REV-ERBα Inhibits the PTGS2 Expression in Bovine Uterus Endometrium Stromal and Epithelial Cells Exposed to Ovarian Steroids

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Abstract. The nuclear receptor REV-ERBα (encoded by NR1D1) has a critical role in metabolism and physiology as well as circadian rhythm. Here, we investigated the possible contribution of clock genes including NR1D1 to the secretion of prostaglandin F\(_2\)α (PGF\(_2\)α) from bovine uterine stromal (USCs) and epithelial cells (UECs) by modulating the expression of PTGS2. The circadian oscillation of clock genes in the cells was weak compared with that reported in rodents, but the expression of BMAL1, PER1, and NR1D1 was changed temporally by treatment with ovarian steroids. Significant expression of clock genes including NR1D1 was detected in USCs exposed to progesterone. NR1D1 was also significantly expressed in UECs exposed to estradiol. The expression of PTGS2 was suppressed in USCs exposed to progesterone, while the expression was initially suppressed in UECs exposed to estradiol and then increased after long-term exposure to estradiol. BMAL1 knockdown with specific siRNA caused a significant decrease in the transcript levels of NR1D1 and PTGS2 in USCs, but not in UECs. The production of PGF\(_2\)α also decreased in USCs after BMAL1 knockdown, while its level did not significantly change in UECs. The transcript level of PTGS2 was increased by treatment with the antagonist of REV-ERBα in both cell types, but the agonist was ineffective. In these two cell types treated with the agonist or antagonist, the PGF\(_2\)α production coincided well with the PTGS2 expression. Collectively, these results indicate that REV-ERBα plays an inhibitory role in the expression of PTGS2 in both bovine USCs and UECs treated with ovarian steroids.

Key words: Bovine uterus endometrium cells, Clock genes, Prostaglandin F\(_2\)α, PTGS2 gene, REV-ERBα

In cows and sheep, luteolysis is induced by prostaglandin F\(_2\)α (PGF\(_2\)α), which is secreted in a pulsatile mode from the uterine endometrium during the luteal phase to the follicular phase. Progesterone (P\(_2\)), estradiol (E\(_2\)), and oxytocin have been regarded as the critical factors regulating the secretion of PGF\(_2\)α from the endometrium. It has been demonstrated that oxytocin promotes the secretion of PGF\(_2\)α as a pulse generator of its secretion in the endometrium [1, 2]. However, the critical roles of P\(_2\) and E\(_2\) in the secretion of PGF\(_2\)α are still unclear [3, 4]. It is generally accepted that ovarian steroids modulate the sensitivity of the endometrium to oxytocin by regulating the expression of the oxytocin receptor [5–7]. Conversely, several studies object to the role of oxytocin in luteolysis [8–10], and it was proposed that oxytocin is not essential for PGF\(_2\)α secretion [3, 11]. Therefore, existence of another regulator(s) of the PGF\(_2\)α secretion in the endometrium was postulated [4], but no regulator has not been identified.

Prostaglandin G/H synthetase (PTGS) is the key rate-limiting enzyme converting arachidonic acid into PGG2 and PGH2, which are the precursors for PGF\(_2\)α and other metabolites. PTGS has two isoforms, PTGS1 and PTGS2. In the bovine endometrium, PGF\(_2\)α is synthesized mostly by PTGS2 [12]. The promoter region of the bovine PTGS2 gene contains the E-box element and REV-ERBα/RORα responsive element (RORE), which are the circadian clock-controlled cis-regulatory elements.

The cellular clock components CLOCK and BMAL1 bind to the E-box enhancer and induce expression of the nuclear receptor REV-ERBα (encoded by NR1D1), resulting in repression of transcription of BMAL1 through direct binding to RORE located in the BMAL1 promoter [13]. In addition to regulating each other to sustain oscillations, the core clock proteins also entrain the rhythmic expression of numerous genes through binding to the E-box, RORE, and D-box at their promoters, which have been called clock-controlled genes (CCGs) and found to comprise a large family. The peripheral oscillators control the expression of downstream CCGs that are expressed in tissue-specific relationships. REV-ERBα has a critical role in the regulation of metabolism and physiology as well as circadian rhythms [14]. The cellular level of heme, identified as a physiological ligand for REV-ERBα [15], oscillates in a circadian manner [16]. SRR278 recently became available as a synthetic antagonist of REV-ERBα [17]. Based on recent studies, we raised the possibility that the PTGS2 gene is a downstream CCG in bovine uterus endometrial cells.

We reported that circadian rhythmicity is weak in the rat uterus luminal epithelium as revealed by immunohistochemistry, although a strong immunostaining signal of PER2 protein is detected in the epithelial cell layer compared with that in the stromal cell layer [18]. Since regulation of the circadian clockwork may be different between stromal cells and epithelial cells, the two cell types for the
circular clockwork need to be analyzed separately. In the present study, we extended our recent investigations to explore the possible contribution of the circadian clockwork to the secretion of PGF₂α from the bovine endometrium by modulating the expression of the PTGS2 gene.

Materials and Methods

Isolation and culture of bovine USCs and UECs

Bovine uteri were collected from a slaughterhouse and transferred to laboratory on ice. The two cell types were isolated from the uteri of cows showing the luteal stage at days 11 to 17 as determined by ovarian morphology [19]. The caruncles were physically dissected from the endometrium of the bovine uterus. Tissue pieces were treated with 0.1% collagenase (Wako, Tokyo, Japan) at 37 °C for 30 min and cultured for 1 week in DMEM/F12 (Invitrogen, Carlsbad, CA, USA) supplemented with 10% charcoal-stripped FBS (Biological Industries, Kibbutz Be’er Haemek, Israel) with 1× antibiotic-antimycotic mixed solution (AA; Nacalai Tesque, Kyoto, Japan). USCs and UECs migrated from the tissue pieces and separately proliferated in a monolayer (Supplementary Fig. 1: on-line only) [20]. USCs and UECs in primary culture were separated with trypsin-EDTA. USCs and UECs were pooled with 0.05% and 0.25% trypsin-EDTA, respectively. Both cell types separated (4.0×10⁵ cells) were seeded (1:250) for 1 h at room temperature. Immunostaining was detected under a fluorescence microscope (Nikon, Japan). The USCs were and cultured for 1 week in DMEM/F12 (Invitrogen, Carlsbad, CA, USA) and DAPI (Sigma-Aldrich) diluted in blocking solution as a negative control. After washing several times with PBS, they were incubated with secondary antibodies (Santa Cruz Biotechnology, CA, USA) and DAPI (Sigma-Aldrich) diluted in blocking buffer. Goat serum was substituted for the primary antibody for an additional 24 h. The cells were maintained with transfection medium for 24 h. The medium was replaced with a medium supplemented with 1× ITS, 1× AA and 0.1% BSA. After 24 h in culture, the medium was removed, and the BMAL1-specific siRNA and non-silencing RNA were diluted in Opti-MEM were transfected into cells using Lipofectamine® RNAiMAX reagent (Life Technologies, Grand Island, NY, USA) according to the manufacturer’s protocol. Both the BMAL1-specific siRNA and non-silencing RNA were used at a final concentration of 100 nM. The cells were maintained with transfection medium for an additional 24 h. The medium was replaced with a medium supplemented with 1× AA, 1× ITS, and 0.1% BSA. Then, USCs and UECs were cultured with 100 nM P₄ and 100 nM E₂, respectively, for 12 h and synchronized with forskolin.

Treatment with heme and SR8278

USCs and UECs were cultured with 50 μM heme (Sigma-Aldrich) or 10 μM SR8278 (Sigma-Aldrich) dissolved in DMSO in the presence of steroid hormones after synchronization with forskolin. As a control, each cell was treated with 0.1% DMSO instead of heme and SR8278.

RNA extraction and RT-qPCR

Cultured cells were harvested at indicated time points, and total RNA was isolated using an RNeasy Mini Kit (Qiagen) according to the manufacturer’s protocol. RNA samples were treated with RNase-free DNase (Qiagen). The cDNAs were generated by RT with Oligo (dT)₁₅ and Random Primers using a GoTaq® 2-Step RT-qPCR System (Promega, Madison, WI, USA). The primer sets used for the RT-qPCR are listed in Supplementary Table 2 (on-line only). All primer pairs were designed to span introns to prevent amplification of products from genomic DNA. RT-qPCR was performed in a 50-μl
volume containing a 20-ng cDNA sample in GoTaq® qPCR Master Mix and 250 nM specific primers with an Mx3000P Real-time qPCR System (Agilent Technologies, Santa Clara, CA, USA) using the parameters described in our previous report [22]. The relative quantification of gene expression was analyzed from the measured threshold cycles (Ct) using the comparative cycle threshold (ΔCt) method [18]. The ΔCt for each sample was normalized to the average level of the constitutively expressed housekeeping gene GAPDH. Gene expression was then normalized to the level of the gene of interest in the control samples.

**PGF₂α assay**

Culture supernatants were collected at 48 h after synchronization. Then the PGF₂α contents were measured using EIA kits (Cayman Chemical, Ann Arbor, MI, USA) according to the manufacturer’s instructions. The intra-assay and inter-assay variabilities were <10%.

**Data analysis and statistics**

Data are expressed as the means ± SEM of at least three independent experiments, each performed with duplicate samples. The statistical analyses were performed by one-way ANOVA with Tukey’s multiple comparison test or the Student’s t test, as indicated using the SigmaPlot software (Ver. 12.0; Systat Software, San Jose, CA, USA). Differences were considered significant at P<0.05 or less. Rhythmicity in gene expression was determined by the single Cosinor method using Timing Series Single 6.3 (Expert Soft Tech.) [23].

**Results**

**Bioluminescence activity in rat and bovine USCs transfected with the mouse Per1-Luc vector**

To investigate whether the cellular clockwork functions in bovine uterus cells, we first analyzed mouse Per1 promoter activity as an indicator of the clockwork. There are three E-box sites and one CRE in the mouse Per1 promoter region (Fig. 1A). The rat USCs exposed to P₄ were used as a positive control, in which a robust circadian clockwork has been confirmed [18, 24]. Real-time monitoring of bioluminescence clearly revealed that there were clear differences in oscillation profiles between rat and bovine USCs. Rat USCs displayed a sharp peak until approximately 30 min after synchronization. Thereafter, the promoter activity in rat USCs showed stable oscillation for 5 days. Conversely, bovine USCs displayed high activity immediately after synchronization, and then the activity in bovine USCs decreased and showed only several small peaks (Fig. 1B).

**Expression of core clock genes in bovine USCs**

We next analyzed the temporal changes of the clock gene transcript levels over the course of 48 h using bovine USCs. After synchronization with forskolin, the clock genes PER1 and NR1D1 displayed no significant expression in the absence of P₄ (Fig. 2). BMAL1 only showed significantly high expression at 6 h (P<0.05). However, these clock gene transcripts showed no diurnal rhythms. P₄ was added to the culture medium, because the stroma is comprised
of progesterone-targeting cells and is fitted to the luteal stage. In the presence of 100 nM P₄, significant expression of three clock genes was detected (P<0.01) (Fig. 2). Several peaks of clock gene transcripts were observed until 48 h, but their diurnal rhythms were not significant, except in the case of PER1 (Cosinor, P=0.0006). The relative expression of NR1D1 was high in the presence of P₄, especially at 24 to 48 h (P<0.05).

Expression of core clock genes in bovine UECs

We also analyzed the temporal changes in the clock gene transcripts in UECs. After synchronization, the clock genes PER1 and NR1D1 displayed no significant expression in the absence of E₂ (Fig. 3), but BMAL1 displayed significant expression (P<0.05) and diurnal rhythms (Cosinor, P=0.0013). E₂ was also added to the culture medium, because the epithelium is comprised of estrogen-targeting cells. In the presence of 100 nM E₂, NR1D1 displayed a significant expression and peaked at around 30 h (P<0.05) (Fig. 3). PER1 also showed significant expression (P<0.01). However, the diurnal rhythms of PER1 and NR1D1 were not significant, except in the case of BMAL1 (Cosinor, P=0.0365).

Expression of PTGS2 in bovine USCs and UECs

The expression level of PTGS2 was investigated in bovine USCs and UECs. After synchronization, PTGS2 displayed significant expression in both cell types. As shown in Fig. 4, however, different responses of the two cell types to steroid hormones were observed. In the USCs exposed to P₄, PTGS2 displayed significantly high expression and peaked at 6 to 12 h (P<0.01) (Fig. 4A). In addition, the diurnal rhythm of the PTGS2 transcript was significant (Cosinor, P=0.0009). The expression level of PTGS2 was low at 30 to 48 h in the presence of P₄, whereas it was high in the absence of P₄. In the UECs exposed to E₂, PTGS2 also showed significant expression and peaked at 48 h (P<0.01) (Fig. 4B). However, the diurnal rhythm of the PTGS2 transcript was not significant. The expression of PTGS2 was suppressed until 30 h in the presence of E₂ compared with the absence of E₂. After long exposure to E₂ (48 h), the PTGS2 transcript level was dramatically increased (P<0.01).

Effect of BMAL1 knockdown on the expression of PTGS2 in bovine USCs and UECs

We used BMAL1-specific siRNA to investigate whether the PTGS2 expression is controlled under BMAL1 transcriptional regulation in the two bovine cell types. BMAL1 associated with CLOCK or NPAS2 promotes the transcription of genes such as NR1D1 through binding to the E-box at the promoter region. The transfection of BMAL1-specific siRNA caused a significant decrease in the BMAL1 transcript level of both the USCs (P<0.01) and the UECs (P<0.05) (Fig. 5). Concomitantly, the NR1D1 transcript level was significantly decreased in the USCs (P<0.01), while it did not change in the UECs. The PTGS2 transcript level was also significantly decreased in the USCs (P<0.05). Conversely, the UECs displayed no downregulation of the PTGS2 transcript after BMAL1 knockdown.

Fig. 2. Expression profiles of core clock gene transcripts over the course of 48 h in bovine USCs. After synchronization with forskolin, total RNA samples were collected at 6 h interval from cells cultured with (bottom) or without (upper) the presence of P₄. RT-qPCR analyses of transcript levels were performed using their specific primers. The relative transcript level was normalized to GAPDH and expressed relative to the first time point (0 h). Each value represents the mean ± SEM of three independent experiments. The statistical analyses were performed by one-way ANOVA with Tukey’s multiple comparison tests. * P<0.05 vs. 0 h.
Fig. 3. Expression profiles of core clock gene transcripts over the course of 48 h in bovine UECs. After synchronization with forskolin, total RNA samples were collected at 6 h interval from cells cultured with (bottom) or without (upper) the presence of estradiol. RT-qPCR analyses of transcript levels were performed using their specific primers. The relative transcript level was normalized to GAPDH and expressed as relative to the first time point (0 h). Each value represents the mean ± SEM of three independent experiments. The statistical analyses were performed by one-way ANOVA with Tukey’s multiple comparison tests. * P<0.05 vs. 0 h.

Fig. 4. Expression of the PTGS2 gene in bovine USCs and UECs. After synchronization with forskolin, total RNA samples were collected at 6 h interval from USCs (A) and UECs (B) cultured with or without the presence of ovarian steroids. RT-qPCR analyses of transcript levels were performed using their specific primers. The relative transcript level was normalized to GAPDH and expressed as relative to the first time point (0 h). Each value represents the mean ± SEM of three independent experiments. The statistical analyses were performed by one-way ANOVA with Tukey’s multiple comparison tests. * P<0.05 vs. 0 h.
Effects of heme and SR8278 on the PTGS2 expression in bovine USCs and UECs

To further investigate the regulation of PTGS2 expression, we treated bovine USCs and UECs with the agonist (heme) or antagonist (SR8278) of REV-ERBα. As shown in Fig. 6, the Ptgs2 transcript level was dramatically increased by SR8278 in both cell types. Conversely, treatment with heme did not alter the expression. During treatment with heme or SR8278, different transcript levels of the clock genes BMAL1 and NR1D1 were observed. The NR1D1 transcript level was greatly increased by SR8278 in the USCs but not in the UECs. However, the BMAL1 transcript level was not changed by SR8278 in the USCs and UECs, probably due to the absence of the REV-ERBα action. Treatment with heme increased the NR1D1 transcript levels in both cell types, although their increases were very small. Treatment with heme also increased the BMAL1 transcript level in the USCs.

Production of PGF2α by bovine USCs and UECs

To further test whether the PTGS2 expression is regulated by BMAL1 and/or REV-ERBα, we determined the production of PGF2α in culture media after treatment with BMAL1-specific siRNA and the agonist or antagonist of REV-ERBα. As shown in Fig. 7A, the level of PGF2α significantly decreased in USCs after the transfection of BMAL1-specific siRNA (P<0.05), and this was coincident with the decreased transcript level of PTGS2. Conversely, the level of PGF2α did not significantly change in UECs transfected with BMAL1-specific siRNA, in which the transcript level of PTGS2 remained unchanged. In both cell types treated with heme or SR8278, the production of PGF2α was well reflected by the expression of PTGS2. As shown in Fig. 7B, the level of PGF2α increased approximately twofold in the presence of SR8278. Conversely, treatment with heme caused no significant changes in the PGF2α level.

Discussion

The regulation of PGF2α production in the bovine uterus endometrium during the estrus cycle remains poorly understood, although P4, E2 and oxytocin are well known as the regulatory hormones [3, 4, 11]. In the present study, we focused on control of the cellular circadian clockwork related to PGF2α production in bovine USCs and UECs. We demonstrated that the nuclear receptor REV-ERBα plays an inhibitory role in PGF2α secretion, which is mediated through direct inhibition of PTGS2 expression in both cell types. We also showed that BMAL1 promotes PGF2α secretion as a heterodimer with CLOCK, which is mediated through the transactivation of the PTGS2 expression in USCs. The secretion of PGF2α may be balanced by the inhibitory or stimulatory transcriptional regulation of REV-ERBα and BMAL1/CLOCK, respectively.

Circadian clockwork systems generate cellular rhythms in physiological functions via identified transcriptional and posttranscriptional regulatory processes. The cellular clock components CLOCK and
BMAL1 bind to the E-box enhancer and positively drive the expression of the *Period* genes (*Per1-3*) and the *Cryptochrome* genes (*Cry1-2*). In turn, PER and CRY proteins heterodimerize and undergo phosphorylation. The PER-CRY complexes translocate to the nucleus and repress the activity of CLOCK-BMAL1 heterodimers [25, 26]. Further adding to the complexity, CLOCK-BMAL1 heterodimers induce expression of the nuclear receptor REV-ERBα (encoded by *NR1D1*), resulting in repression of the transcription of *BMAL1* through direct binding to RORE located in the *BMAL1* promoter [13]. The conservative transcriptional feedback loop resides in the ovine circadian clock [27], and the circadian expression of the core clock genes *BMAL1*, *PER2*, and *Cry1* is generated in the ovine liver [28]. It was thus expected that clock genes would also be driven in oscillatory patterns in bovine uterus endometrial cells, which would be similar to murine cells [18, 29]. Our present results showed that the circadian clockwork machinery functions in bovine USCs exposed to P₄, while it was weak compared to that in rat (Fig. 1B). We also showed that the bovine *PER1* transcript level exhibited a significant diurnal rhythm in bovine USCs exposed to P₄ (Fig. 2). However, comprehensively, the diurnal rhythms of the clock gene expression were not significant in bovine USCs and UECs in the presence or absence of steroid hormones, except for *PER1* and *BMAL1* under some conditions (Figs. 2 and 3). Therefore, it is supposed that the circadian rhythm of clock genes, at least, that we observed may be weak in both USCs and UECs.

In regard to the oscillation, the superiority of clock genes and strength of circadian oscillation in the uterus may depend on cell types and physiological states. An immunohistochemical analysis revealed that the PER2 protein expression is constitutive in epithelial cells but not in the stromal cells [23]. In addition, the circadian rhythm of clock genes was reported to be significant for *Cry1* and not for *Per1*, *Per2* or *Bmal1* in the mouse uterus during the late stage of pregnancy [30]. Moreover, there may be differences among animal species. Most of the clock genes displayed no significant rhythms in bovine lymphocytes [31], unlike murine lymphocytes [32].

In the present study, the diurnal rhythms of clock genes were not particularly significant, but steroid hormones differentially affected the temporal changes in clock gene expression in both the USCs and UECs. In the USCs, the transcript levels of *NR1D1* increased, especially at 24 to 48 h after synchronization in the presence of P₄ (Fig. 2). In the UECs, the transcript levels of *NR1D1* and *PER1* changed significantly in the presence of E₂ (Fig. 4). As revealed by chromatin immunoprecipitation followed by a massive parallel sequencing (ChIP-seq) analysis coupled with microarrays in the mouse uterus, progesterone receptor binding sites are abundant near the coding regions of clock genes (*Clock*, *Npas2*, *Cry1*, *Per1*, and *Nr1d2*) [33]. The phase of *Per2* oscillation in the uterus from *Per2::Luc* knock-in mice is affected by E₂, and the *Per2* oscillation in the uterus during the mouse estrus cycle is modulated by fluctuating E₂ and P₄ [29, 34]. These findings, taken together with our present...
data, indicate that the expression of clock genes affected by steroid hormones may alter the expression of clock-controlled genes and modulate physiological functions in endometrial cells. Here we found that the transcript level of PTGS2 significantly decreased with circadian oscillation in USC during exposure to E2 for 48 h, while its transcript level increased in UECs after exposure to E2 for 48 h (Fig. 4). Consequently, we propose that the PTGS2 expression in USC is regulated by the circadian clockwork and E2. It is possible that other clock genes that we did not analyze in Fig. 1 may cause circadian oscillation in the PTGS2 expression in USC. Conversely, the circadian clockwork in UEC may not affect the PTGS2 expression. Incidentally, the transcript level of PTGS2 significantly increased in the absence of P4 and E2 (Fig. 4), but the expression may result from the action of the forskolin used as a resetting factor for the clockwork. It is known that PTGS2 expression is induced by cyclic AMP [35, 36].

BMAL1 transactivates the target genes by binding of the heterodimer with CLOCK to the E-box element (5'-CACGTG-3') on the promoter region of the responsive clock genes such as PER, NR1D1, DBP and RORα [26, 27]. There are functional E-box elements in the promoter region of the rat PTGS2 gene [37], and our recent study demonstrated that Bmal1 knockdown causes a significant decrease in the Ptgs2 expression and PGF2α production in rat ovarian granulosa cells [22]. In the promoter region of the bovine PTGS2 gene, also there are also several E-box sites [38]. In the present study, Bmal1 knockdown caused significant decreases in PTGS2 expression and PGF2α production in the USC in the presence of P4 (Figs. 5 and 7). Conversely, Bmal1 knockdown had no significant effect on the PTGS2 expression and PGF2α production in the UEC in the presence of E2 (Figs. 5 and 7). In the UECs, Bmal1 knockdown also had no effect on NR1D1 expression. This finding may indicate that Bmal1 transactivation in the PTGS2 and NR1D1 genes is weak in UECs exposed to E2. Actually, it has been reported that E2 disrupts the circadian expression of Per1 and Per2, which are promoted by Bmal1, in the liver, kidney and uterus of rats [39]. In the present results, the synchronization of USC exposed to P4 caused a significant increase in Bmal1 transcripts after 6 h, while the UEC exposed to E2 displayed no significant increase in Bmal1 transcripts (Figs. 2 and 3). These results suggest that the effect of Bmal1 knockdown is weak in the E2-treated UECs, probably through E2 inhibition of the transcriptional activity of Bmal1. Taken together with the present data, these findings suggest that the expression of bovine PTGS2 is controlled under Bmal1 or its responsive clock genes in USC, but not UEC, in the presence of ovarian steroids.

Interestingly, when the transcript level of NR1D1 was high in the USC and UEC in the presence of P4 or E2, the transcript level of PTGS2 was low. We therefore focused on the possible regulation of PTGS2 expression by REV-ERBα. The bovine PTGS2 gene has two ROREs in the promoter region within −3000 bp upstream from the transcription start site (AC_000173). We analyzed the expression of PTGS2 using the antagonist (SR8278) and agonist (heme) of REV-ERBα. The agonist was ineffective, while the antagonist resulted in increased transcript levels of PTGS2 in both cell types in the presence of P4 or E2 (Fig. 6). At least, these results indicate that REV-ERBα represses PTGS2 gene expression.

Concomitantly, PGF2α production completely coincided with the PTGS2 transcript level (Fig. 7). It is also of interest that the antagonist clearly enhanced the PTGS2 expression in the UECs, in which the circadian regulation of PTGS2 was weak as revealed by Bmal1 knockdown. In bovine UECs, therefore, PTGS2 expression is dominantly controlled under REV-ERBα, but not the circadian clockwork, in the presence of E2. Unlike UECs, however, bovine USC is controlled under both REV-ERBα and the circadian clockwork. Our finding that treatment with the antagonist increased the transcript level of NR1D1 in the USC and supports the autoregulation of NR1D1 expression as reported previously [40, 41]. However, it is reasonable that the antagonist had no significant effect on the transcript level of Bmal1 in the USC, which has been found to be repressed by REV-ERBα [13]. Unexpectedly, however, treatment with heme increased the Bmal1 transcript level in the USC in the present study, and the mechanism remains to be investigated.

In conclusion, the circadian oscillation of clock genes is partially weak in bovine USC and UEC, but ovarian steroid hormones may exert differential influences on the expression of the clock genes and the PTGS2 gene. Bmal1 knockdown decreased both the PTGS2 expression and PGF2α production in USC in the presence of P4, indicating circadian regulation of the PTGS2 expression. However,
the PTGS2 expression in UECs is mostly independent of the circadian clockwork. The PTGS2 expression was commonly suppressed in both cell types by REV-ERBα in the presence of steroid hormones. The present findings contribute to our understanding of the intercellular mechanisms underlying the PTGS2 expression and PGF$_2\alpha$ production in bovine uterus endometrium cells.

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