

mRNA and Protein Expressions of Prostaglandin E₂ Receptors (EP₂ and EP₄), Cyclooxygenase-2 and Prostaglandin E Synthase in the Cervix of Cyclic Bitches and those with Pyometra

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Abstract

Prostaglandins play a vital role in regulation of cervical patency. Prostaglandin E₂ (PGE₂) synthesis is regulated by cyclooxygenase (COX) and prostaglandin E synthase (PGES). PGE₂ acts through prostaglandin E receptors (EP), EP₂ and EP₄, to stimulate muscle relaxation. The aim of this study was to investigate mRNA expressions (EP₂, EP₄, COX-2, and PGES) and protein expressions (EP₂, EP₄, and COX-2) in the bitch cervix. Two groups of bitches, normal cyclic bitches and bitches with pyometra, were studied. Cyclic bitches were categorized into anestrus (n = 10), estrus (n = 7), and diestrus (n = 11), whereas bitches with pyometra were defined as open- (n = 18) or closed-cervix pyometra (n = 8) depending on the presence or absence of vaginal discharge, respectively. Cervices from the internal to external os were collected immediately after ovariohysterectomy. RNA extraction from cervical tissue was determined for levels of EP₂, EP₄, COX-2, and PGES mRNA using real-time qPCR. Western blot was performed to evaluate the protein expressions of EP₂, EP₄, and COX-2. There were no differences of mRNA and protein expressions in the bitch cervix among the stages of the estrous cycle. However, the expressions of PGES mRNA was higher in the cervix of bitches with open-cervix than closed-cervix pyometra ($p < 0.05$). The differences of protein expressions of EP₂, EP₄, and COX-2 were not observed. Our findings suggest that mRNA and protein expressions of the enzymes involved in PGE₂ synthesis and PGE₂ receptors are not influenced by hormonal status during the estrous cycle whereas PGES mRNA expression is likely associated with cervical relaxation in the bitches with pyometra.

Keywords: cervical patency, dog, prostaglandins, transcription

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บทคัดย่อ

การแสดงออกของเมสเซนเจอร์อาร์เอ็นเอของตัวรับพรอสตาแกลนดินอี₂(ซัพไทป์ 2 และ 4) ไซโคลออกซีจีเนส-2 และเอนไซม์พรอสตาแกลนดินอีซินเทส ในคอมดลูกสุนัขที่อยู่ในวงจรการเป็นสัด และในสุนัขเป็นมดลูกอักเสบแบบมีหนอง

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พรอสตาแกลนดินมีความสำคัญในการควบคุมการเปิดปิดของคอมดลูก การผลิตพรอสตาแกลนดินอี₂ (PGE₂) ควบคุมโดยเอนไซม์ไซโคลออกซีจีเนส (COX) และพรอสตาแกลนดินอีซินเทส (PGES) พรอสตาแกลนดินอี₂ทำงานผ่านการจับกับตัวรับฮอร์โมนพรอสตาแกลนดินอี₂ (EP) ซัพไทป์ EP₂ และ EP₄ ทำให้เกิดการคลายตัวของกล้ามเนื้อ การศึกษาครั้งนี้มีวัตถุประสงค์เพื่อตรวจสอบระดับการแสดงออกของเมสเซนเจอร์อาร์เอ็นเอ คือ EP₂ EP₄ COX-2 และ PGES ในคอมดลูกของสุนัขระยะต่างๆ ของวงจรการเป็นสัด และในสุนัขที่มีปัญหาหมดลูกอักเสบแบบมีหนอง ทำการศึกษาในสุนัขปกติจำนวนทั้งหมด 28 ตัว โดยแบ่งออกเป็น 3 กลุ่ม คือ แอนเอสตรัส (10 ตัว) เอสตรัส (7 ตัว) และไดเอสตรัส (11 ตัว) ส่วนสุนัขกลุ่มที่มีปัญหาหมดลูกเป็นหนองจำนวน 26 ตัว แบ่งออกเป็น 2 กลุ่ม คือ มดลูกเป็นหนองแบบคอมดลูกเปิด (18 ตัว) และแบบคอมดลูกปิด (8 ตัว) โดยดูจากการพบหรือไม่พบของเหลวไหลจากช่องคลอด เก็บคอมดลูกจากช่องเปิดด้านในถึงช่องเปิดด้านนอกหลังการทำหมันโดยตัดตรงไขและมดลูกออก สกัดอาร์เอ็นเอจากตัวอย่างคอมดลูกแล้วนำมาตรวจสอบระดับการแสดงออกของ EP₂ EP₄ COX-2 และ PGES ด้วยวิธี quantification real-time PCR (qPCR) จากการศึกษาพบว่า การแสดงออกของเมสเซนเจอร์อาร์เอ็นเอที่สนใจไม่มีความแตกต่างกันในสุนัขในแต่ละระยะของวงจรการเป็นสัด แต่การแสดงออกของเมสเซนเจอร์อาร์เอ็นเอของPGES ในกลุ่มสุนัขที่มีปัญหาหมดลูกเป็นหนองแบบคอมดลูกเปิดมีค่ามากกว่าในกลุ่มคอมดลูกปิด ($p < 0.05$) ดังนั้น ระดับฮอร์โมนที่เปลี่ยนแปลงในแต่ละระยะของวงจรการเป็นสัด น่าจะไม่มีผลต่อการแสดงออกของยีนที่เกี่ยวข้องกับการสร้างพรอสตาแกลนดินอี₂และตัวรับฮอร์โมนพรอสตาแกลนดินอี₂ ซัพไทป์ 2 และ 4 แต่ PGES น่าจะมีส่วนเกี่ยวข้องกับกลไกการเปิดของคอมดลูกในสุนัขที่มีปัญหาหมดลูกเป็นหนองแบบคอมดลูกเปิด

คำสำคัญ: ภาวะเปิดปิดของคอมดลูก สุนัข พรอสตาแกลนดิน ทรานสคริปชัน

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Introduction

Relaxation of the cervix is regulated by complex mechanism. Current knowledge about mechanism of cervical relaxation arises from the studies of pregnancy and parturition in humans (Timmons et al., 2010), rats (Chien and Macgregor, 2003), rabbits (Fukuda et al., 2007) and sheep (Kershaw-Young et al., 2009). In women, understanding of the control of cervical relaxation is crucial for the management of labor including its induction in case of prolonged pregnancy and treatment of undesired preterm births. In sheep, cervical relaxation may facilitate transcervical intrauterine artificial insemination (Kershaw et al., 2007). The cervical relaxation is regulated by serum hormonal concentrations, prostaglandin synthesis, and extracellular matrix remodeling (Kershaw-Young et al., 2009). In bitches, relationship between hormonal status and cervical patency is partly known. In

general, progesterone induces closure of the cervical canal and estrogen is capable of opening the canal during estrus which is important in fertilization process (Silva et al., 1995). Moreover, prostaglandin E₂ (PGE₂) was shown to induce cervical ripening in human when administered intravaginally (Feltovich et al., 2005). Biosynthesis of PGE₂ is regulated mainly by two enzymes, cyclooxygenase (COX) which converts arachidonic acid to prostaglandin H₂ (PGH₂), and prostaglandin E synthase (PGES) which converts PGH₂ to PGE₂. There are two forms of COX, COX-1 and COX-2. COX-1 is a constitutive enzyme, whereas COX-2 is specific to inflammatory process (Tamada et al., 2012) and can be regulated by hormonal changes (Kowalewski et al., 2006). Studies in baboons and sheep revealed that cervical glandular epithelial cells were the major source of COX-2 mRNA (Wu et al., 2004; Wu et al., 2005). Moreover, a previous study in sheep showed that COX-2 mRNA was highly expressed in the cervix at estrus when serum estradiol

concentrations were high, indicating a relationship between PGE₂ and estradiol (Kershaw et al., 2007). Prostaglandin E₂ exerts its role by coupling to prostaglandin E receptors (EP); EP₁, EP₂, EP₃ and EP₄. EP₁ and EP₃ are involved in the contraction of smooth muscle, whereas EP₂ and EP₄ function to induce smooth muscle relaxation (Narumiya et al., 1999). EP₄ mRNA expression in the rat cervix was shown to be involved in cervical remodeling at the term time (Feltovich et al., 2005).

In bitches, pyometra is a common uterine disease which affects 25% of adult animals before they reach 10 years of age (Verstegen et al., 2008). The disease is classified into two categories; open- and closed-cervix pyometra. Clinical signs of pyometra depend primarily on whether the cervix is patent enough to allow the drainage of purulent fluid in uterus (Pretzer, 2008). Bitches with closed-cervix pyometra suffer from enlarged uteri and risk of uterine rupture. Cervical patency is a key to decide whether medical treatment is possible for pyometra bitches. To release pus from the uterus, aglepristone, an antiprogesterin along with prostaglandins are reported to successfully induce cervical relaxation (Fieni et al., 2001). However, the exact mechanism of the induction of cervical relaxation in the bitch is unknown. In our previous study, the number of neutrophils was significantly higher in the bitches with open-cervix compared to that with closed-cervix pyometra (Kunkitti et al., 2011). Moreover, induction of cervical relaxation by neutrophil infiltration was also demonstrated in rabbits at the term time and was reported to be mediated by EP₄ (Fukuda et al., 2007). Taken together, we hypothesized that there were associations between PGE₂ [via its receptors (EP₂ and EP₄)], enzymes involved in PGE₂ synthesis (COX-2 and PGES), and various stages of the estrous cycle which were influenced by sex steroid hormones. Moreover, the corresponding relationships might exist also in bitches affected with open- and closed-cervix pyometra. The present study aimed to investigate mRNA expressions (EP₂, EP₄, COX-2 and PGES) and protein expressions (EP₂, EP₄, and COX-2) in normal cyclic bitches during different stages of the estrous cycle and those with pyometra.

Materials and Methods

Animals: Twenty eight bitches of various breeds with an average age of 2.1±0.8 years (ranging from 1-4 years) subjected to routine spaying were divided into 3 stages of estrous cycle; anestrus (n = 10), estrus (n = 7), and diestrus (n = 11), on the basis of presence or absence of large follicles or corpora lutea on the

ovaries, serum progesterone concentrations and vaginal cytology (Table 1). Another group of 28 bitches diagnosed as having uterine content by ultrasonography were divided into open-cervix (n = 18) and closed-cervix pyometra (n = 10) according to presence or absence of vaginal discharge, respectively. The bitches affected with pyometra had an average age of 7.0±3.9 years (ranging from 2-15 years).

Cervical tissue collection: Cervical tissue from each animal was collected immediately after ovariohysterectomy and prepared as previously described (Kunkitti et al., 2011). In brief, after collection the cervixes were longitudinally cut into 2 parts. The cervical tissue was then cut into 0.1 g pieces and frozen in liquid nitrogen immediately and stored at -80°C until used for RNA and protein extraction.

RNA extraction, reverse transcription and real-time qPCR: Cervical tissues were pulverized with sterile mortar and pestle. Total RNA was extracted from frozen cervical tissue using RNeasy Mini Kit (QIAGEN, Valencia, CA, USA) at room temperature following the manufacturer's instructions. The RNA concentration and purity were accessed using spectrophotometer at 260 and 280 nm (Nanadrop ND-2000, Wilmington, Delaware, USA). After extraction RNA was stored at -80°C. To ensure complete removal of any trace amounts of genomic DNA, DNA digestion was performed with RNase-free DNase set (1 U/μg RNA, Promega, Madison, USA) at 37°C for 30 min. Subsequently, single-stranded complementary DNA (cDNA) synthesis was performed using Omniscript First-Strand cDNA Synthesis Kit according to the guidelines supplied by the manufacturer (Invitrogen, Carlsbad, CA, USA). Ten μl of extracted RNA was incubated with 2 μl of random primer (100 μM), 2 μl of 5 mM deoxynucleotide triphosphates (dNTP) mix, 2 μl of 10x Buffer RT, 0.25 μl of RNase inhibitor (40 units/μl), 1 μl of Omniscript RT and 2.75 μl of RNase free water at 37°C for 60 min. Selected negative control samples were prepared by including all reagents as above, minus the reverse transcriptase. A master mix of RT reagent was prepared once to minimize potential variation.

For quantification of mRNA expression of EP₂, EP₄, COX-2, and PGES, the quantitative real-time PCR (qPCR) standard curve method was employed as previously described (Swangchan-Uthai et al., 2011). To standardize the quantification method, an endogenous RN18S1 was chosen as reference gene. The primer pairs of interested genes were inferred from published canine sequences as shown in Table 2. The primers were then tested by

Table 1 Criteria used to determine the stage of estrous cycle, ovarian structure, appearance of vaginal cytology, serum progesterone level, and number of healthy cyclic bitches.

	Anestrus	Estrus	Diestrus
Dominant ovarian structure	Absence of ovarian activity	Follicles	Corpora lutea
Majority of cells in the vaginal cytology	Basal cells	Cornified cells	Non-cornified cells
Serum progesterone (ng/ml)	< 1	2-15	> 15
(n)	10	7	11

n indicates the number of animals within each group

conventional PCR amplification using Platinum PCR supermix (22 U/ml complexed recombinant Taq DNA polymerase with Platinum® Taq Antibody, 22 mM Tris-HCl (pH 8.4), 55 mM KCl, 1.65 mM MgCl₂, 220 μM dGTP, 220 μM dATP, 220 μM dTTP, 220 μM dCTP, and stabilizers) containing Tag polymerase (Invitrogen; Invitrogen Ltd. UK), 50 ng cDNA and 20 μM primers. The hot-start PCR reaction was run for 2 min at 95°C (activation of Taq polymerase), followed by 38 cycles, each one comprising a denaturing step at 95°C for 30 sec, annealing at 62.5°C (for EP₂ and EP₄) or 64.1°C (for COX-2) or 62.5°C (for PGES) for 30 sec, extension at 72°C for 20 sec and final elongation at 72°C for 5 min. The amplification products were separated by electrophoresis through a 2% (w/v) agarose gel (Bio-Rad, CA, USA). The desired PCR products of all interested genes (EP₂, EP₄, COX-2, PGES and RN18S1) were visualized as a single band. The identity of the PCR products was confirmed by DNA sequencing (GATC Biothech, London, UK).

In order to optimize real-time qPCR assay, serial dilutions of external standards and sample to be used in melting curve and annealing temperature analysis were prepared. The purified PCR product of each gene was produced from a conventional PCR amplification and then purified by QIAquick PCR Purification kits in accordance with guidelines supplied by Qiagen (QIAGEN, Valencia, CA, USA). The concentration of purified PCR product was determined by NanoDrop ND-1000 spectrophotometer. In the following stage, the optimal annealing temperature and melting curve analysis were assessed using a temperature gradient feature ranging from 50-65°C.

The transcripts of each gene were determined by an optimized qPCR procedure with a single-plex SYBR Green I assay (CFX 96 Real-Time PCR Detection System, Bio-Rad Lab, Inc, CA, USA). The amplification mixes contained 10 μl of KAPA SYBR FAST qPCR Kits (GRI, Braintree, Essex, UK), 0.5 μl of 20 μM forward and reverse primers mix, 4.5 μl of nuclease free water and 5 μl of unknown sample (50 ng of cDNA). The qPCR reactions for both standards and samples were performed in duplicate in PCR plate. Thermal cycling conditions applied to each assay consisted of an initial Taq activation step at 95°C for 5 min followed by 38 cycles of denaturation at 95°C for 15 sec, annealing temperature as shown in

Table 2, extension at 72°C for 20 sec followed by amplicon-specific fluorescence acquisition reading (range 74-84°C). Absolute concentrations of the PCR product were calculated by comparing the C_q values of the unknown samples to a standard curve using CFX Manager™ Software Version 1.0.1035.131 (Bio-Rad Lab, Inc) and expressed as fg/μg reverse-transcribed RNA.

Western Blot analysis: Frozen cervical tissues were ground to powder with sterile mortar and pestle and treated with lysis buffer containing Tris-Glycine-SDS buffer, sodium, orthovanadate (200mM), and protease inhibitor cocktail set 1 (Calbiochem, Germany). The sample was vortexed and centrifuged at 13,000 rpm at 4°C for 10 min, supernatant were collected and the sample was boiled at 100°C for 5 min. Two μl of cervical lysate solution were used for determination of the protein concentration by spectrophotometry using Protein A280 technique (NanoDrop® ND1000 spectrophotometer, NanoDrop Technologies Inc, Wilmington, Delaware, USA). The rest of lysate was mixed with 5% β-mercaptoethanol (Sigma-Aldrich GmbH, Steinheim, Germany) and 0.02% bromophenol blue (Sigma-Aldrich GmbH, Steinheim, Germany) and stored at -20°C. Protein extracts (30 μg) were resolved on a 12% SDS-PAGE (sodium dodecylsulfate-polyacrylamide gel) with a 4% stack. Proteins were transferred to a polyvinylidene difluoride membrane (BioTrace™ PVDF transfer membrane, MI, USA) and blocked with 5% BSA in TBS-T at room temperature for 1 hour. Immunoblots were performed by using goat polyclonal antihuman EP₂ (sc-22196), goat polyclonal antihuman EP₄ (sc-16022) (Santa Cruz, California, USA), rabbit polyclonal antimurine COX-2 (catalogue 16016 Cayman Chemical, Ann Arbor, Mich), and mouse monoclonal beta actin (AC-15, ab6276, abcam®, Abcam plc, San Francisco, USA) at dilution of 1 : 250, 1 : 250, 1 : 250 and 1 : 5,000, respectively, in clocker solution and incubated at 4°C overnight. Horseradish peroxidase (HRP)-conjugated horse anti-goat IgG (PI-9500, Vector Laboratories, California, USA) and polyclonal rabbit anti-mouse immunoglobulin (DAKO, Glostrup, Denmark) were used as the secondary antibodies at dilution of 1 : 500 and 1 : 1,000 in TBS-T, respectively, and incubated at room temperature for 5 hours with intensive washing in TBS-T between each step.

Table 2 Primer sequences for EP₂, EP₄, Cox-2 and PGES, expected product's length, and specific annealing temperature used for real-time PCR

Primer	Accession number	Primer sequence	Annealing	Product-length (bp)
EP ₂	NM_001003170.1	F: 5'-TTC TCC TGG CTA TTA TGA CC-3'	62.5	273
		R: 5'-ATC TAC TGG CGT TTG ACT G-3'		
EP ₄	NM_001003054.1	5'F: -GGT ACG GGT GTT CAT CAA C-3'	62.5	323
		5'AGA R: AGA GGA GGG TCT GAG ATG TG-3'		
COX-2	NM_001003354.1	5'F: -ACA GGA GAG AAG GAA ATG GC-3'	64.1	250
		5'R: -GGA TTG AGG CAG TGT TGA TG-3'		
PGES	NM_001122854.1	5'F: -ACC ATC TAC CCC TTC CTG T-3'	62.5	214
		5'R: -CTG CTT CCC AGA CGA TCT-3'		

Bound antibodies were developed with diaminobenzidine (DAB) (ImmPACT™ DAB Peroxidase Substrate, Vector Laboratories, California, USA) for 5 min until the brown color of protein band developed. Membrane was scanned with HP scanner (HP Scanjet 2400c, HP, USA) to get the image. The optical density of EP₂, EP₄, and COX-2 bands were measured by using Quantity One Software Program version 4.4.0 (Bio-Rad Laboratories). The specific density of each sample was calculated by subtraction of the background density and divided by the specific density of quality control band.

Statistical analyses: Statistical test of analysis of

variance (ANOVA) using SPSS for Microsoft Windows software (version 19; SPSS Inc., Chicago, IL, USA) was performed to analyze the differences of mRNA and protein expression in bitches during different stages of the estrous cycle (anestrus, estrus and diestrus). Data were tested for homogeneity of variance using Levene's test. Post hoc comparisons were performed using Bonferroni correction to test for significances. All data are expressed as mean \pm SEM. For pyometra groups, t-test was used to analyze differences of mRNA expression between open-cervix and closed-cervix pyometra groups. Values were considered to be statistically significant at $p \leq 0.05$.

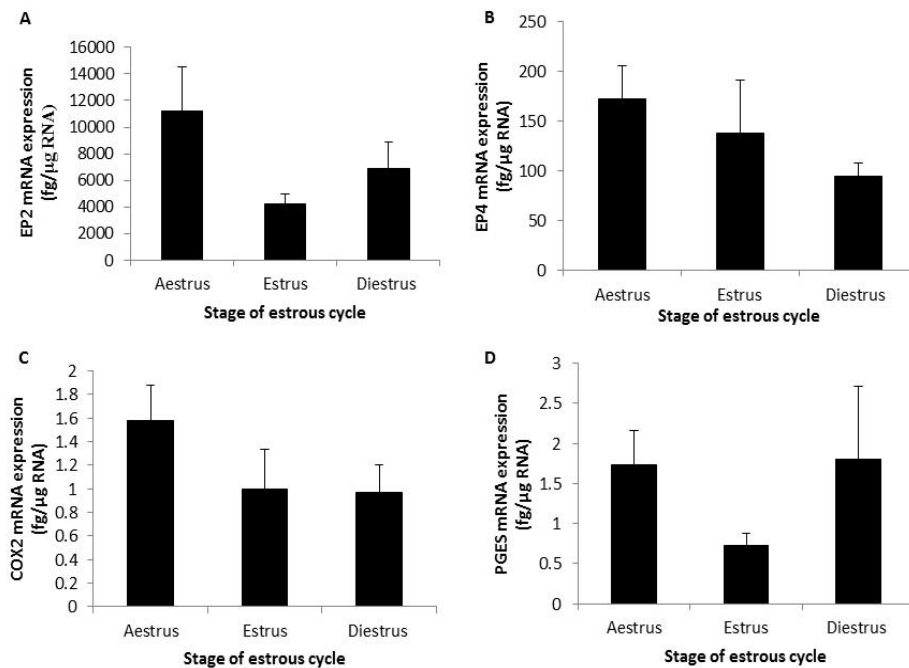


Figure 1 Mean (\pm SEM) mRNA expressions of EP₂, EP₄, COX-2 and PGES in cervixes of healthy bitches during different stages of the estrous cycle

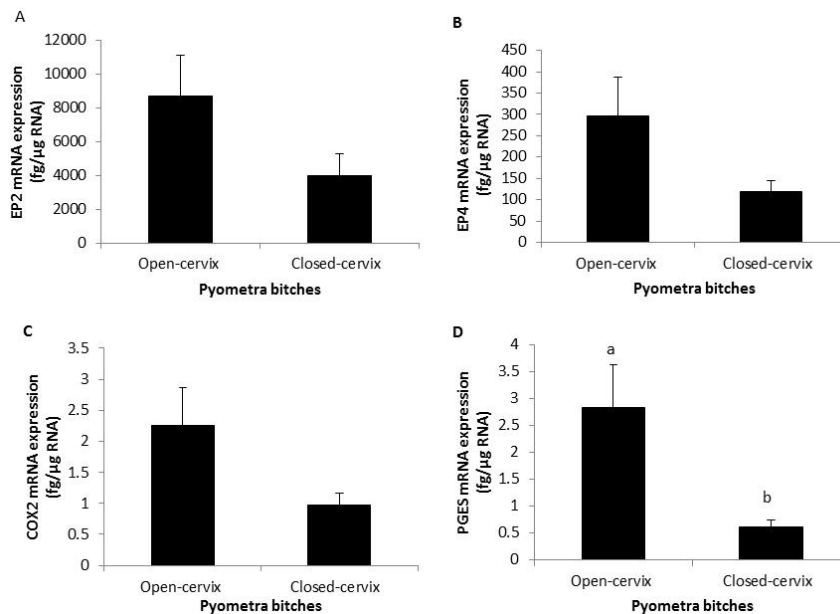


Figure 2 Mean (\pm SEM) mRNA expression of EP₂, EP₄, COX-2 and PGES in cervixes of bitches with open- or closed-cervix pyometra. Bars with different superscripts show significant ($p < 0.05$) differences.

Results

Cervical expression of EP₂, EP₄, COX-2, and PGES mRNA in cyclic and pyometra bitches: The mRNA for EP₂, EP₄, COX-2 and PGES was expressed in cervical tissue of the normal cyclic bitches during all stages of the estrous cycle. However, no differences were observed in the expression of any gene studied among the stages of the estrous cycle when analyzed either as relative number (after normalized with RN18S1) or absolute concentrations (fg cDNA/ μ g RT RNA). The data are presented as absolute numbers in Fig 1. In the bitches with pyometra, PGES mRNA expression in the cervical tissue of open-cervix pyometra was higher than closed-cervix pyometra ($p < 0.05$) whereas the expression of EP₂, EP₄, and COX-2 did not differ between the two groups (Fig 2).

Cervical expression of EP₂, EP₄, and PGES proteins in cyclic and pyometra bitches: The results from western blot confirmed the protein expressions of EP₂, EP₄, and COX-2 in canine cervical tissue during estrous cycle and in bitches with pyometra. EP₂, EP₄, and COX-2 proteins were expressed in anestrus, estrus and diestrus although the differences among them were not observed ($p > 0.05$) (Fig 3). Similarly, there were no differences of EP₂, EP₄, and COX-2 protein expressions between open-cervix and closed-cervix pyometra ($p > 0.05$) (Fig 4).

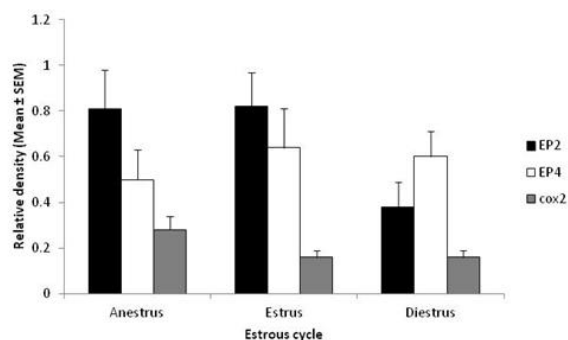


Figure 3 Relative density (Mean \pm SEM) of EP₂ receptor protein expression of canine cervix at estrous cycle

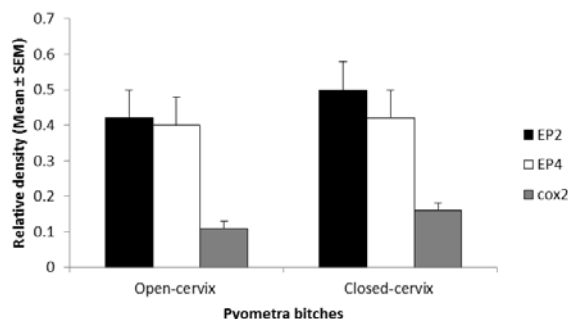


Figure 4 Relative density (Mean \pm SEM) of EP₄ receptor protein expression of canine cervix in bitches with open-cervix pyometra and closed-cervix pyometra

Discussion

In the present study, the cervical mRNA and protein expressions of EP₂, EP₄, COX-2, and PGES were studied in bitches during the various stages of the estrous cycle and those affected with pyometra with the aim to help the understanding of the prostaglandin associated cervical relaxation.

Estradiol and progesterone are two major steroids functioning during the estrous cycle to regulate cervical patency possibly through prostaglandins production (Kershaw et al., 2005; Kershaw et al., 2007; Kershaw-Young et al., 2009). In the present study mRNA expression of COX-2 in the cervix was not influenced by dominated hormones during the estrous cycle. Our results are concordant with the study of COX-2 mRNA expression in the bitch uterus, demonstrating no differences between anestrus and diestrus (Silva et al., 2009), whereas they differ from the studies in sheep, in which estradiol was shown to significantly elevate the COX-2 mRNA expression in the cervix (Zhang et al., 2007; Kershaw-Young et al., 2010). The protein expression of COX-2 in this study did not differ among the stages of estrous cycle. The study in sheep cervix demonstrated that COX-2 protein expression did not increase in cervix treated with estradiol compared to control group (Zhang et al., 2007), which is concordant with our result. On the contrary, the high level of COX-2 protein expression in pre-LH surge was found compared to luteal phase (Falchi and Scaramuzzi, 2013). One possible explanation is that the modulation of COX-2 expression may involve multifactorial regulation. Although the differences in EP₂ mRNA expression were not statistically significant between the estrous and diestrous periods, the considerably lower EP₂ mRNA expression during estrus might resulted from a down regulation by the estradiol during the estrous stage. Similar findings were demonstrated in the baboon cervix in which EP₂ mRNA was lower during labor when the cervix was relaxed than the animals that were not in labor (Smith et al., 2001). Such differences were also observed in the rat uterus (Brodth-Eppley and Myatt, 1998). Interestingly, the EP₂ mRNA expression was regulated by changes in estrogen and progesterone in the mouse uterus in the fashion that the estrogen down-regulated the level of EP₂ mRNA whereas progesterone up-regulated the expression of this receptor (Lim and Dey, 1997). This was also supported by the report in the rat, showing the increase of EP₂ mRNA expression in the myometrium after treatment with progesterone (Dong and Yallampalli, 2000). However, the protein expression of EP₂ did not differ between estrus and diestrus, suggesting that the regulation of EP₂ expression might be modulated at the translation stage. Our results of a lack of differences in EP₄ mRNA expression throughout the estrous cycle are similar to the previous study in the sheep (Kershaw-Young et al., 2009). Although the circulating estradiol concentrations did not seem to influence mRNA and

protein expression of EP₄ in the bitch cervix in the present study, the immunohistochemical study revealed a higher EP₄ expression in the luminal epithelium of the bitch cervix during estrus than anestrus in our previous study (Linharattanaruksa et al., 2013). Moreover, the protein expression of EP₄ in rat cervical tissue increased with advancing gestation and was found highest on the day of parturition when cervix relaxed (Chien and Macgregor, 2003). These lead us to propose that the differential expression of EP₄ during the different stages of the estrous cycle are localized in certain regions and with the whole cervix together tissue, such differences in EP₄ expression become masked.

It has been known that PGE₂ plays an important role in various inflammatory responses (Rocca and FitzGerald, 2002) including cervical relaxation during labor by modification of extracellular matrix, i.e. a decrease in collagen content and an increase in collagen remodeling in the cervix (Rodriguez et al., 2003). In mammalian cervix, proinflammatory cytokines responsible for the changes in extracellular matrix are secreted by various cells including cervical fibroblasts, endothelial cells, and leukocytes such as neutrophils. Although the protein expressions of EP₂ and EP₄ protein did not differ between open- and closed-cervix pyometra in this study, our previous study revealed that immunolocalization of EP₄ expression was higher in the open-cervix than closed-cervix pyometra (Linharattanaruksa et al., 2013). These finding support the notion that EP₄ protein expression in specific tissue layer (in this case luminal epithelium) may be involved in cervical relaxation in the bitches.

In the present study, expression of COX-2 mRNA and protein did not differ between open- and closed-cervix pyometra while the PGES mRNA did, suggesting that a post-COX enzyme mechanism is likely to be involved in the determination of final prostaglandin product (Hafez and Smith, 1982).

In our previous study, the number of neutrophils in the cervix was higher in bitches with open- than closed-cervix pyometra (Kunkitti et al., 2011). In this study, higher COX-2 and PGES mRNA levels were observed in the cervix of bitches with pyometra compared to the normal cyclic bitches, indicating an up-regulated gene transcription. This was also reported in the endometrium of the bitches with pyometra (Silva et al., 2009). COX-2 and PGES are said to be stimulated by proinflammatory cytokines and endotoxins such as lipopolysaccharides (LPS) (Murakami et al., 2000; Helliwell et al., 2004). Moreover, the main proinflammatory cytokine in cervical relaxation is interleukin-8 (IL-8) (Uchiyama et al., 1992; el Maradny et al., 1994; El Maradny et al., 1996), which has chemotactic effect on neutrophils which are the major source of matrix metalloproteinases (MMPs) (Stygar et al., 2002). Furthermore, IL-8 stimulates the activation and degranulation of neutrophils, thus provoking the release of MMPs (van Engelen et al., 2009). MMPs are a family of enzymes that are classified according to substrates such as collagenase, gelatinase, and

stromelysin (Sorsa et al., 2004) that can degrade components of the extracellular matrix. The expression of IL-8 in the cervix is stimulated by PGE₂ (Ito et al., 1994) and the increase in IL-8 concentrations stimulates degranulation of MMPs from neutrophils (Kelly, 2002; Tamada et al., 2012). This, in turn, results in the changes in collagen turn over in extracellular matrix and leads to cervical relaxation. From our results, we propose that the increase in PGES mRNA expression is stimulated by proinflammatory cytokines, resulting in the enhanced production of PGE₂ that subsequently stimulates neutrophil infiltration through the IL-8 and releases MMPs to degrade extracellular matrix causing cervical relaxation.

In conclusion, the cervix of normal bitches during various stages of the estrous cycle expressed the same levels of EP₂ and EP₄ mRNA. Moreover, the biosynthesis of PGE₂ by COX-2 and PGES was not influenced by the stages of the estrous cycle. In addition, PGES seems to control the production of PGE₂ to regulate cervical relaxation in the bitches with open-cervix pyometra.

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