Progesterone and interferon tau regulate leukemia inhibitory factor receptor and IL6ST in the ovine uterus during early pregnancy

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Abstract

The actions of leukemia inhibitory factor (LIF) via LIF receptor (LIFR) and its co-receptor, IL6 signal transducer (IL6ST), are implicated in uterine receptivity to conceptus implantation in a number of species including sheep. The present study determined the effects of the estrous cycle, pregnancy, progesterone (P4), and interferon tau (IFNT) on the expression of LIFR and IL6ST in the ovine uterus.

LIFR mRNA and protein were localized to the endometrial luminal (LE) and superficial glandular epithelia (sGE), whereas IL6ST mRNA and protein were localized primarily in the middle to deep GE. Both LIFR and IL6ST mRNAs and protein were more abundant in pregnant than cyclic ewes and increased from days 10 to 20 of pregnancy. Treatment of ovariectomized ewes with P4 and/or infusion of ovine IFNT increased LIFR and IL6ST in endometrial LE/sGE and GE respectively. Co-expression of LIFR and IL6ST as well as phosphorylated STAT3 was observed only in the upper GE of the endometrium as well as in the conceptus trophectoderm on days 18 and 20. In mononuclear trophoderm and GE cells, LIF elicited an increase in phosphorylated STAT3 and MAPK3/1 MAPK proteins. Collectively, these results suggest that LIFR and IL6ST are both stimulated by IFNT and regulated by P4 in a complex stage- and cell-specific manner, and support the hypothesis that LIF exerts effects on the endometrial GE as well as conceptus trophectoderm during early pregnancy in sheep. Thus, LIF and STAT3 may have biological roles in endometrial function and trophoderm growth and differentiation.

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Introduction

Leukemia inhibitory factor (LIF), a member of the interleukin 6 (IL6, also known as interferon beta 2 (IFNB2)) cytokine family, is a secreted glycoprotein that acts as a polyfunctional cytokine in a variety of tissues and cells types (see (Auernhammer & Melmed 2000) for a review). LIF binds to the LIF receptor (LIFR) with low affinity and subsequently recruits IL6 signal transducer (IL6ST), also known as GP130 as a co-receptor. This heterodimer complex with high affinity for LIF activates janus kinase 1 or 2 (JAK1/2) and tyrosine kinase 2 (TYK2), and then signal transducer and activator of transcription (STAT), particularly STAT3, to regulate target gene expression (see (Shields et al. 1995, Auernhammer & Melmed 2000) for a review). In addition to the JAK–STAT signaling pathway, LIF also activates the MAP kinase (MAPK), protein kinase C (PKC), and phosphatidylinositol 3-kinase (PI3K) pathways. In mice, Lif is expressed exclusively in endometrial GE and plays an essential role in blastocyst implantation via the effects on endometrial LE (Bhatt et al. 1991, Stewart et al. 1992). In the mouse uterus, Lifr and Il6st are co-expressed in the LE, and LIF activates Lifr and then STAT3 at the time of blastocyst attachment (Cheng et al. 2001, Song & Lim 2006). In Lifr null mice, embryos attach to the endometrial LE successfully, but perinatal death occurs (Ware et al. 1995), whereas Il6st null embryos die in utero due to myocardial and hematological defects (Yoshida et al. 1996). In mice, Lif regulates the onset of uterine receptivity to blastocyst implantation and embryogenesis (see (Voglatis & Salamonsen 1999, Cheng et al. 2002, Kimber 2005) for a review). Of particular note is that LIF regulates trophoblast giant cell differentiation in the mouse placenta (Takahashi et al. 2008), and human extravillous trophoblast invasion is stimulated by both LIF and STAT3 (Poehlmann et al. 2005).

LIF, Lifr, and Il6st are implicated in uterine receptivity to implantation in a number of species including humans, primates, rodents, pigs, cattle, mink, and sheep (see (Auernhammer & Melmed 2000, Kimber 2005) for a review). In sheep, endometrial LIF...
cytokines/hormones from the conceptus, such as inter-
largely regulated by P4 from the corpus luteum (CL) and
the peri-implantation period of pregnancy in sheep are
Endometrial functions and epithelial secretions during
et al (Vogiagis et al. 1997a). Although LIF may not be
obligatory for implantation in ruminants, it does appear
to have a role during the establishment of pregnancy
(Vogiagis et al. 1997b). During early pregnancy in sheep,
hatched blastocysts begin to elongate on day 12 to
ultimately form an elongated filamentous conceptus
(embryo and associated extraembryonic membranes) of
~19 cm in length by day 16 (Guillomot 1995, Spencer
et al. 2004a). Blastocyst elongation is accompanied by
the onset of trophoblast giant binucleate cell differen-
tiation that begins on day 14 (Wooding 1992). Those
cells migrate and fuse with the endometrial LE, form
the basis of the cotyledonal area of the placentomes, and
synthesize a number of hormones such as chorionic
somatomammotropin hormone 1 (CSH1 or placental
lactogen) and progesterone (P4). Blastocyst elongation
in sheep requires the uterus and, specifically, secretions
from the endometrial epithelia (Gray et al. 2001).
Endometrial functions and epithelial secretions during
the peri-implantation period of pregnancy in sheep are
largely regulated by P4 from the corpus luteum (CL) and
cytokines/hormones from the conceptus, such as inter-
feron tau (IFNT; Spencer et al. 2004b, 2007). IFNT is
the signal for maternal recognition of pregnancy in
ruminants and is produced between days 10 and 21 of
pregnancy in sheep by the mononuclear trophoblast
cells of the conceptus (Spencer et al. 1996, 2007).
The anti-luteolytic actions of IFNT are required for the
maintenance of a functional CL and continued secretion
of P4, the essential hormone of pregnancy (Bazer et al.
1997). IFNT also induces or stimulates the expression of
a number of genes, termed IFNT-stimulated genes (ISGs),
in a cell-specific fashion within the endometrium, with
emerging biological roles in uterine receptivity to
conceptus development, differentiation, and implanta-
tion (Spencer et al. 2008).

Available results support the working hypothesis that
LIF from the endometrium and conceptus regulate
endometrial function and conceptus development via
LIFR and IL6ST. The expression of LIF mRNA and protein
in the ovine uterus during early pregnancy has been
reported (Vogiagis et al. 1997a, 1997b), but the expres-
sion and hormonal regulation of LIFR and IL6ST
in the ovine uterus and conceptus during early
pregnancy has not been investigated. These studies
were conducted to determine effects of 1) the estrous
cycle and early pregnancy on the expression of LIFR and
IL6ST as well as phosphorylated STAT3 in the ovine
uterus, 2) P4 and IFNT on LIFR and IL6ST expression in
the ovine uterus, and 3) LIF signaling in ovine
trophoblast and endometrial GE cells.

Results

Effects of the estrous cycle and early pregnancy on
the expression of LIFR and IL6ST mRNAs in ovine
endometria (study 1)

Slot-blot hybridization analyses assessed the steady-state
levels of ovine LIFR and IL6ST mRNAs in endometria
from cyclic and pregnant ewes (Fig. 1). In both cyclic
and pregnant ewes, endometrial LIFR mRNA levels
increased after day 10, and the increase was greater in pregnant
than cyclic ewes from days 10 to 16 (day × status,
P<0.01). In pregnant ewes, endometrial LIFR mRNA
levels increased 2.7-fold between days 10 and 14 and
remained abundant thereafter (quadratic effect of day,
P<0.01). Overall, IL6ST mRNA levels were higher in
pregnant than cyclic ewes (status, P<0.04) and
increased 2.8-fold between days 10 and 20 of pregnancy
(linear effect of day, P<0.05).

In situ hybridization analyses determined that LIFR
mRNA (Fig. 2) was most abundant in endometrial

Figure 1  Steady-state levels of LIFR and IL6ST mRNA in
endometria from cyclic and early pregnant ewes as determined
by slot-blot hybridization analysis. In both cyclic and preg-
nant ewes, endometrial LIFR mRNA levels increased after day 10,
and the increase was greater in pregnant than cyclic ewes to day 16
(day × status, P<0.01). (A) In pregnant ewes, endometrial LIFR mRNA
levels increased 2.7-fold between days 10 and 14 and then declined to
day 20 (quadratic effect of day, P<0.01). (B) IL6ST mRNA levels
increased 2.8-fold between days 10 and 20 of pregnancy (linear
effect of day, P<0.05). Data are expressed as LSM relative units (RU)
with S.E.M.
LE/superficial glandular epithelia (sGE) and GE in the upper stratum compactum stroma, whereas IL6ST mRNA (Fig. 3) was most abundant in the middle to deep GE and present at lower abundance in the stroma and LE. In pregnant ewes, LIFR and IL6ST mRNAs increased in endometrial LE/sGE and GE respectively, between days 10 and 16 and remained abundant to day 20. Both LIFR and IL6ST mRNAs were also detected in the trophectoderm of conceptuses on days 18 and 20 of pregnancy. Of particular note is that both LIFR and IL6ST mRNAs were present in the conceptus trophectoderm with IL6ST mRNA being particularly abundant in trophoblast giant binucleate cells (BNC).

**Early P4 treatment induces LIFR and IL6ST mRNAs in endometrial epithelia (study 2)**

This study used a sheep model in which exogenous P4 is administered from day 1.5 post-mating, thereby eliciting a premature increase in the circulating levels of P4 that is correlated with a larger blastocyst size on day 9 and the presence of elongated and filamentous conceptuses on day 12, which produce more IFNT (Satterfield et al. 2006). As shown in Fig. 4A and B, for day 9 ewes, endometrial LIFR mRNA abundance was increased twofold by early P4 (CO versus P4, \( P < 0.03 \)), while IL6ST mRNA was unaffected by this treatment (CO versus P4, \( P > 0.10 \)). In day 12 ewes, LIFR mRNA was also increased (1.6-fold) by P4 (CO versus P4, \( P < 0.05 \)) and IL6ST was not affected (CO versus P4, \( P > 0.10 \)). However, treatment of ewes with the antiprogestin RU486 from days 9 to 12 reduced endometrial LIFR mRNA levels by 2.5-fold (P4 versus P4 + RU486, \( P < 0.005 \); Fig. 4A) and IL6ST mRNA by 2.8-fold (P4 versus P4 + RU486, \( P < 0.02 \); Fig. 4B) compared with P4-treated ewes. In situ hybridization analyses revealed that early P4 increased LIFR mRNA in LE and GE (Fig. 4C) and that RU486 treatment reduced both LIFR and IL6ST mRNA in LE/GE and GE of the endometrium respectively (Fig. 4D).
IFNT stimulates endometrial LIFR and IL6ST expression in ewes treated with P4 (study 3)

In order to determine whether the expression of LIFR and IL6ST in endometria was regulated by P4 and/or IFNT, cyclic ewes were ovariectomized and fitted with intrauterine (i.u.) catheters on day 5, treated with exogenous P4 from days 5 to 16 and given intrauterine infusions of serum proteins as a control (CX) or roIFNT from days 11 to 16. As illustrated in Fig. 5A, LIFR mRNA levels in the endometrium was not affected by P4 (P4\textsubscript{CX} versus P4\textsubscript{ZK}\textsubscript{CX}, P>0.10), whereas IFNT increased LIFR mRNA levels 1.7-fold (P4+CX versus P4+IFN, P<0.04) in the ewes treated with P4, but not in the ewes treated with P4+ZK. Endometrial IL6ST mRNA levels were increased 2.3-fold by P4 (P4+CX versus P4+ZK+CX, P<0.03) and an additional 1.5-fold (P4+CX versus P4+IFN, P<0.05) and 1.4-fold (P4+IFN versus P4+ZK+IFN, P<0.04) respectively in both P4- and P4+ZK-treated ewes (Fig. 5B). In situ hybridization found that IFNT increased LIFR mRNA primarily in LE and sGE (Fig. 5C) and IL6ST mRNA in GE and stroma (Fig. 5D) of the endometrium respectively. In P4+ZK ewes, IFNT increased IL6ST mRNA in the deep GE of the endometrium (Fig. 5D).

Localization of immunoreactive LIFR and IL6ST proteins in the ovine uterus (study 1)

Immunohistochemical analysis indicated that LIFR protein was localized predominantly to endometrial LE/sGE, whereas IL6ST protein was localized primarily in uterine LE and GE (Fig. 6). In early pregnant ewes, both LIFR and IL6ST proteins in endometrial epithelia increased after day 14 and were abundant on day 20 of pregnancy (data not shown). Both LIFR and IL6ST proteins were detected in conceptus trophectoderm with IL6ST protein, particularly abundant in trophoblast giant BNC.
Localization of phosphorylated STAT3 protein in ovine endometrium and conceptus

Immunohistochemical analyses revealed that phosphorylated STAT3 (p-STAT3) protein was present in most endometrial cell types in cyclic and pregnant ewes, but was particularly abundant in the nuclei of endometrial epithelia (Fig. 7A). In uterine LE, p-STAT3 protein increased between days 10 and 12, remained maximal from days 12 to 16, and declined thereafter in pregnant ewes. In the upper GE, p-STAT3 protein increased substantially between days 16 and 18 of pregnancy (Fig. 7A and B). The p-STAT3 protein was also abundant in conceptus trophectoderm and detected in the endoderm (Fig. 7C).

IFNT increase LIFR and IL6ST proteins in ovine trophoblast cells

In oTr1 cells, IFNT increased amounts of LIFR (190 kDa) and IL6ST (130 kDa) proteins by 1.9-fold ($P<0.05$) and 2.2-fold ($P<0.01$) respectively over basal levels at 24-h post-treatment (Fig. 8A and B). In oGE cells, both LIFR and IL6ST proteins were present at all time points, but not affected ($P>0.10$) by IFNT (Fig. 9A and B).

LIF activates STAT3 and MAPK3/1 MAPK phosphorylation in ovine trophoblast and glandular epithelial cells

The oTr1 cells were untreated or treated with LIF for 15 min and then phosphorylated and total STAT3 and MAPK3/1 (p42/p44) MAPK proteins detected in cell lysates by immunoblotting. As shown in Fig. 8C and D, LIF increased the abundance of both p-STAT3 and p-MAPK3/1 MAPK proteins. In response to treatment with 100 ng/ml of recombinant LIF, p-STAT3 abundance increased 5.3-fold ($P<0.01$) over basal levels within 5 min and then decreased to basal levels by 60 min (Fig. 8E). Meanwhile, LIF stimulated a rapid 5.6-fold ($P<0.01$) increase in p-MAPK3/1 MAPK abundance within 15 min that decreased to basal levels between 30 and 60 min (Fig. 8F). In oGE cells, roIFNT did not affect the abundance...
of LIFR or IL6ST proteins (Fig. 9A and B). However, LIF increased the levels of p-STAT3 and p-MAPK3/1 MAPK proteins by 6.1-fold \((P < 0.01)\) and 3.6-fold \((P < 0.01)\) over basal levels respectively within 5 min; the effect was maintained to 90 min (Fig. 9C and D).

**Discussion**

The present studies revealed that both LIFR and IL6ST expression in the ovine endometrium increases during the peri-implantation period of early pregnancy. Co-expression of LIFR and IL6ST mRNA and protein as well as phosphorylated (activated) STAT3 protein was primarily in the superficial and upper glands of the endometrium, as well as in the trophoderm of the conceptus. Vogiagis *et al.* (1997a) found that LIF mRNA and protein were present in relatively constant amounts throughout the estrous cycle and early pregnancy in sheep and localized to all uterine cell types with particular abundance in the LE, and that immunoreactive LIF was present in conceptus trophoderm. Thus, the paracrine and perhaps autocrine actions of LIF within the uterus during early pregnancy in sheep are most likely manifest on the upper glands of the endometrium and conceptus trophoderm. The results of the present studies indicate that the biological effects of LIF on those cells involve activation of STAT3 and MAPK3/1 MAPK signaling pathways to alter gene expression patterns and cell proliferation and differentiation.

The results of the present study found that LIFR and IL6ST in the endometrial LE/GE and GE respectively are stimulated by P4 and IFNT in a complex stage- and cell-specific manner. The induction of many genes by P4, such as galectin 15 \((LGALS15\); Gray *et al.* 2004), cathepsin L1 \((CTSL1\); Song *et al.* 2005), cystatin C \((CST3\; Song *et al.* 2006a), endothelial PAS domain protein 1 \((EPAS1; Song *et al.* 2008a), gastrin-releasing peptide \((GRP; Song *et al.* 2008b), and insulin-like binding proteins 1 and 3 \((IGFBP1\ and IGFBP3; Satterfield *et al.* 2008), in the endometrial LE/SGE of the ovine uterus appears to be indirect and require P4-induced down-regulation of P4 receptors (PGR) in those epithelia (Spencer *et al.* 2004b, 2007), as well as perhaps factors from PGR-positive uterine stromal cells, such as fibroblast growth factor 10 \((FGF10; Chen *et al.* 2000, Satterfield *et al.* 2008). Indeed, the increase in LIFR mRNA abundance in the LE/SGE and upper GE between days 10 and 14 post-estrus/mating in study 1 is coincident with the loss of PGR mRNA and protein in these epithelia (Wathes & Hamon 1993, Spencer *et al.* 1995). Furthermore, in studies 2 and 3, LIFR mRNA increased in endometrial LE/SGE and upper GE of...
P4-treated ewes, but not in the ewes treated with P4 and a PGR antagonist, i.e., ZK 136 317 or RU486. Continuous exposure of the sheep uterus to P4 for 8–10 days down-regulates PGR mRNA and protein in endometrial LE/sGE, but not in stroma or myometrium (Johnson et al. 2000b); however, PGR are present in the endometrial epithelia of the ewes treated with P4 and a PGR antagonist (Johnson et al. 2000b), because PGR antagonists prevent P4 from down-regulating the expression of PGR. Consequently, the increase in LIFR mRNA may be due to P4-induced down-regulation of PGR in LE/sGE between days 10 and 12 of the estrous cycle and pregnancy (Spencer & Bazer 2004, Spencer et al. 2004b). The increase in endometrial LIFR expression by early treatment with P4 in study 2 also occurred coincident with early loss of PGR by endometrial LE/sGE (Satterfield et al. 2006). Similarly, IL6ST is expressed predominantly in endometrial GE as is the case for secreted phosphoprotein 1 (commonly referred to as osteopontin), serpin peptidase inhibitor (also known as uterine milk protein or UTMP), stanniocalcin 1 (STC1), and GRP, which encode proteins secreted into the uterine lumen (Moffatt et al. 1987, Ing & Roberts 1989, Johnson et al. 1999b, 2003, Song et al. 2006b, 2008b). All four of those genes are induced in endometrial GE by the long-term effects of continuous P4 that also requires loss of the PGR as a permissive event preceding IFNT effects to enhance gene expression (Spencer & Bazer 2002, Spencer et al. 2004b). Collectively, available evidence supports the idea that treatment of ewes with PGR antagonists prevents P4-induced loss of PGR in the LE/sGE and GE, as well as stromal-derived progestomedins, and then subsequent induction of gene expression in those epithelia, which, in turn, produces a uterus unsupportive of conceptus development and implantation. Indeed, no blastocysts were recovered from the P4 + RU486-treated ewes in study 2 that had reduced the levels of endometrial LIFR and IL6ST expression (Satterfield et al. 2006). In addition to being an antiprogestin, RU486 or mifepristone is a high-affinity antagonist of the nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor; NR3C1, also known as GR; Baulieu 1989), suggesting that NR3C1 and glucocorticoids may also regulate uterine LE/sGE gene expression. However, little is known of NR3C1 expression and glucocorticoid effects within the ovine uterus during early pregnancy.

Available results support our working hypothesis that uterine LIF regulates endometrial function and conceptus growth and development during the peri-implantation period of pregnancy in sheep. In the present study, LIFR, IL6ST, and phosphorylated STAT3 were found in the upper GE of early pregnancy during the period of conceptus elongation and implantation. Similarly, Lifr and Il6st are co-expressed in the uterine LE of mice (Song & Lim 2006), which responds to LIF from the endometrial GE by phosphorylating STAT3 that is essential for implantation (Cheng et al. 2001, Song & Lim 2006). In the present studies, treatment of ovine endometrial GE cells with LIF increased the abundance of activated phosphorylated STAT3 and MAPK3/1 MAPK proteins. Future studies will determine which genes in the upper GE are the targets of LIF actions.

Novel results from the present studies implicate LIF, LIFR, IL6ST co-receptor, and STAT3 and MAPK3/1 MAPK in the growth and differentiation of conceptus trophectoderm and, in particular, tropheblast giant BNC. In particular, LIFR signaling via STAT3 regulates trophoblast giant cell differentiation in mice (Takahashi et al. 2008).

Figure 6 Immunolocalization of LIFR and IL6ST proteins in the uteri from cyclic and pregnant ewes. Immunoreactive LIFR and IL6ST proteins were localized predominantly near the apical surface of endometrial LE/sGE and all GE respectively in uteri and in conceptus trophectoderm from day 18 pregnant ewes using a rabbit anti-human LIFR polyclonal antibody and a rabbit anti-human gp130 polyclonal antibody. For the IgG control, normal rabbit IgG was substituted for the primary antibody. Sections were not counterstained. LE, luminal epithelium; GE, glandular epithelium; Tr, trophectoderm; M, myometrium; BV, blood vessels; sGE, superficial GE; BNC, binucleate cells. Scale bar, 10 μm.

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Indeed, the polyploid trophoblast giant cells of the mouse placenta are terminally differentiated and mediate trophoblast invasion of maternal decidua (Simmons & Cross 2005). Similarly, human extravillous trophoblast invasiveness can be regulated by LIF and STAT3 (Poehlmann et al. 2005). The trophoblast giant BNC of the ovine placenta are similar to the trophoblast giant cells of the mouse placenta, in that they are polyploid, invasive, and express unique genes such as CSH1 (Hoffman & Wooding 1993). In addition to STAT3, the MAPK3/1 MAPK pathway also plays important roles in differentiation, including embryonic and placental development (Mudgett et al. 2000, Wang et al. 2004, Daoud et al. 2005). Given that little is known about the cellular and molecular mechanisms governing trophoblast growth and differentiation in ruminants, the potential roles of LIF, its receptor complex, STAT3, and MAPK3/1 MAPK in development and differentiation within the sheep conceptus need to be discerned.

Materials and Methods

Animals

Mature crossbred Suffolk sheep (Ovis aries) were observed daily for estrus in the presence of vasectomized rams and used in experiments after they had exhibited at least two estrous cycles of normal duration (16–18 days). At estrus, the ewes were assigned randomly to cyclic or pregnant status. All experimental and surgical procedures were in compliance with the Guide for the Care and Use of Agriculture Animals in Teaching and Research and were approved by the Institutional Animal Care and Use Committee of Texas A&M University.

Experimental design

Study 1

At estrus (day 0), the ewes were mated to either an intact or vasectomized ram and then hysterectomized (n=5 ewes/day) on either day 10, 12, 14, or 16 of the estrous cycle or day 10, 12, 14, 16, 18, or 20 of pregnancy as described previously (Spencer et al. 1999a). At hysterectomy, the uterus was flushed with 20 ml sterile saline. Pregnancy was confirmed on days 10–16 post-mating by the presence of a morphologically normal conceptus(es) in the uterine flushing. It was not possible to obtain uterine flushings on either day 18 or 20 of pregnancy, because the conceptus had firmly adhered to the endometrial LE and basal lamina. At hysterectomy, several sections (≈0.5 cm) from the mid-portion of each uterine horn ipsilateral to the CL were fixed in fresh 4% paraformaldehyde in PBS (pH 7.2) (v/v). After 24 h, the fixed tissues were changed to 70% ethanol (v/v) for 24 h, dehydrated through a graded series of alcohol to xylene, and then embedded in Paraplast Plus (Oxford Labware, St Louis, MO, USA). The remaining endometrium was physically dissected from myometrium, frozen in liquid nitrogen, and stored at −80 °C for subsequent RNA extraction. In monovulatory pregnant ewes, uterine tissue samples were marked as either contralateral or ipsilateral to the ovary bearing the CL and only tissues from the ipsilateral

Figure 7 Immunohistochemical localization of phosphorylated STAT3 protein in endometria from cyclic and pregnant ewes. Immunoreactive p-STAT3 protein was localized using a rabbit anti-mouse phospho-STAT3 (Tyr705) polyclonal antibody. Normal rabbit IgG was substituted for the primary antibody as a negative control. Sections were not counterstained. Immunoreactive p-STAT3 protein was present in the nuclei of endometrial LE, GE, and conceptus trophoderm of pregnant ewes. Interestingly, after day 16 of pregnancy, p-STAT3 protein was predominantly localized to the endometrial upper glands while significantly decreased in the LE. The p-STAT3 protein was also particularly abundant in conceptus trophoderm in pregnant ewes. Localization of immunoreactive p-STAT3 protein in conceptus trophoderm, including binucleate giant cells, was based on cell morphology. LE, luminal epithelium; GE, glandular epithelium; S, stroma; En, endoderm; Tr, trophectoderm. (A and C) Scale bar, 5 μm; (B) 2.5 μm.
uterine horn were used in subsequent analyses. In addition, conceptuses (n=5 per day) were collected on days 13, 14, 15, and 16 of pregnancy by uterine flush and then fixed and embedded in paraffin as described above.

Study 2
As described previously (Satterfield et al. 2006), the ewes were mated at estrus (day 0) to intact rams and then assigned randomly to receive daily i.m. injections from days 1.5 to 9 of either corn oil vehicle (CO; n=6) or 25 mg P4 (n=6). All ewes were hysterectomized on day 9, and uteri processed as described for experiment 1. In a complementary study, the ewes were mated and assigned randomly (n=5 per treatment) to receive daily i.m. injections of P4 and/or a PGR antagonist (ZK 136,317; Schering AG, Berlin, Germany) and intrauterine (i.u.) infusions of control serum proteins and/or recombinant ovine IFNT protein (rolFNT) as follows: 1) 50 mg P4 (days 5–16) and 200 µg control serum (CX) proteins (days 11–16) (P4+CX), 2) P4 plus 75 mg ZK 136,317 (days 11–16) and CX proteins (P4+ZK+CX), 3) P4 and IFNT (2×10^6 antiviral units, days 11–16) (P4+IFN), or 4) P4 plus ZK and IFNT (P4+ZK+IFN). Steroids were administered i.m. daily in corn oil vehicle. Both uterine horns of each ewe received twice daily injections of either CX proteins (50 µg/horn/injection) or rolFNT (5×10^6 antiviral units/horn/injection). The rolFNT was produced in Pichia pastoris and purified as described previously (Van Heeke et al. 1996). CX proteins were prepared for intrauterine injection as described previously (Spencer et al. 1995). This regimen of P4 and rolFNT mimics the effects of P4 from the CL and IFNT from the conceptus on endometrial expression of hormone receptors and ISGs during early pregnancy in sheep (Song et al. 2005, 2006a, 2007, 2008a, 2008b). All ewes were hysterectomized on day 17, and uteri processed as described for study 1.

Study 3
Cyclic ewes (n=20) were checked daily for estrus and then ovariectomized and fitted with indwelling uterine catheters on day 5 as described previously (Johnson et al. 2000a). The ewes were then assigned randomly (n=5 per treatment) to receive daily i.m. injections of P4 and/or a PGR antagonist (ZK 136,317; Schering AG, Berlin, Germany) and intrauterine (i.u.) infusions of control serum proteins and/or recombinant ovine IFNT protein (rolFNT) as follows: 1) 50 mg P4 (days 5–16) and 200 µg control serum (CX) proteins (days 11–16) (P4+CX), 2) P4 plus 75 mg ZK 136,317 (days 11–16) and CX proteins (P4+ZK+CX), 3) P4 and IFNT (2×10^6 antiviral units, days 11–16) (P4+IFN), or 4) P4 plus ZK and IFNT (P4+ZK+IFN). Steroids were administered i.m. daily in corn oil vehicle. Both uterine horns of each ewe received twice daily injections of either CX proteins (50 µg/horn/injection) or rolFNT (5×10^6 antiviral units/horn/injection). The rolFNT was produced in Pichia pastoris and purified as described previously (Van Heeke et al. 1996). CX proteins were prepared for intrauterine injection as described previously (Spencer et al. 1995). This regimen of P4 and rolFNT mimics the effects of P4 from the CL and IFNT from the conceptus on endometrial expression of hormone receptors and ISGs during early pregnancy in sheep (Song et al. 2005, 2006a, 2007, 2008a, 2008b). All ewes were hysterectomized on day 17, and uteri processed as described for study 1.

Study 4
A mononuclear ovine trophectoderm cell line (oTr1), derived from a day 15 conceptus (Farmer et al. 2008, Kim et al. 2008),
was cultured as described previously in DMEM–F12 (Sigma-Aldrich Corp.) that included 10% FBS (v/v), 50 U penicillin, 50 μg streptomycin, 0.1 mM each non-essential amino acids, 1 mM sodium pyruvate, 2 mM glutamine, and 0.7 μM insulin. When cell density in dishes reached about 80% confluence, they were passaged at a ratio of 1:3 and frozen stocks of cells were prepared at each passage. For experiments, monolayer cultures of oTr1 cells (between passages 9 and 13) were grown in culture medium to 90% confluence on 100 mm tissue culture plates. Immortalized ovine endometrial GE (oGE) cells were cultured as described previously (Johnson et al. 1999a). Ovine GE cells were maintained in DMEM–F12 supplemented with 10% FBS (v/v) and antibiotics and then both cell monolayer cultures were grown to 90% confluence on 100 mm tissue culture plates. All cell lines were incubated in serum-free medium for 24 h and then left untreated as a control or treated with roIFNT (10^4 AVU/ml) for the indicated periods of time. Blots were imaged to calculate the normalized values presented in graphs (bottom) by measurements of the levels of mouse a-tubulin (TUBA) protein relative to total proteins. This time-course design was replicated in four independent experiments. (C and D) The oGE cells were starved for 24 h in serum-free medium and then treated with LIF by indicated time (100 ng/ml LIF). Blots were imaged to calculate the normalized values presented in graphs by measurements of the levels of phosphorylated -protein relative to total proteins. All quantitative data are presented as least-squares means (LSM) with overall s.e.m. This time-course design was replicated in three independent experiments.

Cloning of partial cDNAs for ovine LIFR and IL6ST

Partial cDNAs for ovine LIFR and IL6ST mRNAs were amplified by RT-PCR using total RNA from day 18 pregnant endometrium using specific primers based on bovine LIFR mRNA (GenBank accession no. XM_587754; forward, 5’-AGC CAC TGA CCG AGT TTC C-3′; reverse, 5’-ATG GGA AGA AAT TCC TGT GC-3′) and bovine IL6ST mRNA (GenBank accession no. XM-600430; forward, 5’-TGG TGG AAG GGA AAC ATA CC-3′; reverse, 5’-GCT TCT TCA CTC CAG TCA CT-3′). Reverse transcription of total RNA into cDNA was performed as described previously (Taylor et al. 2001). PCR amplification was conducted as follows for LIFR and IL6ST: 1) 95 °C for 5 min; 2) 95 °C for 30 s, 56.5 °C for 40 s, and 72 °C for 1 min for 35 cycles; and 3) 72 °C for 10 min. The partial cDNAs for ovine LIFR and IL6ST PCR products were cloned into pCRII using a T/A Cloning Kit (Invitrogen) and their sequences verified using an ABI PRISM Dye Terminator Cycle Sequencing Kit and ABI PRISM automated DNA sequencer (Applied Biosystems, Foster City, CA, USA).

Slot-blot hybridization analyses

The steady-state levels of mRNA in ovine endometria were assessed by radioactive slot-blot hybridization as described previously (Spencer et al. 1999b). Denatured total endometrial RNA (20 μg) from each ewe was hybridized with radiolabeled antisense cRNA probes. To correct for variation in total RNA loading, a duplicate RNA slot-blot membrane was hybridized with radiolabeled antisense 18S cRNA (pT718S; Ambion, Austin, TX, USA), because 18S RNA content of the endometrium was not affected by day, pregnancy status, or hormonal treatment in any of the studies (data not shown). Following washing, the blots were digested with RNase A and radioactivity associated with slots quantified using a Typhoon 8600 Multimager (Molecular Dynamics, Piscataway, NJ, USA).

RNA isolation

Total cellular RNA was isolated from the frozen endometria or cultured cells using the TRIzol reagent (Gibco-BRL), according to the manufacturer’s recommendations. The quantity and quality of total RNA were determined by spectrometry and denaturing agarose gel electrophoresis respectively.
In situ hybridization analyses

Location of mRNA in uterine sections (5 μm) was determined by radioactive in situ hybridization analysis as described previously (Spencer et al. 1999b). After hybridization, washing and RNase A digestion, slides were dipped in NTB-2 liquid photographic emulsion (Kodak), and exposed at 4°C for 10 days. After development and counterstaining, images of the representative fields were recorded under bright- or dark-field illumination.

Immunohistochemical analyses

Immunohistochemical localization of LIFR and IL6ST proteins in ovine uterus was performed as described previously (Spencer et al. 1999c) using rabbit anti-human LIFR polyclonal IgG (catalog no. sc-659; Santa Cruz Biotechnology Inc., Santa Cruz, CA, USA) at 1:500 dilution (0.4 μg/ml), rabbit anti-human IL6ST polyclonal IgG (catalog no. 06-261; Upstate, Lake Placid, NY, USA) at 1:1000 dilution (1.0 μg/ml), and rabbit anti-mouse phospho-STAT3 (Tyr705) polyclonal IgG (catalog no. 9131; Cell Signaling Technology, Danvers, MA, USA) at 1:100 dilution. Antigen retrieval was performed using the boiling citrate method. Negative controls included substitution of the primary antibody with purified non-immune rabbit IgG at the same final concentration. Sections were not counterstained prior to affixing coverslips.

Whole cell extracts and immunoblot assays were prepared and performed as described previously (Stewart et al. 2001). Proteins in cell lysates were denatured, separated using SDS-PAGE, transferred to nitrocellulose, and western blot analyses performed as described previously (Spencer et al. 1999a) using ECL detection (SuperSignal West Pico, Pierce, Rockford, IL, USA) and X-OMAT AR X-ray film (Kodak), according to the manufacturer’s recommendations. Immunoreactive proteins were detected using anti-human LIFR polyclonal IgG (catalog no. sc-659; Santa Cruz Biotechnology Inc.) at 1:1000 dilution (0.2 μg/ml), anti-human IL6ST polyclonal IgG (catalog no. 06-261; Upstate) at 1:2000 dilution (0.5 μg/ml), anti-mouse phospho-STAT3 (Tyr705) polyclonal IgG (catalog no. 9131; Cell Signaling Technology) at 1:1000 dilution (1.0 μg/ml), anti-human phospho-MAPK3/1 polyclonal IgG (catalog no. 9101; Cell Signaling Technology) at 1:2000 dilution (0.5 μg/ml), anti-rat STAT3 polyclonal IgG (catalog no. S21320; Transduction Laboratories Inc., Lexington, KY, USA) at 1:2500 dilution (1.0 μg/ml), and anti-human MAPK3/1 monoclonal IgG (catalog no. 4695; Cell Signaling Technology) at 1:5000 dilution. Multiple exposures of each western blot were performed to ensure linearity of chemiluminescent signals. Western blots were quantified using a ChemiDoc EQ system and Quantity One software (Bio-Rad).

Statistical analyses

All quantitative data were subjected to least-squares ANOVA using the Statistical Analysis System (SAS Institute, Cary, NC, USA). Slot-blot hybridization data were corrected for differences in sample loading using the 18S rRNA data as a covariate. Data from ewes between days 10 and 16 (study 1) were analyzed for the effects of day, pregnancy status (cyclic or pregnant), and their interaction. Data from studies 2 and 3 were analyzed using orthogonal contrasts (day 9: CO versus P4, day 12: CO versus P4, and day 12: P4 versus P4+RU486 for study 2; P4+CX versus P4+IFN, P4+ZK+CX versus P4+ZK+IFN, P4+CX versus P4+ZK+CX for study 3) to determine the effects of the treatment. All tests of significance were performed using the appropriate error terms according to the expectation of the mean squares for error. P≤0.05 was considered significant. Data are presented as least-squares means with (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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