sup>+/+</sup> sections; however, Tpha displayed a pattern of expression similar to that of the Prl3bl1, with areas of marked cells observed protruding into the labyrinth (Fig. 6, g–j). By Day 12.5, Hand1 encompassed all three major fetal layers of the placenta, marking the outer TGCs, spongiotrophoblasts, and labyrinth in both the control and experimental groups (Fig. 6, k and l).

Finally, glial cells missing 1 (Gcm1) and cathepsin Q (Ctsq) were used to identify various cell types within the labyrinth layer. Gcm1 is specifically expressed in the chorionic trophoblast cell derivatives in the labyrinth, including mononuclear and syncytiotrophoblastic cells that line the maternal blood spaces. As predicted by the spongiotrophoblast layer morphology observed in Nodal<sup>AA</sup> placentas, Gcm1 in situ hybridization produced disbanding of the complementary tissue in the labyrinth, whereas Gcm1 remained uniformly distributed in the Nodal<sup>+/+</sup> controls (Fig. 6, m and n). Gcm1 expression also appears to be more encompassing in the Nodal knockout placentae, with an increased number of positively marked cells throughout the labyrinth. Intriguingly, Ctsq, marking S-TGCs at the site of nutrient/waste exchange, appears much more...
robust and appears to encompass a larger portion of the fetal placenta in the uterine Nodal knockout samples (Fig. 6, o and p). Taken together, these experiments suggest Nodal/D/D placenta contain all of the fetal layers within the maturing placenta, but with moderate alterations in layer organization and increased Gcm1/Ctsq-expressing cells in the labyrinthine compartment.

**Maternal Decidua Basalis in the Developing NodalΔ/Δ Placenta Exhibits Reduced Proliferation and Increased Apoptosis**

As described above, the maternal decidua basalis in NodalΔ/Δ placentae becomes severely compromised by Day 12.5. In order to delineate the underlying cause(s) of the altered morphology and to provide insight into potential roles for uterine-derived NODAL, we examined several processes that can alter placental architecture. Using the PCNA marker, immunohistochemistry was performed on Day 10.5 NodalΔ/D and NodalΔ/+ placental sections. Maternal decidual tissue obtained from NodalΔ/Δ females displayed a significantly reduced level of PCNA nuclear staining in comparison with the robust signal observed in NodalΔ/+ controls (Fig. 7, a–c). Interestingly, uterine tissue immediately adjacent to the muscular myometrium appears relatively unaffected, whereas only a limited number of proliferating cells were observed in the central (Fig. 7, d–f) and antimesometrial (Fig. 7, g–i) decidua basalis of NodalΔ/Δ-derived placenta. In contrast, no difference in marker staining was detected in the fetal trophoblast giant cell, spongiotrophoblast, or labyrinth layers. Immunohistochemistry was also

![FIG. 3. Uterine deletion of Nodal does not affect postimplantation decidualization ability. a) Whole-mount uteri isolated from pregnant NodalΔ/+ and NodalΔ/Δ females on Days 6.5–12.5 postcoitum depicting relative size and quality of conceptus sites. Photographs of compared uteri were taken in the same photographic frame. If pregnancy is obtained, the number (b) and weight (c) of the conceptus site are unaffected in NodalΔ/Δ females when quantified on Day 8.5. Complete data are presented in Supplemental Table S2. Values are mean ± SEM.](https://bioone.org/journals/Biology-of-Reproduction)
performed with an alternate proliferation marker, MKI67, generating a similar pattern of expression with a marked reduction in decidua basalis expression (Supplemental Fig. S1).

In addition to proliferation, the effects of uterine Nodal deletion on apoptosis were investigated by in situ TUNEL assay on Day 10.5 placental sections. Strikingly, few apoptotic cells were detected in placentas isolated from Nodal\textsuperscript{+/\textsuperscript{+}} controls; however, abundant positively marked cells were observed throughout the maternal decidua basalis in Nodal\textsuperscript{+/\textsuperscript{-}} placentae (Fig. 8). Interestingly, a high concentration of apoptotic cells was positioned adjacent to the mesometrial aspect of the trophoblast giant cell layer. For example, several sections displayed numerous positive cells situated between the giant cell layer and uterine lumen (Fig. 8h). Taken together, the reduced maternal decidua basalis appears to be the product of reduced proliferation combined with increased cell death prior to Day 12.5 postcoitum.

The Parturition Cascade in Pregnant Nodal\textsuperscript{+/\textsuperscript{+}} Females Is Disrupted prior to the Onset of Labor

In mice, parturition is known to be regulated at the maternal-fetal interface by the production of prostaglandins derived from the cyclooxygenase (COX or PTGS)/PGFS/mPGES, and PGIS). Ultimately, the production of PGF\textsubscript{2\alpha} results in luteolysis of the ovarian corpora lutea, and subsequently a drop in maternal blood serum progesterone levels. This progesterone withdrawal is absolutely essential in mice for the cervical ripening and uterine contractions that precede birth [23]. Although several components of the parturition cascade have been identified, the precise molecular events that initiate natural parturition remain poorly understood. As a result, our ability to determine the underlying causes and contributing factors of spontaneous and idiopathic preterm birth is limited. As Nodal\textsuperscript{+/\textsuperscript{-}} females experience aberrant placentaation leading to a disrupted maternal-fetal interface prior to the onset of preterm birth, it is possible the parturition cascade has been affected or prematurely initiated because of Nodal deletion. Therefore, assessing the known components of the parturition cascade is a critical primary step toward using the Nodal\textsuperscript{+/\textsuperscript{-}} strain to elucidate the underlying mechanisms of preterm birth.

In order to determine whether the documented components of the parturition cascade are disrupted prior to preterm birth in Nodal\textsuperscript{+/\textsuperscript{-}} females, we first quantified the level of PGFS2 enzyme at the maternal-fetal interface. Interestingly, we observed a significant 2-fold increase of PGFS2 protein within the maternal tissues of Nodal\textsuperscript{+/\textsuperscript{-}} females when quantified by Western blot analysis on Day 16.5 (\(P < 0.02\); Fig. 9a). As a result, histological sections of the ovarian tissue were analyzed and the progesterone concentration in maternal blood serum was quantified by radioimmunoassay. Although we were unable to directly observe luteolysis by histological sectioning (Fig. 9b) or in situ TUNEL assay (data not shown), a significant decline in progesterone concentration was observed prior to preterm birth in the Nodal\textsuperscript{+/\textsuperscript{-}} group (Nodal\textsuperscript{+/\textsuperscript{-}}, 46.87 \pm 8.27 ng/ml; Nodal\textsuperscript{+/\textsuperscript{+}}, 28.58 \pm 3.96 ng/ml; Fig. 9c). Furthermore, four of five blood samples collected from Nodal\textsuperscript{+/\textsuperscript{-}} females on Day 16.5 had a considerably lower progesterone concentration (\(<28.0 \text{ ng/ml}; 0.59\text{-fold}\)) than the mean concentration observed in the control group. As a result, premature progesterone withdrawal occurs in a proportion of the pregnant Nodal\textsuperscript{+/\textsuperscript{-}} population that correlates with the observed rate of preterm birth (11 of 14 preterm; Fig. 2b). These observations indicate that deleting Nodal from the uterus ultimately contributes to a disrupted parturition cascade, leading to an early decline in maternal progesterone and, as a result, preterm birth. Interestingly, the precise point of deviation from the natural cascade occurs upstream of PGFS2 production, extending beyond the well-documented events that are known to mediate parturition.

DISCUSSION

In this study, we describe the generation of a novel transgenic mouse strain with a maternal-specific deletion of Nodal that displays aberrant placentaation, ultimately leading to significant IUGR, preterm birth, and fetal loss. The role of NODAL in facilitating placental development has remained a well-studied topic in trophoblast research; however, most of these studies focus on the role of NODAL derived from an embryonic origin. Indeed, complete ablation of the Nodal gene, in addition to disrupting primitive streak and mesoderm formation, also results in impaired extraembryonic tissues with an increased giant cell number and a loss of spongiotrophoblast and labyrinth [7, 24]. Furthermore, NODAL hypomorphic mice that prolong embryo development beyond chorioallantoic fusion before the onset of lethality also display an expanded giant cell and reduced labyrinth, but unexpectedly contain a larger spongiotrophoblast compartment [25]. The authors of these studies hypothesize that embryonic NODAL may be
involved in redirecting trophoblast fate toward an expansion of the labyrinth while maintaining a thin layer of trophoblast giant cells at the maternal-fetal boundary [26]. More recently, NODAL has been shown to be essential for the in vivo maintenance of the trophoblast stem cell microenvironment by preventing precocious differentiation; however, this role is likely mediated indirectly through FGF4 produced in the embryonic ectoderm [27, 28].

The results presented in this study add a new and important dimension to the role of NODAL signaling during placenta development, because eliminating the uterine contribution of NODAL to the maternal-fetal interface has severe consequences on placenta and reproductive outcome. Strikingly, the placenta of Nodal<sup>−/−</sup> mice have a significantly diminished maternal decidua basalis, and in a few cases displayed irregular extraembryonic characteristics, such as an expanded trophoblast giant cell layer or moderate spongiotrophoblast/labyrinthine disorganization. Further investigation of the underlying mechanisms revealed that increased apoptosis and reduced proliferation within the maternal compartment contributed to the decidua basalis deletion by midgestation (Day 12.5 postcoitum). Several reports have previously implicated the NODAL signaling pathway in mediating apoptosis and proliferation, although the effect of NODAL appears to vary with cell type. For example, Munir et al. [29] demonstrated that Nodal overexpression, acting through activin receptor-like kinase 7 (ALK7) and SMAD2/3, induces apoptosis and inhibits proliferation in human trophoblast cells in vitro (HTR8/SVNeo). Similar proapoptotic effects of Nodal overexpression were also observed in human epithelial ovarian cancer cells [30] and rat ovarian granulosa cells during follicular atresia [31]. However, the opposite effect was observed in orthotopic human breast cancer cells (MDA-MB-231) and melanoma tumors (C8161), because inhibition of NODAL decreased proliferation (as marked by MKI67) and increased apoptosis (TUNEL) [32]. Apoptosis is also extensive in embryonic Nodal mutants on Day 7.5 that fail to undergo mesoderm differentiation, leading the authors to suggest the loss of NODAL signal leads directly to programmed cell death of precursor ectodermal cells [33]. As presented here, the loss of maternal NODAL from the uterus during pregnancy appears to have the latter effect in vivo, because increased apoptosis and decreased proliferation lead to a significant reduction of decidua basalis tissue during placentation.

It is well documented that maternal-fetal interactions are critical for the establishment of pregnancy and generation of a healthy placenta [34, 35]. As placenta proceeds, NODAL is observable in both the developing fetal and maternal compart-
FIG. 6. In situ hybridization marker analysis of the fetal layers in mature Day 12.5 Nodal^{+/+} and Nodal^{+/−} placental sections. a and b) Prl3d1 marking P-TGCs. c and d) Prl3b1 depicting P-TGCs, C-TGCs, and S-TGCs. e and f) Prl2c marking P-TGCs, SpA-TGCs, and spongiotrophoblasts. Although Prl3d1 and Prl2c expression appears unaltered, moderate abnormalities are highlighted with Prl3b1 staining, suggesting increased C-TGCs and/or S-TGCs contained in the fetal compartment of Nodal^{+/−} samples. Prl8a8 (g and h) and Tpbpa (i and j) expression used to mark the spongiotrophoblast layer. Although Prl8a8 produced limited staining that was similar in both Nodal^{+/+} and Nodal^{+/−} placentas, Tpbpa expression displayed spongiotrophoblast cells protruding into the labyrinth layer. k and l) Hand1 expression, used to mark outer TGCs, spongiotrophoblasts, and labyrinth, was unaltered in the Nodal^{+/−} fetal compartment; however, the staining pattern highlights the lack of integration with the maternal uterine endometrium. Gcm1 (m and n) and Ctsq (o and p) expression, marking various cells within the labyrinth, displayed more encompassing and robust signals in Nodal^{+/−} knockout placenta in comparison with the Nodal^{+/+} control sections with moderate staining. All sections are counterstained with Nuclear Fast Red. Bars = 1 mm.
ments, because expression has been detected in the ectoplacental cone, chorion (Day 8.5), and spongiotrophoblast (Day 8.5) in addition to the uterine stroma (Day 8.5) and decidua parietalis (Day 10.5) [12, 26, 28]. As such, it is an interesting observation that Nodal knockout placentae, much like embryonic Nodal mutants, exhibited drastic trophoblast giant cell clustering along the maternal-fetal border on Day 10.5. Although, unexplainably, less apparent on Day 12.5 in Nodal knockout placenta and uncharacterized in null Nodal placenta because of embryonic lethality, this phenotype supports the initial function of NODAL hypothesized by Ma et al. [26] with regard to maintaining a thin giant cell layer. The morphogenetic properties and self-regulating positive/negative feedback loops associated with NODAL signaling make it tempting to hypothesize that a delicate balance of NODAL signal along, or across, the maternal-fetal interface is critical for placenta development [10]. Perhaps, endogenous NODAL protein from both fetal and maternal sources maintains proper placenta histotarchitecture, and disrupting this balance (from either source) severely affects placenta layer formation, as evident from both the Nodal null females described above and the uterine Nodal knockout mice characterized in this study. Although an interesting possibility, it remains to be seen if deleting embryonic or maternal NODAL alters the expression profile of NODAL in neighboring tissue compartments.

Following the placenta malformation, several phenotypes arise during late pregnancy as an apparent result of this placental insufficiency. First, we observed significant IUGR of fetuses developing within the uterine Nodal deleted females. As the source of the nutrients and gas exchange required for fetal development, it is easy to speculate that aberrant placenta led to insufficient nourishment and stunted growth. However, the precise underlying cause(s) remains to be determined. Interestingly, more expansive Ctsq expression, a marker of syncytiotrophoblast cells (SynT-Is), and Gcm1 were observed in the labyrinth of Nodal knockout placentae. Considering functionality, it is not inconceivable that Nodal knockout placenta may have adapted an expanded labyrinth and/or increased the surface of maternal-fetal exchange to compensate for a reduced supply of maternal blood. As one would expect, fetal growth restriction has been associated with a diminished labyrinth phenotype [36]; however, IUGR has also been observed alongside a significantly larger labyrinth layer in the streptozotocin-induced diabetic rat [37]. However, in the diabetic rat strain a thickening of the trophoblastic layers within the labyrinth was also observed and the IUGR was attributed to poor placental transfer.

During proper placental development, the most significant process to occur within the maternal uterine decidual tissue is the remodeling of the spiral arteries by invading trophoblast cells [38, 39]. During midgestation in mice, a subpopulation of interstitial and endovascular trophoblasts invade the maternal compartment and replace the smooth muscle cells that line the uterine arteries, thereby increasing blood flow for nourishment and rendering the arteries unresponsive to maternal vasoconstriction [40]. Although it has yet to be investigated, it is possible this process is compromised in Nodal knockout-derived conceptus, because placentae display a diminished decidua basalis. By removing this decidua layer, invading trophoblasts would undoubtedly experience a different physical route to the uterine arteries in addition to a potentially alternate milieu of cytokines, growth factors, hormones, or other influencing factors (μNK cells) present in the decidual layer. Inadequate or...
shallow invasion may impede blood delivery, whereas increased trophoblast migration could result in uterine hemorrhaging [41]. Interestingly, NODAL signaling itself has recently been implicated in trophoblast migration and invasion. Using both human trophoblast cell culture and first-trimester placental explants in vitro, it was demonstrated that NODAL signals through ALK7 to inhibit both the migratory ability of trophoblast cells and outgrowth of placenta explants [42]. The opposite effect was observed in siRNA knockdown of either Nodal or Alk7 [42]. Although the precise role of NODAL signaling, whether from embryonic or maternal sources, in mediating trophoblast invasion remains to be determined in mice in vivo, it is an interesting link that Nodal D/D females did not support adequate fetal growth during late mid to late pregnancy and also displayed examples of hemorrhaging. As previously discussed, it is possible a complex relationship between the fetal- and maternal-derived NODAL signals plays a critical role in regulating the ability, rate, route, or depth to which trophoblasts invade the uterine tissue.

The most significant phenotype observed in pregnant Nodal+/– females was substantial preterm birth and fetal loss on Day 17.5 of gestation, a phenotype rarely observed in rodents [15]. Strikingly, the only mouse strain to our knowledge that exhibited spontaneous preterm birth also displayed a decreased decidual layer in the mature placenta; however, the reduction appears less pronounced and developed from a different mechanism [43]. By using the same PR-Cre strain and generating a uterine-specific Trp53 knockout strain, Hirota et al. [43] observed terminal differentiation and cellular senescence of uterine decidual cells, leading to reduced decidua basalis and a compromised maternal-fetal interface. Regression of the decidua basalis occurs naturally in rodents during the second half of pregnancy, and as a result the malformations leading to a reduced decidua tissue coincidentally resemble the histoarchitecture of a late-stage placenta around the time of parturition [44, 45]. Moreover, injection of the bacteria Fusobacterium nucleatum, which has been isolated in the amniotic fluid of women delivering prematurely, causes preterm fetal loss in mice [46]. Interestingly, the bacterial infection was first restricted to the lower maternal decidua basalis, where severe inflammation and necrosis were observed before infection spread to neighboring tissues (marginal zone, visceral yolk sac, and amnion) [46]. Taken together, these results suggest prematurely compromising the functional ability of the decidua basalis, whether by deletion or bacterial infection, may lead to preterm delivery and fetal loss in mice. Because the maternal tissue at the placental interface is believed to be the source of the signal(s) that initiate parturition, it is tempting to speculate that abundant, healthy cells within the decidua basalis prevent the production of downstream prostaglandins prior to term, which is then removed naturally during basalis regression.

In the Nodal+/– females, much like the uterine Trp53-deleted mice, we observed an increase of PTGS2 enzyme at the placental interface; however, this was accompanied by a significant decrease in progesterone concentration in circulating maternal blood that was not observed in Hirota et al. [43]. As a result, uterine deletion of Trp53 led to dystocia because

![FIG. 8. Apoptosis is increased in the maternal decidua basalis as a result of uterine Nodal deletion. Immunofluorescent in situ cell death assay marked all nuclei in DNase I-treated positive control placentas isolated from both Nodal+/+ (a) and Nodal+/– (b and c) females on Day 10.5. d–f Minimal to no signal was observed in negative control samples treated without the incorporating enzyme. Experimentally treated sections (TUNEL) displayed minimal staining in Nodal+/+ control samples (g), whereas Nodal+/– placenta (h and i) contained abundant positively marked nuclei in the maternal decidua basalis. Apoptotic cells appeared most concentrated around the antimesometrial (bottom left) aspect of the decidua basalis adjacent to the fetal layers. Bars = 200 μm.](https://bioone.org/journals/Biology-of-Reproduction?term=25 Aug 2019)
uterine contractions occurred without cervical ripening, whereas NodalΔ/Δ mice appeared to deliver without any pronounced distress. This suggests NodalΔ/Δ females, although delivering preterm, may have more closely followed the natural parturition cascade once initiated, complete with progesterone withdrawal and a prepared cervix. The precise point at which the preterm induction of parturition deviates from the natural cascade of events remains to be determined; however, it occurs prior to PTGS2 upregulation and appears to be associated with aberrant placental development. Consequently, the newly generated uterine NodalΔ/Δ knockout mouse strain provides an attractive alternative for preterm birth research as current models, induced by local bacterial inoculation, fail to address the underlying cause(s) of spontaneous and idiopathic preterm birth. The placenta has long been targeted as a major potential contributor to the pathogenesis of premature delivery and adverse conditions associated with pregnancy [47]. Here, we demonstrate that mice lacking a uterine source of NODAL fail to support adequate placental development though mid-gestation, and ultimately experience a spontaneous premature induction of parturition, leading to fetal loss. Complete characterization of the NodalΔ/Δ strain is imperative to the ongoing pursuit of 1) identifying the transduction pathways associated with premature birth and 2) the development of suitable animal models required to advance preterm birth research.

Despite the prevalence, severity, and economic impact of premature birth, very little is understood regarding the causes and mechanisms underlying spontaneous preterm birth. In this study, we describe the generation and analysis of a novel tissue-specific knockout of Nodal in the female reproductive tract of mice. Our results demonstrate that NODAL signaling, emanating from a maternal source in the uterus, is critical for proper placental development, adequate intrauterine growth, and term delivery of healthy offspring. These observations shed new light on the in vivo role of maternal NODAL in the developing placenta, present an interesting link between disrupted decidua basalis formation and premature parturition, and introduce a potentially valuable model toward understanding the complex processes that trigger preterm birth.

ACKNOWLEDGMENT

We thank E.J. Robertson for donating the mouse strains required to generate the NodalΔ/Δ line; J. C. Cross, D. R. Natale, and M. Gasperowicz for assistance with the in situ hybridization procedure/interpretation; and E. Asselin and S. Parent for assistance with apoptosis experiments and interpretation of the data. We would also like to thank B. D. Murphy and his laboratory for help with the progesterone assays.

REFERENCES

11. Park CB, Dufo D. Elsevier trophoblast research award lecture: the