



**Insulin promotes cat preantral follicle growth and antrum formation through temporal expression of genes regulating steroidogenesis and water transport**

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1 **Insulin promotes cat preantral follicle growth and antrum formation through temporal**  
2 **expression of genes regulating steroidogenesis and water transport**

3 **Short title:** Insulin enhances cat follicle growth in vitro

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19 **Abstract**

20 The objectives were to determine the influence of insulin on in vitro (1) viability and growth of  
21 domestic cat ovarian follicles, (2) mRNA expression of genes regulating steroidogenesis  
22 (*Cyp17a1*, *Cyp19a1*, *Star*) and water transport (aquaporins (AQPs); *Aqp1*, *Aqp3*, *Aqp7*,  
23 *Aqp9*) and (3) steroid production (17 $\beta$ -oestradiol, E2; progesterone, P4; androstenedione,  
24 A4). Cat secondary follicles were isolated from ovarian cortices and cultured in 0 (Control), 1,  
25 or 10  $\mu$ g/ml insulin for 14 d (Day 0 = culture onset). Follicle/oocyte viability (based on neutral  
26 red staining), diameter, and antrum formation were assessed every 72 h and at the end of  
27 incubation (Day 14). mRNA expression of steroidogenic and water transport genes were

28 evaluated on Days 0, 6, and 12, and E2, P4, and A4 concentrations in medium on Day 12.  
29 By Day 14, insulin at 1 and 10 µg/ml promoted ( $P < 0.05$ ) antrum formation in  $26.9 \pm 9.0\%$   
30 (mean  $\pm$  SEM) and  $78 \pm 10.2\%$  of follicles, respectively, as well as follicle growth (diameter,  
31  $151.4 \pm 4.5$  and  $169.9 \pm 10.5$  µm) compared to the Control ( $3.3 \pm 3.3\%$  and  $129.1 \pm 6.6$  µm).  
32 High insulin (10 µg/ml) treatment increased ( $P < 0.05$ ) follicle viability compared to the  
33 Control ( $86.0 \pm 9.8$  versus  $38.1 \pm 10.9\%$ ). However, insulin exerted no benefit ( $P > 0.05$ ) on  
34 oocyte diameter. *Cyp17a1* expression on Days 6 and 12 was higher ( $P < 0.05$ ) in follicles  
35 cultured in the low (1 µg/ml) compared to high (10 µg/ml) insulin treatment with both being  
36 similar to the Control. *Star* expression was higher ( $P < 0.01$ ) in low insulin compared to the  
37 Control on Day 6, but this gene was undetectable in the high insulin treatment by Day 12.  
38 Compared to the high dosage, low insulin increased ( $P < 0.05$ ) *Aqp1* expression on Day 6;  
39 however, differences among treatments were not observed on Day 12. By contrast, high  
40 insulin supplementation decreased ( $P < 0.05$ ) transcript level of *Aqp9* compared to the  
41 Control. Only P4 production was influenced by insulin supplementation with concentration  
42 being higher ( $P < 0.05$ ) in the low compared to high dose and Control groups. In summary,  
43 findings indicated that insulin promoted cat ovarian follicle growth and survival in vitro,  
44 including by enhancing antrum formation, with the likely mechanism involving temporal  
45 expression of *Cyp17a1*, *Star*, and *Aqp9* genes.

## 46 1. Introduction

47 The ability to artificially grow a preantral follicle to the antral stage containing a  
48 developmentally competent oocyte has enormous potential for rescuing the valuable  
49 genomes of endangered wildlife species (Comizzoli *et al.* 2009; Songsasen *et al.* 2012) and  
50 preserving fertility of women facing cancer treatments (Hovatta 2004; Barrett and Woodruff  
51 2010). In vitro culture of ovarian tissue also offers a valuable platform for advancing our  
52 understanding of the mechanisms regulating folliculogenesis (Picton *et al.* 2008; West-  
53 Farrell *et al.* 2009). Yet, successful production of live offspring from oocytes recovered from  
54 in vitro grown follicles remains limited to only the mouse (Eppig and O'Brien 1996; Xu *et al.*

55 2006). Attempts to apply mouse protocols to larger-size, more complex animal models  
56 (buffalo (Gupta *et al.* 2008); pig (Wu *et al.* 2001); sheep (Luz *et al.* 2012); goat (Magalhaes  
57 *et al.* 2011); baboon (Xu *et al.* 2011)) have met with limited success in advancing follicle size  
58 and oocyte viability in vitro. Nonetheless, studying non-rodent models has provided insights  
59 into the important roles of endocrine and paracrine controls in ovarian folliculogenesis  
60 (Knight and Glister 2003; Hunter *et al.* 2004).

61 In our laboratory, the primary model for sorting out the complexities of folliculogenesis has  
62 been the domestic cat, because findings have application to conserving felid colonies used  
63 to study human disorders, including hypertrophic cardiomyopathy (Camacho *et al.* 2016) and  
64 ophthalmic diseases (e.g., glaucoma and neuroretinal degenerative diseases) (Narfström *et al.*  
65 2013). Furthermore, what we have learned about the domestic cat has had relevance and  
66 indirect and direct conservation benefits to a host of endangered felid species, including the  
67 clouded leopard (Pelican *et al.* 2006), cheetah (Comizzoli *et al.* 2009; Moulavi *et al.* 2017)  
68 and African lion (Troyer *et al.* 2011). Our specific investigations into follicle culture in the  
69 domestic cat have demonstrated that protein free medium and an agarose gel system  
70 support follicular survival in vitro (Fujihara *et al.* 2012). Addition of growth factors, such as  
71 epidermal growth factor (Fujihara *et al.* 2014) or stem cell factor (Thuwanut *et al.* 2016), to  
72 ovarian cortice culture now is known to improve follicle activation and viability as well as  
73 ovarian cell proliferation.

74 Insulin is a peptide hormone that appears to play multiple roles in regulating folliculogenesis,  
75 oocyte maturation, and embryo development in the few mammals studied to-date (Chaves *et al.*  
76 2011). Insulin is known to act via an insulin receptor that is widely distributed within the  
77 ovarian somatic system, including the granulosa and theca cells of the human (Willis *et al.*  
78 1996), pig (Quesnel 1999), and cow (Shimizu *et al.* 2008). In large mammals, insulin acts  
79 synergistically with FSH to promote follicular cell proliferation and differentiation (Willis *et al.*  
80 1996; Xu *et al.* 2009; Chaves *et al.* 2012), facilitate FSH-dependent steroidogenesis (May *et al.*  
81 *et al.* 1980; Duleba *et al.* 1997), and induce LH receptor expression in granulosa cells (Silva

82 and Price 2002). The only work on the effect of insulin in the cat follicle dates to more than 2  
83 decades ago when Jewgenow and Göritz (1995) determined that insulin enhances  
84 granulosa cell proliferation and proportions of oocytes with an intact germinal vesicle in  
85 cultured preantral follicles. Otherwise, the mechanisms by which insulin may be involved in  
86 preantral follicle development in the cat are unknown. Furthermore, no investigation has ever  
87 been undertaken to determine the role of this peptide hormone on water transport genes that  
88 are known to exist in ovarian follicles. We have been particularly interested in understanding  
89 factors that influence formation of the follicle's antrum. Water transport genes, including  
90 *Aqp1*, *Aqp3*, *Aqp7*, *Aqp8*, and *Aqp9*, have been implicated as involved in antral cavity  
91 establishment in mammals, including the mouse (Huang *et al.* 2006), pig (Skowronska *et al.*  
92 2009), and human (Thoroddsen *et al.* 2011; Lee *et al.* 2016). Meanwhile, studies of other cell  
93 types have revealed that insulin down-regulates *Aqp1*, *Aqp3*, *Aqp7*, and *Aqp9*, including in a  
94 human colon cell line (Asai *et al.* 2006; Higuchi *et al.* 2007), fetal membranes (Bouvier *et al.*  
95 2015), and mouse pancreatic  $\beta$ -cells (Louchami *et al.* 2012).

96 The objectives of our studies here were to examine the influence of insulin on in vitro (1)  
97 viability and growth of cat follicles, (2) mRNA expression of genes regulating steroidogenesis  
98 (Cytochrome P450 family 17 subfamily, a polypeptide 1, *Cyp17a1*; Cytochrome P450 family  
99 19 subfamily, a polypeptide 1, *Cyp19a1*; and steroidogenic acute regulatory protein, *Star*)  
100 and water transport (aquaporins, *Aqp1*, *Aqp3*, *Aqp7*, *Aqp9*), and (3) steroidogenesis (17 $\beta$ -  
101 oestradiol, E2; progesterone, P4; and androstenedione, A4). We hypothesized that insulin  
102 promotes antral formation, growth, and survival in incubated cat secondary follicles, and that  
103 this effect occurs by influencing temporal expression of genes known to regulate  
104 steroidogenesis and water transport.

## 105 **2. Materials and methods**

106 All chemicals used were purchased from Sigma Aldrich (St. Louis, Missouri, USA) unless  
107 stated otherwise.

## 108 2.1 Collection of ovaries

109 Fresh ovaries were obtained from domestic cats as recently described by Songsasen *et al.*  
110 (2017). In brief, ovaries were collected from 40 cats (age, 6 mo – 3 yr) undergoing routine  
111 ovariohysterectomy at local veterinary clinics. Gonads were transported to the laboratory  
112 within 1 to 5 h post-excision at 4°C while immersed in Leibovitz's L-15 medium. Ovaries  
113 were washed twice in Collection Medium (Minimum Essential Medium (MEM) containing 2  
114 mM L-glutamine, 20 mM Hepes, 40 IU/ml penicillin G sodium, 40 µg/ml streptomycin sulfate,  
115 and 3 mg/ml bovine serum albumin) before processing for follicle collection.

## 116 2.2 Isolation and selection of secondary follicles

117 Secondary stage follicles (100 – 200 µm in diameter) were mechanically recovered from  
118 ovarian cortex as described by Jewgenow and Goritz (1995) and within the Collection  
119 Medium. In brief, this involved mechanical dissection of cat ovaries using a cell dissection  
120 sieve and the cell suspension passed through a 100 µm cell strainer. The latter was flushed  
121 with Collection medium to recover all preantral follicles. Isolated secondary follicles with  
122 normal morphology (i.e., round or oval in shape, surrounded by 2 – 3 compact layers of  
123 granulosa cells with an intact basement membrane (Jewgenow and Goritz, 1995)) were  
124 selected under a stereomicroscope (Nikon SMZ-2T, Tokyo, Japan). Each was evaluated for  
125 viability by exposure to 50 µg/ml neutral red stain for 20 min at 37°C (Wongbandue *et al.*  
126 2013). Follicles containing both a neutral red positive oocyte and granulosa cells were  
127 classified as viable (Fig. 1) (Repetto *et al.* 2008).

## 128 2.3 Assessment of follicle/oocyte growth

129 Diameters of each follicle and enclosed oocyte were measured at the onset of in vitro culture  
130 (Day 0) and on Days 3, 6, 9, 12, and 14 using an inverted microscope (Leitz DMIL, Leica  
131 Microsystem, Buffalo Grove, Illinois, USA) with an ocular micrometer. Each follicle was sized  
132 from the outer layer of somatic cells, with the measurements including the widest diameter  
133 and perpendicular width to the initial assessment. The mean of these two metrics was

134 calculated and reported as diameter. Oocyte size, excluding the zona pellucida, was  
135 evaluated using the same method. Relative growth over time was calculated by the value  
136 obtained at each culture assessment divided by that recorded on Day 0. At the end of  
137 incubation (Day 14), the presence or absence of an antrum (a fluid-filled cavity) was  
138 determined, and follicle viability was again assessed by neutral red staining (as above).

#### 139 2.4 In vitro culture of secondary follicles

140 Only morphologically-normal and neutral red positive follicles were encapsulated in 0.5%  
141 alginate hydrogel (Pronova UP MVG; Novamatrix, Sandvika, Norway) using described  
142 methods from our laboratory (Songsasen *et al.* 2017). Each alginate-enclosed follicle was  
143 incubated in 500  $\mu$ l of basic culture medium (MEM with 2 mM L-glutamine, 40 IU/ml penicillin  
144 G sodium, 40  $\mu$ g/ml streptomycin sulfate, 3 mg/ml BSA, 1.9  $\mu$ g/ml human transferrin, and 5  
145  $\mu$ g/ml sodium selenite) supplemented with 1  $\mu$ g/ml FSH (Folltropin-V; Bioniche Animal  
146 Health, Belleville, Ontario, Canada) containing 0 (Control), 1, or 10  $\mu$ g/ml insulin. All follicles  
147 in these three cohorts were incubated in a humidified atmosphere of 5% CO<sub>2</sub> in air for 14 d.  
148 Half of the culture medium was changed every 72 h throughout the experimental interval  
149 with fresh medium supplemented with insulin (0, 1, or 10  $\mu$ g/ml according to treatment  
150 group).

#### 151 2.5 RNA extraction

152 Total RNA was extracted from a group of 20 follicles at the onset of in vitro culture and after  
153 6 or 12 d of incubation (3 replicates/treatment/culture period) using RNeasy plus mini-kit  
154 (Qiagen, Valencia, California, USA) following the manufacturer's protocol. Extracted RNA  
155 was treated by a RapidOut DNA removal kit (Thermo-Scientific, Carlsbad, California, USA)  
156 to avoid genomic DNA contamination. Quantity of extracted RNA was assessed using a  
157 fluorometer (Qubit™ 3.0, Life Technologies, Thermo-Scientific, Carlsbad, California, USA) by  
158 the RNA Spike-in method (Li *et al.* 2015).

#### 159 2.6 Quantitative RT-PCR (qRT-PCR)

160 Complementary DNA was synthesized from mRNA (2.4 ng/sample) using a Transcriptor  
161 High Fidelity cDNA synthesis kit (Roche, Basel, Switzerland) according to the manufacturer's  
162 instructions. Products were stored at -20°C until qPCR analysis. Sequences of gene-  
163 specific primers were referenced from Songsasen *et al.* (2017), except *Aqp9* primers that  
164 were designed by the Beacon Designer Software package (Premier Biosoft, Palo Alto,  
165 California, USA). Primer sequences are described in Table 1. Relative expression of all  
166 genes was normalized to the endogenous control gene  $\beta$ -actin that has been shown to be  
167 more stable than glyceraldehyde-3-phosphate dehydrogenase (*Gapdh*) in RefFinder  
168 software (Xie *et al.* 2012). With the exception of *Aqp7*, each PCR reaction (total volume, 20  
169  $\mu$ l) consisted of 2  $\mu$ l cDNA and 18  $\mu$ l of a reaction mixture containing 10  $\mu$ l of FastStart  
170 Essential DNA green master (Roche, Basel, Switzerland), 1  $\mu$ l each of 10  $\mu$ M forward and  
171 reverse primers, and 6  $\mu$ l of nuclease-free water. For *Aqp7*, 5  $\mu$ M of forward and reverse  
172 primers were used. Reactions were performed with the following settings: 95°C for 10 min  
173 followed by 45 cycles at 95°C for 10 sec, specific annealing temperature (Table 1) for 30  
174 sec, and 72°C for 10 sec. All amplifications were performed in triplicate using LightCycler®  
175 96 (Roche, Basel, Switzerland). Reactions without cDNA were performed in parallel as a  
176 negative control. Primer efficiency was assessed in each gene by serial dilution of DNA.  
177 Calculation of mRNA expression levels was performed by the comparative Ct method using  
178 the amplification efficiency of each gene as a correction factor. Day 0 (non-cultured) follicles  
179 were used as a control group for calculations of relative quantitation. Data were reported as  
180 n-times difference in relation to the fresh, non-cultured group (Livak and Schmittgen 2001).  
181 Data were calculated using Microsoft Excel 2016 software.

## 182 2.7 Assessment of follicle morphology

183 To determine follicular morphology, follicles were processed histologically, as previously  
184 described (West-Farrell *et al.* 2009). Briefly, alginate-enclosed follicles at the end of culture  
185 (Day 14) were placed in a calcium chloride solution (50 mM CaCl<sub>2</sub>, 140 mM NaCl) for 2 min  
186 followed by fixation in 4% paraformaldehyde, 0.1 M sodium cacodylate, 0.1 M sucrose, and

187 10 mM calcium chloride for 4 h (4°C). Each fixed follicle then was stained with 0.5% alcian  
188 blue and dehydrated through a graded series of ethanol solutions (70 – 100%) followed by  
189 embedding in a paraffin block. Serial sections (5 µm) were cut, stained with hematoxylin-  
190 eosin, and evaluated by light microscopy (Olympus BX40; Olympus America, Inc.; 400x) for  
191 determining the morphology of follicle structure, the presence of theca cells and antral  
192 formation.

### 193 2.8 Hormone assays

194 Conditioned medium was collected on Day 12 and then stored at -80°C until shipped to the  
195 Endocrine Technologies Support Core (ETSC) at the Oregon National Primate Research  
196 Center (Beaverton, Oregon, USA) for analysis of total concentrations of E2, P4, and A4  
197 measured using ultra-high performance liquid chromatography-heated electrospray  
198 ionization-tandem triple quadrupole mass spectrometry (LC-MS/MS) on a Shimadzu Nexera-  
199 LCMS-8050 instrument (Kyoto, Japan). For sample preparation, 150 µl of culture medium  
200 was mixed with 100 µl ultrapure water (Honeywell B&J, Muskegon, Michigan, USA)  
201 containing 3.8 ng/ml 17β-oestradiol-D<sub>5</sub>, 1.6 ng/ml progesterone-D<sub>9</sub>, and 0.8 ng/ml  
202 androstene-3,17-dione-2,3,4-C<sub>3</sub> isotopic standards (Cerilliant, Round Rock, Texas, USA)  
203 and added to a 400 µl SLE+ extraction plate (Biotage, Charlotte, North Carolina, USA).  
204 Steroids were eluted with 900 µl dichloromethane (Merck KGaA, Darmstadt, Germany),  
205 dried with forced air, and reconstituted in 50 µl of 25% (v:v) methanol:ultrapure water.  
206 Quality control (QC) pools of normal rhesus macaque serum spiked with E4, P4, and A4  
207 standards at concentrations of 1 to 10 ng/ml were also analyzed. QCs were subjected to the  
208 same SLE+ extraction procedure with four replicates in each assay. For calibration curves,  
209 blank culture medium was spiked with E2, P4, and A4 standards in methanol and diluted  
210 serially to final concentrations from 0.015 to 15 ng/ml in a 12-point curve. Spiked standards  
211 were then subjected to the SLE+ extraction procedure. After the reconstitution step,  
212 samples, standards, and QCs were subjected to LC-MS/MS analysis. Using a Shimadzu  
213 SIL-30CAMP autosampler, 25 µl of each sample were injected onto a Raptor 2.7 µm

214 Biphenyl 50 mm X 2.1 mm column (Restek, Bellefonte, Pennsylvania, USA). The mobile  
215 phase consisted of 0.15 mM ammonium fluoride in water (A) and methanol (B) with a flow  
216 rate of 0.25 ml/min. Using a Shimadzu Nexera LC-30AD system (LC), gradient elution  
217 started at 70% methanol and increased to 100% methanol over 5 min. After  
218 chromatography, the column was re-equilibrated back to 70% methanol for 2.75 min for a  
219 total of 7.75 min per sample. E2, P4, and A4 had retention times of 1.53, 4.48, and 3.52 min,  
220 respectively. E2 was detected in negative ion mode with P4 and A4 detected in positive ion  
221 mode with multiple reaction monitoring (MRM) using a Shimadzu LCMS-8050 tandem triple-  
222 quadrupole MS with heated electrospray ionization (ESI). All MS parameters were optimized  
223 for maximum sensitivity while maintaining analytical robustness prior to sample analysis. The  
224 interface temperature was 300°C, the desolvation line temperature was 150°C, and the heat  
225 block temperature was 500°C. The dynamic range for the E2, P4, and A4 standard curves  
226 was 0.015 to 15 ng/ml. Data processing and analysis were performed using LabSolutions  
227 Software, V5.72 (Shimadzu, Japan). Intra-assay variations for E2 were 1.54% and 0.25% for  
228 replicate 1 and 2, respectively. The respective values for P4 and A4 were 14.8% and 1.6%  
229 (P4) and 16.1% and 1.6% (A4). Because all samples were analyzed using a single assay, no  
230 specific inter-assay variation was calculated. Overall inter-assay variation for these three  
231 assay systems within the ETSC is less than 15%.

## 232 2.9 Experimental design

233 The design was to determine the impact of insulin supplementation on in vitro follicle growth  
234 and survival, mRNA expression of gene regulating steroidogenesis and water transport and  
235 steroidogenesis. Cat secondary follicles (n = 646) were isolated from ovarian cortices and  
236 cultured in 0 (Control), 1, or 10 µg/ml insulin for 14 d (Day 0 = culture onset). Follicle/oocyte  
237 viability (based on neutral red staining), diameter, and antrum formation were assessed  
238 every 72 h and at the end of incubation (Day 14). mRNA expression of steroidogenic  
239 (*Cyp17a1*, *Cyp19a1*, *Star*) and water transport (*Aqp1*, *Aqp3*, *Aqp7*, *Aqp9*) genes were  
240 evaluated on Days 0, 6, and 12 and E2, P4, and A4 concentrations on Day 12.

## 241 2.10 Statistical analysis

242 All data were tested for normality using the Shapiro Wilk normality test and variance  
243 homogeneity using the Barlett's test. Follicle and oocyte growth, absence or presence of an  
244 antrum cavity, and follicle viability data were normally distributed with equal variance.  
245 Comparisons of mean percentages in follicle and oocyte growth within treatment were  
246 analyzed using a repeated measure ANOVA followed by a Tukey's multiple comparison test.  
247 Mean percentages in follicle and oocyte growth, absence or presence of antrum cavity, and  
248 follicle viability among treatment groups were compared using a one way ANOVA followed  
249 by a Tukey's multiple comparison test. Differences in mRNA expression were evaluated  
250 using a Kruskal-Wallis test with a Dunn's multiple comparison test. All statistical analyses  
251 were performed using Graphpad Prism version 5.0 for Windows (GraphPad Software, La  
252 Jolla, California, USA). Differences with a value of  $P < 0.05$  were considered statistically  
253 significant.

## 254 3. Results

255 Insulin enhanced ( $P < 0.05$ ) viability of cultured follicles. Specifically, more neutral red  
256 positive follicles were observed on Day 14 after the high (86%) compared to the Control  
257 (38.1%) or low (59.8%) insulin treatment. Follicles exposed to insulin (1 or 10  $\mu\text{g/ml}$ )  
258 increased in diameter as in vitro culture progressed (Fig. 2a), whereas those cultured without  
259 the hormone remained the same size through the 14 d incubation. Insulin supplementation  
260 dose-dependently increased ( $P < 0.05$ ) the proportion of follicles forming an antrum.  
261 Seventy-eight percent of follicles exposed to high insulin developed a distinctive antral cavity  
262 compared to only 3.3% and 26.9% of those in no and low insulin groups, respectively (Fig.  
263 3a-c, Fig. 4). Histological analysis revealed presence of theca cell layers on follicles (on Day  
264 14) incubated in high insulin supplementation (Fig. 4d). Although sustaining oocyte viability  
265 (based on neutral red staining), supplemental insulin had no influence on oocyte growth; egg

266 diameter on Day 14 in all groups was no different ( $P > 0.05$ ) from that on Day 0 at culture  
267 onset (Fig. 2b).

268 Our evaluation revealed that insulin influenced temporal mRNA expression of steroidogenic  
269 genes across treatment groups, especially on Day 6. Specifically, *Cyp17a1* expression was  
270 higher ( $P < 0.05$ ) in the low compared to high insulin treatment (with the 0 dosage producing  
271 an intermediate, non-significant difference) (Fig. 5a). Similar to what occurred on Day 6,  
272 mRNA levels on Day 12 were increased ( $P < 0.01$ ) by exposure to low compared to high  
273 insulin concentration. Although *Cyp19a1* mRNA level was similar ( $P > 0.05$ ) among Control  
274 and treatment groups (Fig. 5b), *Star* expression in follicles cultured for 6 d in low insulin was  
275 higher ( $P < 0.01$ ) than the no insulin counterpart. There was no evidence of *Star* mRNA  
276 expression by Day 12 in the presence of high insulin (Fig. 5c).

277 In contrast to what occurred for steroidogenic genes, expression of *Aqp3* and *Aqp7* was  
278 unaffected ( $P > 0.05$ ) by treatment (Fig. 6). However, *Aqp1* expression was up-regulated ( $P$   
279  $< 0.01$ ) on Day 6 in the low compared to high insulin condition. Although insulin had no effect  
280 on *Aqp9* expression on Day 6, transcript level of this gene was influenced ( $P < 0.05$ ) by high  
281 insulin supplementation with down-regulation on Day 12 compared to the Control (Fig. 6).

282 Analysis of spent medium collected on Day 12 revealed that E2 and A4 concentrations were  
283 not different ( $P > 0.05$ ) between the Control and either the low or high insulin treatment  
284 groups (Fig. 7a&c). However, low insulin increased progesterone concentration compared to  
285 no ( $P < 0.01$ ) or high ( $P < 0.001$ ) insulin counterparts (Fig. 7b).

286

#### 287 **4. Discussion**

288 Our study in the cat model examined secondary ovarian follicles cultured in vitro and added  
289 to the informational database by making three main discoveries. First, we observed a dose-  
290 dependent response of insulin on antrum formation, growth, follicle survival and theca cell

291 differentiation. Secondly, insulin assisted in sustaining oocyte viability without influencing  
292 actual growth and ultimate size of the egg. Lastly, insulin affected temporal expression of  
293 specific genes regulating steroidogenesis and water transport, while having an additional  
294 effect (at low dosage) on enhanced progesterone production in vitro. Collectively, these  
295 findings revealed that insulin appeared to be a key endocrine factor in successful  
296 folliculogenesis in the domestic cat.

297 Earlier studies have demonstrated the important roles of insulin in ovarian follicle activation  
298 and growth both in vivo and in vitro (Selvaraju *et al.* 2003; Rossetto *et al.* 2016). In the  
299 mouse, insulin promotes primordial follicular assembly and activation by stimulating the  
300 PI3K/Akt signaling pathway (Zhang *et al.* 2010). Insulin also enhances cell proliferation and  
301 differentiation of incubated goat preantral follicles (Chaves *et al.* 2012) and facilitates FSH-  
302 dependent steroidogenesis in cultured pig granulosa cells (May *et al.* 1980). Insulin also is  
303 known to play a key role in in vitro activation of primordial follicles enclosed within incubated  
304 ovarian cortices in the rat (Kezele *et al.* 2002), goat (Chaves *et al.* 2011), cow (Fortune *et al.*  
305 2010), and human (Louhio *et al.* 2000). Supplemental insulin also has been found to  
306 enhanced survival of secondary stage, cultured follicles of the dog (Serafim *et al.* 2013) and  
307 goat (Ferreira *et al.* 2016), in both cases by promoting formation of the follicular antrum.  
308 Goat oocytes within such insulin-exposed follicles are better able to resume meiosis and  
309 ultimately achieve metaphase II (Silva *et al.* 2017). Our findings confirmed that impact of  
310 insulin on incubated, immature follicles appeared conserved across species. Cat secondary  
311 follicles reacted similarly to those of the dog (another carnivore; Serafim *et al.* 2013), goat  
312 (Chaves *et al.* 2012; Ferreira *et al.* 2016), and human (Louhio *et al.* 2000). More specifically,  
313 supplemental insulin sustained follicular and oocyte viability while increasing follicle size by  
314 30% above control values. There also was an affirmation on influence of this hormone  
315 (especially at high dosage) to enhance antrum formation and enlargement, likely by  
316 stimulating theca cell differentiation that, in turn, facilitated flow of extrafollicular fluid into the  
317 antral cavity. This speculation is supported by earlier studies of the mouse and human where

318 either insulin or insulin-like-growth factor I is known to promote ovarian follicle growth by  
319 inducing theca cell differentiation and proliferation (Young and McNeilly 2010), probably by  
320 regulating cell metabolism through signal transduction pathways, such as Ras-MAPK and  
321 PI3K-Akt (Avruch 1998).

322 Insulin dose-dependency appeared focused strictly on oocyte survival (based on neutral red  
323 staining) with no influence on the growth of gamete itself. Oocyte diameter at onset of culture  
324 in our study (~65  $\mu\text{m}$ ) was consistent with that of eggs derived from in vivo-developed,  
325 secondary cat follicles (Reynaud *et al.* 2009). However, our cultured follicles on Day 14  
326 produced oocytes (also ~65  $\mu\text{m}$ ), even in the presence of high insulin, that were far smaller  
327 in size than in vivo-derived counterparts from late secondary (~86  $\mu\text{m}$ ) or early antral (~108  
328  $\mu\text{m}$ ) stages (Reynaud *et al.* 2009). This finding was contrary to that reported in the goat  
329 where supplementing preantral follicles with insulin increased both diameter and ability to  
330 resume meiosis of the resident oocyte over an 18 d incubation (Ferreira *et al.* 2016). The  
331 differences between what was observed in the goat and cat models probably was related to  
332 the stage of the donor follicle. For example, it is known that the diameter of oocytes within  
333 primordial goat follicles is unaffected in vitro by exposure to insulin (Chaves *et al.* 2011).  
334 Therefore, we speculate that oocytes from more advanced follicles are likely to be more  
335 responsive to an insulin stimulus, a possibility that deserves further study. Alternatively,  
336 there simply may be species variabilities in sensitivity at the oocyte level to this peptide  
337 hormone, a possibility that will be understood as the influence of insulin is explored in other  
338 animal models.

339 One mechanism whereby insulin stimulates follicle growth is by up-regulating genes that  
340 control steroidogenesis, including *Star* (facilitates transport of cholesterol required for  
341 steroidogenesis), *Cyp11a1* (converts cholesterol to pregnenolone), and *Cyp17a1* (converts  
342 pregnenolone to dehydroepiandrosterone, DHEA) (Young and McNeilly 2010). In the present  
343 study, insulin, especially at a low concentration increased mRNA expression of *Star* and  
344 *Cyp17a1* after 6 d of culture. The up-regulation of *Star* during low insulin exposure was

345 confirmed physiologically by a parallel increase in P4 concentration over the entire  
346 incubation period. However, the up-regulation of *Cyp17a1* in low insulin failed to translate  
347 into increased A4 concentration in culture. This inability of insulin supplementation to  
348 influence A4 production suggested that the cat may be similar to the human where the  
349 P450c17 enzyme is unable to efficiently convert 17 $\beta$ -hydroxyprogesterone to A4, a finding in  
350 contrast to that observed in cattle and rodents (Miller *et al.* 2006). Despite the stimulating  
351 effect of low insulin exposure on *Cyp17a1*, the higher dosage had no influence on this gene  
352 and, furthermore, diminished *Star* expression by the end of culture. There is early evidence  
353 in the cow that a lower concentration of insulin supplementation enhances E2 and P4  
354 production in granulosa cell cultures, whereas increased insulin has no impact (Spicer *et al.*  
355 1993). In the present study, the undetectable level of *Star* transcript and low P4  
356 concentration at Day 12 in the presence of high insulin suggested that persistent elevations  
357 of this steroidogenic transcript and P4 production are not a prerequisite for antrum formation.  
358 In fact, up-regulation of *Star* mRNA and P4 production has been shown to be associated  
359 with poor antrum formation in incubated mouse preantral follicles (West-Farrell *et al.* 2009).

360 In the present study, we demonstrated for the first time that insulin influenced temporal  
361 expression of water transport genes within the incubated mammalian follicle. We observed  
362 an absence of *Aqp7* by Day 6 when cat follicles were exposed to high insulin. However, the  
363 transcript was detected at the level similar to the low (or control) insulin counterparts on Day  
364 12. It is known that *Aqp7* is located in sheep follicular cells (Sales *et al.* 2015; Lee *et al.*  
365 2016). Therefore, the increase in this transcript in high insulin treatment was likely the result  
366 of granulosa cell proliferation associated with insulin supplementation (Jewgenow and Göritz  
367 1995) rather than the direct impact of this hormone on the water transport gene.

368 Our finding that high insulin suppressed transcription of *Aqp9* was similar to previous  
369 observations made for human fetal membrane (Bouvier *et al.* 2015) and placental tissue  
370 (Castro Parodi *et al.* 2011). These particular in vitro studies determined that insulin increases  
371 phosphorylation of Akt proteins, a process that then impairs the intracellular phosphorylation

372 pathway and down-regulates *Aqp9* expression. However, it also is noteworthy that immuno-  
373 localization of this water transport gene is associated with formation of the follicular antrum  
374 in sheep (Sales *et al.* 2015). Thus, future studies should examine the impact of insulin on  
375 protein expression of AQP9 in incubated cat follicles to verify its inter-relationship to insulin  
376 in antral formation. Finally, for *Aqp1*, the transcript level increased only in the presence of  
377 low insulin and only on Day 6, an effect lost by Day 12. In the human, mRNA and protein  
378 expression of AQP1 is known to increase during the late follicular phase and post-ovulation,  
379 suggesting that this gene is likely most associated with the peri-ovulatory period, ovulation,  
380 and corpus luteum formation (Thoroddsen *et al.* 2011). Therefore, the role of AQP1 in the  
381 cat may well be the same (or quite similar to the human), coming into functional play at the  
382 end of folliculogenesis.

383 In summary, this study helped provide another level of understanding about control of  
384 folliculogenesis, including how to advance ovarian follicle (and resident oocyte) development  
385 in an artificial microenvironment. Our findings in the cat model add credence to observations  
386 made in eight other mammalian species that insulin is a key regulator of growth and  
387 differentiation of secondary follicles, and dose dependently. It appeared that insulin's  
388 stimulating mechanism was through ensuring appropriate temporal expression of *Cyp17a1*  
389 and *Star* as well as progesterone production. Earlier investigations (Edashige *et al.* 2000;  
390 McConnell *et al.* 2002; Skowronska *et al.* 2009) have suggested that AQPs, especially *Aqp1*,  
391 *Aqp3*, *Aqp7*, *Aqp8*, and *Aqp9*, may play a role in antral cavity formation. But such efforts  
392 have focused on examining AQP localization within the ovary (Edashige *et al.* 2000; Lee *et al.*  
393 *et al.* 2016; Skowronska *et al.* 2009; Thoroddsen *et al.* 2011). Ours was the first to examine  
394 these water transport genes in the follicle itself, demonstrating yet another new mechanism  
395 whereby insulin has influence through temporal mRNA expression of two (*Aqp1* and *Aqp9*)  
396 of these five transcripts. This finding also provided encouragement for the need to identify  
397 other key regulators of AQPs expression during folliculogenesis as antral cavity expansion is  
398 fundamental to follicular maturation. Likely candidates include ovarian steroids, cyclic

399 adenosine monophosphate, forskolin, and prostaglandins (Hua *et al.* 2013). We are  
400 confident that building upon this collective knowledge will lead to the ability to create an in  
401 vitro system that permits appropriate antral cavity expansion to allow producing oocytes that  
402 can mature, fertilize, and develop into a viable embryo.

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#### 410 **Conflicts of interest**

411 The author declares that there is no conflict of interest.

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599

## 600 Figure Legends

601 **Fig. 1.** Micrographs of (a) (non-viable, neutral red negative) and (b) (viable, neutral red  
602 positive cat follicles at Day 14 of in vitro culture. Bar =150  $\mu\text{m}$ .

603 **Fig. 2.** Diameter ( $\mu\text{m}$ ); Mean  $\pm$  SEM of secondary follicle (a) and oocytes (b) cultured for 14  
604 d in medium supplemented with 0, 1 or 10  $\mu\text{g/ml}$  insulin. <sup>A,B,C,D,E</sup> Superscripts indicate  
605 significant difference among culture days within the same treatment,  $P < 0.05$ . <sup>a,b,c</sup> indicate  
606 significant difference among treatments within the same culture day,  $P < 0.05$ .

607 **Fig. 3.** Micrographs of cat follicles cultured in the absence of insulin (a), 1  $\mu\text{g/ml}$  (b), and 10  
608  $\mu\text{g/ml}$  (c) insulin. Bar = 150  $\mu\text{m}$ . Black arrow head indicates antral cavity.

609 **Fig. 4.** Histological images of non-cultured follicle (a), cultured follicles on Day 14 with insulin  
610 supplementation at 0 (b), 1 (c) and 10 (d)  $\mu\text{g/ml}$ . Bar = 100  $\mu\text{m}$ . O, oocyte; GC, granulosa  
611 cells; a, antrum; black arrow head, theca cells.

612 **Fig. 5.** Relative expression (based on the fresh, non-cultured control) of gene regulating  
613 steroidogenesis (*Cyp17a1* (a), *Cyp19a1* (b) and *Star* (c) in follicles at Day 6 and 12 of culture  
614 in medium supplemented with insulin (0, 1 or 10  $\mu\text{g/ml}$ ). Bars show mean  $\pm$  SEM. Asterisks  
615 indicate significant levels. \*  $P \leq 0.05$ , \*\*  $P \leq 0.01$ , \*\*\*  $P \leq 0.001$ .

616 **Fig. 6.** Relative expression (based on the fresh, non-cultured control) of gene regulating  
617 water transport (*Aqp1* (a), *Aqp3* (b), *Aqp7* (c) and *Aqp9* (d) in follicles at Day 6 and 12 of  
618 culture in medium supplemented with insulin (0, 1 or 10  $\mu\text{g/ml}$ ). Bars show mean  $\pm$  SEM.  
619 Asterisks indicate significant levels. \*  $P \leq 0.05$ , \*\*  $P \leq 0.01$ .

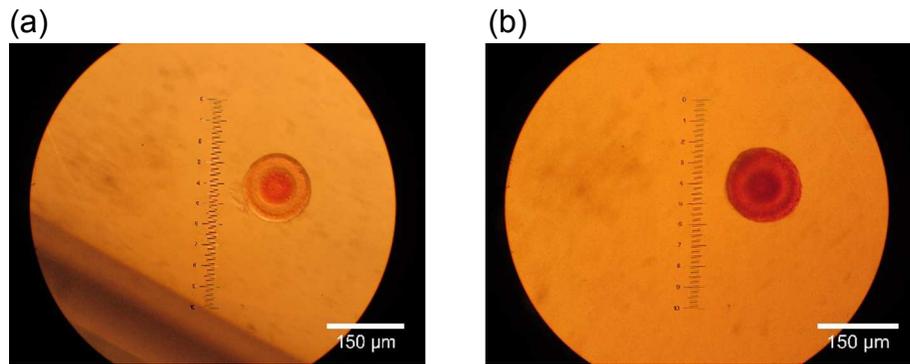
620 **Fig. 7.** Oestradiol (a), progesterone (b) and androstenedione (c) production at Day 12 of  
621 culture by cat follicles cultured in medium supplemented with insulin (0, 1 or 10  $\mu\text{g/ml}$ ). Bars  
622 show mean  $\pm$  SEM. Asterisks indicate significant levels. \*\*  $P < 0.01$ , \*\*\*  $P < 0.001$ .

623

624

For Review Only

Fig. 1



For Review Only

Fig. 2

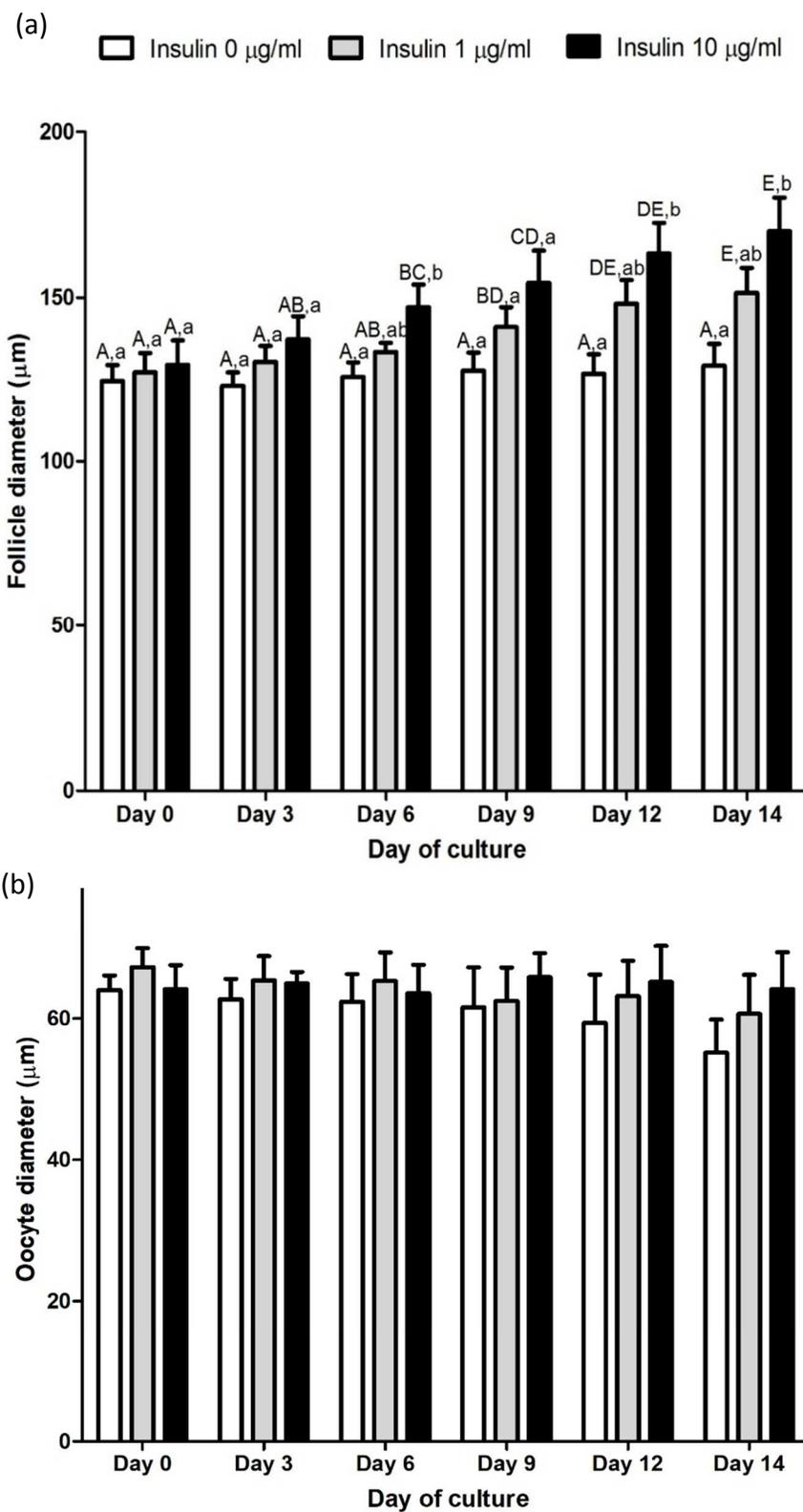


Fig. 3

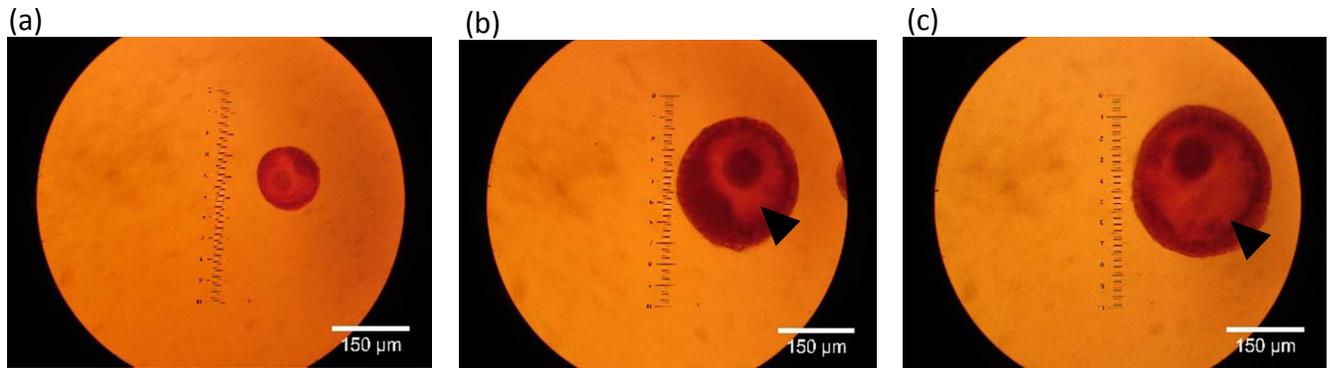


Fig. 4

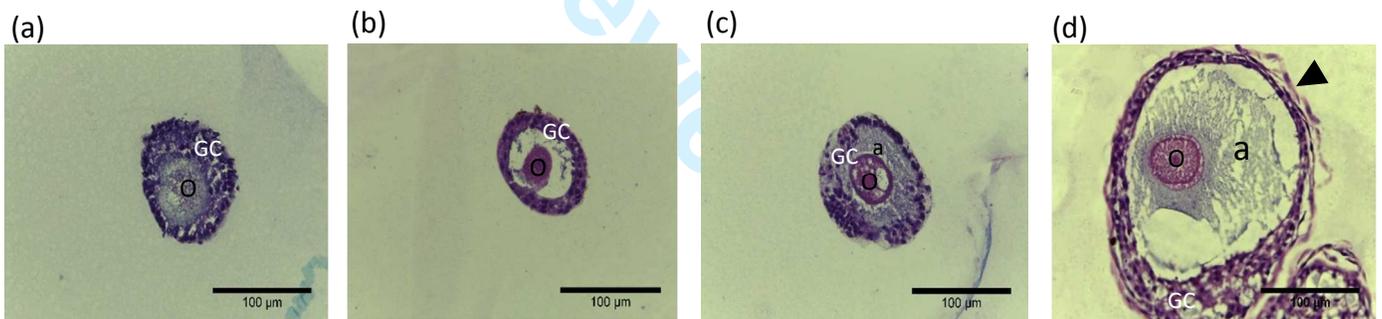


Fig. 5

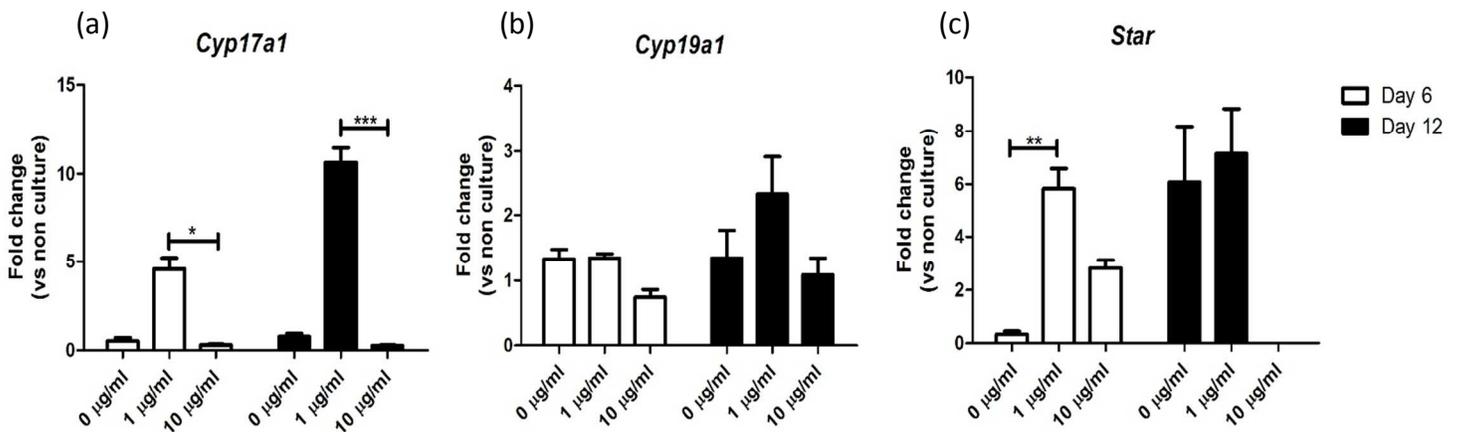


Fig. 6

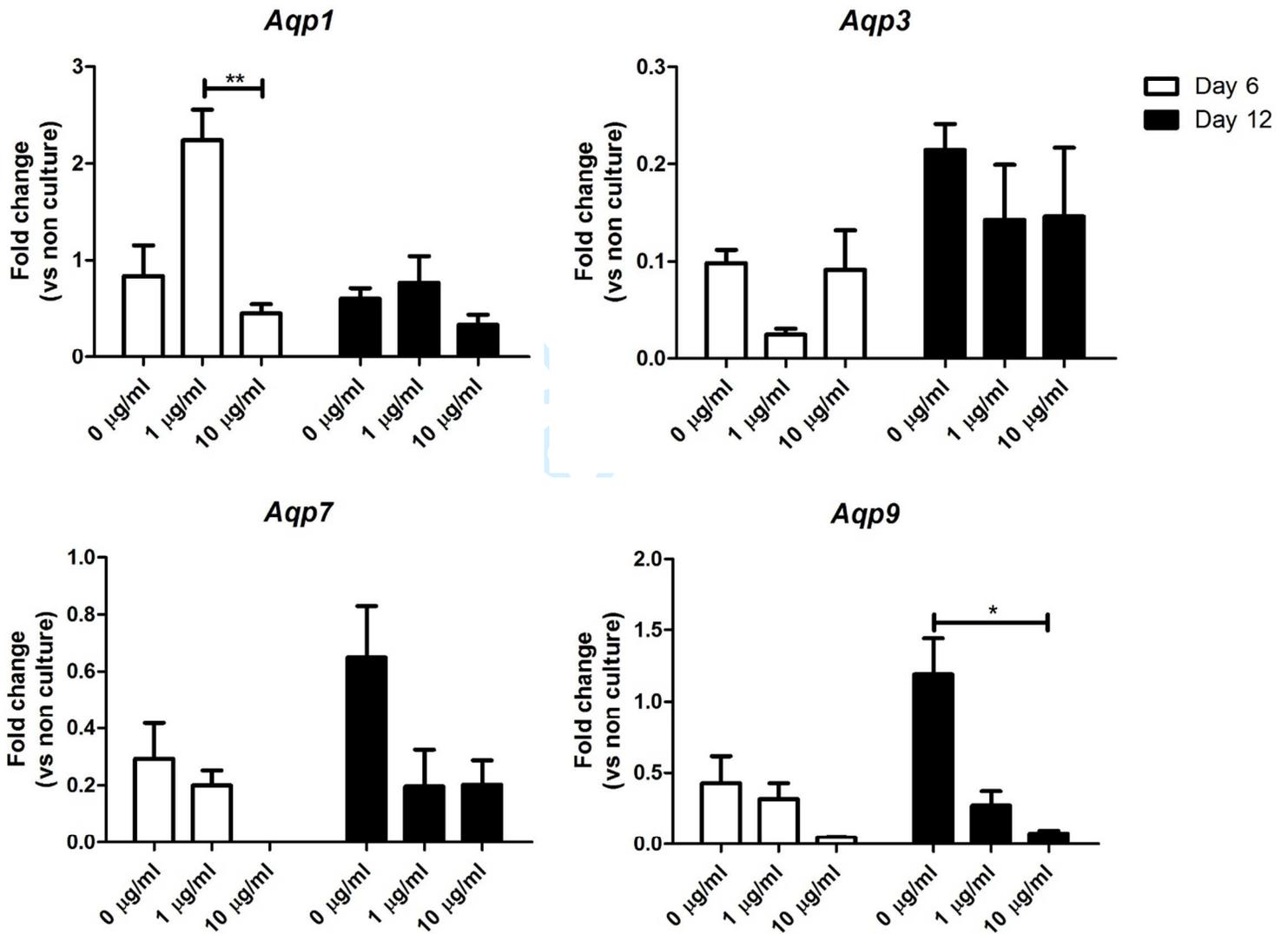


Fig. 7

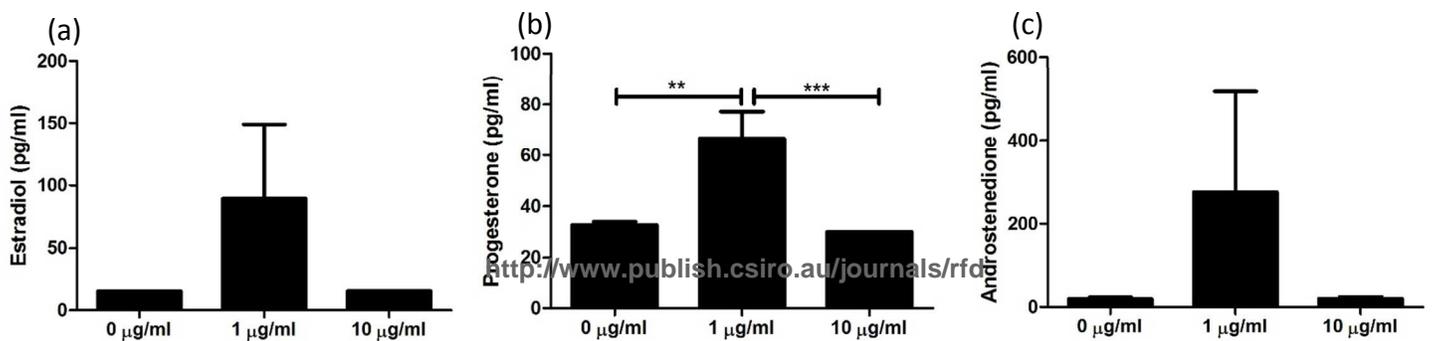


Table 1. List of primers used in this study

Gene	Sense	Sequence 5'-3'	Accession number	Annealing temperature (°C)	Product length (bp)	Primer efficiency
<i>β-actin</i>	Forward	ATCCACGAGACCACCTTC	AB051104.1	57	75	1.077
	Reverse	CACCGTGTTAGCGTAGAG				
<i>Gapdh</i>	Forward	CATCACCATCTTCCAGGA	NM_001009307	57	81	1.009
	Reverse	CCAGTAGACTCCACAACA				
<i>Cyp17a1</i>	Forward	CCGAGATGAGTTGCTGAG	NM_001009371.2	57	105	0.87
	Reverse	GAGTTCATCCTGGCTTGG				
<i>Cyp19a1</i>	Forward	CAATCCTGCTGCTCACTG	GU306147.1	57	84	0.917
	Reverse	CCATGCAATAGCCAGGAC				
<i>Star</i>	Forward	ATGGAAGCGATGGGAGAG	NM_001246196.1	57	90	1.066
	Reverse	CAACTCGTGGGTGATGAC				
<i>Aqp1</i>	Forward	GGCTCGTCAGTGATTACTC	XM_003982907.3	60	103	0.924
	Reverse	CCAGGATGAAGTCGTAGATG				
<i>Aqp3</i>	Forward	ATCTATGCCTTGGCTCAG	XM_011288588.1	59	96	1.056
	Reverse	CTCATTCTTGGCGAAGTC				
<i>Aqp7</i>	Forward	GCATGTCCTGGAAGAAGT	XM_006939211.2	57	78	1.321
	Reverse	AGTAGATGGTGGCAGAAG				
<i>Aqp9</i>	Forward	GTCTTGAAGAGCACCTTAGC	XM_003987104.3	57.5	85	1.038
	Reverse	CAACAGAGCCACATCCAA				