

The expression of fibroblast growth factor receptors during early bovine conceptus development and pharmacological analysis of their actions on trophoblast growth *in vitro*

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Abstract

The overall aim of this work was to examine the expression profiles for fibroblast growth factor receptors (FGFRs) and describe their biological importance during bovine pre- and peri-implantation conceptus development. *FGFR1* and *FGFR2* mRNAs were detected at 1-, 2-, 8-cell, morula and blastocyst stages whereas *FGFR3* and *FGFR4* mRNAs were detected after the 8-cell stage but not earlier. The abundance of *FGFR1*, *FGFR3*, and *FGFR4* mRNAs increased at the morula and blastocyst stages. Immunofluorescence microscopy detected FGFR2 and FGFR4 exclusively in trophoblast cells whereas FGFR1 and FGFR3 were detected in both trophoblast cells and inner cell mass in blastocysts. Neither transcripts for *FGF10* nor its receptor (*FGFR2b*) were temporally related to interferon τ (*IFNT*) transcript profile during peri- and postimplantation bovine conceptus development. A series of studies used a chemical inhibitor of FGFR kinase function (PD173074) to examine FGFR activation requirements during bovine embryo development. Exposing embryos to the inhibitor (1 μ M) beginning on day 5 post-fertilization did not alter the percentage of embryos that developed into blastocysts or blastocyst cell numbers. The inhibitor did not alter the abundance of *CDX2* mRNA but decreased ($P < 0.05$) the relative abundance of *IFNT* mRNA in blastocysts. Exposing blastocysts to the inhibitor from days 8 to 11 post-fertilization reduced ($P < 0.05$) the percentage of blastocysts that formed outgrowths after transfer to Matrigel-coated plates. In conclusion, each FGFR was detected in bovine embryos, and FGFR activation is needed to maximize *IFNT* expression and permit outgrowth formation.

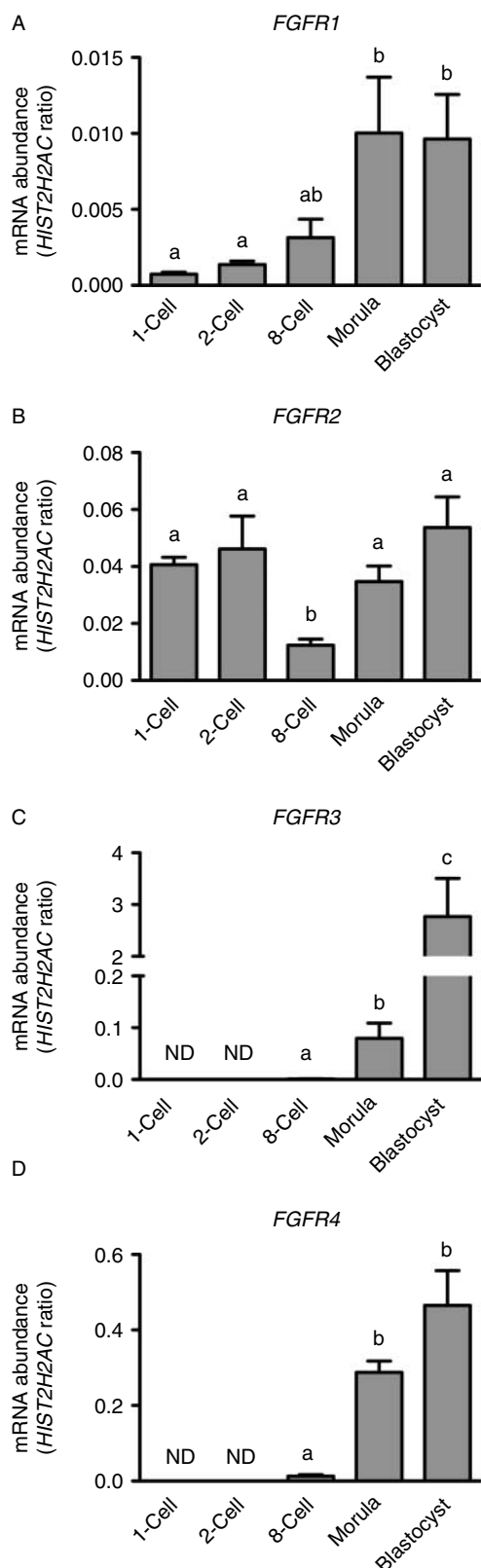
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Introduction

Fibroblast growth factors (FGFs) encompass a large class of autocrine, paracrine, endocrine, and intracrine factors. More than 20 genes encode FGFs in mammals, including bovids (Elsik *et al.* 2009, Zimin *et al.* 2009, Oulion *et al.* 2012). The FGFs interact with a group of tyrosine kinase receptors encoded by four genes in mammals (termed *FGFR1/2/3/4*). Alternative splicing events observed in several species generate an array of receptor isoforms with disparate ligand binding and signaling capabilities (Powers *et al.* 2000, Bottcher & Niehrs 2005). One predominant splicing event occurs within the third IgG-like extracellular domain in three of these receptors (*FGFR1/2/3*), and the excision of one or two exons generates receptor subtypes that recognize different FGFs in various mammals, including ruminants

(Johnson *et al.* 1991, Chen *et al.* 2000, Elsik *et al.* 2009, Zimin *et al.* 2009).

Several actions for FGFs have been described during embryogenesis. FGFs are required for the emergence and proliferation of extraembryonic endoderm in mice, cattle, and humans (Kuijk *et al.* 2008, Cockburn & Rossant 2010, Yamanaka *et al.* 2010, Yang *et al.* 2011a). Maintenance of trophoblast lineage is also controlled by FGFs. One of the first described activities in this regard was the necessity for FGF4 to maintain trophoblast stem cells in an undifferentiated state in mice (Feldman *et al.* 1995, Tanaka *et al.* 1998). Not all mammals show this need for FGF4 or another FGF to stimulate trophoblast stem cell proliferation and block differentiation. Trophoblast cells from the rhesus monkey and common vole (*Microtus rossiaeneridionalis*) proliferate without differentiation in the absence of exogenous factors, including



FGFs (Vandevoort *et al.* 2007, Grigor'eva *et al.* 2009). Likewise, trophoblast cells derived from ungulates (cattle, sheep, and pigs) proliferate in the absence of FGFs (Talbot *et al.* 2000, Shimada *et al.* 2001, La Bonnardiere *et al.* 2002, Dunlap *et al.* 2006, Michael *et al.* 2006).

Although exogenous FGFs are not required for trophoblast cell proliferation and survival, FGF activities exist in trophoblast cells. Several FGFs stimulate interferon τ (IFNT) production. Trophoblast cell-derived IFNT is the maternal recognition of pregnancy hormone in ruminants (Ealy & Yang 2009). Several FGFs (e.g. FGF1, FGF2, FGF7, and FGF10) stimulate *IFNT* mRNA and protein production in bovine trophoblast cell lines and blastocysts through a PKC- δ -dependent mechanism (Michael *et al.* 2006, Cooke *et al.* 2009). FGF2 and FGF10 also stimulate migration of bovine and ovine trophoblast cells (Yang *et al.* 2011b). Collectively, these observations indicate that FGF signals influence trophoblast cell behavior as these cells rapidly proliferate, prepare for adhesion to the uterine lining, and produce IFNT.

The need for FGF signals during the initial stages of bovine embryo development is not clear. An FGF that has been examined recently is FGF2, or basic FGF. Transcripts for *FGF2* and several of the *FGFR* subtypes that react with FGF2 have been identified in bovine embryos during early development (Daniels *et al.* 2000, Cooke *et al.* 2009). The uterine endometrium also produces FGF2 throughout the estrous cycle and early pregnancy in sheep and cattle, and immunoreactive FGF2 is detected in uterine flushes during diestrus (Michael *et al.* 2006, Ocon-Grove *et al.* 2008). In some studies, providing FGF2 during bovine embryo culture improved subsequent blastocyst formation (Larson *et al.* 1992, Neira *et al.* 2010). However, previous studies from this laboratory failed to detect positive effects of FGF2 on blastocyst formation unless large amounts of recombinant protein were provided (500–1000 ng/ml; Fields *et al.* 2011). The overall aim of this work was to resolve whether embryo-derived FGFs and FGFR signaling is essential during early embryo development in cattle. Specific objectives were to describe the expression of *FGFRs* during early and pre-/peri-implantation conceptus development in cattle and define early developmental events that require FGFR activity.

Figure 1 The relative abundance of *FGFR1/2/3/4* mRNAs throughout early bovine conceptus development. Total cellular RNA was extracted from IVP bovine embryos collected either 24 h after fertilization (1-cell; presumptive zygotes) or at the 2-cell, 8-cell, morula or blastocyst stages ($n=5$ replicate studies, ten embryos/time point/replicate). Quantitative RT-PCR was completed to determine the relative abundance of *FGFR1/2/3/4* (A, B, C and D respectively). Data are presented relative to the abundance of the reference transcript (*HIST2H2AC*). Different superscripts depict differences in mRNA abundance within each panel ($P<0.05$).

Results

Expression profiles for FGFR1/2/3/4 during pre-implantation conceptus development

The ontogeny of *FGFR* expression at the initial stages of bovine embryo development has not been examined previously. Therefore, a study was completed to describe the expression profiles for each *FGFR* throughout early embryogenesis (Fig. 1). Abundance of *HIST2H2AC* mRNA was consistent from the 1-cell to blastocyst stage and was used as the endogenous control. Transcripts for *FGFR1* were detected throughout early development, but the relative abundance of *FGFR1* mRNA was greater ($P < 0.05$) in morulae and blastocysts than 1- and 2-cell embryos (Fig. 1A). Similar levels of *FGFR2* mRNA were detected throughout early development with the exception of 8-cell embryos, which contained less ($P < 0.05$) mRNA than other stages (Fig. 1B). Transcripts for *FGFR3* and *FGFR4* were not detected in 1- and 2-cell embryos but were detected in 8-cell embryos (Fig. 1C and D). The relative abundance of *FGFR3* and *FGFR4* mRNA increased ($P < 0.05$) in morulae and blastocysts.

Immunolocalization of FGFRs in bovine blastocysts

Immunofluorescence was used to examine the localization of each FGFR protein from *in vitro*-produced (IVP) embryos. Immunoreactive FGFR1, FGFR2,

FGFR3, and FGFR4 could not be detected in 1-, 2-, or 8-cell embryos (data not shown), but immunoreactivity for each receptor was detected at the blastocyst stage (Fig. 2). Morulae were not examined. FGFR1 and FGFR3 proteins were detected in both the inner cell mass and the trophoblast cells whereas FGFR2 and FGFR4 localized to the trophoblast cells.

Expression profiles of selected transcripts during peri- and postimplantation periods

The association between FGF10 and IFNT was of interest because both are produced by the peri-implantation conceptus around the time when IFNT production is maximal, suggesting that FGF10 may assist in the control of peak IFNT production (Cooke *et al.* 2009). Also, the FGF10 receptor, termed *FGFR2b* (or keratinocyte growth factor receptor, a spliced variant of the *FGFR2* subfamily), is produced by trophoblast (TE) during the peri-implantation period in sheep (Chen *et al.* 2000), but its expression throughout early embryo development remained unexplored.

A biphasic pattern of *IFNT* mRNA abundance was detected throughout pre-, peri-, and post-attachment periods of bovine conceptus development (Fig. 3A). *IFNT* mRNA was detected in blastocysts, and mRNA abundance increased ($P < 0.05$) in ovoid conceptuses collected at day 14 of pregnancy. The relative abundance

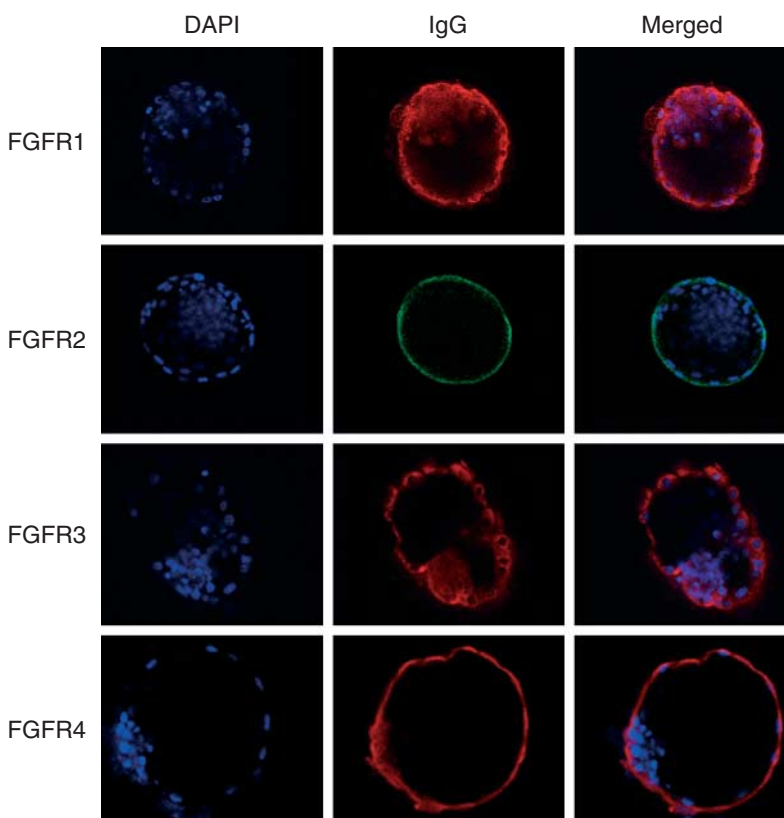


Figure 2 Localization of immunoreactive FGFR1/2/3/4 protein within bovine blastocysts. Representative photomicrographs of blastocysts exposed to antibodies for FGFR1, FGFR2, FGFR3, or FGFR4. The left column contains nuclear DAPI staining for each blastocyst, the center column contains the antibody-specific immunofluorescence, and the right column contains the overlay of DAPI and immunoreactive stains (100 \times magnification).

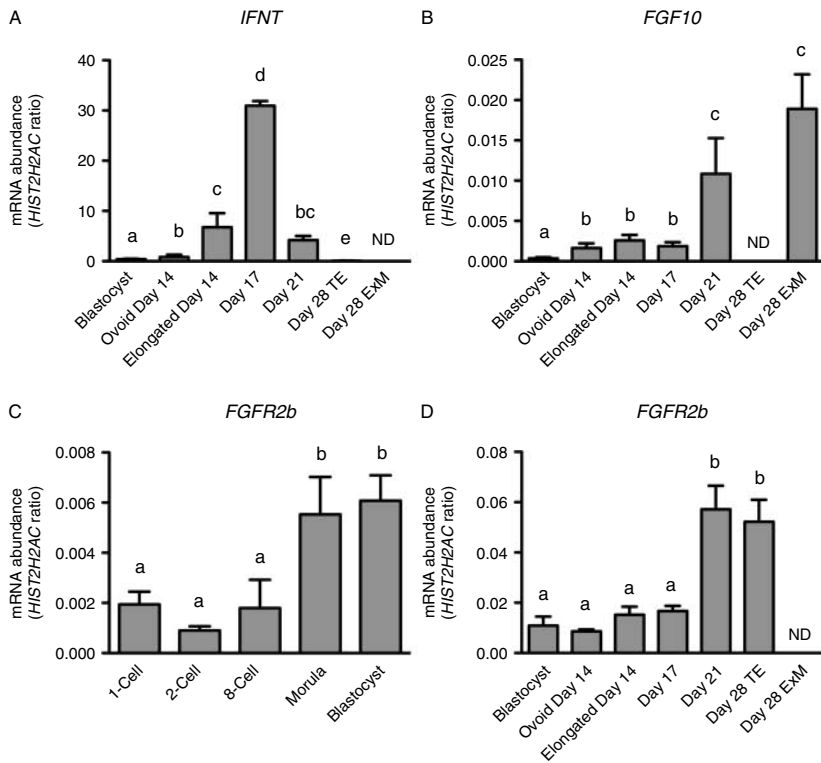


Figure 3 Transcript profiles for *IFNT*, *FGF10*, and the cognate *FGF10* receptor (*FGFR2b*) throughout early conceptus development. Total cellular RNA was extracted from IVP bovine embryos collected either 24 h after fertilization (1-cell; presumptive zygotes) or at the 2-cell, 8-cell, morula or blastocyst (day 8 post-IVF) stages ($n=5-6$ replicate studies, ten embryos/time point/replicate). At day 8 post-IVF ($n=6$ blastocyst pools), from conceptuses collected from superovulated cows at day 14 (ovoid or elongating; $n=6$ conceptus pools) and day 17 ($n=6$ conceptus pools) post-insemination, and from conceptuses collected from non-superovulated cows at day 21 ($n=5$ samples) and day 28 ($n=3$ samples) post-insemination. At day 28, trophoblast (TE) and extraembryonic mesoderm were separated before snap-freezing and were processed as separate samples. (A) *IFNT* mRNA abundance between days 8 and 28; (B) *FGF10* mRNA abundance between days 8 and 28; (C) *FGFR2b* mRNA abundance between days 1 and 8; and (D) *FGFR2b* mRNA abundance between days 8 and 28. Transcripts of interest are presented relative to the abundance of a reference transcript (*HIST2H2AC* for early embryo; *GAPDH* for days 8–28 conceptuses). Different superscripts depict differences in mRNA abundance within each panel ($P<0.05$).

of *IFNT* mRNA increased ($P<0.05$) further in elongating conceptuses collected at day 14. Maximal amounts of *IFNT* mRNA were detected in elongated conceptuses collected at day 17. *IFNT* mRNA was detected at day 21 and in TE at day 28, albeit at very low levels. No *IFNT* mRNA was detected in extraembryonic mesoderm (ExM) at day 28.

Both *FGF10* and *FGFR2b* mRNAs were detected throughout all the stages of conceptus development. However, neither expression pattern mirrored that of *IFNT*. The transcript abundance for *FGF10* was low in blastocysts and increased ($P<0.05$) in conceptuses collected at day 14 (Fig. 3B). The relative abundance of *FGF10* mRNA was unchanged in ovid and elongating conceptuses collected at day 14 and conceptuses collected at day 17 and was increased ($P<0.05$) at days 21 and 28. *FGF10* mRNA was only detected in ExM at day 28. Two studies examined the expression profiles for *FGFR2b*. The first study examined *FGFR2b* mRNA abundance during the initial stages of bovine embryonic development (Fig. 3C). *FGFR2b* mRNA was detected in 1-, 2-, and 8-cell embryos, and its relative abundance increased ($P<0.05$) at morula and blastocyst stages. RNA collected at subsequent stages of bovine conceptus development (Fig. 3D) determined that the relative abundance of *FGFR2b* mRNA remained unchanged between the blastocyst stage and day 17. An increase ($P<0.05$) in *FGFR2b* mRNA abundance was detected at day 21 and in TE at day 28. No *FGFR2b* mRNA was detected in ExM.

***FGFR* signaling requirements for embryo development and *IFNT* expression**

The requirement of *FGFR* signaling during pre-implantation embryo development was examined by blocking *FGFR* activation with PD173074, a cell-permeable *FGFR* kinase inhibitor used by this laboratory and others to examine *FGFR*-mediated events in bovine tissues (Yang *et al.* 2011a, Kuijk *et al.* 2012, Zhang & Ealy 2012). This compound competitively inhibits ATP binding to receptor kinase regions of *FGFRs* (Mohammadi *et al.* 1998, Skaper *et al.* 2000). Studies have not been completed to verify the specificity of this compound to bovine *FGFRs*, but this specificity is probable given the high degree of sequence conservation in *FGFR* tyrosine kinase regions of cattle and humans (>98% amino acid sequence identity with corresponding human *FGFR* kinase domains). A pilot study verified that PD173074 inhibited *FGF2*-dependent responses in a bovine trophoblast cell line (CT1). Cells were exposed to 10 ng/ml *FGF2* and various concentrations of PD173074. In non-PD173074-treated controls, *FGF2* increased ($P<0.05$) *IFNT* mRNA abundance by 5.0 ± 1.6 -fold. No significant changes in *FGF2*-induced *IFNT* mRNA abundance were detected by providing 10 or 100 nM PD173074, but exposing cells to 1 μ M PD173074 for 24 h before *FGF2* treatment prevented the *FGF2* effect (0.81 ± 0.15 -fold effect vs control).

Exposing embryos to 1 μ M PD173074 from days 5 to 8 post-IVF did not affect blastocyst development rate and

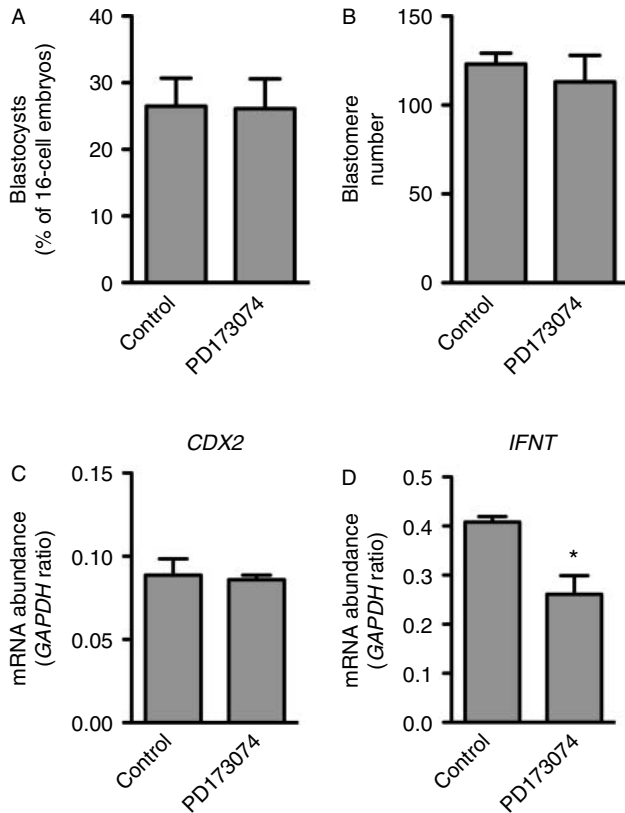


Figure 4 Inhibition of FGFR activity with PD173074 does not affect embryo development or trophoblast gene expression during *in vitro* culture. Bovine embryos were generated by IVP. Embryos containing ≥ 8 blastomeres were collected at day 5 post-IVF and incubated in medium containing 1 μM PD173074 or carrier only (control). In one study, rates of blastocyst formation were determined at day 8 (A) and blastocysts were fixed and stained to determine blastomere numbers (B) ($n=6$ replicate studies, 28–31 embryos/treatment/replicate). In another study, blastocysts ($n=4$ replicate studies, 10–15 blastocysts/treatment/replicate) were collected and RNA was extracted at day 8 and qRT-PCR was used to determine the abundance of *CDX2* (C) and *IFNT* (D) transcripts relative to the abundance of the reference transcript (*GAPDH*). The asterisk depicts differences between PD173074-treated and control samples ($P<0.05$).

total cell numbers in blastocysts (Fig. 4A and B). Also, no changes in mRNA abundance of *CDX2*, a trophoblast lineage marker, were observed (Fig. 4C). However, PD173074 treatment decreased ($P<0.05$) *IFNT* mRNA abundance (Fig. 4D).

Interruption in blastocyst outgrowth development following FGFR inhibition

The need for FGFR signals after blastocyst formation was examined by assessing the ability of blastocysts to adhere to Matrigel-coated plates and form trophoblast outgrowths (Fig. 5). Individual blastocysts were incubated in growth medium containing 1 μM PD173074 or carrier only from days 8 to 11 post-IVF, then medium was exchanged, and blastocysts were cultured without

treatments thereafter. In controls, trophoblast outgrowths were evident in a low proportion of blastocysts ($< 3\%$) as early as day 10. Additional outgrowths were detected thereafter until day 15 (Fig. 5A). No additional outgrowths were formed after day 15. Exposure to PD173074 delayed ($P<0.05$) the time when outgrowth development was first observed (day 12). The treatment also decreased ($P<0.05$) the percentage of blastocysts that formed outgrowths at each day of examination (Fig. 5A). A large variation in outgrowth size (i.e. surface area) was evident in both treatments (Fig. 5B). A numerical reduction in outgrowth size was observed between controls and PD173074-treated blastocysts, but this outcome was not statistically significant ($P=0.15$).

Discussion

The first major focus of this work was to identify stages when bovine embryos are potentially responsive to FGFs by describing the ontogeny of *FGFR* mRNA and protein production during bovine embryogenesis. Differences in

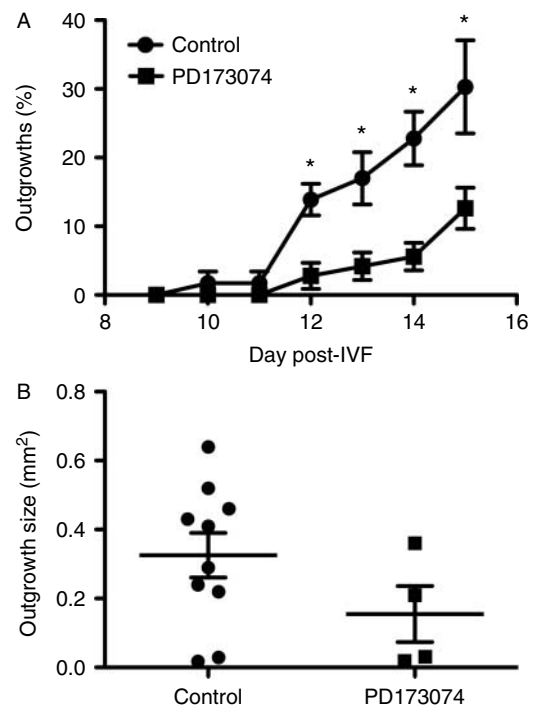


Figure 5 Exposing blastocysts to PD173074 compromises subsequent outgrowth formation. Bovine embryos were generated by IVP. Blastocysts were collected at day 8 post-IVF and incubated in individual wells of a 24-well plate containing Matrigel basement membrane matrix with medium containing 1 μM PD173074 or carrier only (control; $n=6$ replicate studies, 10–14 blastocysts/treatment/replicate). At day 11 post-IVF, medium was exchanged with medium lacking PD173074. The incidence of blastocyst outgrowth formation was examined daily until day 15 (A). Size of outgrowths was determined at day 15 (B). Asterisk (*) indicates differences in outgrowth formation due to treatment within day ($P<0.05$).

expression profiles exist between *FGFR* subtypes. Of particular note is the presence of *FGFR1* and *FGFR2* transcripts throughout early embryonic development vs the presence of *FGFR3* and *FGFR4* transcripts only after embryonic genome activation (8- to 16-cell stage in bovine embryos; Telford *et al.* 1990). Transcripts found in embryos before embryonic genome activation are synthesized by the maternal genome before ovulation and stored in the cytoplasm during fertilization and the first several days of embryogenesis (Gilchrist *et al.* 2008). Therefore, both maternal and embryonic *FGFR1* and *FGFR2* transcripts exist in the bovine embryo whereas only embryonic transcripts were detected for *FGFR3* and *FGFR4*. The loss of *FGFR2* mRNA at the 8-cell stage likely reflects the use and degradation of maternal transcripts before embryonic transcription begins. Transcripts for *FGFR1*, *FGFR3*, and *FGFR4* exhibited marked increases in their relative abundance at the blastocyst stage in cattle when compared with their abundance at the 8-cell stage. The pattern of *FGFR2* expression was different in this regard, and no dramatic changes in overall transcript abundance occurred after embryonic genome activation.

It is unclear what roles *FGFR1* and *FGFR2* may be playing in early bovine embryo development. The major spliced variants for these receptors react with numerous FGFs, including FGF2 and FGF10 (Powers *et al.* 2000, Bottcher & Niehrs 2005), and their presence likely contributes to the embryotrophic activities for FGF2 during early bovine embryogenesis (Larson *et al.* 1992, Neira *et al.* 2010). Interestingly, the necessity for *FGFR1* and *FGFR2* activity is not evident until after blastocyst formation in mice. Early embryogenesis occurs normally in knock-out models of each receptor, and loss of *FGFR1* function induces a postimplantation embryonic lethal phenotype characterized by defects in mesoderm and endoderm migration and cell fate determination (Deng *et al.* 1994, 1997, Yamaguchi *et al.* 1994) whereas loss of *FGFR2* function generates a post-blastocyst stage embryonic lethality characterized by lack of visceral endoderm and reduced TE mass (Arman *et al.* 1998). Epiblast-derived FGF4 interacting with the *FGFR2c*-spliced variant is responsible for these activities. Variants of *FGFR2* also appear important for conceptus development in ruminants. FGF2, which reacts with *FGFR2c* and several other *FGFRs*, is produced by the endometrial epithelium and peak secretion occurs around the time of conceptus elongation in sheep (Michael *et al.* 2006, Ocon-Grove *et al.* 2008). Also, the other major *FGFR2*-spliced variant, *FGFR2b*, is expressed in bovine, ovine, and porcine TE before implantation and its primary ligands (FGF7 and FGF10) are produced in endometrium before and during implantation (Chen *et al.* 2000, Ka *et al.* 2001, Cooke *et al.* 2009, Yang *et al.* 2011a). In the sheep uterus, FGF10 production from the uterine stroma is controlled by progesterone and its interaction with *FGFR2b* in the luminal epithelium is associated with uterine events

that control early conceptus development (Chen *et al.* 2000, Satterfield *et al.* 2008). Also, immature binucleate cells contain *FGFR2* transcripts, and perhaps endometrial FGF10 regulates trophoblast differentiation, migration, and hormone production (Pfarrer *et al.* 2006).

Not only did *FGFR3* and *FGFR4* mRNA profiles differ from the other *FGFRs* but the relative transcript abundance of these *FGFRs* was much greater than the other receptors. At the blastocyst stage, *FGFR3* mRNA abundance was 15- to 300-fold greater than *FGFR2* and *FGFR1* respectively. Similarly, *FGFR4* mRNA was 10- to 40-fold greater in abundance than *FGFR2* and *FGFR1* respectively. Neither absolute mRNA concentrations nor adjustments to the relative abundance measurements were made here; therefore, direct comparisons between these transcripts cannot be completed. However, the high expression of these transcripts suggests that these receptors may be important during early embryogenesis. It is unclear what these functions may be. *FGFR3* reacts with several FGFs (FGF1 and FGF9 for *FGFR3b*; FGF1, FGF2, FGF4, FGF8, and FGF9 for *FGFR3b*; Itoh & Ornitz 2004), and it is expressed through gestation in human and rodent placentae and localizes to extraembryonic endoderm and trophoblast giant cells in mice (Rappolee *et al.* 1998, Anteby *et al.* 2005). Mutations in *FGFR3* function in mice and humans are associated with skeletal dysplasia, notably achondroplasia during fetal development and urothelial tumorigenesis in adulthood (Iyer & Milowsky 2012, Laederich & Horton 2012). No spliced variants exist for *FGFR4*. Numerous FGFs interact with *FGFR4* (e.g. FGF1, FGF2, FGF4, FGF6, FGF8, and FGF9; Itoh & Ornitz 2004), and it is expressed throughout gestation in the mouse and human placenta (Rappolee *et al.* 1998, Anteby *et al.* 2005). In the human placenta, *FGFR4* mRNA localizes to several trophoblast cell types at the decidual-trophoblast border, suggesting a role in maintaining this interface (Anteby *et al.* 2005). *FGFR4* is also needed during neural development and is linked with various cancers in several species (Marchal *et al.* 2009, Ota *et al.* 2010, Tenhagen *et al.* 2012).

Detecting *FGFR* proteins at the blastocyst stage is consistent with the transcript profiles for *FGFR3* and *FGFR4* but it is not clear why immunoreactive *FGFR1* and *FGFR2* were not detected at earlier stages of development. Perhaps posttranscriptional events (e.g. RNA silencing) limit *FGFR* protein translation during early stages of embryo development. Alternatively, perhaps the sensitivity of detection was insufficient to visualize immunoreactivity at these early stages. Nonetheless, the detection of each *FGFR* transcript and protein at the blastocyst stage suggests that each major *FGFR* subtype is available to interact with FGFs at this stage. *FGFR2* exhibits a trophoblast-specific localization pattern in mice, pigs, and sheep (Haffner-Krausz *et al.* 1999, Chen *et al.* 2000, Ka *et al.* 2007). This work demonstrated the same expression profile in cattle.

The localization patterns of other FGFRs have not been characterized previously at blastocyst stage. These outcomes indicate that FGFR4 localizes solely to the trophoblast cell in blastocysts whereas trophoblast and inner cell mass cells express FGFR1 and FGFR3.

The expression profile for *FGFR2b* and one of its ligands, *FGF10*, was examined throughout the pre-, peri-, and postimplantation stages in cattle to examine a potential linkage between this FGF ligand/receptor system and peak *IFNT* expression in peri-attachment conceptuses. Recent work from this laboratory detected an increase in the relative abundance of embryonic *FGF10* mRNA around the time of bovine conceptus elongation (Cooke *et al.* 2009), thereby implicating FGF10 as a potential mediator of the rapid surge in IFNT production during elongation. However, work presented herein found no correlations in expression patterns. The *IFNT* mRNA profile was identical to that reported by others (Kubisch *et al.* 1998, Ealy *et al.* 2001, Robinson *et al.* 2006). A pronounced increase in *IFNT* mRNA occurred with elongation, and maximal transcript abundance was evident at day 17 whereas the *FGF10* mRNA profile remained unchanged around the time of conceptus elongation (days 14–17). Also, *FGFR2b* mRNA abundance remained unchanged during conceptus elongation. Although FGF10 and FGF2b do not appear to be principle players defining the pattern on *IFNT* expression, this and other FGFs certainly appear to play a role in regulating the constitutive production of IFNT in ruminant TE (Michael *et al.* 2006, Cooke *et al.* 2009). Also, work presented herein found that blocking FGFR kinase activity reduces *IFNT* mRNA abundance. No changes in *CDX2* mRNA, a trophoblast lineage marker, were noted, indicating that the number and overall transcriptional activity of trophoblast cells is not altered with this inhibitor. Rather, this outcome supports the hypothesis that blastocyst-derived FGFs (e.g. FGF2 and FGF10) mediate constitutive IFNT production in cattle. With that said, to date, no studies have directly examined the necessity for FGFR signals during peak *IFNT* expression in ruminants. Work at this critical stage of pregnancy is needed before we can claim whether FGF signaling is required for maximal IFNT production or if these signals are only being used before the peak in IFNT production at days 14–17 in cattle.

The second major focus of this work was to describe functions for FGFRs during early embryonic development. The necessity for specific FGFRs has not been described in the cow, but as described previously, loss-of-function mutation studies on mice determined that FGFR1 and FGFR2 are vital for post-blastocyst survival and FGFR3 and FGFR4 are important after implantation (Deng *et al.* 1994, Yamaguchi *et al.* 1994, Arman *et al.* 1998, Iyer & Milowsky 2012, Laederich & Horton 2012). Present work failed to detect any adverse developmental effects by inhibiting FGFR activity before blastocyst formation. A previous study using another FGFR kinase

domain inhibitor (SU5402) observed that fewer cultured embryos formed blastocysts at day 7 but not at day 8 post-fertilization (Fields *et al.* 2011). Blastocyst formation at day 7 was not examined in this project, but no differences in blastocyst formation, blastomere numbers, and the expression of *CDX2* were detected at day 8 post-fertilization in embryos exposed to PD173074. Therefore, FGFR inhibition seems to impact the timing of blastocyst formation but not overall blastocyst formation, embryonic numbers, and lineage commitment to trophoblast cells. It remains possible that FGFs function, at least in part, as cooperative factors during early embryonic development in cattle. One recent study found that the positive effect of FGF2 supplementation on *in vitro* bovine blastocyst development was enhanced when it was co-supplemented with other factors, such as insulin-like growth factors or colony-stimulating factor 2 (Neira *et al.* 2010). Another study failed to detect a benefit of FGF2 supplementation on *in vitro* bovine embryo development unless it was co-cultured with transforming growth factor β (Larson *et al.* 1992).

The last study examined potential impacts of inhibiting FGFR signals after blastocyst formation. Bovine blastocysts attach to basement membrane matrices, such as Matrigel, when cultured in medium containing serum (Talbot *et al.* 2007, Yang *et al.* 2011a). Exposing blastocysts to the FGFR inhibitor delayed the onset of outgrowth formation and reduced the overall rate of outgrowth formation. The size of the outgrowths at day 15 was not statistically different between groups. This is not surprising as so few outgrowths were established after exposure to the FGFR inhibitor. Observing such small outgrowths at day 15 could reflect that FGFR inhibition compromised trophoblast cell growth potential. Alternatively, observing smaller outgrowths at day 15 could simply reflect the delayed ontogeny of outgrowth formation. FGF2 and FGF10 stimulate bovine and ovine trophoblast cell migration across trans-well inserts (Yang *et al.* 2011b). Therefore, FGFR signaling may mediate the chemotactic, adhesive, migratory, and/or proliferative activities required for changes in trophoblast cell morphology, adhesion and attachment, and conceptus elongation during peri-implantation development. However, it remains untested whether post-blastocyst stage development is compromised by FGFR signal interference *in utero*.

One aspect of the outgrowth work that remains unresolved involves pinpointing the precise timing for FGFR signal control of outgrowth formation. Temporary reductions in FGFR protein abundance have been noted by others following PD173074 treatment (Azuma *et al.* 2011, Lamont *et al.* 2011). If similar PD173074-induced reductions in FGFR expression also occur in bovine blastocysts, then these embryos may be unresponsive to endogenous FGF signals after removal of the inhibitor at day 11 post-IVF. *FGFR* mRNA profiles and FGFR activity assessments were not examined during and after

PD173074 treatment. Therefore, it is not known whether the effects observed resulted from FGFR signal inhibition between days 8 and 11 post-IVF or if continued inhibition of FGFR activity after day 11 was responsible for the outcomes.

In summary, these observations provide new insights into the necessity for FGFR signaling during early embryo development in cattle. Transcripts for *FGFR1* and *FGFR2* were detected before embryonic genome activation and all four *FGFR* subtypes were detected after genome activation. Immunoreactive proteins for each FGFR localized to trophoblast cells at the blastocyst stage. FGFR1 and FGFR3 proteins were detected in the inner cell mass in blastocysts. Interference of FGFR signaling did not impact development to the blastocyst stage and blastomere numbers in blastocysts. However, this report identified that FGFR activity mediates *IFNT* expression in blastocysts and maximizes blastocyst outgrowth formation and spreading. This work implicates embryo-derived FGFs and FGFR signaling as important components for IFNT production and trophoblast cell adhesion in cattle.

Materials and Methods

In vitro embryo production

Oocyte maturation, fertilization, and embryo culture was completed as described previously (Loureiro *et al.* 2009, Zhang *et al.* 2010, Fields *et al.* 2011). In brief, ovaries were obtained from a local slaughterhouse (Central Beef Industries, Center Hill, FL, USA). Pools of COCs ($n=10-20$) were collected and matured in 50 μ l drops of oocyte maturation medium (OMM; TCM199 containing Earle's salts (Invitrogen Corp.), 25 μ g/ml porcine FSH (Folltropin-V, Bioniche Life Sciences, Belleville, ON, Canada), 2 μ g/ml estradiol 17 β , 0.2 mM sodium pyruvate, 50 μ g/ml gentamicin sulfate, 1 mM glutamine, and 1 mg/ml polyvinyl alcohol (Sigma-Aldrich)). After 21–22 h, COCs were placed in fertilization medium (TL-Fert (Caisson, Sugar City, ID, USA) containing 0.6% (w/v) essentially fatty acid-free BSA and 1 mM Na pyruvate) and incubated with Percoll gradient-purified bovine spermatozoa for 8–10 h at 38.5 °C (5% CO₂ in humidified air). A pool of semen from four bulls was used for all studies. After 8 h of fertilization, cumulus cells were removed by vortexing in 1000 U/ml hyaluronidase (Sigma-Aldrich) and putative zygotes were cultured in groups of 25–30 in 50 μ l drops of serum-free mSOF-BE (Millipore, Billerica, MA USA; Fields *et al.* 2011). Drops were covered with mineral oil and maintained at 38.5 °C in 5% CO₂, 5% O₂, and 90% N₂.

For transcript ontogeny studies, presumptive zygotes (1-cell) and 2-cell embryos were collected 24 h after fertilization (day 1), and 8-cell, morulae and blastocysts were collected at days 3, 5, and 8 post-IVF respectively. Pools of embryos ($n=10$ /pool) were generated at each collection time point. Embryos were processed immediately to extract total cellular RNA using the PicoPure RNA Isolation Kit (MDS Analytical Technologies, Sunnyvale, CA, USA).

Bovine conceptus collections

Day 14 conceptuses were collected from superovulated Holstein cows ($n=9$) nonsurgically and sorted based on size (ovoid vs elongating; $n=3-5$ conceptuses/pool; six pools) as described previously (Cooke *et al.* 2009). Approximately half of the conceptuses collected at day 14 were ovoid and the remaining elongating conceptuses ranged in size from ~0.5–3 cm in length. Day 17 conceptuses were collected from superovulated Holstein cows ($n=6$) by flushing excised uteri following killing (Cooke *et al.* 2009). All conceptuses were elongated and ranged in size from 5 to 45 cm. conceptuses were pooled in small groups ($n=3-5$ /pool; six pools) and snap-frozen in liquid nitrogen.

Day 21 and 28 conceptuses were collected from excised reproductive tracts of non-superovulated Holstein cows ($n=5$ and 3 cows respectively) after killing. Estrous was synchronized and induced by administering a GNRH analog (100 μ g Cystorelin, Merial Limited, Duluth, GA, USA) and inserting an intravaginal progesterone-containing device (Eazi-Breed CIDR; Pfizer Corp.) for 7 days. Lutalyse (25 mg, Pfizer Corp.) was administered at the time of CIDR removal and the GNRH analog was provided 56 h later. Cows were inseminated with Holstein semen (Genex Cooperative, Inc., Shawano, WI, USA) 16 h later. At day 21, the embryo proper was excised and the entire TE from each cow was collected and snap-frozen in liquid nitrogen. At day 28, the embryo was excised and the TE and ExM was separated and snap-frozen. The TRIzol Plus RNA Purification System containing PureLink spin columns (Invitrogen Corp.) were used to extract RNA from all samples.

Quantitative RT-PCR

RNA concentrations and integrity (A_{260}/A_{280} ratio ≥ 1.8) were determined using the Nano Drop 2000 Spectrophotometer (Thermo Scientific, Wilmington, DE, USA). Quantitative RT-PCR (qRT-PCR) was completed using a 7300 Fast Real-Time PCR System (Applied Biosystems) as described previously (Cooke *et al.* 2009, Zhang *et al.* 2010, Yang *et al.* 2011a). In brief, samples were incubated with RNase-free DNase (New England Biolabs, Ipswich, MA, USA) and reverse transcribed (High-Capacity cDNA RT Kit, Applied Biosystems) and amplified with SYBR Green PCR Master Mix reagent (Applied Biosystems) and normal PCR conditions (40–50 cycles of 95 °C for 15 s and 60 °C for 1 min). Primer pairs (Table 1) were validated in previous work for adequate primer efficiency and correctness of amplicon sequence (Cooke *et al.* 2009, Zhang *et al.* 2010, Yang *et al.* 2011a). Amplification of a single PCR product for each sample was examined by dissociation curve analysis. Also, the exclusion of reverse transcriptase was included as a negative control for each sample. Histone HIST2H2AC (*HIST2H2AC*) was used as the transcript reference control for studies examining changes in transcript abundance from 1-cell to blastocyst stages and *GAPDH* was used as the reference control for studies from blastocysts to day 28 of gestation. The abundance of each reference control transcript was unchanged during the specified stages of development similar to that described previously by others (Robert *et al.*

Table 1 Primers used for qRT-PCR.

Gene of interest	Primer sequences (5'–3')
<i>FGF10</i>	F: AGAGGACAGAAAACCGAAGGAAA R: GGTATACTGCATCTGCAATCATTG
<i>FGFR1</i>	F: TGGTCACAGCCACGCTCTGC R: GAACATCGTCCCGCAGCCGA
<i>FGFR2</i>	F: GACCTGGTGTCTGTACCTACCA R: CTGGCAGCTAAATCTCGATGAA
<i>FGFR2b</i>	F: GTGGAAAAGAACGGCAGTAAATA R: GAACTATTTATCCCCGAGTGCTTG
<i>FGFR3</i>	F: GCAGCGGCTACAGGTGCTCA R: CAGGCCGCTCCAGTAAGGG
<i>FGFR4</i>	F: GCAGACGCTCCTCACCCGAC R: CGAGACTCACGAGGCCAGCG
<i>HIST2H2AC (H2a)</i>	F: GTCGTGGCAAGCAAGGAG R: GATCTCGGCCGTTAGGTACTC
<i>GAPDH</i>	F: ACCAGAAGACTGTGGATGG R: CAACAGACACGTTGGGAGTG
<i>IFNT</i>	F: GATCCTTCTGGAGTGGYTG R: GCCCGAATGAACAGACTCYC

F, forward primer (sense); R, reverse primer (antisense); Y, insertion of a C or T nucleotide. Primers were validated in previous work for amplification efficiency and correctness of amplification (Cooke *et al.* 2009, Zhang *et al.* 2010, Yang *et al.* 2011a).

2002, Purcell *et al.* 2009). Data were normalized based on the ratio of transcript abundance for the gene of interest to that of the reference control ($2^{-CT \text{ gene of interest}/2^{-CT \text{ reference control}}}$).

Immunofluorescence and confocal microscopy

IVP bovine embryos were fixed with 4% (v/v) paraformaldehyde in PBS for 15 min, permeabilized for 15 min with 0.25% Triton X-100 in PBS, and blocked with PBS containing 5% (w/v) BSA. Embryos were incubated overnight at 4 °C with primary antibody (FGFR1, FGFR3, and FGFR purchased from Abcam (Cambridge, MA, USA), FGFR2 (1:200, Abnova, Taipei City, Taiwan), FGFR3 (1:200, Abcam), and FGFR4 (1:100, ab65974, Abcam)). Each preparation was diluted in Tris-buffered saline containing 0.1% (v/v) Tween 20 (TBST) and 1% (w/v) BSA. After washing, embryos were incubated in secondary antibody (anti-mouse IgG conjugating FITC (1:1000, Abcam) or anti-rabbit IgG conjugating Alexa Fluor 555 (1:1000, Cell Signaling Technology, Danvers, MA, USA)) prepared in TBST-BSA for 1 h at room temperature. Nuclei were labeled with 4',6-diamidino-2-phenylindole (DAPI) (1 µg/ml). Fluorescence signals were visualized with a Zeiss Pascal LSM5 Confocal Laser Scanning Microscope (Zeiss, Göttingen, Germany). Western blotting was completed with bovine cell lysates (CT1 cells and Madin-Darby bovine kidney (MDBK) cells) to verify that antibodies recognized a single protein band of the approximate molecular weight specified for each FGFR (data not shown).

FGFR inhibition during early embryo development

In one study, ≥ 16 -cell embryos were collected at day 5 post-IVF and transferred to mSOF medium containing PD173074 (1 µM, Stemgent, Cambridge, MA, USA) or vehicle only (0.005% DMSO) ($n=6$ replicate studies, 28–31 embryos/treatment/replicate). At day 8, embryos were examined for

their progression to the blastocyst stage, and blastocysts were stained with DAPI to determine blastomere numbers as described earlier.

In another study, pools of blastocysts derived from cultures containing or lacking PD173074 were collected and RNA was extracted as described previously ($n=4$ replicate studies; 10–15 blastocysts/treatment/replicate). Effects of PD173074 treatment on *NANOG*, *GATA4*, *CDX2*, and *IFNT* mRNA abundance were examined by qRT-PCR as described previously (Zhang *et al.* 2010, Yang *et al.* 2011a).

FGFR inhibition and outgrowth formation

Blastocyst outgrowth cultures were completed as described previously (Yang *et al.* 2011a). Blastocysts were collected at day 8 post-IVF and individual blastocysts were placed into Matrigel-coated wells (0.95 cm²) in 500 µl DMEM containing high glucose (4.5 g/l), 10% FBS, and either 1 µM PD173074 or vehicle only (0.005% DMSO) ($n=6$ replicate studies, 10–14 blastocysts/treatment/replicate). Cultures were incubated at 38.5 °C in a 20% oxygen environment. After 3 days' exposure to treatment (i.e. day 11 post-IVF), medium was removed and replaced with DMEM containing 10% fetal bovine serum (FBS) but lacking treatments. Cultures were removed from the incubator daily from days 9 to 15 post-IVF to examine the onset of outgrowth formation as described previously (Yang *et al.* 2011a). At day 15 post-IVF, the surface area of a subset of the outgrowths was determined by tracing the outline of the outgrowths using a Nikon SMZ1500 stereomicroscope and Nikon DXM-1200F digital camera and quantifying surface area using NIS-Elements Software (Nikon, Melville, NY, USA).

Statistical analyses

Data were analyzed by ANOVA using the general linear model of the Statistical Analysis System (SAS Institute, Inc., Cary, NC, USA). Differences between individual means were compared using pairwise comparisons (Probability of Difference (PDIFF) Analysis in SAS). Relative abundances of selected transcripts were analyzed over time and across treatments after log-transformation. Percentage data were arcsine transformed. Data are presented as arithmetic mean \pm S.E.M.

Declaration of interest

The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of the research reported.

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