Glucose transporter 1 expression accompanies hypoxia sensing in the cyclic canine corpus luteum

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Abstract
The canine corpus luteum (CL) functions as a source of progesterone (P₄) and 17β-oestradiol (E₂); however, the transport of energy substrates to maintain its high hormonal output has not yet been characterised. This study involved the localisation and temporal distribution of the facilitative glucose transporter 1 and the quantification of the corresponding protein (GLUT1) and gene (SLC2A1) expression. Some GLUT1/SLC2A1 regulatory proteins, such as hypoxia-inducible factor 1α (HIF1A) and fibroblast growth factor 2 (FGF2); mRNAs, such as HIF1A, FGF2 and vascular endothelial growth factor A (VEGFA); and VEGFA receptors 1 and 2 (FLT1 and KDR) were also analysed from days 10 to 70 after ovulation. Additionally, plasma P₄ and E₂ levels were assessed via chemiluminescence. Moreover, the canine KDR sequence has been cloned, thereby enabling subsequent semi-quantitative PCR analysis. Our results demonstrate time-dependent variations in the expression profile of SLC2A1 during dioestrus, which were accompanied by highly correlated changes (0.84 < r < 0.98; P < 0.03) in the gene expression of HIF1A, VEGF and FLT1 as well as in P₄ plasma concentrations. FGF2 mRNA correlated with E₂ plasma concentrations (r = 0.61; P = 0.01). Our data reveal that the glucose transporter is regulated throughout the CL lifespan and suggest that CL depends on the sensing of hypoxia and the status of luteal vascularisation. Moreover, time-dependent expression of GLUT1/SLC2A1 may lie underneath increased metabolic and energetic requirements for sustaining P₄ production.

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Introduction
The reproductive cycle of non-pregnant dogs is distinct from other species and is characterised by a long corpus luteum (CL) phase (dioestrus), which can last over 60–80 days with regression occurring despite the presence of a uterine luteolysin (Hoffmann et al. 1992). During this time, the CL undergoes morpho-endocrinological changes in response to gonadotrophic stimuli and local regulatory factors (Hoffmann et al. 2004, Kowalewski et al. 2008a, 2009, Papa & Hoffmann 2011). Morphological changes following ovulation until late in dioestrus (Sonnack 2009) as well as changes in steroid hormone, prostaglandin and cytokine levels have been described to act as local regulatory factors (Engel et al. 2005, Kowalewski et al. 2008a, 2008b, Papa & Hoffmann 2011). The lifespan of the CL depends on energetic supply (Downing et al. 1995), which may be regulated by steroid hormones (Frolova et al. 2009): in endometrial cells, progesterone (P₄) directly regulates the expression of glucose transporter type 1 (SLC2A1 gene/GLUT1 protein) through its receptor (Kim & Moley 2009), activating the signalling pathway Akt/PKA/PRKAA and increasing the expression and translocation of GLUT1 (Kim & Moley 2009), the most ubiquitously distributed facilitative glucose transporter responsible for taking up glucose at basal conditions (Palfreyman et al. 1992). Besides steroid hormones, the hypoxia-inducible factor 1α (HIF1A) has been implicated as a potent inducer of GLUT1 and of its gene SLC2A1 (Takagi et al. 2009).
samples were collected every other day to determine the oscillation over dioestrus, mirroring that of CL-pO2 and the steroid hormone profile (Concannon et al. 1998). Seven groups (n=4 animals per group) were established. The CLs were harvested via ovariohysterectomy on days 10, 20, 30, 40, 50, 60 and 70 after ovulation (p.o.), covering the entire period of dioestrus. The experimental protocol, including anaesthesia (acepromazine, 0.2 mg/kg i.m.; xylazine, 3 mg/kg and ketamine, 5–8 mg/kg i.v.) and surgery, was approved by the Committee of Ethics in the Use of Animals of the Faculty of Veterinary Medicine and Animal Science, University of Sao Paulo, Sao Paulo, Brazil (protocol number 1432/2008). After collection, the CL were dissected from the surrounding ovarian tissue and immediately frozen in liquid nitrogen for total RNA and protein extraction or fixed in 4% buffered formalin for 24 h for immunohistochemistry. The following parameters were assessed: VEGF, FLT1, KDR, SCL2A1, HIF1A and FGF2 mRNA expression and GLUT1, HIF1A and FGF2 protein expression. Blood samples (5 ml) were collected on the day of surgery prior to anaesthesia for measurement of 17β-oestradiol (E2) and P4 levels.

Molecular cloning of canine KDR

As the sequence of canine KDR has not yet been reported, homology cloning was performed as described previously (Kowalewski & Hoffmann 2008), using mRNA derived from four different bitches to determine the cDNA coding of canine KDR. Primers for qualitative PCR were derived from the alignment of the predicted canine KDR sequence (GI: 73975290; www.ncbi.nlm.nih.gov/genome/guide/dog/index.html) with predicted bovine and available mouse and pig sequences (GenBank accession numbers: bovine GI: 61884824; mouse GI: 27777647 and pig GI: 7160277). A 4068-bp cDNA fragment PCR product of the predicted open reading frame (ORF) of canine KDR was amplified. Total RNA was isolated from canine CL with TRIzol Reagent according to the manufacturer’s protocol ( Gibco-BRL, Life Technologies). DNase treatment and RT-PCR were performed using the GeneAmp Gold RNA PCR Kit (Perkin-Elmer Applied Biosystems GmbH, Weiterstadt, Germany) as described previously (Kowalewski et al. 2006). The annealing temperature was 58.5 °C. PCR products were separated on a 2% ethidium bromide-stained agarose gel, purified using the Qiaex II gel extraction system (Qiagen GmbH), ligated into the pGEM-T vector (Promega), amplified in XL1 BLUE competent cells (Stratagene, La Jolla, CA, USA) and sequenced on both strands (SRD, Oberursel, Germany) with T7 and Sp6 sequencing primers. For every experiment, autoclaved water was used instead of RNA as negative control. RNA integrity and the assay procedure were tested via amplification of the reference gene glyceraldehyde-3-phosphate dehydrogenase. Finally, the cloned cDNA sequence was submitted to GenBank with access number DQ269018.1 Canis familiaris KDR, complete cds. The prediction of the amino acid sequence and sequence comparison was performed using ChromasPro version 1.2 oligo Software (Technelysium Pty. Ltd., Brisbane, Queensland, Australia).

Materials and methods

Dogs and experimental design

Twenty-eight healthy mongrel female dogs belonging to ‘Santuário’ dog shelter (Sao Paulo, Brazil) were included in the study. After the onset of pro-oestrous bleeding, blood samples were collected every other day to determine the P4 concentrations. The day of ovulation was considered the day when P4 plasma concentrations reached 5 ng/ml (Concannon et al. 1989). Seven groups (n=4 animals per group) were established. The CLs were harvested via ovariohysterectomy on days 10, 20, 30, 40, 50, 60 and 70 after ovulation (p.o.), covering the entire period of dioestrus. The experimental protocol, including anaesthesia (acepromazine, 0.2 mg/kg i.m.; xylazine, 3 mg/kg and ketamine, 5–8 mg/kg i.v.) and surgery, was approved by the Committee of Ethics in the Use of Animals of the Faculty of Veterinary Medicine and Animal Science, University of Sao Paulo, Sao Paulo, Brazil (protocol number 1432/2008). After collection, the CL were dissected from the surrounding ovarian tissue and immediately frozen in liquid nitrogen for total RNA and protein extraction or fixed in 4% buffered formalin for 24 h for immunohistochemistry. The following parameters were assessed: VEGF, FLT1, KDR, SCL2A1, HIF1A and FGF2 mRNA expression and GLUT1, HIF1A and FGF2 protein expression. Blood samples (5 ml) were collected on the day of surgery prior to anaesthesia for measurement of 17β-oestradiol (E2) and P4 levels.

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**RNA extraction and RT**

The CLs were homogenised with TRIzol Reagent using a Bio-gen Pro 200 homogeniser (Pro Scientific, Inc., Oxford, CT, USA). This step was followed by chloroform/isopropanol/ethanol extraction, as recommended by the manufacturer (Invitrogen). RNA concentration and quality were assessed via spectrometry using a BioPhotometer (Eppendorf, Hamburg, Germany), and integrity verification was performed with a 2% agarose gel. Following the DNase treatment, 1 μg total RNA per sample was reverse transcribed using a Superscript III Kit (Invitrogen).

**Real-time PCR**

Real-time PCR analyses were performed using an ABI 7500 Sequence Detection System (PE Applied Biosystems) as described previously (Campos et al. 2010) with some modifications to match dog-specific conditions, such as the low concentrations of available cDNA. SLC2A1, HIF1A, VEGFA, FLT1, KDR and FGF2 primers and probes were designed using the Assays-by-Design service from Applied Biosystems (Table 1). Cyclophilin A was used as the reference gene, as determined by NormFinder Software (Arhus, Århus, Denmark; Andersen et al. 2004). In 96-well plates, 125 ng cDNA diluted in 2.5 μl nuclease-free water were added to a mixture containing 6.25 μl TaqMan Universal PCR Master Mix buffer (2X, Applied Biosystems). Additionally, 0.5 μl of both forward and reverse primers (900 mM), 250 mM probe (Applied Biosystems) and 3.25 μl water were added to a final volume of 12.5 μl. All plates were sealed with MicroAmp Optical Adhesive Covers (Applied Biosystems) following the complete mixture of all reagents and subsequent centrifugation. The following cycling parameters were applied: 2 min at 50°C, 10 min at 95°C and 40 cycles of 15 s at 95°C (denaturation) and 1 min at 60°C (annealing and extension). PCR assays for target genes were conducted at least in quadruplicate for each sample, and the expression level was determined using relative quantification via linear regression of the fluorescence data. The ratios were calculated using the equation ‘relative expression = N0 (target gene)/N0 (cyclophilin A)’ with N0 values calculated using the LinRegPCR 7.0 (Linear Regression PCR) program (Ramakers et al. 2003, Roussel et al. 2007), followed by calculation using the 2−ΔΔCt method (Kowalewski et al. 2006).

### Table 1 List of primers for real-time (TaqMan) PCR.

<table>
<thead>
<tr>
<th>Gene</th>
<th>Primers</th>
<th>Sequences</th>
<th>Probes</th>
<th>GenBank numbers</th>
</tr>
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<tbody>
<tr>
<td>SLC2A1</td>
<td>Forward</td>
<td>5'-CACCCAGAGTCCCCCCCTCTATCA-3'</td>
<td>CACCCAGACTTCCAC</td>
<td>XM539554</td>
</tr>
<tr>
<td></td>
<td>Reverse</td>
<td>5'-GTGCCACCTCTGAGACTCTG-3'</td>
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<td>HIF1A</td>
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<td>5'-GCTTGCTGGAGACAACTATCT-3'</td>
<td>CAGGACACAAAGACTG</td>
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<tr>
<td></td>
<td>Reverse</td>
<td>5'-ACATCCCTATAAACGGAGACTCTCAAG-3'</td>
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<tr>
<td>VEGFA</td>
<td>Forward</td>
<td>5'-GTGCCAAGCAGAGCTGCATGCG-3'</td>
<td>CATGCCAGAAGACTG</td>
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<td></td>
<td>Reverse</td>
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<tr>
<td>FLT1</td>
<td>Forward</td>
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<td>AAAGCCTGAGACTAATCTGCTC</td>
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</tr>
<tr>
<td></td>
<td>Reverse</td>
<td>5'-TGTCGATCTTCAGAGACCCTCGAT-3'</td>
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<tr>
<td>KDR</td>
<td>Forward</td>
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<td>Reverse</td>
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<tr>
<td>FGF2</td>
<td>Forward</td>
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<td></td>
<td>Reverse</td>
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<td>Cyclophilin A</td>
<td>Forward</td>
<td>ID C603986523_gH</td>
<td></td>
<td>XM843227.1</td>
</tr>
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</table>

**Immunohistochemistry**

Localisation of GLUT1, HIF1A and FGF2 expression was assessed via IHC on 2 μm tissue sections prepared from four CL per dog using one section per CL and four dogs per group to assure description accuracy. The antisera used were as follows: for GLUT1, a polyclonal antibody raised in goat against human (C-20, sc-1605, dilution 1:150, Santa Cruz Biotechnology); for HIF1A, a polyclonal antibody raised in rabbit against human (NB100-134, dilution 1:400, Novus Biologicals, Littleton, CO, USA); and for FGF2, a mouse MAB (clone bFm-2, dilution 1:100, Upstate, Lake Placid, NY, USA). Standard procedures for embedding and processing CL tissue have been described previously (Mariani et al. 2006). Negative controls were prepared using IgG isotype control antibodies (Normal rabbit IgG for HIF1A and normal goat IgG for GLUT1; Santa Cruz Biotechnologies), while positive controls were human placenta for GLUT1 (Leon-Villalapalo et al. 2005) and HIF1A (according to the manufacturer’s protocol) and bovine placenta for FGF2 (Prado et al. 2004).

**Western blotting and quantification**

Luteal homogenates were prepared with NET-2 lysis buffer (50 mM Tris–HCl (pH 7.4), 300 mM NaCl and 0.05% NP-40) containing 1 μl/ml protease inhibitor cocktail (Sigma–Aldrich) using a Polytron (Brinkman Instruments, Westbury, NY, USA) and were centrifuged at 10 000 g for 10 min at 4°C. The supernatants were collected, and the protein concentrations were determined using the Bradford method (Bradford 1976). Total protein was solubilised in sample buffer (25 mmol/l Tris–Cl, pH 6.8, 1% SDS, 5% β-mercaptoethanol, 10% glycerol and 0.01% bromophenol blue) and incubated at 95°C for 5 min prior to loading onto the gel. Twenty-five micrograms of protein were loaded onto 8 or 12% SDS-polyacrylamide gels (Mini Protean II System, Bio-Rad Laboratories, Inc.) for the quantification of HIF1A and GLUT1 protein respectively. After electrophoresis, the proteins were transferred onto a PVDF membrane (Bio-Rad Laboratories, Inc.), and the membrane was
incubated in blocking buffer containing 5% non-fat dry milk for 1 h at room temperature. The membrane was then probed with primary antibodies (anti-GLUT1, 1:500, C-20, sc-1605, Santa Cruz Biotechnology; anti-HIF1A, dilution 1:500, NB100-134, Novus Biologicals and anti-ACTB, Clone AC-15, dilution 1:500, A1978, Sigma–Aldrich Co., as the reference protein) overnight at 4 °C, followed by probing with Ig–HRP antibodies (anti-rabbit IgG for HIF1A and ACTB and anti-goat IgG for GLUT1; Amersham Biosciences) diluted in a 2.5% non-fat dried milk solution for 1 h at room temperature. The immunocomplexes were then visualised using ECL, as recommended by the manufacturer (Amersham Biosciences). The validation of both antibodies for canine tissue was performed using human placenta. The proteins were examined by measuring the specific bands using a ChemiDoc MP Imaging System (Bio-Rad Laboratories) and normalised to β-actin (ACTB; 42 kDa) using ImageJ Software (Bio-Rad Laboratories).

**Determination of plasma P₄ and E₂ concentrations**

After collection, blood samples (5 ml) were centrifuged for 10 min at 300 g, 4 °C. The serum samples were stored at −20 °C until P₄ and E₂ determination by validated chemiluminescence immunoassay. The low limit detection of the P₄ and E₂ assays was 0.03 ng/ml and 0.5 pg/ml respectively. The inter-assay coefficient of variation (CV) for P₄ and E₂ was 6.93 and 7.03% respectively. The intra-assay CV was <10% for both hormones.

**Statistical analysis**

All the experiments were performed at least three times with a minimum of three repeats, including western blotting analyses. Dependent variables (i.e. steroid production and gene and protein expression of SLC2A1/GLUT1, HIF1A, VEGFA, FLT1, KDR and FGF2) were analysed by Kruskal–Wallis test followed by Dunn’s multiple comparison test. The correlations between hormone concentrations and gene or protein expression levels were determined using the Pearson’s Correlation test. Response variables were tested according to their homogeneity and normality of variances. Data are presented as mean ± S.E.M. Statistical analyses were performed using the GraphPad Prism 4 program (GraphPad Software, Inc.). Differences with P value <0.05 were considered significant.

**Results**

**Homology cloning of canine KDR**

The available predicted sequence of canine KDR was used for the homology cloning procedure. Consequently, the canine-specific sequence was amplified, cloned and submitted to GenBank under access number GI: 82548234. This sequence comprises 4068 nucleotides of a predicted ORF of canine KDR, which encodes a 1355 amino acid protein with a deduced molecular weight of 152 kDa. BLAST analysis showed 97, 92, 90 and 85% homology with human (GI: 231570519), pig (GI: 7160277), bovine (GI: 61884824) and mouse (GI: 27777647) KDR sequences respectively. According to the published canine genome sequence, the KDR sequence is located on chromosome 13.

**Expression of SLC2A1-, HIF1A-, FGF2-, VEGFA-, FLT1- and KDR mRNA**

The expression of six target genes directly involved in the response of the CL against fluctuations in substrate availability and oxygen tension in luteal cells was investigated. Dioestrus had an effect of time on the expression of SLC2A1 (P<0.002), HIF1A (P<0.001), FGF2 and the VEGF system (P=0.002; Fig. 1). SLC2A1 (Fig. 1A) and HIF1A (Fig. 1B) expression levels increased on day 20 p.o., decreased at mid dioestrus (days 30 and 40 p.o.), increased again on days 50 and 60 p.o. (P<0.05) and were significantly down-regulated at the beginning of anoestrus (day 70 p.o.; P<0.05). The FGF2 expression increased on day 30 p.o. and decreased thereafter until day 60 p.o. (P<0.05; Fig. 1C). VEGFA (Fig. 1D) and FLT1 (Fig. 1E) expression levels were significantly elevated on days 20 and 60 p.o., while the KDR expression levels were elevated on days 20 and 40 p.o. (P<0.05; Fig. 1F).

**Spatial expression of GLUT1, HIF1A, and FGF2 assessed via IHC**

GLUT1 and HIF proteins were localised in the dog CL over dioestrus. Immunopositive staining could be observed restricted to the cytoplasm of luteal, glut1 and HIF proteins were localised in the dog CL over dioestrus. Immunopositive staining could be observed restricted to the cytoplasm of luteal,

\[ \text{Fig. 1 SLC2A1 (A), HIF1A (B), FGF2 (C), VEGFA (D), FLT1 (E) and KDR (F) expression levels in the canine CL (n=28; four per group) determined via real-time (TaqMan) PCR. RGE, relative gene expression (mean ± S.E.M.) normalised to cyclophilin A. Bars with different letters represent significant differences (P<0.05); 10–70: days after ovulation.} \]
endothelial and stromal cells in all phases studied (days 10–70 p.o.; Figs 2 and 3). Besides the cytoplasm staining, the nuclear staining of HIF1A from day 30 until 60 could also be observed. However, no positive staining could be observed in the negative control. Positive control (human placenta, PC; Figs 2 and 3) showed a marked positive staining.

Positive immunostaining for FGF2 was observed in the cytoplasm of luteal, endothelial and stromal cells (Fig. 4); positive staining was observed primarily in stromal cells on day 10 p.o. and in luteal cells on day 20 p.o. By day 30 p.o., luteal cells displayed marked positive immunostaining, while stromal cells were primarily negative. By days 50 and 60, FGF2 signals appeared weaker; however, at day 70, the cytoplasmic staining levels were evident again. Bovine CL served as positive control (Prado et al. 2004), and the negative control revealed no staining for FGF2 (Insert on Fig. 4).

Quantification of GLUT1 and HIF1A protein expression via western blotting and the correlation with the respective gene expression levels

We observed that time had an effect on the expression of both GLUT1 (P=0.04) and HIF1A (P<0.0001; Fig. 5). GLUT1 expression increased on day 20 (P<0.05), decreased on day 30 and showed a tendency to increase on day 40 p.o., but no further variations until day 70 p.o. (Fig. 5B; P>0.05) were observed. This expression pattern highly correlates with the SCL2A1 expression during the first half of dioestrus (r=0.83; P=0.009). The HIF1A expression (Fig. 5D) showed an increase on day 30 p.o. followed by a further increase on day 60 p.o. and a final decrease on day 70 p.o. (P<0.05). In contrast to GLUT1, HIF1A protein was negatively correlated with its mRNA expression in the same period (r= −0.86; P=0.005).

Plasma steroid hormone profiles

P₄ plasma concentrations were highest on day 20 and displayed a distinct and continuous decrease thereafter (Fig. 6A; P<0.05). The concentrations of E₂ increased from days 10 to 40 p.o. followed by a gradual decrease thereafter (Fig. 6B; P<0.05).

The correlation between hormone concentrations and gene expression

A significant positive correlation during the first half of dioestrus was observed between P₄ levels and the expression levels of all genes studied (Table 2), except for FGF2, whose expression pattern positively correlated with E₂ levels throughout the entire observation period (r=0.61; P=0.01). Positive and significant correlation was observed among the expressions of HIF1A and SCL2A1, HIF1A and VEGF, VEGFA and FLT1, VEGF and SCL2A1, and FLT1 and SCL2A1 (Table 2).

Correlations of hormone concentrations and protein expression assessed by western blotting

During the first half of dioestrus, the GLUT1 expression was positively correlated with P₄ plasma concentration (r=0.86; P=0.005) and negatively correlated with the expression of HIF1A (r= −0.77; P=0.02), while both
proteins showed no significant correlation with the E₂ plasma concentration (r = -0.15; P = 0.73 and r = -0.38; P = 0.39 respectively).

**Discussion**

According to our hypothesis, the expression of HIF1A at the mRNA level, which is a factor sensitive to decreased tissue/cell O₂ concentrations, was positively correlated with the expression of SLC2A1, VEGFA, the VEGFA receptor FLT1 and FGF2 during the entire period of dioestrus. Additionally, the mRNA expression of these factors accompanied fluctuations of P₄ concentrations during the first half of dioestrus, thereby indicating the importance of these factors during CL formation.

These observations of the up-regulation of the ‘glucose transport system’ matching that of factors that play a role in angiogenesis raise the question of the underlying triggering mechanisms. Although hypoxia occurs during the initial phase of CL formation (Nishimura et al. 2010), the function of P₄ and perhaps that of E₂ should also be considered.

In addition to its function as an endocrine factor, the observations in cattle suggest that P₄ may also act as a local luteotrophic factor, capable of exerting a positive feedback loop on its receptor (Schams & Berisha 2004). Observations in dogs, in which the application of a P₄ receptor inhibitor results in preterm luteolysis, further support the hypothesis concerning a luteotrophic function of P₄ in the canine CL (Kowalewski et al. 2009, 2010).

It has also been reported that P₄ directly regulates SCL2A1 expression in endometrial cells (Frolova et al. 2009, Kim & Moley 2009) via its own receptor (Frolova et al. 2009), thereby activating the intracellular signalling pathway and enhancing GLUT1 expression levels and translocation to the plasma membrane (Kim & Moley 2009). Both studies suggest an opposite function for E₂, i.e. the down-regulation of SCL2A1/GLUT1, when tested alone or in combination with P₄. Moreover, blocking the oestrogen receptor 1 (ESR1) with ICI 182 780 restored the expression of SCL2A1/GLUT1 (Kim & Moley 2009). Incorporating these data into the context of the canine luteal function, it is possible that P₄ acts in the same way by enhancing SCL2A1/GLUT1 expression via signalling through its receptor (Hoffmann et al. 2004, Papa & Hofmann 2011), which results in an increased availability of glucose, thereby reinforcing the concept that increased luteal glucose uptake (Palfreyman et al. 1992) corresponds to a higher steroidogenic output. In contrast to what has been observed for the dog CL in this study, Nishimoto et al. (2006) described, in cattle, no cycle-related SCL2A1 expression in the early or mid luteal phase but a decrease in the late luteal phase. These differences may also rely on the local interplay between P₄ and E₂, which reaches its highest levels in cows when the CL regresses, but not during the strumal (S) cells at 10, 20, 30, 50, 60 and 70 days after ovulation. Bars = 20 μm.

**Figure 4** FGF2 staining in the canine CL assessed by immunohistochemistry. Positive signals were observed as indicated by the brown colour in the cytoplasm of luteal (L), endothelial (E) and stromal (S) cells at 10, 20, 30, 50, 60 and 70 days after ovulation. Bars = 20 μm.

**Figure 5** Protein expression of GLUT1 (A and B) and HIF1A (C and D) in the canine CL during dioestrus (n = 28; four animals per group). Electrophoresis images are representative of three independent experiments. The total protein isolated from luteal homogenates was examined with specific antibodies and normalised to ACTB expression. The data are expressed as the mean ± S.E.M. Bars with different letters indicate a significant difference (P < 0.05).
The data are presented as the mean ± S.E.M. Asterisks or different letters indicate a significant difference (P < 0.05).

early or mid luteal phase, in which P$_4$ governs alone (revised by Sartori & Barros (2011)).

E$_2$ levels were positively correlated with the FGF2 expression pattern, which seems to contribute to maintaining angiogenesis when VEGFA starts decreasing. Both angiogenic factors play complementary roles in CL vascularisation, as already described for cattle (Schams & Berisha 2004), and VEGFA responds to hypoxia (Neeman et al. 1997). Additionally, Kihira et al. (2011) described FGF2 as an enhancer of SLC2A1 expression in cultured 3T3-L1 adipocytes, but further studies are necessary to characterise species and tissue specificities concerning the function of FGF2 in this respect.

The role of hypoxia during CL formation was recently addressed in cattle (Nishimura et al. 2010) and seemed to relate directly to the formation of the vascular bed by inducing the expression of VEGF. VEGFA protein and its receptors are expressed in the canine CL throughout dioestrus with a decrease after day 40 p.o. and unaltered receptor (FLT1 and KDR) protein expression (Mariani et al. 2006), which was confirmed in this study for expression at the mRNA level. In addition to its paramount role in angiogenesis, VEGFA may also be considered a luteotrophic factor, as it enhances P$_4$ production in bovine placental cells in vitro (Sousa et al. 2012) and induces STAR expression in bovine luteal cells (Yamashita et al. 2008). In this study, VEGFA expression was highly correlated, at the mRNA level (r = 0.85; P = 0.01), with plasma P$_4$ levels, thereby suggesting the function of a luteotrophic factor in dogs. The HIF1A expression accompanied that of VEGFA and SLC2A1 as stated above. According to our findings, the canine CL detected the first O$_2$ imbalance at day 30 p.o., as revealed by western blotting analysis of HIF1A, which did not decrease until day 60 p.o., when it experienced a further and abrupt increase. This corroborates with findings by Hoffmann et al. (2004), who observed a decreased density of luteal cells from day 30 of dioestrus onwards. Similarly, Nishimura et al. (2008) reported a decrease in blood perfusion to bovine CL followed first by hypoxia and then by functional and finally structural luteolysis. The presence of the HIF1A protein in the nuclei on day 50 p.o., concomitant to increased levels of HIF1A mRNA and subsequent to increased HIF1A protein on day 60 p.o., matches a moment in the CL lifespan, in which levels of luteal P$_4$ are decreasing and first signs of structural regression can be observed (Sonack 2009). The correlation observed between the expression levels of HIF1A, VEGFA and SLC2A1 at the mRNA level suggests a functional inter-relationship that results in the formation of GLUT1 protein. However, further evidence must be provided, and the sequence of events is unclear.

While our data concerning expression at the mRNA level seem to yield a rather clear picture, the whole situation becomes somewhat less clear when taking the protein data into account. Therefore, the concentrations of GLUT1 protein seem to be parallel to some extent to the relative gene expression of SLC2A1. Concerning the HIF1A protein, there was a negative correlation with its

**Table 2** Correlation coefficients between steroid production and gene expression in canine CL during dioestrus.

<table>
<thead>
<tr>
<th>Variables</th>
<th>Pearson’s r</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>P$_4$ vs HIF1A</td>
<td>0.78</td>
<td>0.03$^a$</td>
</tr>
<tr>
<td>P$_4$ vs SLC2A1</td>
<td>0.79</td>
<td>0.03$^a$</td>
</tr>
<tr>
<td>P$_4$ vs VEGFA</td>
<td>0.85</td>
<td>0.01$^a$</td>
</tr>
<tr>
<td>P$_4$ vs FLT1</td>
<td>0.90</td>
<td>0.005$^b$</td>
</tr>
<tr>
<td>P$_4$ vs KDR</td>
<td>0.76</td>
<td>0.04$^a$</td>
</tr>
<tr>
<td>P$_4$ vs FGF2</td>
<td>0.05</td>
<td>0.84</td>
</tr>
<tr>
<td>E$_2$ vs HIF1A</td>
<td>-0.38</td>
<td>0.39</td>
</tr>
<tr>
<td>E$_2$ vs SLC2A1</td>
<td>-0.15</td>
<td>0.73</td>
</tr>
<tr>
<td>E$_2$ vs VEGFA</td>
<td>-0.15</td>
<td>0.73</td>
</tr>
<tr>
<td>E$_2$ vs FLT1</td>
<td>-0.21</td>
<td>0.64</td>
</tr>
<tr>
<td>E$_2$ vs KDR</td>
<td>0.38</td>
<td>0.39</td>
</tr>
<tr>
<td>E$_2$ vs FGF2</td>
<td>0.61</td>
<td>0.01$^b$</td>
</tr>
<tr>
<td>HIF1A vs SLC2A1</td>
<td>0.93</td>
<td>0.002$^b$</td>
</tr>
<tr>
<td>HIF1A vs VEGFA</td>
<td>0.98</td>
<td>0.03$^b$</td>
</tr>
<tr>
<td>HIF1A vs FLT1</td>
<td>0.84</td>
<td>0.01$^b$</td>
</tr>
<tr>
<td>HIF1A vs FGF2</td>
<td>-0.37</td>
<td>0.18</td>
</tr>
<tr>
<td>SLC2A1 vs VEGFA</td>
<td>0.84</td>
<td>0.001$^b$</td>
</tr>
<tr>
<td>SLC2A1 vs FLT1</td>
<td>0.83</td>
<td>0.007$^b$</td>
</tr>
<tr>
<td>VEGFA vs FLT1</td>
<td>-0.21</td>
<td>0.46</td>
</tr>
<tr>
<td>VEGFA vs KDR</td>
<td>0.93</td>
<td>0.002$^b$</td>
</tr>
<tr>
<td>VEGFA vs FGF2</td>
<td>0.53</td>
<td>0.21</td>
</tr>
<tr>
<td>VEGFA vs GLUT1</td>
<td>0.17</td>
<td>0.55</td>
</tr>
</tbody>
</table>

$^a$Correlated in first half of dioestrus (days 10, 20 and 30 p.o.).

$^b$Correlated throughout dioestrus.
expression at the mRNA level; this observation suggests other post-translational regulatory factors, which may become activated in the ageing CL, and stresses the likely importance of P4 concerning the up-regulation of SCL2A1, as was emphasised by observations on day 20, indicating that a function-associated O2 imbalance may not occur prior to approximately day 60, which represents the time point when Sonnack (2009) observed the first signs of structural luteolysis.

By presenting the expression of GLUT1 and its associated regulatory proteins, our data suggest new regulatory factors possibly involved in canine CL. This concerns mostly the first half of dioestrus, on the one hand, when the canine CL is being formed and passes through its highest steroidogenic and metabolic capacity. On the other hand, for the second half of canine dioestrus (Okkens et al. 1990), prolactin appears to be the most important luteotrophic factor.

In conclusion, our data reveal a local time-dependent system comprising hypoxia sensing, induction of angiogenesis and glucose uptake, orchestrated by or influencing P4 secretion, especially in the first half of dioestrus in the canine CL.

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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