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Effects of intrauterine devices on proteins in the uterine lavage fluid of mares

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ABSTRACT

Intrauterine devices block luteolysis in cyclic mares, but the underlying mechanism is unknown. To clarify the mechanisms, the protein profile of the endometrial secretome was analyzed using two-dimensional difference gel electrophoresis (2D-DIGE). Twenty-seven mares were classified according to whether they were inseminated (AI) or had an intrauterine device (IUD), a water-filled plastic sphere, inserted into the uterus on Day 3 after ovulation. Uterine lavage fluids were collected on Day 15 from pregnant inseminated mares (AI-P; n = 8), non-pregnant inseminated mares (AI-N; n = 4), and mares with IUD (n = 15). The IUD group was further divided into prolonged (IUD-P; n = 7) and normal luteal phase (IUD-N; n = 8) groups on the basis of ultrasound examinations, serum levels of progesterone and PGFM on Days 14 and 15, and COX-2 results on Day 15. Four mares from each group were selected for the 2D-DIGE analyses. Ten proteins had significantly different abundance among the groups, nine of the proteins were identified. Malate dehydrogenase 1, increased sodium tolerance 1, aldehyde dehydrogenase 1A1, prostaglandin reductase 1, albumin and hemoglobin were highest in pregnant mares; T-complex protein 1 was highest in non-pregnant mares; and annexin A1 and 6-phosphogluconolactonase were highest in IUD mares. The results suggest that the mechanism behind the intrauterine devices is likely related to inflammation.

1. Introduction

Intrauterine devices (IUDs) are used as a method to suppress estrus behavior in competing mares. The underlying mechanisms of inducing prolonged luteal phases have not been completely elucidated, but embryo simulation by contact with the endometrial wall and endometrial inflammation have been suggested [1–3].

The hypothesis of embryo simulation was initially proposed for three reasons. First, the size of the plastic device is identical to that of an embryo during the time frame of maternal recognition of pregnancy. Secondly, the device can move slightly in the uterine lumen [2], and embryo movement is mandatory for blocking luteolysis [4] during maternal recognition of pregnancy in the mare. Thirdly, the device is in contact with the endometrium, similar to an embryo.

It has been shown that embryo contact with the endometrium – which is enhanced by moving around in the uterus – is involved in the inhibition of luteolysis by attenuating the secretion of $PGF_{2\alpha}$. Specifically, contact of the embryo with the endometrium triggers mechanotransduction mechanisms that induce changes in endometrial protein abundance during pregnancy [5].

Although inflammation is a logical explanation for the effectiveness of IUDs, the evidence for this is not consistent. After IUD use for one year in wild horses, all mares had chronic endometritis at the time of IUD removal [6]. In previous IUD experiments in mares, non-echogenic intrauterine fluid was reported during IUD treatment [1,2], but it was not associated with inflammation in endometrial biopsy samples obtained after IUD removal [1,2,7,8]. It is possible that the mares had previous inflammation which was resolved by the time the biopsies were taken, or at least acute inflammation had already been resolved and turned chronic. It is

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also possible that the diagnostic methods used to detect inflammation in the previous studies were not sensitive enough.

It has been shown that IUDs suppress cyclooxygenase-2 (COX-2) [3], leading to the inhibition of $PGF_{2\alpha}$ release and maintenance of the corpus luteum (CL) [2]. However, the events preceding COX-2 inhibition remain unknown. We do not know how the presence of an IUD is mediated to the endometrium to suppress COX-2. Likewise, differences between mares in the efficacy of the devices to prolong luteal function have yet to be elucidated. However, adequate perfusion and drainage of the endometrium seem to increase the efficacy of the devices to inhibit luteolysis [8].

Uteroferrin staining was increased in endometrial biopsies of mares in which the presence of an IUD resulted in prolonged CL function [8]. This may indicate inflammation, but it also shows that the presence of a device in the uterus induces changes in the composition of endometrial secretions. Other uterine proteins, such as annexin 2, eukaryotic initiation factor 4A1, protein disulphide isomerase, superoxide dismutase and transketolase have been described to be involved in processes of endometrial inflammation in bovine species [9].

During early pregnancy, endometrial secretions – mostly consisting of proteins – are essential. They play a crucial role in implantation and development of the conceptus [10]. Changes in the composition across the estrus cycle are thought to occur to provide the most appropriate environment in the different events of a successful pregnancy [10].

The aim was to gain new insights into the mechanisms by which IUDs prevent luteolysis. Our hypothesis was that the protein composition in endometrial secretions on Day 15 after ovulation differs between pregnant, non-pregnant and IUD mares. For this purpose, a proteomic study using two-dimensional difference gel electrophoresis (2D-DIGE) analysis [11], which allows to compare simultaneously multiple protein samples in the same gel thus reducing the experimental and analytical time, was performed on uterine lavage fluids collected previously [3] from pregnant and non-pregnant mares, and from mares with an IUD exhibiting a prolonged or normal luteal phase.

2. Material and methods

2.1. Animals

Twenty-seven mares (Finnhorses and four warmbloods) from Equine College Ypäjä and MTT Agrifood Research Ypäjä (Finland) were initially included in the present study. The mean age was 9.6 years (ranging from 4 to 17 years); live weights ranged from 500 to 590 kg. The mares had foaled 0 to 7 times, had no history of reproductive failure, and were clinically normal. They were ranked by age, number of foalings and breed, and then assigned alternately into two groups: the inseminated group (AI) (n = 12; mean age 9 years; mean number of foalings 0.75) and the intrauterine device group (IUD) (n = 15; mean age 10.3 years; mean number of foalings 1). These groups were further divided into four sub-groups depending on the results of serum progesterone, COX-2 and ultrasound examination [2]: pregnant (AI-P; n = 8; mean age 6.1 years) and non-pregnant (AI-N; n = 4; mean age 14.8 years); prolonged (IUD-P; n = 7; mean age 9.3 years) and normal luteal phase (IUD-N; n = 8; mean age 10.8 years).

The permission for animal experimentation was granted by the provincial government of Southern Finland (number 1102101).

2.2. Experimental design

Experimental protocol is shown in Fig. 1. The mares included in the study were examined every other day by transrectal palpation and ultrasonography (SonoSite Vet 180 Plus with a 4 MHz linear array transducer; Sono Site Inc., Bothell, WA, USA). Once in early estrus, the examinations were performed daily until ovulation was detected. The ovulation day was assigned as Day 0.

When a ≥35-mm follicle was observed by ultrasound, an injection of 1500 IU of hCG (Chorulon®, Intervet International B·V.,

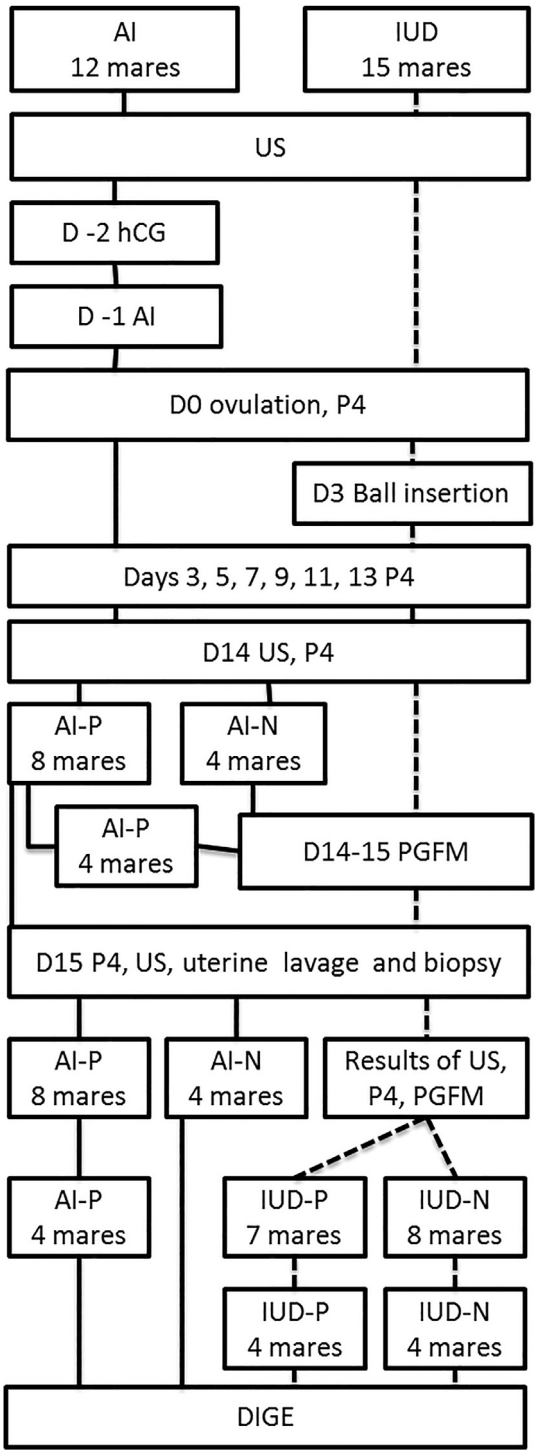

Fig. 1. Experimental protocol for collecting uterine lavage fluid for two-dimensional difference gel electrophoresis (2D-DIGE). AI: artificial insemination; IUD: intrauterine device; US: ultrasound examination; P4: progesterone; AI-P: pregnant mares; AI-N: non-pregnant mares; PGFM: 15-ketodihydro-$PGF_{2\alpha}$; COX-2: cyclooxygenase 2; IUD-P: prolonged luteal phase; IUD-N: normal luteal phase.

Boxmeer, The Netherlands) was given to time ovulation. The mares in the AI group were inseminated approximately 24 h after hCG administration with a proven stallion. In the IUD group, the device was inserted in the uterus on Day 3 after ovulation using the double-glove technique [12]. The device was a water-filled polypropylene ball, 20 mm in diameter [2].

Blood samples for progesterone were obtained on Days 0, 3, 5, 7, 9, 11, 13, 14, and 15 after ovulation and analyzed by means of the Spectria Progesterone radioimmunoassay (RIA) kit (Orion Diagnostica, Espoo, Finland), using the 1270 Rackgamma counter (Wallac Oy, Turku, Finland). The detection limit of the equipment was 0.7 nmol/L. Intra- and inter-assay coefficients of variations for low, medium and high levels of progesterone were 11.5%, 3.0% and 3.8% (intra-), and 7.8%, 5.1% and 4.8% (inter-) respectively. In addition, serial blood samples were obtained to determine serum levels of 15-ketodihydro-$PGF_{2\alpha}$ (PGFM) on Days 14 and 15 after ovulation, as previously described [3] and analyzed according to Granström and Kindahl [13]. The detection limit of the assay was 60 pmol/L. The inter- and intra-assay coefficients of variation were 11.7% and 6.6 respectively.

On Day 14, the mares were examined by transrectal palpation and ultrasonography to determine the stage of the estrus cycle, the presence or absence of an embryo in the AI mares, and the location of the device in the IUD mares.

On Day 15, 30 ml of warm (37 °C) phosphate buffered saline (PBS; pH 7.0) was infused into the uterus via a Foley catheter, and the uterus was briefly massaged per rectum. After 5 min of equilibration, the fluid was allowed to drain into a sterile centrifuge tube [13]. The lavage fluid was kept on ice until centrifuged; after centrifugation, the supernatant was collected and stored at −80 °C until analyzed. Lavage fluid was used for protein analyses by 2-DIGE techniques [14].

2.3. 2D-DIGE analysis

2.3.1. Animal selection for 2D-DIGE analysis

For 2D-DIGE analysis, four mares from each of the four groups were selected. The selection criterion for AI-N mares was the absence of an embryo, and for AI-P mares the presence of an embryo and high serum progesterone. In the IUD mares, serum progesterone and plasma PGFM concentrations, and endometrial COX-2 expression were used to determine a normal or prolonged luteal phase. PGFM concentrations of 60–100 pmol/L were defined as low, 101–200 pmol/L as intermediate, and >200 pmol/L as high. Thus, four mares with progesterone concentrations between 1 and 5 nmol/L on Day 15, two to five distinctive PGFM pulse releases (368–739 pmol/L), and positive expression for COX-2 in immunoblotting and immunohistochemistry were included in the normal luteal phase group (IUD-N), while four mares with progesterone concentrations between 14 and 26 nmol/L, mostly low PGFM values (60/64 values low, 3/64 intermediate, and one value of 256 pmol/L), and negative expression for COX-2 were included in the prolonged luteal phase group (IUD-P) [3]. Mean ages in AI-P, AI-N, IUD-P and IUD-N groups for 2D-DIGE analysis were 5.5, 14.8, 10.5 and 8.8 years, respectively. A workflow for the 2D-DIGE analysis of uterine lavage fluid is shown in Supplementary Fig. S1.

2.3.2. Sample preparation and CyDye labelling

Proteins from the uterine lavage samples were first treated with 0.1 U chondroitinase ABC and 0.1 U betaglucuronidase to remove glycans. Proteins were then precipitated with trichloroacetic acid-acetone precipitation and solubilized in 50 μl of labelling buffer (7 M urea, 2 M thiourea, 4% cholamidopropyl [dimethylammoniol]-1-propanesulfonate hydrate (CHAPS), 30 mM Tris). Protein concentration was measured by using a 2D Quant Kit (GE Healthcare) following the manufacturer's instructions. The samples were then labelled with Cy2, Cy3 and Cy5 dyes (CyDye DIGE Fluor minimal dyes, GE Healthcare) according to the Ettan two-dimensional difference gel electrophoresis (DIGE) protocol (Supplementary Fig. S1). Briefly, 50 μg of protein from each sample was labelled with 400 pmol of the Cy3 and Cy5 dyes. An internal standard was established by combining 25 μg of each sample and labelled with Cy2 dye. The labelling reaction was incubated for 30 min on ice in the dark, and stopped by adding 1 mM lysine to the reaction following a 10-min incubation period.

2.3.3. Two-dimensional gel electrophoresis

Labelled proteins were analyzed by DIGE as described earlier [15]. An immobilized pH gradient (IPG) strip (24 cm, pH 3–10, nonlinear, GE Healthcare) was used for isoelectric focusing. IPG strips were loaded with 150 μg of protein in total by using the cup-loading method. Isoelectric focusing was performed using IPGPhor (GE Healthcare) at 20 °C as follows: 3 h at 150 V, 3 h at 300 V, linear ramping to 10 000 V and 10 000 V for 50 000 Vh with a maximum current of 75 μA per strip. After focusing, the isoelectric strips were prepared for the second-dimension gels by incubation in equilibrium buffer I (50 mM Tris pH 8.8, 6 M urea, 30% glycerol, 2% sodium dodecyl sulphate (SDS), 0.2% bromophenol blue, with added 10 mg/ml dithiothreitol (DTT)) solution for 15 min. This was followed by incubation in equilibrium buffer II (50 mM Tris pH 8.8, 6 M urea, 30% glycerol, 2% SDS, 0.2% bromophenol blue, supplemented with 25 mg/ml iodoacetamide) for another 15 min. The prepared IPG strips were then placed on 12% sodium dodecyl sulphate (SDS) polyacrylamide gels (SDS-PAGE) and sealed with overlay agarose (Bio-Rad). Electrophoresis was initiated at 50 V for 30 min, followed by 300 V for 3 h. The gels were scanned between low-fluorescence glass plates using an FLA-5100 laser scanner (Fujifilm) at wavelengths 473 (for Cy2), 532 (for Cy3), and 635 nm (Cy5) using voltages of 420, 410 and 400 V, respectively. After scanning, the gels were silver stained as previously described [16]. Each evaluated group had four biological replicates.

2.3.4. Image analysis and statistical processing of the data

The gel images were analyzed and statistically assessed using DeCyder 7.0 software (GE Healthcare). First, the gels were automatically analyzed using the batch processor function to normalize the Cy2, Cy3 and Cy5 images from each gel. Spot volumes were calculated based on the intensity of the signal of each spot (Cy3 or Cy5), and compared to Cy2 volumes (internal standard) to correct the inter-gel variations. In the biological variation module, the Cy2 images of all eight gels were matched and the spot volumes were compared. Approximately 7000 separate spots were detected on each gel. Protein spots demonstrating at least a 1.5-fold difference in average spot volume ratios between groups in all biological replicates were selected and analyzed with mass spectrometry. Spot volume ratios were calculated using one-way ANOVA, with a *P*-value of less than 0.05 as the selection criteria.

2.3.5. Protein identification

Protein spots of interest were manually cut from the gel and digested in-gel using trypsin (Trypsin Gold, Mass spectrometry grade, Promega) as earlier described [17,18]. The samples were first concentrated and desalted on a C_{18} trap column (PROTECOL, SGE Analytical Science, Griesham, Germany) followed by peptide separation on a PepMap 100 C_{18} analytical column (LC Packings, Sunnyvale, CA). MS/MS of peptides was performed on a hybrid quadruple/TOF mass spectrometer with Nanospray II source (QSTAR Elite, applied Biosystems, Foster City, CA). The identification of proteins was performed using the local Mascot version 2.2 (matrix science, London, UK) against the in-house database. The

search criteria included digestion with one missed cleavage allowed, as a fixed modification carbamidomethyl modification of cysteine and as a variable modification oxidation of methionine.

2.3.6. Verification of identified proteins

All individual samples included in 2D-DIGE analysis from each group were pooled and used for validation by Western blot analysis (Fig. 4). SDS-PAGE was carried out in 12% polyacrylamide gels using a vertical slab gel apparatus under non-reducing conditions (Bio-Rad TetraCell) as described previously [19]. A 20-μl aliquot of each pooled sample was loaded to the gel, and proteins were separated by electrophoresis at 100 V for 3 h. Proteins were transferred to a PVDF membrane (Immobilon, Amersham) using a semidry blotting apparatus (Bio-Rad). Membranes were blocked for 1 h using 5% bovine serum albumin in Tris-buffered saline containing 0.1% Tween-20 (TBST), and probed using polyclonal anti-6-phosphogluconolactonase (6PGL C14200, Assay Biotech, 1:1000), monoclonal anti-increased sodium tolerance 1 (IST1, clone C7, antibodies-online, 1:1000), polyclonal anti-prostaglandin reductase 1 (PTGR1, C16862, Assay Biotech, 1:1000), polyclonal anti-aldehyde dehydrogenase 1A1 (ALDH1A1, bs-6509R, antibodies-online, 1:500), polyclonal *anti*-malate dehydrogenase 1 (MDH1, ABIN2783316, antibodies-online, 1:500) or polyclonal *anti*-annexin A1 (ANXA1, bs-1562R, antibodies-online, 1:1000), in TBST at 4 °C, respectively. The signals were detected using horseradish peroxidase-conjugated secondary anti-rabbit (sc-2004, Santa Cruz, 1:2000) or anti-mouse (P0447, Daco, 1:1000) and SupserSignal West Dura Chemiluminescent Substrate (Thermo Scientific), and the intensities were quantified with a chemiluminescent image analyzer LAS3000 (Fujifilm). There was no commercial antibody available against the T-complex protein 1 subunit theta (TCP1) and therefore the biological verification of the protein was not conducted.

2.3.7. Gene ontology analysis

To gain further insight into the role of these proteins, gene ontology (GO) analysis was conducted with the FunRich analysis tool [20]. Proteins were mapped for molecular function, cellular component and biological process of GO terms.

3. Results

3.1. 2D-DIGE

In the 2D-DIGE analysis, approximately 7000 different spots were visualized in gels. Ten of these spots had different ($P < 0.05$) abundance in the uterine lavage fluids between AI-P mares and the other groups (Fig. 2). Nine of the ten spots were identified by LC-MS/MS: in addition to albumin and hemoglobin, TCP1, 6PGL, IST1, PTGR1, ALDH1A1, MDH1, and ANXA1 (Table 1). Of the total ten proteins, seven were highest in the AI-P group, one in the AI-N group, one in the IUD-N group, and one in the IUD-P group (Fig. 3; Table 2).

Annexin A1 was up-regulated in IUD mares, with the IUD-P mares showing the highest values, while it was down-regulated in pregnant mares (Table 2; Fig. 3). In contrast, IST1, ALDH1A1, PTGR1, MDH1, albumin and hemoglobin, as well as the non-identified protein, were up-regulated in pregnant mares, while down-regulated in non-pregnant mares. In addition to ANXA1, TCP1 and 6PGL were down-regulated in pregnant mares (Fig. 3).

The average ratio of 2D-DIGE expression of the different identified proteins was calculated by using pregnant mares as the control group. The average ratio between non-pregnant and pregnant mares was significantly different in all identified proteins. The average ratio between IUD-N and pregnant mares was significantly different in TCP-1, ANXA1 and 6PGL. Finally, the average ratio between the IUD-P and pregnant mares was significantly different in TCP-1, IST1, MDH1, and ANXA1 (Table 2).

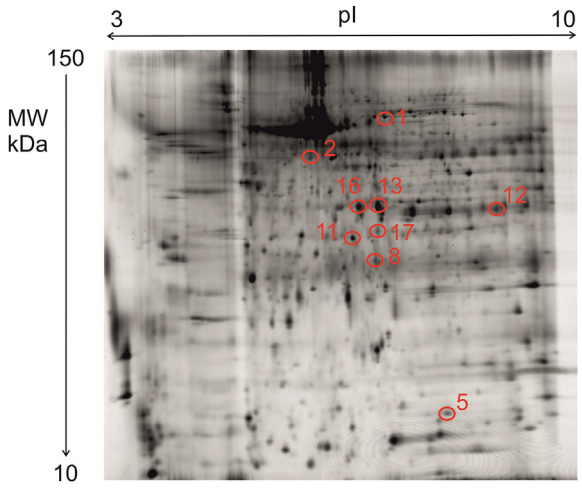

Fig. 2. A representative 2D-DIGE gel image of the endometrial secretome of mares. Proteins with different abundance are marked with red circles. 1: non-identified protein; 2: T-complex protein (TCP1); 5: hemoglobin; 8: 6-phosphogluconolactonase (6PGL); 11: increased sodium tolerance 1 (IST1); 12: prostaglandin reductase 1 (PTGR1); 13: aldehyde dehydrogenase 1A1 (ALDH1A1); 16: malate dehydrogenase 1 (MDH1); 17: annexin A1 (ANXA1). (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

All identified proteins were within the expected size and pI ranges in the 2D analysis. Western blot results verified the identification of the proteins (Fig. 4).

3.2. GO annotations

The top ten GO terms enriched for the cellular component, molecular function and biological process of all identified proteins are shown in Fig. 5. Statistically significant GO terms are listed in Supplementary Table S1. The most prominent cellular component GO terms were extrinsic component of endosome membrane (GO:0031 313), extrinsic component of external side of plasma membrane (GO:0031 232) and phagocytic cup (GO:0001891). For the molecular function, the most enriched GO terms were phospholipase A2 inhibitor activity (GO:0019 834), retinal dehydrogenase activity (GO:0001758), and calcium-dependent phospholipid binding (GO:0005544). The proteins were enriched in 56 biological process GO terms, of which the most prominent ones were regulation of interleukin-1 production (GO:0032 612), negative regulation of T-helper 2 cell differentiation (GO:0045 629), and positive regulation of T-helper 1 cell differentiation (GO:0045 627).

4. Discussion

Pregnant mares had the highest endometrial levels of MDH1, IST1, ALDH1A1 and PTGR1. GO analysis of molecular function of these proteins revealed significant enrichment in oxidoreductases: oxidases and dehydrogenases.

MDH1 is a cytosolic protein involved in the Krebs cycle and NADH metabolic processes that transform malate into oxaloacetate. Literature on the role of MDH1 in female reproduction is scarce. Higher endometrial levels of MDH1 have been observed in pregnant mares compared with cyclic mares on day 13 after ovulation [21]. This protein is crucial for the proper development of the embryo in mice [22] and sows [23]. Considering that the embryo is a highly replicating structure, it can be hypothesized that MDH1

Table 1
Proteins identified by LC-MS/MS following 2D-DIGE analysis.

Spot no	Identified protein	Accession number	Theoretical pI/MW (Da)	Matched peptides	Sequence coverage (%)	MASCOT score
2	TCP1	Q4R5J0	5.5/59.7	4	8	43
8	6PGL	OP5RR6	5.6/27.5	6	27.1	38
11	IST1	Q3ZBV1	5.23/39.7	1	2.4	41
12	PTGR1	Q29073	8.39/35.7	3	10.3	52
13	ALHD1A1	P15437	6.43/54.7	1	2.2	60
16	MDH1	P40925	6.91/36.4	4	11.9	93
17	ANXA1	Q8HZM6	5.67/38.7	6	16.7	111

pI: isoelectric point; MW: molecular weight; TCP1: T-complex protein 1; 6PGL: 6-phosphogluconolactonase; IST1: increased sodium tolerance 1; PTGR1: prostaglandin reductase 1; ALDH1A1: aldehyde dehydrogenase 1A1; MDH1: malate dehydrogenase 1; ANXA1: annexin A1.

might be involved in fulfilling the glucose, glutamine and oxidative phosphorylation demands of the equine embryo.

IST1 is a member of the endosomal sorting complexes required for transport (ESCRT), specifically ESCRT-III [24,25]. The GO analysis revealed that the microtubule organizing center was the most enriched component for IST1. It has been shown that the depletion of IST1 inhibits cellular division [26], suggesting that IST1 is involved in the cytokinesis phase of cellular reproduction. It is hence possible that the presence of an embryo induces the production and/or release of IST1 in the uterine lumen. Furthermore, it can be hypothesized that the higher levels of IST1 in the uterine lumen may be involved in the cellular multiplication of the growing embryo. According to the literature, this is the first time that this protein is described in equine uterine fluid.

ALDH1A1 is a cytosolic enzyme that metabolizes retinal to retinoic acid [27]. Its molecular functions include retinal, aldehyde, and benzaldehyde dehydrogenase activity, and it participates in retinoid and retinol metabolic processes. Retinoid acid is crucial for the proper development of the embryo. Both deficiency and excess of this molecule are linked with teratogenic abnormalities during embryogenesis [28–30]. Retinoic acid is involved in the processes of neurogenesis, cardiogenesis and body axis extension, as well as in the development of the forelimb buds, foregut and eye [27]. Thus, the high expression of ALDH1A1 in the uterine lumen of pregnant mares can be explained by the presence of the developing embryo.

Since these proteins, MDH1, IST1, and ALDH1A1, are all involved in either cellular replication, embryogenesis or metabolic pathways, it seems logical to assume they also play a role in conceptus development.

PTGR1 is a cytosolic prostaglandin reductase involved in PG-metabolism. As it has been stated above, PTGR1 was up-regulated in pregnant mares, which is in agreement with a previous study [21]. Its molecular functions include 2-alkenal reductase [NAD(P)] with 15-oxo -PGE1, -PGE2 or -PGE2-α as substrates, 13-prostaglandin reductase, which produces the transient PGF metabolite, and 15-oxoprostaglandin 13-oxidase activity. The latter enzyme initiates metabolic inactivation of leukotriene B_4 (LTB_4) [31], which is known to be involved in many inflammatory processes [32] including neutrophil recruitment [33]. During the period of implantation, the human endometrium shows signs of inflammatory processes, such as the presence of interleukin 1 (IL1), IL6, IL8, leukemia inhibitory factor and tumor necrosis factor [34], demonstrating that some steps of inflammatory pathways are necessary for the proper establishment of pregnancy. However, some important differences have been observed between implantation inflammation and inflammation in response to disease or injury. The most outlined difference is the lack of neutrophils during implantation [35]. The present results suggest that the inhibition of LTB_4 by PTGR1 might be involved either in the maternal recognition of pregnancy or pregnancy maintenance.

ANXA1 and 6PGL were up-regulated in IUD-P and IUD-N groups. GO analysis of these proteins shows that they are involved in phospholipase A2 (PLA2) inhibitor activity, calcium-dependent phospholipid binding, protein binding, bridging, calcium ion binding, and structural molecule activity. All the ten mostly enriched biological processes and cellular components were associated with annexin A1, as well as the most important molecular function, PLA2 inhibitor activity. Hence, annexin A1 appears to be the most significant component of endometrial secretomics at the time of sampling in our study.

Annexin A1 is a calcium/phospholipid-binding protein that has several functions including promotion of membrane fusion, involvement in exocytosis, and regulation of PLA2 activity [36]. Phospholipase A2 induces the release of arachidonic acid, which is the precursor molecule of prostaglandins, through the action of cyclooxygenases. In the present study, Annexin A1 was down-regulated in pregnant mares. However, previous studies have shown that this specific protein is up-regulated in the intrauterine fluid during early pregnancy in sows [37], sheep [38] and mares [21], linking its action to maternal recognition of pregnancy. The main difference between the studies performed in mares is the different sampling time. In the present study, the mares were sampled on Day 15 after ovulation, while in the study of Smits et al. [21] they were sampled on Day 13. Since maternal recognition of pregnancy in the mare occurs between days 12 and 14 after ovulation [21], it is possible that ANXA1 might be involved in the process of preventing luteolysis by inhibition of PLA2. Once maternal recognition has taken place, ANXA1 levels might decrease again similar to the present results. This hypothesis is sustained by an earlier study [39], which demonstrated that proteomic expression of uterine fluid in pregnant heifers varies depending on the day of pregnancy.

Annexin A1, an anti-inflammatory mediator, may be induced by glucocorticoids in inflammatory cells, and shares with these drugs many anti-inflammatory effects. It is important in the resolution of inflammation and is therefore induced in inflammatory conditions [40]. Annexin A1 inhibits inducible nitric oxide synthetase (iNOS) in macrophages and COX-2 in activated microglia. The inhibition of iNOS expression may be caused by the stimulation of IL-10 release induced by annexin A1 in macrophages [40]. Like glucocorticoids, annexin A1 exerts profound inhibitory effects on both neutrophil and monocyte migration in inflammation. Annexin A1 has been recently identified as one of the signals on apoptotic cells to be recognized and ingested by phagocytes, thus it may contribute to the safe post-apoptotic clearance of dead cells [41]. Since ANXA1 had the highest abundance in IUD mares, it seems likely that the presence of IUDs in the uterine lumen provokes inflammation, which in turn induces annexin A1 release contributing to the inhibition of luteolysis. The highest abundance of annexin A1 was detected in IUD-P mares, which suggests that an intense inflammation may increase the efficacy of the device.

6PGL is an intermediate enzyme in the pentose phosphate

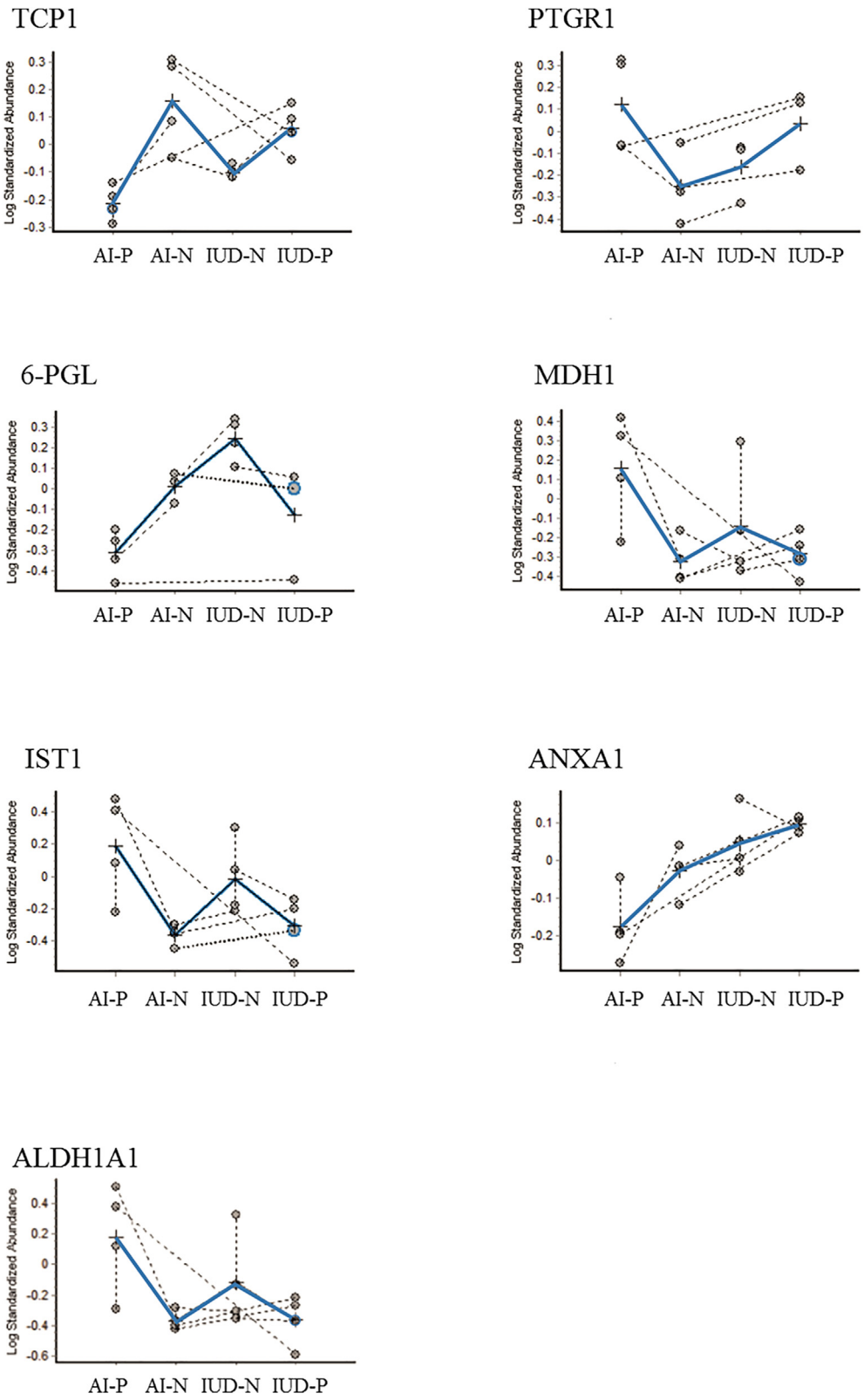

Fig. 3. Graphical representation of the standardized log abundance of the identified proteins in the endometrial secretome from each group of mares. TCP1: T-complex protein 1; PTGR1: prostaglandin reductase 1; 6PGL: 6-phosphogluconolactonase MDH1: malate dehydrogenase 1; IST1: increased sodium tolerance 1; ANXA1: annexin A1; ALDH1A1: aldehyde dehydrogenase 1A1. AI-P: pregnant mares; AI-N: non-pregnant mares; IUD-N: device mares with normal luteal phase; IUD-P: device mares with prolonged luteal phase.

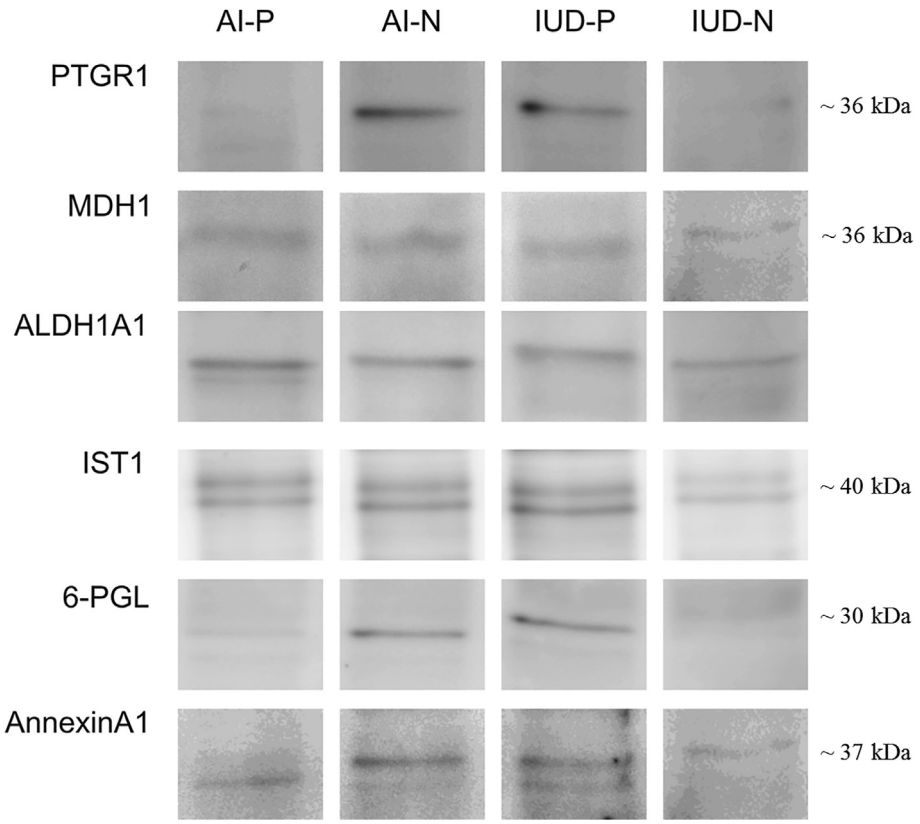

Fig. 4. Western blotting confirmation of 2D-DIGE results for proteins 6PGL, IST1, PTGR1, ALDH1A, MDH1 and Annexin A1. A 20-μl aliquot of pooled samples were used for each verification. AI-P: pregnant mares; AI-N: non-pregnant mares; IUD-P: device mares with prolonged luteal phase; IUD-N: device mares with normal luteal phase.

pathway (PPP) that transforms 6-phosphogluconolactone to 6-phosphogluconate [42]. During pregnancy – mainly during implantation – glucose consumption is increased to meet ATP requirements [43], and the PPP plays a key role to cover these necessities. In the present study, 6PGL showed a lower expression in pregnant mares (AI-P) compared to non-pregnant mares (AI-N). This result disagrees with that of Smits et al. [21] who observed higher concentrations of 6PGL in uterine fluid on day 13 of pregnancy in comparison with cyclic mares on the same day after ovulation. Once again, a possible explanation for this difference could be the fact that the mares were sampled on different days of pregnancy. Expression of 6PGL was similar in IUD and non-pregnant mares. Thus, the presence of the device in the uterus did not induce any change in the expression of 6PGL compatible with a pregnancy.

T-complex protein 1 subunit theta is a cytosolic protein that belongs to the T-complex protein 1 (TCP-1) chaperone family. It participates in the folding of protein complexes [44,45], and is involved in cell growth, proliferation and apoptosis [46] and inflammation [47]. In the present study, pregnant mares showed the lowest expression of TCP-1, whereas AI-N mares had the highest expression.

Finally, hemoglobin and albumin were also present in higher abundance in intrauterine fluid samples from pregnant mares. The role of hemoglobin and albumin in intrauterine fluid is controversial. Since intrauterine fluid contains abundant blood proteins, some studies consider their presence as contamination [48]. However, some other studies have demonstrated the presence of hemoglobin in human endometrium and suggested a role during implantation [49,50]. Higher concentrations of hemoglobin in intrauterine fluid from pregnant mares have been previously described [21], which is in accordance with our results. However, further research is warranted to establish the possible role of hemoglobin in the pregnant mare. Uterine concentration of albumin is increased in acute iatrogenic endometritis in mares [51], and its presence has been reported both in pregnant and non-pregnant mares [52], but no role in normal early pregnancy has been described to date.

Given these results, it appears that the presence of an embryo or IUD induces changes in the protein composition of endometrial secretions on Day 15 after ovulation. In the study by Klohonatz et al. [5], the contact of the embryo/IUD with the endometrial wall induced the formation of adhesion molecules that are involved in mechanisms of mechano-transduction. The released adhesion

Table 2
Average ratios of 2D-DIGE analyses between pregnant mares (AI-P) and either non-pregnant (AI-N) or device (IUD) mares.

Spot nº	Identified protein	AI-N vs AI-P	IUD-N vs AI-P	IUD-P vs AI-P
		Average ratio, one-way ANOVA (p-value)		
2	TCP-1	2.46 (0.0064)	1.29 (0.016)	1.88 (0.0025)
8	6PGL	2.08 (0.0064)	3.60 (0.00036)	1.68 (0.27)
11	IST1	−4.21 (0.015)	−1.69 (0.35)	−3.51 (0.037)
12	PTGR1	−2.49 (0.03)	−2.05 (0.11)	−1.27 (0.6)
13	ALDH1A1	−4.31 (0.023)	−1.96 (0.26)	−4.07 (0.33)
16	MDH1	−3.376 (0.021)	−1.85 (0.21)	−3.09 (0.029)
17	ANXA1	1.40 (0.041)	1.67 (0.012)	1.84 (0.0014)

AI-P: pregnant mares; AI-N: non-pregnant mares IUD-N: device mares with normal luteal phase; IUD-P: device mares with prolonged luteal phase; TCP1: T-complex protein 1; 6PGL: 6-phosphogluconolactonase; IST1: increased sodium tolerance 1; PTGR1: prostaglandin reductase 1; ALDH1A1: aldehyde dehydrogenase 1A1; MDH1: malate dehydrogenase 1; ANXA1: annexin A1.

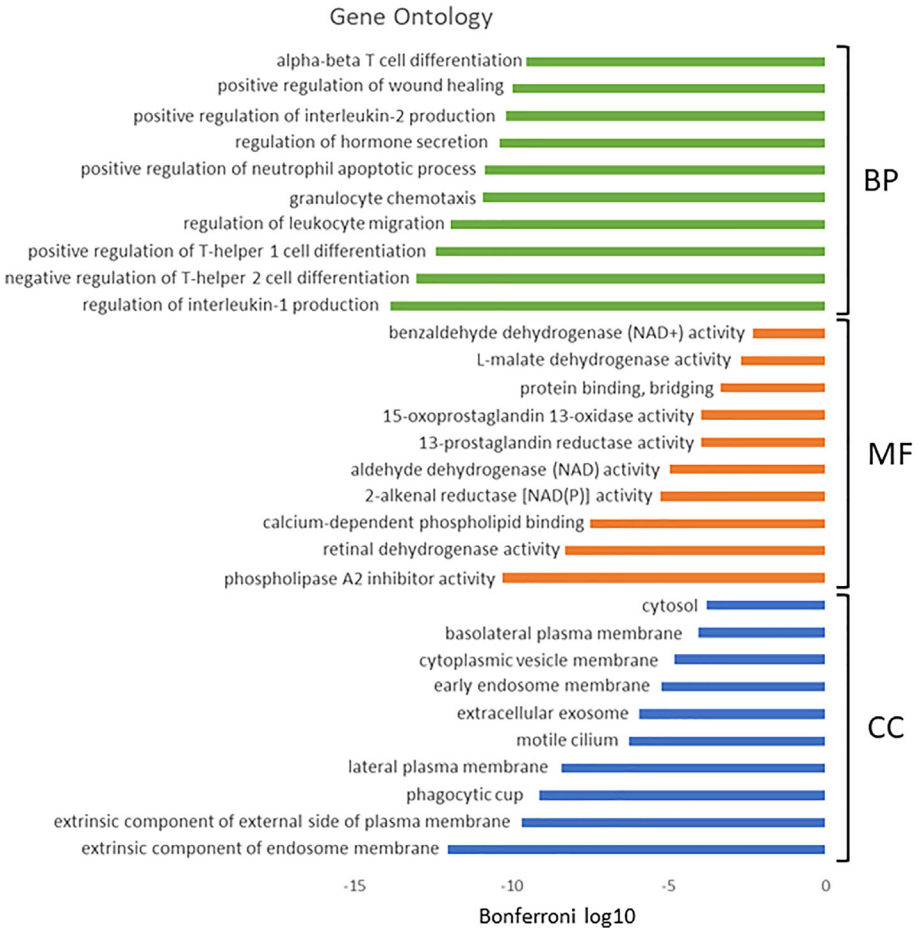

Fig. 5. Gene ontology (GO) classification of the identified proteins. Proteins were grouped into three main GO categories: biological process (BP), molecular function (MF) and cellular component (CC). Bonferroni corrected p-values were transformed by log 10.

molecules differed between embryos and IUDs However, unlike our results, Klohonatz et al. [5] found that the IUD did not block $PGF_{2\alpha}$ release. A possible explanation for this disagreement is the fact that the former study was performed *in vitro*, while ours was done *in vivo*.

Annexin A1 proved to be the most important protein in the endometrial secretomics in this study, as all major biological processes were due to annexin A1. Moreover, they were related to the regulation of inflammation or immune reactions: differentiation of T-cells, leukocyte migration, granulocyte chemotaxis, neutrophil apoptosis and interleukin production. The high levels of annexin A1 in IUD mares suggest that the IUD caused inflammation, which subsequently induced annexin A1 to down-regulate the inflammation. Since annexin A1 is a PLA2 inhibitor, it also prevented COX-2 and subsequent $PGF_{2\alpha}$ release. This is likely the mechanism by which IUDs block the luteolysis.

The present study has some limitations, such as the low number of mares in all groups, as well as the subgroup heterogeneity in terms of age. Another point to consider is the possibility of a delayed [53] or partial luteolysis [54], making Day 15 maybe too early for luteolysis to be completed in some non-pregnant mares.

The protein composition of endometrial secretions differed between pregnant and IUD-P mares, and Annexin A1, an inflammatory mediator, was up-regulated in IUD-mares. In conclusion, the results of the present study suggest that intrauterine devices cause endometrial inflammation which contributes to the inhibition of luteolysis.

Declaration of competing interest

The authors declare that no conflict of interest exists.

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CRediT authorship contribution statement

M.M. Rivera del Alamo: All authors contributed to the planning of the study, carried out the animal experiments, Writing - original draftwrote the draft of the manuscript. **T. Katila:** All authors contributed to the planning of the study. **M. Palviainen:** All authors contributed to the planning of the study, performed the DIGE analysis and analyzed the data. all authors contributed to the writing of the manuscript and approved it. **T. Reilas:** All authors contributed to the planning of the study, carried out the animal experiments.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.theriogenology.2021.02.001.

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